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Supplementary Material

Identification of protein agents that may be associated with reducing of the regrowth of the axillary buds of sugarcane and may be limit for the longevity of cane fields

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Table S1. Total and differential proteome of the axillary bud of the RB867515 sugarcane cultivar at the first cutting stage.

Table S2. Total and differential proteome of the axillary bud of the RB867515 sugarcane cultivar at the third cutting stage.

Table S3. Total and differential proteome of the axillary bud of the RB867515 sugarcane cultivar at the fifth cutting stage.

Table S4. Differentially expressed protein (down-regulated) in axillary buds of the RB867515 sugarcane cultivar at the first cut compared to third cutting stage.

Table S5. Differentially expressed protein (up-regulated) in axillary buds of the RB867515 sugarcane cultivar at the third cut compared to first cutting stage.

Table S6. Differentially expressed protein (down-regulated) in axillary buds of the RB867515 sugarcane cultivar at the first cut compared to fifth cutting stage.

Table S7. Differentially expressed protein (up-regulated) in axillary buds of the RB867515 sugarcane cultivar at the fifth cut compared to first cutting stage.

Table S8. Differentially expressed protein (down-regulated) in axillary buds of the RB867515 sugarcane cultivar at the third cut compared to fifth cutting stage.

Table S9. Differentially expressed protein (up-regulated) in axillary buds of the RB867515 sugarcane cultivar at the fifth cut compared to third cutting stage.

Table S10. The 77 proteins detected only in the axillary buds of the RB867515 sugarcane at first cutting stage within functional categories based on their biological process and subcellular localization.

Table S11. The 39 proteins detected only in the axillary buds of the RB867515 sugarcane at third cutting stage within functional categories based on their biological process and subcellular localization.

Table S12. The 44 proteins detected only in the axillary buds of the RB867515 sugarcane at fifth cutting stage within functional categories based on their biological process and subcellular localization.

Table S13. The 33 proteins detected only in the axillary buds of the RB867515 sugarcane at fifth and third cutting stages within functional categories based on their biological process and subcellular localization.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
1/A0A1D6LAW0/UP7305_Z_mays	D Elongation factor 2	11/11	473	11	94813	*Zea mays*
2/A0A1D6GIG4/UP7305_Z_mays	D Tubulin alpha chain	6/4	372	17	50071	*Triticum aestivum*
3/A0A1D6P848/UP7305_Z_mays	D Sucrose synthase	14/10	542	24	91108	*Zea mays*
4/A0A1D6EJ77/UP7305_Z_mays	D Clathrin heavy chain	4/4	145	3	195605	*Zea mays*
5/A0A1D6Q5B1/UP7305_Z_mays	D Phenylalanine ammonia-lyase	8/3	297	15	75926	*Zea mays*
6/A0A1D6FRN4/UP7305_Z_mays	D Putative mediator of RNA polymerase II transcription subunit 37c	7/1	343	17	68360	*Zea mays*
7/REF_HEVBR/SwissProt	X Rubber elongation factor protein	1/1	57	11	14713	*Hevea brasiliensis*
8/A0A1D6GQ45/UP7305_Z_mays	D Cell division cycle protein 48	4/4	153	6	69832	*Zea mays*
9/B6UF55/UP7305_Z_mays	D 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	12/4	539	18	82279	*Zea mays*

10/A0A1D6I6T7/UP7305_Z_mays	^{D} Heat shock protein 90-2	5/5	211	9	77671	*Zea mays*
11/A0A1D6NVZ7/UP7305_Z_mays	^{D} Transketolase	2/2	82	3	79444	*Zea mays*

Table S1. Total and differential proteome of the axillary bud of the RB867515 sugarcane cultivar at the first cutting stage.

Table S1 - Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
12/A0A1D6GYM1/UP7305_Z_mays	^{D} Luminal-binding protein 2	3/1	111	6	60635	*Zea mays*
13/A0A1D6FN97/UP7305_Z_mays	^{D} Heat shock 70 kDa protein 14	3/3	111	7	45195	*Zea mays*
14/A0A1D6EGA6/UP7305_Z_mays	^{D} Aconitate hydratase	2/2	67	2	94038	*Zea mays*
15/BIP4_ORYSJ/SwissProt	^{D} Heat shock 70 kDa protein BIP4	2/1	107	3	74438	*Oryza sativa* subsp. *japonica*
16/A0A1D6H9F2/UP7305_Z_mays	^{B} TUDOR-SN protein 1	1/1	73	2	49468	*Zea mays*
17/A0A096R6Z8/UP7305_Z_mays	^{D} Heat shock 70 kDa protein 6 chloroplastic	1/1	49	1	73148	*Zea mays*
18/A0A1D6FEZ2/UP7305_Z_mays	^{D} Phospholipase D	1/1	44	2	83385	*Zea mays*
19/A0A1D6N717/UP7305_Z_mays	^{X} Alpha-1,4 glucan phosphorylase	1/1	53	1	77875	*Zea mays*
20/A0A1D6L0J1/UP7305_Z_mays	^{D} Lipoxygenase	1/1	81	1	96845	*Zea mays*
21/A0A1D6KE29/UP7305_Z_mays	^{D} Heat shock protein 70	11/5	498	27	71447	*Zea mays*

22/SDHA_ORYSJ/SwissProt	[D] Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	2/2	160	4	69494	*Oryza sativa* subsp. *japonica*
N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
23/A0A1D6FHT8/UP7305_Z_mays	[D] ATP citrate synthase	6/6	263	8	66504	*Zea mays*
24/A0A1D6DW07/UP7305_Z_mays	[D] D-3-phosphoglycerate dehydrogenase	2/2	110	4	64984	*Zea mays*
25/B6SXW8/UP7305_Z_mays	[D] RuBisCO large subunit-binding protein subunit alpha	3/2	149	7	61419	*Zea mays*
26/A0A096S0J0/UP7305_Z_mays	[D] Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha	1/1	92	2	68229	*Zea mays*
27/A0A1D6FGX5/UP7305_Z_mays	[D] Aspartyl-tRNA synthetase	1/1	71	2	59639	*Zea mays*
28/A0A1D6JSM9/UP7305_Z_mays	[X] T-complex protein 1 subunit gamma	1/1	62	1	58500	*Zea mays*
29/A0A1D6F5B9/UP7305_Z_mays	[D] Protein disulfide-isomerase	2/2	60	5	61141	*Zea mays*
30/A0A1D6FI28/UP7305_Z_mays	[D] 3-hydroxyacyl-CoA dehydrogenase	1/1	59	3	72964	*Zea mays*
31/A0A1D6L4F0/UP7305_Z_mays	[X] Exhydrolase II	1/1	56	2	73960	*Zea mays*
32/A0A1D6EC19/UP7305_Z_mays	[A] Diadenosine tetraphosphate synthetase	1/1	55	2	63383	*Zea mays*

Table S1 - Cont.

Table S1 - Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
33/C0P905/UP7305_Z_mays	^{X} Glucan endo-1,3-beta-D-glucosidase	1/1	55	2	53994	*Zea mays*
34/A0A1D6FSJ2/UP7305_Z_mays	^{X} 60S ribosomal protein L24	1/1	46	6	21113	*Zea mays*
35/A0A1D6JFG2/UP7305_Z_mays	^{X} Beta-D-xylosidase	1/1	52	1	82773	*Zea mays*
36/A0A1D6EL67/UP7305_Z_mays	^{D} ADP-ribosylation factor A1F	1/1	49	7	21298	*Zea mays*
37/A0A1D6NUS9/UP7305_Z_mays	^{D} Acyl-coenzyme A oxidase	1/1	62	4	32559	*Zea mays*
38/ILVB1_MAIZE/SwissProt	^{X} Acetolactate synthase 1, chloroplastic	1/1	48	2	69172	*Zea mays*
39/A0A096RF51/UP7305_Z_mays	^{D} DEAD-box ATP-dependent RNA helicase 52	1/1	46	2	68556	*Zea mays*
40/P49087/UP7305_Z_mays	^{D} V-type proton ATPase catalytic subunit A	4/4	158	11	62198	*Zea mays*
41/A0A1D6K5D2/UP7305_Z_mays	^{D} Nucleoredoxin1	1/1	72	2	64030	*Zea mays*
42/A0A1D6GJ72/UP7305_Z_mays	^{D} Phosphoglucomutase	2/2	68	4	68576	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
43/B6T4R3/UP7305_Z_mays	^{D} UTP--glucose-1-phosphate uridylyltransferase	5/5	282	13	52227	*Zea mays*
44/A0A1D6P248/UP7305_Z_mays	^{D} Vacuolar proton pump subunit B	6/4	272	16	55448	*Zea mays*
45/ATPAM_BETVU/SwissProt	^{D} ATP synthase subunit alpha, mitochondrial	3/3	169	6	55246	*Beta vulgaris*
46/VATB2_HORVU/SwissProt	^{X}V-type proton ATPase subunit B 2	4/4	224	13	53806	*Hordeum vulgare*
47/C0P567/UP7305_Z_mays	^{D} Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta	4/2	160	10	61640	*Zea mays*
48/ENO_ORYSJ/SwissProt	^{D} Enolase	5/5	291	12	48285	*Oryza sativa* subsp. *japonica*
49/A0A1D6NMU3/UP7305_Z_mays	^{X} Ubiquitin carboxyl-terminal hydrolase	1/1	144	6	41416	*Zea mays*
50/A0A1D6HR41/UP7305_Z_mays	^{X} Pyridoxal 5'-phosphate synthase-like subunit PDX1.2	1/1	27	1	44219	*Zea mays*
51/B4FBP0/UP7305_Z_mays	^{D} T-complex protein 1 subunit eta	2/2	120	7	60718	*Zea mays*
52/A0A1D6QHK0/UP7305_Z_mays	^{A} Pyruvate kinase	3/3	119	10	52618	*Zea mays*
53/A0A1D6HN61/UP7305_Z_mays	^{D} Leucine aminopeptidase 2 chloroplastic	3/3	113	6	62181	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
54/A0A1D6KMC8/UP7305_Z_mays	^{X} Dihydroxy-acid dehydratase chloroplastic	1/1	113	3	66497	*Zea mays*
55/CH61_MAIZE/UP7305_Z_mays	^{D} Chaperonin CPN60-1, mitochondrial	3/1	111	7	61458	*Zea mays*
56/A0A1D6FKV6/UP7305_Z_mays	^{D} Ketol-acid reductoisomerase	3/3	133	7	63213	*Zea mays*
57/A0A1D6FMC0/UP7305_Z_mays	^{D} Importin subunit alpha	3/2	130	7	64522	*Zea mays*
58/C0HGT5/UP7305_Z_mays	^{D} T-complex protein 1 subunit delta	1/1	93	4	58096	*Zea mays*
59/ATPBM_MAIZE/SwissProt	^{D} ATP synthase subunit beta, mitochondrial	8/5	423	21	59181	*Zea mays*
60/A0A1D6FI07/UP7305_Z_mays	^{X} Dihydrolipoyl dehydrogenase	2/2	70	5	44851	*Zea mays*
61/CATA_SECCE/SwissProt	^{D} Catalase	2/2	94	6	57077	*Secale cereale*
62/A0A1D6DYK5/UP7305_Z_mays	^{D} Polyadenylate-binding protein RBP45C	1/1	65	2	48979	*Zea mays*
63/UGDH4_ORYSJ/SwissProt	^{D} UDP-glucose 6-dehydrogenase 4	5/1	270	16	53391	*Oryza sativa* subsp. *japonica*
64/A0A1D6FAH0/UP7305_Z_mays	^{X} T-complex protein 1 subunit epsilon	2/2	60	7	61109	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
65/TBB_CICAR/SwissProt	[D] Tubulin beta chain	5/5	185	11	51171	*Cicer arietinum*
66/A0A1D6JVQ5/UP7305_Z_mays	[B] Peptidylprolyl isomerase	1/1	51	2	47904	*Zea mays*
67/A0A1D6E7X7/UP7305_Z_mays	[D] Glucose-6-phosphate dehydrogenase (NADP(+))	2/2	50	9	27709	*Zea mays*
68/A0A1D6KPH6/UP7305_Z_mays	[D] Aminoaldehyde dehydrogenase 1b	1/1	48	2	55843	*Zea mays*
69/A0A1D6L6F3/UP7305_Z_mays	[D] Glucose-6-phosphate isomerase	1/1	42	2	48918	*Zea mays*
70/A0A1D6GPS2/UP7305_Z_mays	[X] Pre-mRNA-processing factor 19	1/1	41	2	60914	*Zea mays*
71/ATPA_SACHY/SwissProt	[X] ATP synthase subunit alpha, chloroplastic	1/1	40	2	55773	*Saccharum* hybrid
72/A0A1D6IX59/UP7305_Z_mays	[X] Beta-glucosidase, chloroplastic	1/1	39	1	52535	*Zea mays*
73/TCPZA_ARATH/SwissProt	[X] T-complex protein 1 subunit zeta	1/1	38	2	59426	*Arabidopsis thaliana*
74/FB250_ARATH/SwissProt	[X] F-box protein At5g03100	1/1	37	2	35271	*Arabidopsis thaliana*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
75/A0A1D6Q9M3/UP7305_Z_mays	[D] Aldehyde dehydrogenase2	1/1	34	2	26211	*Zea mays*
76/C0PHR4/UP7305_Z_mays	[D] Adenosylhomocysteinase	7/4	237	19	53884	*Zea mays*
77/K7TSD2/UP7305_Z_mays	[D] Serine hydroxymethyltransferase	2/1	93	5	57881	*Zea mays*
78/AMYB_MAIZE/SwissProt	[D] Beta-amylase	1/1	75	3	55487	*Zea mays*
79/A0A1D6HFQ3/UP7305_Z_mays	[D] Chaperonin 60 subunit beta 2 chloroplastic	1/1	57	6	17770	*Zea mays*
80/EF1A_ORYSJ/SwissProt	[D] Elongation factor 1-alpha	4/1	133	14	49604	*Oryza sativa* subsp. *japonica*
81/A0A1D6LSP0/UP7305_Z_mays	[D] Elongation factor gamma1	1/1	71	4	47098	*Zea mays*
82/B7ZY32/UP7305_Z_mays	[D] DUF642 domain-containing protein	1/1	51	6	14960	*Zea mays*
83/A0A0B4J303/UP7305_Z_mays	[D] Eukaryotic initiation factor4a	1/1	60	6	47238	*Zea mays*
84/A0A1D6F6Z2/UP7305_Z_mays	[A] T-complex protein 1 subunit theta	1/1	43	4	29684	*Zea mays*
85/A0A1D6F1W9/UP7305_Z_mays	[X] Phospho-2-dehydro-3-deoxyheptonate aldolase	1/1	45	3	41118	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
86/A0A096PQR7/UP7305_Z_mays	[D] Cytochrome P450 CYP74A19	1/1	45	3	53248	*Zea mays*
87/A0A1D6FV26/UP7305_Z_mays	[B] Glutamate--cysteine ligase	1/1	39	5	38071	*Zea mays*
88/A0A1D6IXG3/UP7305_Z_mays	[X] Citrulline--aspartate ligase	1/1	38	2	46015	*Zea mays*
89/PS17_PINST/SwissProt	[D] Putative cytochrome c oxidase subunit II PS17 (Fragments)	1/1	34	50	1707	*Pinus strobus*
90/B4G0K4/UP7305_Z_mays	[D] Phosphoglycerate kinase	10/9	336	36	42470	*Zea mays*
91/C0PC61/UP7305_Z_mays	[D] Transaldolase	4/4	146	11	46363	*Zea mays*
92/A0A1D6H3Y9/UP7305_Z_mays	[X] Proteasome component4	1/1	80	7	31580	*Zea mays*
93/B4FLJ3/UP7305_Z_mays	[D] Isocitrate dehydrogenase [NADP]	2/2	79	6	46411	*Zea mays*
94/A0A1D6HTM2/UP7305_Z_mays	[A] 60S ribosomal protein L4-1	4/3	153	14	36321	*Zea mays*
95/A0A1D6HPL2/UP7305_Z_mays	[D] 3-ketoacyl-CoA thiolase 2 peroxisomal	3/3	113	8	36936	*Zea mays*
96/A0A1D6FZ20/UP7305_Z_mays	[D] UBP1-associated protein 2C	1/1	78	5	42200	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
97/A0A1D6FUX8/UP7305_Z_mays	[B] S-adenosylmethionine synthase	3/3	93	7	51644	*Zea mays*
98/A0A1D6IYG5/UP7305_Z_mays	[A] Obg-like ATPase 1	1/1	62	4	46058	*Zea mays*
99/A0A1D6JZR5/UP7305_Z_mays	[D] LL-diaminopimelate aminotransferase chloroplastic	2/2	79	5	52087	*Zea mays*
100/B4F9B2/UP7305_Z_mays	[D] Acetyl-CoA acetyltransferase, cytosolic 1 (Thiolase)	2/1	68	9	41618	*Zea mays*
101/CHS5_SORBI/SwissProt	[B] Chalcone synthase 5	1/1	41	3	44070	*Sorghum bicolor*
102/ADH1_ORYSJ/SwissProt	[D] Alcohol dehydrogenase 1	1/1	69	5	41699	*Oryza sativa* subsp. *japonica*
103/A0A1D6ELX4/UP7305_Z_mays	[D] Monodehydroascorbate reductase homolog1	1/1	45	11	14585	*Zea mays*
104/ALFC2_ORYSJ/SwissProt	[D] Fructose-bisphosphate aldolase 2, cytoplasmic	4/1	177	7	39137	*Oryza sativa* subsp. *japonica*
105/A0A1D6L4P1/UP7305_Z_mays	[X] Protein STRICTOSIDINE SYNTHASE-LIKE 3	1/1	33	3	59693	*Zea mays*
106/A0A1D6GPH0/UP7305_Z_mays	[D] Malate dehydrogenase	3/3	211	17	33521	*Zea mays*
107/G3PC1_HORVU/SwissProt	[D] Glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic	3/2	156	16	36605	*Hordeum vulgare*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
108/SCRK1_ORYSI/SwissProt	^{D} Fructokinase-1	4/4	155	16	34878	*Oryza sativa* subsp. *indica*
109/B4FFH8/UP7305_Z_mays	^{D} Adenosine kinase	4/4	179	17	37539	*Zea mays*
110/A0A1D6LDS1/UP7305_Z_mays	^{D} Fructokinase-2	4/4	126	13	36170	*Zea mays*
111/A0A1D6MDY4/UP7305_Z_mays	^{A} V-type proton ATPase subunit C	1/1	77	4	39756	*Zea mays*
112/SCRK7_ARATH/SwissProt	^{X} Probable fructokinase-7	2/1	76	5	37233	*Arabidopsis thaliana*
113/A0A1D6ESW5/UP7305_Z_mays	^{D} Pyruvate dehydrogenase E1 component subunit beta	2/2	76	6	37682	*Zea mays*
114/A0A1D6F125/UP7305_Z_mays	^{D} UDP-arabinopyranose mutase 3	1/1	72	3	42246	*Zea mays*
115/GBLPA_ORYSJ/SwissProt	^{D} Guanine nucleotide-binding protein subunit beta-like protein A	5/5	241	14	36665	*Oryza sativa* subsp. *japonica*
116/COMT1_SACOF/SwissProt	^{D} Caffeic acid 3-O-methyltransferase	3/3	158	9	39838	*Saccharum officinarum*
117/A0A1D6LBH9/UP7305_Z_mays	^{D} Late embryogenesis abundant protein group 2	3/3	123	17	29322	*Zea mays*
118/A0A1D6JQM9/UP7305_Z_mays	^{A} 40S ribosomal protein Sa-1	2/2	65	7	28786	*Zea mays*

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
119/C0PNU9/UP7305_Z_mays	[X] Protein binding protein	1/1	34	2	31083	*Zea mays*
120/A0A1D6EZI3/UP7305_Z_mays	[B] Succinyl-CoA ligase alpha-chain 2	1/1	66	23	5271	*Zea mays*
121/B4FMW6/UP7305_Z_mays	[X] Aspartyl protease AED3	1/1	45	1	45280	*Zea mays*
122/A0A1Q0ZFB6/UP7305_Z_mays	[X] Alba DNA/RNA-binding protein	1/1	43	3	36593	*Zea mays*
123/RAB7_MESCR/SwissProt	[D] Ras-related protein Rab7A	1/1	38	5	23516	*Mesembryanthemum crystallinum*
124/GSA_BRANA/UP7305_Z_mays	[X] Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic	1/1	42	2	50562	*Brassica napus*
125/A0A1D6HJJ4/UP7305_Z_mays	[D] Glutamine synthetase	1/1	42	2	40876	*Zea mays*
126/B4G195/UP7305_Z_mays	[X] Glutamate-oxaloacetate transaminase5	1/1	39	2	49619	*Zea mays*
127/A0A1D6K1B9/UP7305_Z_mays	[B] Hydroxyproline-rich glycoprotein family protein	1/1	47	3	41036	*Zea mays*
128/Q84TL7/UP7305_Z_mays	[D] Legumin-like protein	1/1	51	3	38047	*Zea mays*
129/A0A1D6FBT4/UP7305_Z_mays	[X] Transcription factor Pur-alpha 1	1/1	35	2	43177	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
130/B6TEK2/UP7305_Z_mays	^{A} GroES-like zinc-binding alcohol dehydrogenase family protein	1/1	43	3	39052	*Zea mays*
131/B4F7W6/UP7305_Z_mays	^{A} GDSL esterase/lipase	1/1	46	3	42051	*Zea mays*
132/RABG1_ARATH/SwissProt	^{D} Ras-related protein RABG1	1/1	38	5	23823	*Arabidopsis thaliana*
133/B6TQ06/UP7305_Z_mays	^{D} Aminomethyltransferase	1/1	29	4	44406	*Zea mays*
134/RLA0_MAIZE/SwissProt	^{D} 60S acidic ribosomal protein P0	2/2	114	13	34597	*Zea mays*
135/A0A1D6G0Z9/UP7305_Z_mays	^{D} Ribokinase	1/1	78	3	37978	*Zea mays*
136/A0A1D6MWW9/UP7305_Z_mays	^{D} 60S ribosomal protein L2	1/1	82	7	17905	*Zea mays*
137/A0A1D6ECS1/UP7305_Z_mays	^{D} Phosphoenolpyruvate carboxylase family protein	2/2	55	20	13850	*Zea mays*
138/A0A1D6K371/UP7305_Z_mays	^{B} Nascent polypeptide-associated complex alpha subunit-like protein	2/2	81	17	19099	*Zea mays*
139/K7TFA7/UP7305_Z_mays	^{D} Putative oxidoreductase, aldo/keto reductase family protein	1/1	54	6	34649	*Zea mays*
140/A0A1D6E930/UP7305_Z_mays	^{D} 14-3-3-like protein GF14-6	1/1	48	2	31041	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
141/IFRH_MAIZE/SwissProt	[D] Isoflavone reductase homolog IRL	2/2	90	8	32831	*Zea mays*
142/PILR4_THUPL/SwissProt	[B] Bifunctional pinoresinol-lariciresinol reductase	1/1	47	3	34834	*Thuja plicata*
143/A0A1D6DVE8/UP7305_Z_mays	[B] Protein-serine/threonine phosphatase	1/1	45	2	34798	*Zea mays*
144/A0A1D6JMR6/UP7305_Z_mays	[B] 60S ribosomal protein L5-1	1/1	55	3	33179	*Zea mays*
145/A0A1D6M5S1/UP7305_Z_mays	[D] Aldo-keto reductase family 4 member C9	1/1	45	2	39115	*Zea mays*
146/B4FK56/UP7305_Z_mays	[D] Peroxidase	2/2	72	9	36545	*Zea mays*
147/A0A1D6KU62/UP7305_Z_mays	[D] Ras-related protein Rab-18	1/1	38	4	27585	*Zea mays*
148/A0A1D6PD08/UP7305_Z_mays	[D] L-ascorbate peroxidase	6/4	246	22	30847	*Zea mays*
149/Q6TM44/UP7305_Z_mays	[X] Germin-like protein	1/1	41	10	22101	*Zea mays*
150/A0A1D6I845/UP7305_Z_mays	[D] Proteasome subunit beta	3/3	138	15	24653	*Zea mays*
151/A0A1D6PVR8/UP7305_Z_mays	[X] 40S ribosomal protein S3-1	4/4	114	18	28696	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
152/GSTF1_MAIZE/SwissProt	[D] Glutathione S-transferase 1	3/3	81	13	24034	*Zea mays*
153/A0A1D6NHH6/UP7305_Z_mays	[X] GTP-binding nuclear protein	2/2	83	11	25440	*Zea mays*
154/C0PH34/UP7305_Z_mays	[D] 60S ribosomal protein L6	2/2	96	12	24223	*Zea mays*
155/A3FMB9/UP7305_Z_mays	[D] Proteasome subunit alpha type	2/2	94	10	27382	*Zea mays*
156/A0A1D6GF42/UP7305_Z_mays	[X] 40S ribosomal protein S2-1	1/1	53	5	30027	*Zea mays*
157/B6TPA4/UP7305_Z_mays	[X] Carnitine racemase/catalytic	1/1	46	5	25869	*Zea mays*
158/A0A1D6FVM4/UP7305_Z_mays	[X] ULP_PROTEASE domain-containing protein	1/1	45	1	117912	*Zea mays*
159/A0A1D6ENH9/UP7305_Z_mays	[D] Ras-related protein RABA4c	1/1	44	4	25143	*Zea mays*
160/PMM_ORYSI/SwissProt	[A] Phosphomannomutase	1/1	42	7	28403	*Oryza sativa* subsp. *indica*
161/B4F848/UP7305_Z_mays	[X] 20 kDa chaperonin chloroplastic	1/1	40	7	25796	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
162/C0HHH9/UP7305_Z_mays	[A] Stress-response A/B barrel domain-containing protein UP3	1/1	39	4	26448	*Zea mays*
163/A0A1D6PI62/UP7305_Z_mays	[X] 40S ribosomal protein S3a	2/2	61	7	34634	*Zea mays*
164/A0A1D6KEX3/UP7305_Z_mays	[X] Adenine phosphoribosyltransferase	1/1	39	9	16873	*Zea mays*
165/A0A1D6KQ94/UP7305_Z_mays	[X] Co-chaperone protein SBA1	1/1	35	8	15736	*Zea mays*
166/A0A1D6L3U5/UP7305_Z_mays	[D] Aluminum induced protein with YGL and LRDR motifs	1/1	38	2	41034	*Zea mays*
167/COP52_ORYSJ/SwissProt	[X] Putative copper transporter 5.2	1/1	31	5	17936	*Oryza sativa* subsp. *japonica*
168/B4FB66/UP7305_Z_mays	[X] 40S ribosomal protein S5-2	1/1	57	6	22297	*Zea mays*
169/AOC_ORYSI/UP7305_Z_mays	[D] Allene oxide cyclase, chloroplastic	1/1	38	3	26206	*Oryza sativa* subsp. *indica*
170/CYPH_MAIZE/SwissProt	[D] Peptidyl-prolyl cis-trans isomerase	2/2	101	15	18565	*Zea mays*
171/A0A1D6LMW9/UP7305_Z_mays	[B] Endoplasmin-like protein	2/2	69	2	92572	*Zea mays*
172/LOX2_ORYSJ/SwissProt	[A] Linoleate 9S-lipoxygenase 2	1/1	47	1	97294	*Oryza sativa* subsp. *japonica*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
173/A0A1D6H0T3/UP7305_Z_mays	^{D} 26S proteasome non-ATPase regulatory subunit 2 homolog	1/1	45	1	95571	*Zea mays*
174/A0A1D6F8K9/UP7305_Z_mays	^{D} Coatomer subunit gamma	1/1	38	4	30142	*Zea mays*
175/A0A1D6H701/UP7305_Z_mays	^{D} Alpha-aminoacylpeptide hydrolase	1/1	33	1	60323	*Zea mays*
176/TAD3_ARATH/SwissProt	^{A} tRNA-specific adenosine deaminase TAD3	1/1	32	2	45697	*Zea mays*
177/A0A1D6IV93/UP7305_Z_mays	^{X} Agamous-like MADS-box protein AGL8	1/1	29	3	29077	*Zea mays*
178/A0A1D6FQA7/UP7305_Z_mays	^{B} Gibberellin receptor GID1A	1/1	29	2	35017	*Zea mays*
179/A0A1D6NQP7/UP7305_Z_mays	^{B} Chalcone-flavonone isomerase family protein	1/1	50	5	25446	*Zea mays*
180/A0A1D6J4Q3/UP7305_Z_mays	^{X} Translation elongation factor EF1A/initiation factor IF2gamma family protein	1/1	54	2	46081	*Zea mays*
181/PMG1_ARATH/SwissProt	^{D} 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1	2/1	62	3	60770	*Arabidopsis thaliana*
182/A0A1D6KNM8/UP7305_Z_mays	^{X} Phosphoglycerate dehydrogenase	1/1	43	1	69667	*Zea mays*
183/C4J4W3/UP7305_Z_mays	^{X} Hsp70-Hsp90 organizing protein 3	1/1	40	1	65563	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
184/A0A1D6GY43/UP7305_Z_mays	ᴰ Translationally controlled tumor1	1/1	54	8	20328	*Zea mays*
185/A0A1D6F4V8/UP7305_Z_mays	ᵡ 26S proteasome regulatory subunit 4 homolog A	1/1	58	3	41048	*Zea mays*
186/A0A1D6FL86/UP7305_Z_mays	ᵡ Putative calcium-dependent protein kinase family protein	1/1	57	4	44614	*Zea mays*
187/A0A1D6N395/UP7305_Z_mays	ᴰ Selenium-binding protein 3	1/1	50	4	29130	*Zea mays*
188/A0A1D6DZS2/UP7305_Z_mays	ᴮ UDP-N-acetylglucosamine diphosphorylase 2	1/1	59	2	49205	*Zea mays*
189/A0A1D6JPH3/UP7305_Z_mays	ᴰ Glutathione reductase	1/1	36	2	59553	*Zea mays*
190/A0A1D6NUR0/UP7305_Z_mays	ᵡ Carotenoid 910(9'10')-cleavage dioxygenase 1	1/1	34	1	69195	*Zea mays*
191/A0A1D6FQ43/UP7305_Z_mays	ᴰ Guanosine nucleotide diphosphate dissociation inhibitor	1/1	49	5	51286	*Zea mays*
192/A0A1D6LJP0/UP7305_Z_mays	ᴰ 6-phosphogluconate dehydrogenase, decarboxylating	1/1	49	3	55248	*Zea mays*
193/A0A1D6M1D4/UP7305_Z_mays	ᵡ Eukaryotic peptide chain release factor subunit 1-1	1/1	48	2	49026	*Zea mays*
194/B6TQC0/UP7305_Z_mays	ᴰ 3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase	1/1	48	2	46584	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
195/C0HDR0/UP7305_Z_mays	^{B} Histidinol dehydrogenase, chloroplastic	1/1	43	3	51496	*Zea mays*
196/A0A1D6EAA2/UP7305_Z_mays	^{D} Regulator of chromosome condensation2	1/1	37	2	29232	*Zea mays*
197/GME1_ORYSI/SwissProt	^{X} GDP-mannose 3,5-epimerase 1	2/2	86	7	43180	*Oryza sativa* subsp. *indica*
198/ACT_MESVI/SwissProt	^{X} Actin	3/2	123	8	41791	*Mesostigma viride*
199/K7V9P7/UP7305_Z_mays	^{X} Beta-ketoacyl-[acyl-carrier-protein] synthase I	1/1	63	2	51721	*Zea mays*
200/A0A1D6KN99/UP7305_Z_mays	^{D} 12-oxo-phytodienoic acid reductase7	1/1	52	2	37278	*Zea mays*
201/B6TN48/UP7305_Z_mays	^{D} 3-hydroxyisobutyryl-CoA hydrolase-like protein 5	1/1	51	1	43135	*Zea mays*
202/A0A1D6H7L0/UP7305_Z_mays	^{X} 26S protease regulatory subunit 8 homolog B	1/1	50	3	41699	*Zea mays*
203/A0A1D6GVM3/UP7305_Z_mays	^{X} Delta-aminolevulinic acid dehydratase (Porphobilinogen synthase)	2/2	58	5	46434	*Zea mays*
204/A0A1D6HNF6/UP7305_Z_mays	^{B} Aspartate transaminase	1/1	41	2	46492	*Zea mays*
205/A0A1D6DUW9/UP7305_Z_mays	^{D} 26S proteasome non-ATPase regulatory subunit 7 homolog A	1/1	48	3	35966	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
206/RABD1_ARATH/UP7305_Z_mays	[D] Ras-related protein	1/1	71	7	22995	*Arabidopsis thaliana*
207/A0A1D6HDG0/UP7305_Z_mays	[B] Succinate-CoA ligase subunit beta	1/1	39	1	40725	*Zea mays*
208/ACT4_SOLLC/SwissProt	[X] Actin-105 (Fragment)	1/1	35	4	37362	*Solanum lycopersicum*
209/A0A1D6NZT3/UP7305_Z_mays	[A] Uncharacterized conserved protein (UCP030210)	1/1	32	5	45907	*Zea mays*
210/C4J5P0/UP7305_Z_mays	[D] Aspartyl protease AED1	1/1	55	2	51276	*Zea mays*
211/A0A1D6HI32/UP7305_Z_mays	[X] Thioredoxin reductase	1/1	52	4	37630	*Zea mays*
212/FBRL2_ARATH/SwissProt	[X] rRNA 2'-O-methyltransferase fibrillarin 2	1/1	51	3	33803	*Arabidopsis thaliana*
213/A0A1D6QTN1/UP7305_Z_mays	[A] NAD(P)-linked oxidoreductase superfamily protein	1/1	48	7	18913	*Zea mays*
214/A0A1D6FKF4/UP7305_Z_mays	[D] Aspartic proteinase A1	1/1	52	4	56800	*Zea mays*
215/A0A1D6H1H5/UP7305_Z_mays	[B] Hydroxymethylbilane synthase	1/1	42	3	46158	*Zea mays*
216/B8A2X5/UP7305_Z_mays	[D] Pectinesterase	3/3	98	6	60684	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
217/CYSK_MAIZE/SwissProt	^{D} Cysteine synthase	2/2	74	7	34299	*Zea mays*
218/A0A1D6HNQ2/UP7305_Z_mays	^{D} Oxidoreductase zinc-binding dehydrogenase family protein	1/1	49	2	35976	*Zea mays*
219/A0A1D6FR00/UP7305_Z_mays	^{X} Elongation factor 1-beta	1/1	55	3	27466	*Zea mays*
220/TPIC_SPIOL/SwissProt	^{X} Triosephosphate isomerase, chloroplastic	1/1	46	4	34787	*Spinacia oleracea*
221/A0A1D6G511/UP7305_Z_mays	^{X} 40S ribosomal protein S6-1	1/1	45	7	13533	*Zea mays*
222/CAMT1_MAIZE/SwissProt	^{X} Caffeoyl-CoA O-methyltransferase 1	1/1	36	6	29016	*Zea mays*
223/PCNA_MAIZE/SwissProt	^{D} Proliferating cell nuclear antigen	2/2	73	10	29609	*Zea mays*
224/P45633/UP7305_Z_mays	^{X} 60S ribosomal protein L10	1/1	78	5	25359	*Zea mays*
225/DOT2_ARATH/SwissProt	^{X} SART-1 family protein DOT2	1/1	54	1	94086	*Arabidopsis thaliana*
226/B6SHT0/UP7305_Z_mays	^{B} OB-fold nucleic acid binding domain containing protein	1/1	62	6	15544	*Zea mays*
227/B6T6G1/UP7305_Z_mays	^{D} 60S ribosomal protein L12	1/1	76	9	17805	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
228/A0A1D6F0E2/UP7305_Z_mays	^{D} Eukaryotic translation initiation factor 5A	1/1	47	7	15487	*Zea mays*
229/RL11_ORYSI/SwissProt	^{B} 60S ribosomal protein L11	1/1	53	7	20994	*Zea mays*
230/A0A1D6GZY9/UP7305_Z_mays	^{D} Cleavage and polyadenylation specificity factor (CPSF) A subunit protein	2/2	95	2	132541	*Zea mays*
231/A0A1D6EYG6/UP7305_Z_mays	^{A} HOPM interactor 7	1/1	52	1	122829	*Zea mays*
232/SKM1_ARATH/SwissProt	^{X} Leucine-rich repeat receptor-like serine/threonine-protein kinase SKM1	1/1	38	1	107464	*Arabidopsis thaliana*
233/A0A1D6IQM5/UP7305_Z_mays	^{D} E1 ubiquitin-activating enzyme	1/1	55	1	113830	*Zea mays*
234/A0A1D6HN05/UP7305_Z_mays	^{A} T-complex protein 1 subunit alpha	1/1	41	2	42446	*Zea mays*
235/A0A1D6HNE6/UP7305_Z_mays	^{X} DNA helicase	1/1	39	2	82318	*Zea mays*
236/A0A1D6NQE9/UP7305_Z_mays	^{D} Non-reducing end alpha-L-arabinofuranosidase	1/1	31	4	44052	*Zea mays*
237/A0A1D6GZE7/UP7305_Z_mays	^{X} RuvB-like helicase	1/1	62	3	50233	*Zea mays*
238/B4F922/UP7305_Z_mays	^{B} Acyltransferase	1/1	60	3	47893	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
239/A0A1D6ECT0/UP7305_Z_mays	[D] Aldehyde dehydrogenase family 7 member B4	1/1	41	6	23630	*Zea mays*
240/A0A1D6MQV8/UP7305_Z_mays	[B] Glycine hydroxymethyltransferase	1/1	80	11	10741	*Zea mays*
241/PRS6B_ARATH/SwissProt	[X] 26S proteasome regulatory subunit 6B homolog	1/1	74	4	45894	*Arabidopsis thaliana*
242/A0A1D6MRA8/UP7305_Z_mays	[D] Zea CEFD homolog1	2/2	64	5	52474	*Zea mays*
243/A0A1D6M0K3/UP7305_Z_mays	[X] GOLD domain-containing protein	1/1	26	3	49812	*Zea mays*
244/A0A1D6ETA7/UP7305_Z_mays	[D] ATPase 100193266	1/1	101	4	39908	*Zea mays*
245/A0A1D6E501/UP7305_Z_mays	[D] 3-isopropylmalate dehydrogenase	2/2	93	9	43132	*Zea mays*
246/A0A1D6G3W9/UP7305_Z_mays	[A] UDP-D-apiose/UDP-D-xylose synthase 2	1/1	71	2	45261	*Zea mays*
247/AT9_ORYSJ/SwissProt	[A] Acyl transferase 9	1/1	49	2	46535	*Oryza sativa* subsp. *japonica*
248/A0A1D6NT98/UP7305_Z_mays	[D] Uncharacterized protein (Membrane protein – UniProtKB)	1/1	42	1	68147	*Zea mays*
249/LDHA_HORVU/SwissProt	[X] L-lactate dehydrogenase A	1/1	72	3	37840	*Hordeum vulgare*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
250/A0A1D6FSS5/UP7305_Z_mays	^{D} NAD(P)H dehydrogenase (quinone)	1/1	59	6	19170	*Zea mays*
251/A0A1D6KNS0/UP7305_Z_mays	^{X} Cinnamoyl CoA reductase1	1/1	32	3	45016	*Zea mays*
252/A0A1D6EGZ7/UP7305_Z_mays	^{X} ARM repeat superfamily protein	1/1	32	3	47837	*Zea mays*
253/A0A1D6HJS1/UP7305_Z_mays	^{B} Pyruvate dehydrogenase E1 component subunit alpha	1/1	67	3	43016	*Zea mays*
254/A0A1D6FN07/UP7305_Z_mays	^{D} UDP-glucuronic acid decarboxylase 4	1/1	46	5	21307	*Zea mays*
255/A0A1D6EKR8/UP7305_Z_mays	^{D} Spermidine synthase 2	1/1	68	4	35264	*Zea mays*
256/A0A1D6DT56/UP7305_Z_mays	^{X} NADPH-protochlorophyllide oxidoreductase	1/1	54	3	41525	*Zea mays*
257/KDSA2_ARATH/UP7305_Z_mays	^{D} 2-dehydro-3-deoxyphosphooctonate aldolase 2	1/1	51	2	31998	*Zea mays*
258/B4F7V1/UP7305_Z_mays	^{D} 3-deoxy-8-phosphooctulonate synthase	1/1	51	2	32126	*Zea mays*
259/KCAB_ARATH/SwissProt	^{X} Probable voltage-gated potassium channel subunit beta	1/1	40	3	36744	*Arabidopsis thaliana*
260/B4FVD5/UP7305_Z_mays	^{X} V-type proton ATPase subunit E3	1/1	39	4	26727	*Zea mays*

Table S1 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
261/A0A1D6MQ90/UP7305_Z_mays	[X] 26S proteasome regulatory subunit RPN11	1/1	35	2	31682	*Zea mays*
262/A0A1D6MLF6/UP7305_Z_mays	[D] Triose phosphate isomerase4	4/4	252	27	27958	*Zea mays*
263/RS8_MAIZE/SwissProt	[X] 40S ribosomal protein S8	2/2	134	13	25155	*Zea mays*
264/A0A1D6G8L3/UP7305_Z_mays	[B] Triose phosphate isomerase5	1/1	41	6	24871	*Zea mays*
265/RIC1_ORYSJ/SwissProt	[D] Ras-related protein RIC1	2/2	88	13	22690	*Oryza sativa* subsp. *japonica*

X: Detected proteins only at first cut; D: Detected proteins at all cuts; B: Detected proteins only at first and third cuts; **A**: Detected proteins only at first and fifth cuts.

Table S2. Total and differential proteome of the axillary bud of the RB867515 sugarcane cultivar at the third cutting stage.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
1/A0A1D6IQ26/UP7305_Z_mays	^{D} Clathrin heavy chain	3/3	139	2	195242	*Zea mays*
2/A0A1D6LAW0/UP7305_Z_mays	^{D} Elongation factor 2	10/6	547	14	94813	*Zea mays*
3/A0A1D6Q5B1/UP7305_Z_mays	^{D} Phenylalanine ammonia-lyase	8/4	278	13	75926	*Zea mays*
4/A0A1D6GGA0/UP7305_Z_mays	^{D} Tubulin alpha chain	1/1	63	3	46258	*Zea mays*
5/A0A1D6P848/UP7305_Z_mays	^{D} Sucrose synthase	5/5	275	9	91108	*Zea mays*
6/A0A1D6N531/UP7305_Z_mays	^{D} Lipoxygenase	4/4	131	5	99495	*Zea mays*
7/A0A1D6KGM2/UP7305_Z_mays	^{D} 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	4/2	283	9	82279	*Zea mays*
8/A0A1D6PUK7/UP7305_Z_mays	^{D} Aconitate hydratase (aconitase)	3/3	107	4	104138	*Zea mays*
9/A0A1D6FNB8/UP7305_Z_mays	^{D} Heat shock 70 kDa protein 14	2/2	100	3	95515	*Zea mays*
10/A0A096S9C5/UP7305_Z_mays	^{B} Ribonuclease	1/1	73	1	99011	*Zea mays*
11/A0A1D6ES19/UP7305_Z_mays	^{D} Heat shock protein 90-2	2/2	94	3	80407	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
12/A0A1D6H701/UP7305_Z_mays	^{D} Alpha-aminoacylpeptide hydrolase	2/2	68	3	60323	*Zea mays*
13/A0A1D6GYL9/UP7305_Z_mays	^{D} Luminal-binding protein	1/1	62	3	59016	*Zea mays*
14/A0A1D6EL67/UP7305_Z_mays	^{D} ADP-ribosylation factor A1F	1/1	51	7	21298	*Zea mays*
15/PS17_PINST/SwissProt	^{D} Putative cytochrome c oxidase subunit II PS17 (Fragments)	1/1	43	50	1707	*Pinus strobus*
16/TKTC_MAIZE/SwissProt	^{D} Transketolase, chloroplastic	2/2	96	3	73347	*Zea mays*
17/A0A1D6QG34/UP7305_Z_mays	^{D} E1 ubiquitin-activating enzyme	2/2	103	5	81253	*Zea mays*
18/A0A1D6KE24/UP7305_Z_mays	^{D} Heat shock protein 70	7/1	304	20	65311	*Zea mays*
19/A0A1D6FHT8/UP7305_Z_mays	^{D} ATP citrate synthase	3/3	161	5	66504	*Zea mays*
20/A0A1D6DW07/UP7305_Z_mays	^{D} D-3-phosphoglycerate dehydrogenase	3/3	105	6	64984	*Zea mays*
21/A0A1D6H1R5/UP7305_Z_mays	^{D} V-ATPase 69 kDa subunit	2/2	93	5	55167	*Zea mays*
22/A0A096S0J0/UP7305_Z_mays	^{D} Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha	1/1	62	2	68229	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
23/SDHA_ORYSJ /SwissProt	^{D} Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	2/2	127	4	69494	*Oryza sativa* subsp. *japonica*
24/C0P790/UP7305_Z_mays	^{C} Eukaryotic translation initiation factor 3 subunit B	1/1	67	1	83062	*Zea mays*
25/BIP4_ORYSJ/SwissProt	^{D} Heat shock 70 kDa protein BIP4	3/2	152	4	74438	*Zea mays*
26/A0A1D6L1Y9/UP7305_Z_mays	^{D} Phosphoglucomutase	3/1	137	9	70703	*Zea mays*
27/A0A1D6NQE9/UP7305_Z_mays	^{D} Non-reducing end alpha-L-arabinofuranosidase	1/1	55	4	44052	*Zea mays*
28/A0A096R6Z8/UP7305_Z_mays	^{D} Heat shock 70 kDa protein 6 chloroplastic	3/3	109	5	73148	*Zea mays*
29/A0A1D6K5D2/UP7305_Z_mays	^{D} Nucleoredoxin1	1/1	55	2	64030	*Zea mays*
30/A0A1D6FI28/UP7305_Z_mays	^{D} 3-hydroxyacyl-CoA dehydrogenase	1/1	47	3	72964	*Zea mays*
31/A0A1D6NUS9UP7305_Z_mays	^{D} Acyl-coenzyme A oxidase	1/1	62	4	32559	*Zea mays*
32/A0A1D6KZB9/UP7305_Z_mays	^{Y} Tetratricopeptide repeat (TPR)-like superfamily protein	1/1	33	1	73005	*Zea mays*
33/A0A1D6F5B9/UP7305_Z_mays	^{D} Protein disulfide-isomerase	2/2	65	3	61141	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
34/A0A1D6FQA7/UP7305_Z_mays	^{B} Gibberellin receptor GID1A	1/1	43	2	35017	*Zea mays*
35/A0A1D6GWE1/UP7305_Z_mays	^{B} Shepherd-like1	2/2	87	4	92874	*Zea mays*
36/PDC2_ORYSI/SwissProt	^{C} Pyruvate decarboxylase 2	3/3	145	6	65889	*Oryza sativa* subsp. *indica*
37/B4FAL8/UP7305_Z_mays	^{D} Selenium-binding protein 3	2/2	60	5	54659	*Zea mays*
38/VATB1_ARATH/SwissProt	^{D} V-type proton ATPase subunit B1	8/6	376	22	54188	*Arabidopsis thaliana*
39/B6T4R3/UP7305_Z_mays	^{D} UTP--glucose-1-phosphate uridylyltransferase	9/8	394	24	52227	*Zea mays*
40/ENO_ORYSJ/SwissProt	^{D} Enolase	9/2	376	26	48285	*Oryza sativa* subsp. *japonica*
41/ATPBM_MAIZE/SwissProt	^{D} ATP synthase subunit beta, mitochondrial	8/8	307	17	59181	*Zea mays*
42/C0HGT5/UP7305_Z_mays	^{D} T-complex protein 1 subunit delta	2/2	107	11	58096	*Zea mays*
43/UGDH5_ORYSJ/SwissProt	^{D} UDP-glucose 6-dehydrogenase 5	4/4	193	12	53455	*Oryza sativa* subsp. *japonica*
44/C0P567/UP7305_Z_mays	^{D} Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta	1/1	82	2	61640	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
45/A0A1D6FKV6/UP7305_Z_mays	[D] Ketol-acid reductoisomerase	4/4	127	9	63213	*Zea mays*
46/K7UGM3/UP7305_Z_mays	[D] Catalase	2/2	97	5	56941	*Zea mays*
47/TCPH_ARATH/SwissProt	[D] T-complex protein 1 subunit eta	1/1	63	3	60195	*Arabidopsis thaliana*
48/A0A1D6HN61/UP7305_Z_mays	[D] Leucine aminopeptidase 2 chloroplastic	2/2	103	5	62181	*Zea mays*
49/B4FM07/UP7305_Z_mays	[Y] Thioredoxin-dependent peroxiredoxin	1/1	37	5	28318	*Zea mays*
50/B6SXW8/UP7305_Z_mays	[D] RuBisCO large subunit-binding protein subunit alpha	1/1	75	2	61419	*Zea mays*
51/A0A1D6LJS9/UP7305_Z_mays	[D] Chaperonin 60 subunit beta 2 chloroplastic	1/1	39	2	62041	*Zea mays*
52/A0A1D6FU93/UP7305_Z_mays	[Y] Arginyl-tRNA synthetase	1/1	38	1	67511	*Zea mays*
53/A0A1D6E7X7/UP7305_Z_mays	[D] Glucose-6-phosphate dehydrogenase (NADP$^+$)	3/3	85	13	27709	*Zea mays*
54/A0A1D6HYS3/UP7305_Z_mays	[Y] Phosphoglucosamine mutase family protein	1/1	63	5	20237	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
55/C0PHR4/UP7305_Z_mays	D Adenosylhomocysteinase	5/3	138	11	53884	*Zea mays*
56/A0A1D6N1Z8/UP7305_Z_mays	D 6-phosphogluconate dehydrogenase, decarboxylating	7/7	234	17	52908	*Zea mays*
57/A0A0B4J3C2/UP7305_Z_mays	D Elongation factor 1-alpha	2/2	74	4	49478	*Zea mays*
58/B4G0K4/UP7305_Z_mays	D Phosphoglycerate kinase	5/5	165	17	42470	*Zea mays*
59/A0A1D6DTX6 /UP7305_Z_mays	Y Protein DJ-1 homolog D	1/1	39	3	35815	*Zea mays*
60/A0A1D6ER22/UP7305_Z_mays	D Aldehyde dehydrogenase family 7 member B4	1/1	55	2	55365	*Zea mays*
61/A0A1D6GN16/UP7305_Z_mays	C Putative serine protease EDA2	1/1	57	2	55538	*Zea mays*
62/A0A096PQR7/UP7305_Z_mays	D Cytochrome P450 CYP74A19	1/1	50	3	53248	*Zea mays*
63/GLYC4_ARATH/SwissProt	D Serine hydroxymethyltransferase 4	3/2	126	8	52141	*Arabidopsis thaliana*
64/A0A1D6LSP0/UP7305_Z_mays	D Elongation factor gamma1	1/1	47	4	47098	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
65/A0A1D6MRA8/UP7305_Z_mays	^{D} Zea CEFD homolog1	1/1	46	5	52474	*Zea mays*
66/A0A1D6ENE6/UP7305_Z_mays	^{D} Guanosine nucleotide diphosphate dissociation inhibitor	1/1	45	4	55745	*Zea mays*
67/A0A1D6PRL0/UP7305_Z_mays	^{C} Apyrase 1	1/1	44	2	52164	*Zea mays*
68/AMYB_MAIZE/SwissProt	^{D} Beta-amylase	2/2	79	5	55487	*Zea mays*
69/GLYM_PEA/SwissProt	^{Y} Serine hydroxymethyltransferase, mitochondrial	1/1	41	2	57371	*Pisum sativum*
70/A0A096SSY4/UP7305_Z_mays	^{D} Tubulin beta chain	1/1	41	2	50663	*Zea mays*
71/C0P6C5/UP7305_Z_mays	^{C} Threonine synthase	1/1	40	3	57919	*Zea mays*
72/C0PC61/UP7305_Z_mays	^{D} Transaldolase	3/3	124	8	46363	*Zea mays*
73/B4FWP0/UP7305_Z_mays	^{D} Fructose-bisphosphate aldolase	5/5	168	25	38891	*Zea mays*
74/A0A1D6E501/UP7305_Z_mays	^{D} 3-isopropylmalate dehydrogenase	3/3	98	13	43132	*Zea mays*
75/A0A1D6ETA7/UP7305_Z_mays	^{D} ATPase 100193266	1/1	66	4	39908	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
76/A0A1D6KN99/UP7305_Z_mays	[D] 12-oxo-phytodienoic acid reductase7	2/2	64	5	37278	*Zea mays*
77/A0A1D6L117/UP7305_Z_mays	[C] Tryptophanyl-tRNA synthetase	1/1	61	4	28162	*Zea mays*
78/B6TN48/UP7305_Z_mays	[D] 3-hydroxyisobutyryl-CoA hydrolase-like protein 5	1/1	54	2	43135	*Zea mays*
79/A0A1D6JZR5/UP7305_Z_mays	[D] LL-diaminopimelate aminotransferase chloroplastic	1/1	59	2	52087	*Zea mays*
80/C0PCC1/UP7305_Z_mays	[B] Chalcone synthase C2	1/1	55	4	36017	*Zea mays*
81/A0A1D6FCW7/UP7305_Z_mays	[D] Putative acetyl-CoA acetyltransferase cytosolic 2	1/1	46	3	46208	*Zea mays*
82/C4J4E4/UP7305_Z_mays	[D] Monodehydroascorbate reductase homolog1	1/1	45	5	46817	*Zea mays*
83/A0A1D6HNF6/UP7305_Z_mays	[B] Aspartate transaminase	1/1	44	2	46492	*Zea mays*
84/A0A1D6FUX8/UP7305_Z_mays	[B] S-adenosylmethionine synthase	1/1	44	1	51644	*Zea mays*
85/B4FLJ3/UP7305_Z_mays	[D] Isocitrate dehydrogenase [NADP]	2/2	61	6	46411	*Zea mays*
86/A0A1D6PNA2/UP7305_Z_mays	[Y] U2 snRNP auxiliary factor large subunit	1/1	30	4	38886	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
87/A0A1D6KLI4/UP7305_Z_mays	[D] UDP-glucuronic acid decarboxylase 5	1/1	49	7	21962	*Zea mays*
88/B4FRJ1/UP7305_Z_mays	[D] Malate dehydrogenase	4/4	194	26	35789	*Zea mays*
89/A0A1D6LER1/UP7305_Z_mays	[D] Glyceraldehyde-3-phosphate dehydrogenase	3/3	161	13	35809	*Zea mays*
90/SCRK1_ORYSI/SwissProt	[D] Fructokinase-1	3/3	123	11	34878	*Oryza sativa* subsp. *indica*
91/MDHM2_ARATH/SwissProt	[C] Malate dehydrogenase 2, mitochondrial	2/1	89	8	36024	*Arabidopsis thaliana*
92/COMT1_SACOF/SwissProt	[D] Caffeic acid 3-O-methyltransferase	2/2	91	9	39838	*Saccharum officinarum*
93/A0A1D6HJS1/UP7305_Z_mays	[B] Pyruvate dehydrogenase E1 component subunit alpha	1/1	76	3	43016	*Zea mays*
94/RGP1_ORYSJ/SwissProt	[D] UDP-arabinopyranose mutase 1	2/2	88	8	41835	*Oryza sativa* subsp. *japonica*
95/A0A1D6LBH9/UP7305_Z_mays	[D] Late embryogenesis abundant protein group 2	2/2	74	8	29322	*Zea mays*
96/RLA0_MAIZE/SwissProt	[D] 60S acidic ribosomal protein P0	2/2	96	14	34597	*Zea mays*
97/K7UXK5/UP7305_Z_mays	[D] Putative alcohol dehydrogenase superfamily protein	1/1	80	3	39196	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
98/CYSK_MAIZE/SwissProt	^{D} Cysteine synthase	1/1	59	3	34299	*Zea mays*
99/SPL8_ARATH/UP7305_Z_mays	^{Y} Squamosa promoter-binding-like protein 8	1/1	41	2	37261	*Zea mays*
100/A0A1D6EZI3/UP7305_Z_mays	^{B} Succinyl-CoA ligase alpha-chain 2	1/1	53	23	5271	*Zea mays*
101/GBLPA_ORYSJ/SwissProt	^{D} Guanine nucleotide-binding protein subunit beta-like protein A	4/4	205	15	36665	*Oryza sativa* subsp. *japonica*
102/A0A1D6LDS1/UP7305_Z_mays	^{D} Fructokinase-2	4/2	135	13	36170	*Zea mays*
103/A0A1D6G0Z9/UP7305_Z_mays	^{D} Ribokinase	2/2	91	6	37978	*Zea mays*
104/A0A1D6FKF4/UP7305_Z_mays	^{D} Aspartic proteinase A1	3/3	140	9	56800	*Zea mays*
105/A0A1D6Q3V1/UP7305_Z_mays	^{D} 60S ribosomal protein L6	1/1	81	12	12696	*Zea mays*
106/A0A1D6FQM0/UP7305_Z_mays	^{C} Alpha/beta-hydrolases superfamily protein	1/1	80	16	11663	*Zea mays*
107/A0A1D6P3Y5/UP7305_Z_mays	^{D} Proteasome subunit beta	1/1	104	7	26154	*Zea mays*
108/A0A1D6H5M9/UP7305_Z_mays	^{Y} ATP-dependent DNA helicase	1/1	68	24	8239	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
109/A0A1D6MWW9/UP7305_Z_mays	^{D} 60S ribosomal protein L2	1/1	74	7	17905	*Zea mays*
110/B6UAK0/UP7305_Z_mays	^{C} Probable 6-phosphogluconolactonase	1/1	77	5	34874	*Zea mays*
111/A0A1D6MLF6/UP7305_Z_mays	^{D} Triose phosphate isomerase4	3/3	220	24	27958	*Zea mays*
112/B6TAJ3/UP7305_Z_mays	^{D} Proteasome subunit alpha type	1/1	80	4	30282	*Zea mays*
113/A0A1D6PD08/UP7305_Z_mays	^{D} L-ascorbate peroxidase	2/2	63	12	30847	*Zea mays*
114/A0A1D6E930/UP7305_Z_mays	^{D} 14-3-3-like protein GF14-6	1/1	38	3	31041	*Zea mays*
115/B4FB55/UP7305_Z_mays	^{C} Ras-related protein ARA-3	3/3	120	16	24038	*Zea mays*
116/RIC1_ORYSJ/SwissProt	^{D} Ras-related protein RIC1	2/1	78	13	22690	*Oryza sativa* subsp. *japonica*
117/A0A1D6KU62/UP7305_Z_mays	^{D} Ras-related protein Rab-18	1/1	68	4	27585	*Zea mays*
118/RABG1_ARATH/SwissProt	^{D} Ras-related protein RABG1	1/1	68	5	23823	*Arabidopsis thaliana*
119/YPTV5_VOLCA/SwissProt	^{D} GTP-binding protein yptV5	1/1	68	5	23381	*Volvox carteri*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
120/A0A1D6FNG1/UP7305_Z_mays	^{C} Superoxide dismutase	3/3	118	11	26419	*Zea mays*
121/B4FJB2/UP7305_Z_mays	^{D} Ras-related protein RABA4a	2/2	78	10	24099	*Zea mays*
122/EXPA1_ARATH/SwissProt	^{C} Expansin-A1	1/1	46	3	26957	*Arabidopsis thaliana*
123/AOC_ORYSI/SwissProt	^{D} Allene oxide cyclase, chloroplastic	1/1	46	3	26206	*Oryza sativa* subsp. *indica*
124/RABD1_ARATH/SwissProt	^{D} Ras-related protein RABD1	1/1	42	7	22995	*Arabidopsis thaliana*
125/CYPH_MAIZE/SwissProt	^{D} Peptidyl-prolyl cis-trans isomerase	3/3	162	15	18565	*Zea mays*
126/B4FN19/UP7305_Z_mays	^{D} 60S ribosomal protein L12-3	3/3	111	22	17925	*Zea mays*
127/A0A1D6FHA9/UP7305_Z_mays	^{B} Nucleic acid-binding OB-fold-like protein	1/1	56	3	27030	*Zea mays*
128/A0A1D6F0E2/UP7305_Z_mays	^{D} Eukaryotic translation initiation factor 5A	1/1	61	8	15487	*Zea mays*
129/B7ZY32/UP7305_Z_mays	^{D} DUF642 domain-containing protein	1/1	50	6	14960	*Zea mays*
130/A0A1D6QSC9/UP7305_Z_mays	^{C} Glycine cleavage system H protein	1/1	45	8	19817	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
131/A0A1D6FNK4/UP7305_Z_mays	^{B} 60S ribosomal protein L11-1	1/1	41	8	14224	*Zea mays*
132/A0A1D6KDZ6/UP7305_Z_mays	^{Y} Translocon-associated protein beta (TRAPB) family pro	1/1	40	5	22107	*Zea mays*
133/B4FMB1/UP7305_Z_mays	^{C} DUF538 family protein	1/1	60	4	17499	*Zea mays*
134/A0A1D6MK62/UP7305_Z_mays	^{D} Phospholipase D	3/3	138	6	77695	*Zea mays*
135/A0A1D6HBU2/UP7305_Z_mays	^{C} Glycerophosphodiester phosphodiesterase	1/1	59	1	81765	*Zea mays*
136/A0A1D6KE00/UP7305_Z_mays	^{Y} Thaumatin-like protein	1/1	42	1	118090	*Zea mays*
137/A0A1D6GB94/UP7305_Z_mays	^{D} Phosphoenolpyruvate carboxylase	1/1	41	1	109040	*Zea mays*
138/A0A1D6E267/UP7305_Z_mays	^{C} Fasciclin-like arabinogalactan protein 10	1/1	39	3	44168	*Zea mays*
139/A0A1D6FRN4/UP7305_Z_mays	^{D} Putative mediator of RNA polymerase II transcription subunit 37c	6/1	245	10	68360	*Zea mays*
140/HS704_ARATH/Swiss Prot	^{Y} Heat shock 70 kDa protein 4	6/5	203	12	71456	*Arabidopsis thaliana*
141/A0A1D6MSC4/UP7305_Z_mays	^{D} Peroxidase	1/1	73	4	37579	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
142/C0P5E7/UP7305_Z_mays	^{Y} Leukotriene A-4 hydrolase-like protein	1/1	49	2	68240	*Zea mays*
143/A0A1D6ICM8/UP7305_Z_mays	^{Y} SKU5 similar 4	1/1	51	2	61378	*Zea mays*
144/A0A1D6NDJ4/UP7305_Z_mays	^{C} Malic enzyme	1/1	41	3	65868	*Zea mays*
145/CH60_BRANA/SwissProt	^{D} Chaperonin CPN60-like 1, mitochondrial	1/1	34	3	62829	*Brassica napus*
146/ATPAM_MAIZE/SwissProt	^{D} ATP synthase subunit alpha, mitochondrial	2/2	117	6	55431	*Zea mays*
147/A0A1D6FSA7/UP7305_Z_mays	^{Y} Protein RETICULATA-RELATED 6 chloroplastic	1/1	38	1	61907	*Zea mays*
148/A0A1D6MQV8/UP7305_Z_mays	^{B} Glycine hydroxymethyltransferase	2/1	81	25	10741	*Zea mays*
149/A0A1D6HP32/UP7305_Z_mays	^{D} Glutathione reductase cytosolic	2/2	62	6	57389	*Zea mays*
150/A0A1D6JE05/UP7305_Z_mays	^{Y} Coproporphyrinogen oxidase	1/1	52	3	38083	*Zea mays*
151/A0A1D6NU66/UP7305_Z_mays	^{Y} Telomere-associated protein RIF1	1/1	41	1	69208	*Zea mays*
152/OBP1A_ARATH/SwissProt	^{Y} Oil body-associated protein 1A	1/1	41	2	27447	*Arabidopsis thaliana*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
153/A0A1D6EAA2/UP7305_Z_mays	[D] Regulator of chromosome condensation2 (Ultraviolet-B receptor UVR8)	1/1	38	3	29232	*Zea mays*
154/A0A1D6L8I1/UP7305_Z_mays	[Y] Uncharacterized protein (Putative Galactose-binding domain-containing protein - UniProtKB)	1/1	38	4	41166	*Zea mays*
155/B4FT32/UP7305_Z_mays	[Y] Diaminopimelate decarboxylase 2 chloroplastic	1/1	32	1	53771	*Zea mays*
156/B4FBK3/UP7305_Z_mays	[D] Eukaryotic initiation factor 4A	1/1	47	2	46895	*Zea mays*
157/A0A1D6ESW5/UP7305_Z_mays	[D] Pyruvate dehydrogenase E1 component subunit beta	1/1	39	3	37682	*Zea mays*
158/A0A1D6H0T3/UP7305_Z_mays	[D] 26S proteasome non-ATPase regulatory subunit 2 homolog	1/1	35	1	95571	*Zea mays*
159/A0A1D6HDK4/UP7305_Z_mays	[D] Adenosine kinase	3/3	142	15	27540	*Zea mays*
160/A0A1D6JMR6/UP7305_Z_mays	[B] 60S ribosomal protein L5-1	1/1	32	3	33179	*Zea mays*
161/A0A1D6IYD6/UP7305_Z_mays	[C] Glyoxalase I	2/2	79	6	36506	*Zea mays*
162/A0A1D6HDG0/UP7305_Z_mays	[B] Succinate-CoA ligase subunit beta	1/1	42	2	40725	*Zea mays*
163/LGUL_ORYSJ/SwissProt	[C] Lactoylglutathione lyase	1/1	41	3	32875	*Oryza sativa* subsp. *japonica*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
164/A0A1D6DUW9/UP7305_Z_mays	^{D} 26S proteasome non-ATPase regulatory subunit 7 homolog A	1/1	51	3	35966	*Zea mays*
165/IFRH_MAIZE/SwissProt	^{D} Isoflavone reductase homolog IRL	3/3	102	11	32831	*Zea mays*
166/PILR4_THUPL/SwissProt	^{B} Bifunctional pinoresinol-lariciresinol reductase	1/1	59	3	34834	*Thuja plicata*
167/FABI2_ORYSJ/SwissProt	^{Y} Enoyl-[acyl-carrier-protein] reductase [NADH] 2, chloroplastic	1/1	54	3	39167	*Oryza sativa* subsp. *japonica*
168/Q84TL7/UP7305_Z_mays	^{D} Legumin-like protein	1/1	54	3	38047	*Zea mays*
169/A0A1D6HW85/UP7305_Z_mays	^{C} Nitrile-specifier protein 1	1/1	46	3	40635	*Zea mays*
170/A0A1D6EKR8/UP7305_Z_mays	^{D} Spermidine synthase 2	1/1	44	4	35264	*Zea mays*
171/A0A1D6FNY6/UP7305_Z_mays	^{D} Aldo-keto reductase family 4 member C9	1/1	38	5	16712	*Zea mays*
172/E1AFV5/UP7305_Z_mays	^{C} Beta-1,3-glucanase	2/2	92	10	36068	*Zea mays*
173/B6SKA0/UP7305_Z_mays	^{D} Glutathione S-transferase	2/2	48	12	24020	*Zea mays*
174/A0A1D6FGX5/UP7305_Z_mays	^{D} Aspartyl-tRNA synthetase	1/1	70	2	59639	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
175/A0A1D6IT39/UP7305 _Z_mays	[Y] Aluminum-induced protein homolog1	1/1	60	16	12359	*Zea mays*
176/A0A1D6FSS5/UP730 5_Z_mays	[D] NAD(P)H dehydrogenase (quinone)	1/1	76	6	19170	*Zea mays*
177/A0A1D6FLR1/UP730 5_Z_mays	[D] Spliceosome RNA helicase BAT1 isoform 1	1/1	39	2	52857	*Zea mays*
178/A0A1D6NMI8/UP730 5_Z_mays	[Y] Thioredoxin family Trp26	2/2	65	12	24902	*Zea mays*
179/K7VFF7/UP7305_Z_ mays	[C] Glutaredoxin-dependent peroxiredoxin	1/1	80	7	23860	*Zea mays*
180/K7TFG6/UP7305_Z_ mays	[Y] Cyclin superfamily protein, putative	1/1	36	1	44803	*Zea mays*
181/A0A1D6GZY9/UP730 5_Z_mays	[D] Cleavage and polyadenylation specificity factor (CPSF) A subunit protein	2/2	72	1	132541	*Zea mays*
182/A0A1D6GQ42/UP730 5_Z_mays	[D] Cell division cycle protein 48	2/2	86	3	90803	*Zea mays*
183/A0A1D6KTZ2/UP730 5_Z_mays	[Y] Chaperonin2	3/3	75	5	60983	*Zea mays*
184/A0A1D6M7L9/UP730 5_Z_mays	[Y] Assimilatory sulfite reductase	1/1	40	1	70336	*Zea mays*
185/A0A1D6FF26/UP730 5_Z_mays	[Y] 2-hydroxyacyl-CoA lyase	1/1	39	1	71527	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
186/A0A1D6MRK0/UP7305_Z_mays	D Betaine aldehyde dehydrogenase 2 mitochondrial	1/1	75	17	19118	*Zea mays*
187/A0A1D6I642/UP7305_Z_mays	D Glucose-6-phosphate isomerase	1/1	68	2	48331	*Zea mays*
188/A0A1D6IYM8/UP7305_Z_mays	B UDP-N-acetylglucosamine diphosphorylase 2	1/1	67	2	53902	*Zea mays*
189/A0A1D6NYE7/UP7305_Z_mays	D Restorer of fertility2	1/1	33	2	64098	*Zea mays*
190/B4F8S9/UP7305_Z_mays	C Uncharacterized protein (Fasciclin-like arabinogalactan protein 15 – UniProtKB)	2/2	65	7	50125	*Zea mays*
191/A0A1D6FV26/UP7305_Z_mays	B Glutamate--cysteine ligase	1/1	80	5	38071	*Zea mays*
192/IMA1A_ORYSJ/Swiss Prot	D Importin subunit alpha-1a	2/2	73	4	58162	*Oryza sativa* subsp. *japonica*
193/K7VX77/UP7305_Z_mays	Y Phosphotransferase	1/1	57	3	55001	*Zea mays*
194/B4G1P9/UP7305_Z_mays	D 3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase	2/2	81	5	46433	*Zea mays*
195/A0A1D6PA07/UP7305_Z_mays	C Beta-adaptin-like protein C	1/1	32	1	95514	*Zea mays*
196/A0A1D6HPL2/UP7305_Z_mays	D 3-ketoacyl-CoA thiolase 2 peroxisomal	1/1	44	6	36936	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
197/KDSA2_ARATH/Swiss Prot	^{D} 2-dehydro-3-deoxyphosphooctonate aldolase 2	1/1	49	2	31998	*Arabidopsis thaliana*
198/B4F7V1/UP7305_Z_mays	^{D} 3-deoxy-8-phosphooctulonate synthase	1/1	49	2	32126	*Zea mays*
199/A0A1D6K1B9/UP7305_Z_mays	^{B} Hydroxyproline-rich glycoprotein family protein	1/1	47	3	41036	*Zea mays*
200/A0A1D6HNQ2/UP7305_Z_mays	^{D} Oxidoreductase zinc-binding dehydrogenase family protein	1/1	46	2	35976	*Zea mays*
201/C4J5P0/UP7305_Z_mays	^{D} Aspartyl protease AED1	1/1	39	2	51276	*Zea mays*
202/A0A1D6G992/UP7305_Z_mays	^{D} Phosphoglycerate mutase	2/1	79	3	61993	*Zea mays*
203/A0A1D6G8L3/UP7305_Z_mays	^{B} Triose phosphate isomerase5	1/1	39	6	24871	*Zea mays*
204/A0A1D6FZF8/UP7305_Z_mays	^{D} oxidoreductase, aldo/keto reductase family protein	1/1	37	4	37750	*Zea mays*
205/A0A1D6PF20/UP7305_Z_mays	^{B} 26S proteasome non-ATPase regulatory subunit 4	1/1	59	2	48460	*Zea mays*
206/A0A1D6K370/UP7305_Z_mays	^{B} Nascent polypeptide-associated complex alpha subunit-like protein	1/1	55	6	22545	*Zea mays*
207/A0A1D6FTA3/UP7305_Z_mays	^{C} Ras-related protein RABG3f	1/1	43	5	22374	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
208/A0A1D6PIQ7/UP7305_Z_mays	^{Y} Eukaryotic translation initiation factor 3 subunit K	1/1	42	4	27923	*Zea mays*
209/API5_ORYSJ/SwissProt	^{Y} Apoptosis inhibitor 5-like protein API5	1/1	38	1	60176	*Oryza sativa* subsp. *japonica*
210/A0A1D6JIH1/UP7305_Z_mays	^{C} Pre-mRNA cleavage factor Im 25 kDa subunit	1/1	35	6	23457	*Zea mays*
211/A0A1D6GY43/UP7305_Z_mays	^{D} Translationally controlled tumor1	2/2	76	13	20328	*Zea mays*
212/CFI_MAIZE/Swissprot	^{B} Chalcone--flavonone isomerase	1/1	51	5	24406	*Zea mays*
213/A0A1D6QHJ6/UP7305_Z_mays	^{D} Aluminum induced protein with YGL and LRDR motifs	1/1	34	3	38614	*Zea mays*
214/A0A1D6DYK5/UP7305_Z_mays	^{D} Polyadenylate-binding protein RBP45C	1/1	46	2	48979	*Zea mays*
215/SODC_ANACO/Swiss Prot	^{Y} Superoxide dismutase [Cu-Zn]	3/3	115	16	15280	*Ananas comosus*
216/A0A1D6E5L0/UP7305_Z_mays	^{C} Ras-related protein18A1	1/1	56	5	21581	*Zea mays*
217/B4G227/UP7305_Z_mays	^{C} Peptide-N4-(N-acetyl-beta-glucosaminyl) asparagine amidase A protein	1/1	48	2	67783	*Zea mays*
218/A8WER4/UP7305_Z_mays	^{Y} ZCN2	1/1	34	5	19501	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
219/B4F922/UP7305_Z_mays	[B] Acyltransferase	2/2	56	6	47893	*Zea mays*
220/A0A1D6GLG2/UP7305_Z_mays	[B] Serine/threonine-protein phosphatase	1/1	40	1	105932	*Zea mays*
221/GAPN_ARATH/Swiss Prot	[C] NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	1/1	26	4	53710	*Arabidopsis thaliana*
222/TPS7_PHYDL/SwissProt	[Y] Trans-alpha-bergamotene synthase	1/1	33	2	63908	*Phyla dulcis*
223/A0A1D6L6R8/UP7305_Z_mays	[B] Histidinol dehydrogenase chloroplastic	1/1	31	7	26585	*Zea mays*
224/A0A1D6QRC6/UP7305_Z_mays	[C] Fumarylacetoacetase	1/1	26	5	41938	*Zea mays*
225/A0A1D6H1H5/UP7305_Z_mays	[B] Hydroxymethylbilane synthase	1/1	39	3	46158	*Zea mays*
226/A0A1D6EW83/UP7305_Z_mays	[C] Ras-related protein RABH1b	1/1	43	7	15909	*Zea mays*
227/IAAT_MAIZE/SwissProt	[Y] Alpha-amylase/trypsin inhibitor	1/1	46	5	22973	*Zea mays*
228/LOX1_HORVU/Swiss Prot	[C] Linoleate 9S-lipoxygenase 1	1/1	30	1	96447	*Zea mays*
229/A0A1D6H284/UP7305_Z_mays	[Y] 4-coumarate--CoA ligase 1	1/1	37	2	62506	*Zea mays*

Table S2 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
230/A0A1D6NT98/UP7305_Z_mays	^{D} Uncharacterized protein (Membrane protein – UniProtKB)	1/1	41	1	68147	*Zea mays*
231/A0A1D6HNP5/UP7305_Z_mays	^{D} Proliferating cell nuclear antigen	1/1	45	10	16672	*Zea mays*
232/A0A1D6P2Q0/UP7305_Z_mays	^{C} Transducin/WD40 repeat-like superfamily protein	1/1	45	4	28752	*Zea mays*
233/A0A1D6FZ20/UP7305_Z_mays	^{D} UBP1-associated protein 2C	1/1	39	5	42200	*Zea mays*
234/GCSP_PEA/SwissProt	^{Y} Glycine dehydrogenase (decarboxylating), mitochondrial	1/1	34	1	115411	*Pisum sativum*
235/A0A1D6EGS0/UP7305_Z_mays	^{Y} Protein transport protein Sec24-like CEF	1/1	23	1	117330	*Zea mays*
236/A0A1D6JKV2/UP7305_Z_mays	^{Y} Actin-related protein 4	1/1	39	3	38583	*Zea mays*
237/PUB25_ARATH/SwissProt	^{Y} U-box domain-containing protein 25	1/1	35	1	46654	*Arabidopsis thaliana*
238/B6TQ06/UP7305_Z_may	^{D} Aminomethyltransferase	1/1	20	4	44406	*Zea mays*
239/A0A1D6HJJ4/UP7305_Z_may	^{D} Glutamine synthetase	1/1	42	4	40876	*Zea mays*
240/A0A1D6F8L6/UP7305_Z_may	^{D} Coatomer subunit gamma	1/1	66	1	99656	*Zea mays*

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
241/A0A1D6LVE5/UP7305_Z_may	^{C} Gibberellin receptor GID1L2	1/1	38	4	34811	*Zea mays*
242/B8A2X5/UP7305_Z_mays	^{D} Pectinesterase	1/1	36	1	60684	*Zea mays*
243/A0A1D6GPP6/UP7305_Z_mays	^{C} Heterogeneous nuclear ribonucleoprotein 1	1/1	92	3	48323	*Zea mays*

Table S2 – Cont.

Y: Detected proteins only at third cut; D: Detected proteins at all cuts; B: Detected proteins only at first and third cuts; C: Detected proteins only at third and fifth cuts.

Table S3. Total and differential proteome of the axillary bud of the RB867515 sugarcane cultivar at the fifth cutting stage.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
1/A0A1D6LAW0/UP7305_Z_mays	^{D} Elongation factor 2	12/12	546	17	94813	*Zea mays*
2/CLH1_ORYSJ/SwissProt	^{D} Clathrin heavy chain 1	6/4	255	5	194534	*Zea mays*
3/A0A1D6GZY9/UP7305_Z_mays	^{D} Cleavage and polyadenylation specificity factor (CPSF) A subunit protein	2/2	99	2	132541	*Zea mays*
4/A0A1D6P848/UP7305_Z_mays	^{D} Sucrose synthase	7/6	260	11	91108	*Zea mays*
5/A0A1D6EYZ1/UP7305_Z_mays	^{A} HOPM interactor 7	1/1	58	1	104180	*Zea mays*
6/ENO_ORYSJ/SwissProt	^{D} Enolase	9/2	412	26	48285	*Oryza sativa* subsp. *japonica*
7/A0A1D6PTE3/UP7305_Z_mays	^{D} Adenosylhomocysteinase	6/4	225	29	26295	*Zea mays*
8/A0A1D6JY65/UP7305_Z_mays	^{Z} Heat shock cognate 70 kDa protein 2	1/1	43	2	65343	*Zea mays*
9/C0P5Y3/UP7305_Z_mays	^{D} 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	9/4	452	21	84781	*Zea mays*
10/A0A1D6IQM5/UP7305_Z_mays	^{D} E1 ubiquitin-activating enzyme	2/2	81	1	113830	*Zea mays*
11/A0A1D6Q5B1/UP7305_Z_mays	^{D} Phenylalanine ammonia-lyase	7/3	263	13	75926	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
12/A0A1D6ES19/UP7305_Z_mays	^{D} Heat shock protein 90-2	2/2	83	3	80407	*Zea mays*
13/A0A1D6N531/UP7305_Z_mays	^{D} Lipoxygenase	6/5	186	8	99495	*Zea mays*
14/A0A1D6PUK7/UP7305_Z_mays	^{D} Aconitate hydratase	6/1	218	9	104138	*Zea mays*
15/A0A1D6GGA0/UP7305_Z_mays	^{D} Tubulin alpha chain	2/2	87	8	46258	*Zea mays*
16/A0A1D6H0T3/UP7305_Z_mays	^{D} 26S proteasome non-ATPase regulatory subunit 2 homolog	5/5	111	7	95571	*Zea mays*
17/A0A1D6H701/UP7305_Z_mays	^{D} Alpha-aminoacylpeptide hydrolase	2/2	81	3	60323	*Zea mays*
18/A0A1D6M007/UP7305_Z_mays	^{D} Heat shock 70 kDa protein 14	2/2	74	3	94528	*Zea mays*
19/A0A1D6ECS1/UP7305_Z_mays	^{D} Phosphoenolpyruvate carboxylase 1	2/2	110	22	13850	*Zea mays*
20/A0A1D6MK62/UP7305_Z_mays	^{D} Phospholipase D	2/2	90	5	77695	*Zea mays*
21/C0PDC7/UP7305_Z_mays	^{Z} Chaperone protein ClpB1	1/1	53	2	101284	*Zea mays*
22/LOX1_HORVU/UP7305_Z_mays	^{C} Linoleate 9S-lipoxygenase 1	2/2	51	3	96447	*Hordeum vulgare*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
23/TAD3_ARATH/UP7305_Z_mays	[A] tRNA-specific adenosine deaminase TAD3	1/1	50	2	45697	*Zea mays*
24/LOX2_ORYSJ/SwissProt	[A] Linoleate 9S-lipoxygenase 2	2/1	49	3	97294	*Oryza sativa* subsp. *japonica*
25/A0A1D6NVZ7/UP7305_Z_mays	[D] Transketolase	2/2	81	3	79444	*Zea mays*
26/A0A1D6GCT9/UP7305_Z_mays	[Z] Protein EXPORTIN 1A	1/1	44	1	123719	*Zea mays*
27/A0A1D6HTM2/UP7305_Z_mays	[A] 60S ribosomal protein L4-1	1/1	34	2	36321	*Zea mays*
28/B6T3V0/UP7305_Z_mays	[Z] Ferredoxin-related	1/1	34	3	24446	*Zea mays*
29/CGEP_ORYSJ /SwissProt	[Z] Probable glutamyl endopeptidase, chloroplastic	1/1	32	2	104400	*Oryza sativa* subsp. *japonica*
30/PS17_PINST/SwissProt	[D] Putative cytochrome c oxidase subunit II PS17 (Fragments)	1/1	33	50	1707	*Pinus strobus*
31/A0A1D6E312/UP7305_Z_mays	[Z] Argonaute1c	1/1	31	1	58007	*Zea mays*
32/A0A1D6KE29/UP7305_Z_mays	[D] Heat shock protein 70	13/4	526	30	71447	*Zea mays*
33/A0A1D6N7I4/UP7305_Z_mays	[D] Putative mediator of RNA polymerase II transcription subunit 37c	10/1	440	22	71142	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
34/A0A1D6FHT8/UP7305_Z_mays	^{D} ATP citrate synthase	3/3	200	5	66504	*Zea mays*
35/BIP4_ORYSJ/SwissProt	^{D} Heat shock 70 kDa protein BIP4	3/2	177	4	74438	*Oryza sativa* subsp. *japonica*
36/A0A1D6QS46/UP7305_Z_mays	^{D} V-ATPase 69 kDa subunit	3/3	146	7	67665	*Zea mays*
37/SDHA_ORYSJ/SwissProt	^{D} Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	2/2	133	4	69494	*Oryza sativa* subsp. *japonica*
38/A0A1D6L1Y8/UP7305_Z_mays	^{D} Phosphoglucomutase1	3/3	115	9	66493	*Zea mays*
39/A0A1D6NDJ3/UP7305_Z_mays	^{C} Malic enzyme	2/2	89	4	67301	*Zea mays*
40/A0A1D6DW07/UP7305_Z_mays	^{D} D-3-phosphoglycerate dehydrogenase	3/3	96	7	64984	*Zea mays*
41/B4FK56/UP7305_Z_mays	^{D} Peroxidase	2/2	87	6	36545	*Zea mays*
42/A0A1D6EC20/UP7305_Z_mays	^{A} Glycine--tRNA ligase mitochondrial 1	1/1	67	5	30725	*Zea mays*
43/A0A1D6NUS9/UP7305_Z_mays	^{D} Acyl-coenzyme A oxidase	1/1	78	4	32559	*Zea mays*
44/A0A096R6Z8/UP7305_Z_mays	^{D} Heat shock 70 kDa protein 6 chloroplastic	2/2	62	3	73148	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
45/A0A1D6K5D2/UP7305_Z_mays	^{D} Nucleoredoxin1	1/1	56	2	64030	*Zea mays*
46/A0A1D6FI28/UP7305_Z_mays	^{D} 3-hydroxyacyl-CoA dehydrogenase	2/2	93	3	72964	*Zea mays*
47/A0A1D6NQE9/UP7305_Z_mays	^{D} Non-reducing end alpha-L-arabinofuranosidase	2/1	103	8	44052	*Zea mays*
48/C0P790/UP7305_Z_mays	^{C} Eukaryotic translation initiation factor 3 subunit B	1/1	62	1	83062	*Zea mays*
49/A0A1D6GPU9/UP7305_Z_mays	^{D} Chaperonin 1	1/1	46	4	29777	*Zea mays*
50/A0A1D6I3K9/UP7305_Z_mays	^{Z} Endo-1,3(4)-beta-glucanase	1/1	41	3	82719	*Zea mays*
51/A0A1D6HN04/UP7305_Z_mays	^{A} T-complex protein 1 subunit alpha	1/1	55	7	45938	*Zea mays*
52/B6T4R3/UP7305_Z_mays	^{D} UTP--glucose-1-phosphate uridylyltransferase	10/9	414	28	52227	*Zea mays*
53/A0A1D6P248/UP7305_Z_mays	^{D} Vacuolar proton pump subunit B	7/6	361	20	55448	*Zea mays*
54/C0HGT5/UP7305_Z_mays	^{D} T-complex protein 1 subunit delta	4/4	315	21	58096	*Zea mays*
55/A0A1D6FKV6/UP7305_Z_mays	^{D} Ketol-acid reductoisomerase	4/4	174	9	63213	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
56/UGDH5_ORYSJ/SwissProt	[D] UDP-glucose 6-dehydrogenase 5	5/5	205	15	53455	*Oryza sativa* subsp. *japonica*
57/CATA3_MAIZE/UP7305_Z_mays	[Z] Catalase isozyme 3	4/1	127	14	57159	*Zea mays*
58/CATA2_HORVU/SwissProt	[Z] Catalase isozyme 2	3/2	110	7	57390	*Hordeum vulgare*
59/Q8S4W9/UP7305_Z_mays	[C] Pyruvate decarboxylase	4/4	175	10	65990	*Zea mays*
60/AMPL2_ORYSJ/SwissProt	[D] Leucine aminopeptidase 2, chloroplastic	3/3	105	6	62179	*Oryza sativa* subsp. *japonica*
61/A0A1D6MRK0/UP7305_Z_mays	[D] Betaine aldehyde dehydrogenase 2 mitochondrial	1/1	102	17	19118	*Zea mays*
62/A0A1D6KSE9/UP7305_Z_mays	[D] T-complex protein 1 subunit eta	2/1	77	20	17712	*Zea mays*
63/A0A1D6N395/UP7305_Z_mays	[D] Selenium-binding protein 3	2/2	70	8	29130	*Zea mays*
64/CATA1_HORVU/SwissProt	[D] Catalase isozyme 1	2/1	63	5	57063	*Zea mays*
65/RUBA_RICCO/SwissProt	[D] RuBisCO large subunit-binding protein subunit alpha (Fragment)	1/1	59	3	52461	*Ricinus communis*
66/A0A1D6I642/UP7305_Z_mays	[D] Glucose-6-phosphate isomerase	1/1	59	2	48331	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
67/A0A1D6NR86/UP7305_Z_mays	^{D} Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta	1/1	54	2	63451	*Zea mays*
68/A0A1D6QHK0/UP7305_Z_mays	^{A} Pyruvate kinase	1/1	53	5	52618	*Zea mays*
69/ATPAM_ARATH/SwissProt	^{D} ATP synthase subunit alpha, mitochondrial	1/1	54	4	55296	*Arabidopsis thaliana*
70/A0A1D6Q9M3/UP7305_Z_mays	^{D} Aldehyde dehydrogenase2	1/1	41	2	26211	*Zea mays*
71/A0A1D6E7X7/UP7305_Z_mays	^{D} Glucose-6-phosphate dehydrogenase (NADP^{+})	2/2	68	9	27709	*Zea mays*
72/A0A1D6IWN4/UP7305_Z_mays	^{Z} Shikimate dehydrogenase	1/1	38	1	62956	*Zea mays*
73/A0A1D6FGX5/UP7305_Z_mays	^{D} Aspartyl-tRNA synthetase	1/1	64	2	59639	*Zea mays*
74/AMYB_MAIZE/SwissProt	^{D} Beta-amylase	1/1	86	3	55487	*Zea mays*
75/K7V938/UP7305_Z_mays	^{Z} Putative carboxylesterase 2	1/1	51	3	31561	*Zea mays*
76/A0A1D6F8L6/UP7305_Z_mays	^{D} Coatomer subunit gamma	1/1	47	1	99656	*Zea mays*
77/ATPBM_MAIZE/SwissProt	^{D} ATP synthase subunit beta, mitochondrial	10/10	465	23	59181	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
78/A0A1D6MRA8/UP7305_Z_mays	^{D} Zea CEFD homolog1	1/1	102	5	52474	*Zea mays*
79/B4G0K4/UP7305_Z_mays	^{D} Phosphoglycerate kinase	5/5	220	19	42470	*Zea mays*
80/A0A1D6LJP0/UP7305_Z_mays	^{D} 6-phosphogluconate dehydrogenase, decarboxylating	2/2	71	5	55248	*Zea mays*
81/A0A1D6FQ43/UP7305_Z_mays	^{D} Guanosine nucleotide diphosphate dissociation inhibitor	1/1	56	5	51286	*Zea mays*
82/A0A1D6QHJ6/UP7305_Z_mays	^{D} Aluminum induced protein with YGL and LRDR motifs	1/1	39	3	38614	*Zea mays*
83/A0A1D6PRL0/UP7305_Z_mays	^{C} Apyrase 1	1/1	52	2	52164	*Zea mays*
84/A0A1D6GN16/UP7305_Z_mays	^{C} Putative serine protease EDA2	1/1	36	2	55538	*Zea mays*
85/K7TSD2/UP7305_Z_mays	^{D} Serine hydroxymethyltransferase	2/2	93	5	57881	*Zea mays*
86/A0A1D6QRC6/UP7305_Z_mays	^{C} Fumarylacetoacetase	1/1	30	5	41938	*Zea mays*
87/ALF_MAIZE/SwissProt	^{D} Fructose-bisphosphate aldolase, cytoplasmic isozyme	4/4	183	13	39036	*Zea mays*
88/C0PC61/UP7305_Z_mays	^{D} Transaldolase	3/3	135	10	46363	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
89/A0A0B4J303/UP7305_Z_mays	[D] Eukaryotic initiation factor4a	1/1	98	6	47238	*Zea mays*
90/B4FLJ3/UP7305_Z_mays	[D] Isocitrate dehydrogenase [NADP]	2/2	98	6	46411	*Zea mays*
91/A0A1D6KN99/UP7305_Z_mays	[D] 12-oxo-phytodienoic acid reductase7	3/3	97	10	37278	*Zea mays*
92/A0A1D6DZK5/UP7305_Z_mays	[Z] Adenosylmethionine aminotransferase1	1/1	68	2	56004	*Zea mays*
93/A0A1D6ELG3/UP7305_Z_mays	[D] Polyadenylate-binding protein	1/1	64	2	60354	*Zea mays*
94/A0A1D6NT98/UP7305_Z_mays	[D] Uncharacterized protein (Membrane protein – UniProtKB)	1/1	53	1	68147	*Zea mays*
95/A0A1D6ELX4/UP7305_Z_mays	[D] Monodehydroascorbate reductase homolog1	1/1	49	11	14585	*Zea mays*
96/B4FJB2/UP7305_Z_mays	[D] Ras-related protein RABA4a	1/1	49	5	24099	*Zea mays*
97/B4F9B2/UP7305_Z_mays	[D] Acetyl-CoA acetyltransferase, cytosolic 1	1/1	46	2	41618	*Zea mays*
98/A0A1D6HPL2/UP7305_Z_mays	[D] 3-ketoacyl-CoA thiolase 2 peroxisomal	1/1	43	6	36936	*Zea mays*
99/A0A1D6MDY2/UP7305_Z_mays	[A] V-type proton ATPase subunit C	1/1	42	6	29124	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
100/A0A1D6KPD0/UP7305_Z_mays	[D] Regulator of chromosome condensation (RCC1) family protein	1/1	41	2	36195	*Zea mays*
101/B6TN48/UP7305_Z_mays	[D] 3-hydroxyisobutyryl-CoA hydrolase-like protein 5	2/2	61	4	43135	*Zea mays*
102/A0A1D6E501/UP7305_Z_mays	[D] 3-isopropylmalate dehydrogenase	1/1	64	6	43132	*Zea mays*
103/A0A1D6JZR5/UP7305_Z_mays	[D] LL-diaminopimelate aminotransferase chloroplastic	1/1	34	2	52087	*Zea mays*
104/A0A1D6IYG5/UP7305_Z_mays	[A] Obg-like ATPase 1	1/1	77	4	46058	*Zea mays*
105/MDHC_BETVU/SwissProt	[D] Malate dehydrogenase, cytoplasmic	4/4	183	17	35810	*Beta vulgaris*
106/PMM_ORYSI/SwissProt	[A] Phosphomannomutase	1/1	55	7	28403	*Oryza sativa* subsp. *indica*
107/SCRK1_ORYSI/SwissProt	[D] Fructokinase-1	4/1	146	14	34878	*Zea mays*
108/COMT1_SACOF/SwissProt	[D] Caffeic acid 3-O-methyltransferase	4/4	149	10	39838	*Saccharum officinarum*
109/G3PC1_HORVU/SwissProt	[D] Glyceraldehyde-3-phosphate dehydrogenase4	3/2	115	16	36605	*Hordeum vulgare*
110/A0A1D6HDK5/UP7305_Z_mays	[D] Adenosine kinase	4/4	165	22	27789	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
111/A0A1D6LBH9/UP7305_Z_mays	^{D} Late embryogenesis abundant protein group 2	3/3	108	13	29322	*Zea mays*
112/A0A1D6PDH9/UP7305_Z_mays	^{D} UDP-glucuronic acid decarboxylase 5	2/2	56	7	39116	*Zea mays*
113/A0A1D6GLV8/UP7305_Z_mays	^{D} UDP-arabinopyranose mutase 3	1/1	44	12	18379	*Zea mays*
114/A0A1D6FKF4/UP7305_Z_mays	^{D} Aspartic proteinase A1	3/3	176	9	56800	*Zea mays*
115/SCRK2_ORYSI/SwissProt	^{D} Fructokinase-2	3/1	132	11	35893	*Oryza sativa* subsp. *indica*
116/K7TFA7/UP7305_Z_mays	^{D} Putative oxidoreductase, aldo/keto reductase family protein	2/2	92	11	34649	*Zea mays*
117/GBLPA_ORYSJ/SwissProt	^{D} Guanine nucleotide-binding protein subunit beta-like protein A	6/1	309	13	36665	*Oryza sativa* subsp. *japonica*
118/CYSK_MAIZE/SwissProt	^{D} Cysteine synthase	2/2	62	8	34299	*Zea mays*
119/IFRH_MAIZE/SwissProt	^{D} Isoflavone reductase homolog IRL	2/2	74	6	32831	*Zea mays*
120/A0A1D6LVE5/UP7305_Z_mays	^{C} Gibberellin receptor GID1L2	1/1	54	4	34811	*Zea mays*
121/Q84TL7/UP7305_Z_mays	^{D} Legumin-like protein	2/2	111	8	38047	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
122/A0A1D6IYD6/UP7305_Z_mays	C Glyoxalase I	1/1	59	3	36506	*Zea mays*
123/A0A1D6EKR8/UP7305_Z_mays	D Spermidine synthase 2	1/1	52	4	35264	*Zea mays*
124/B4FTN5/UP7305_Z_mays	Z Metal-dependent protein hydrolase	1/1	49	3	43011	*Zea mays*
125/A0A1D6HNQ2/UP7305_Z_mays	D Oxidoreductase zinc-binding dehydrogenase family protein	1/1	48	2	35976	*Zea mays*
126/A0A1D6QTN1/UP7305_Z_mays	A NAD(P)-linked oxidoreductase superfamily protein	1/1	47	7	18913	*Zea mays*
127/A0A1D6HNP5/UP7305_Z_mays	D Proliferating cell nuclear antigen	1/1	50	5	16672	*Zea mays*
128/RLA0_MAIZE/SwissProt	D 60S acidic ribosomal protein P0	2/2	68	7	34597	*Zea mays*
129/PGIP1_ORYSJ/SwissProt	Z Polygalacturonase inhibitor 1	1/1	36	4	36012	*Oryza sativa* subsp. *japonica*
130/A0A1D6P2Q0/UP7305_Z_mays	C Transducin/WD40 repeat-like superfamily protein	1/1	42	4	28752	*Zea mays*
131/A0A1D6HKP7/UP7305_Z_mays	Z Annexin	1/1	47	2	45684	*Zea mays*
132/A0A1D6MLF6/UP7305_Z_mays	D Triose phosphate isomerase4	3/3	144	20	27958	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
133/A0A1D6PD08/UP7305_Z_mays	[D] L-ascorbate peroxidase	5/3	202	15	30847	*Zea mays*
134/E1AFV5/UP7305_Z_mays	[C] Beta-1,3-glucanase	2/2	136	10	36068	*Zea mays*
135/A3FMB9/UP7305_Z_mays	[D] Proteasome subunit alpha type	2/2	72	10	27382	*Zea mays*
136/A0A1D6I845/UP7305_Z_mays	[D] Proteasome subunit beta	3/2	162	20	24653	*Zea mays*
137/A0A1D6FQM0/UP7305_Z_mays	[C] Alpha/beta-Hydrolases superfamily protein	2/2	102	25	11663	*Zea mays*
138/GSTF1_MAIZE/UP7305_Z_mays	[D] Glutathione S-transferase 1	2/2	58	13	24034	*Zea mays*
139/A0A1D6F519/UP7305_Z_mays	[D] UBP1-associated protein 2C	1/1	58	5	25880	*Zea mays*
140/A0A1D6Q3V1/UP7305_Z_mays	[D] 60S ribosomal protein L6	1/1	68	12	12696	*Zea mays*
141/ACLB1_ARATH/SwissProt	[Z] ATP-citrate synthase beta chain protein 1	1/1	57	2	66342	*Arabidopsis thaliana*
142/A0A1D6LSP0/UP7305_Z_mays	[D] Elongation factor gamma1	1/1	54	4	47098	*Zea mays*
143/A0A096SSY4/UP7305_Z_mays	[D] Tubulin beta chain	1/1	65	2	50663	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
144/A0A0B4J3C2/UP7305_Z_mays	^{D} Elongation factor 1-alpha	1/1	52	2	49478	*Zea mays*
145/A0A1D6L8E8/UP7305_Z_mays	^{Z} Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex	1/1	44	2	53355	*Zea mays*
146/A0A1D6LLB2/UP7305_Z_mays	^{A} GDSL esterase/lipase	1/1	41	2	37713	*Zea mays*
147/A0A1D6NY34/UP7305_Z_mays	^{Z} Putative threonine aldolase family protein	1/1	38	2	46800	*Zea mays*
148/1433A_SOYBN/SwissProt	^{D} 14-3-3-like protein A	1/1	35	11	29145	*Glycine max*
149/A0A1D6MWW9/UP7305_Z_mays	^{D} 60S ribosomal protein L2	1/1	34	7	17905	*Zea mays*
150/A0A1D6G992/UP7305_Z_mays	^{D} Phosphoglycerate mutase	1/1	40	1	61993	*Zea mays*
151/A0A1D6FNG1/UP7305_Z_mays	^{C} Superoxide dismutase	4/4	124	18	26419	*Zea mays*
152/CFIS2_ARATH/SwissProt	^{C} Pre-mRNA cleavage factor Im 25 kDa subunit 2	1/1	78	7	23043	*Arabidopsis thaliana*
153/A0A1D6GY43/UP7305_Z_mays	^{D} Translationally controlled tumor1	2/2	74	13	20328	*Zea mays*
154/A0A1D6E5L0/UP7305_Z_mays	^{C} Ras-related protein18A1	1/1	56	5	21581	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
155/A0A1D6KU62/UP7305_Z_mays	^{D} Ras-related protein Rab-18	1/1	56	4	27585	*Zea mays*
156/RABG1_ARATH/SwissProt	^{D} Ras-related protein RABG1	1/1	56	5	23823	*Arabidopsis thaliana*
157/RAB7_MESCR/SwissProt	^{D} Ras-related protein Rab7A	1/1	56	5	23516	*Mesembryanthemum crystallinum*
158/A0A1D6NB04/UP7305_Z_mays	^{Z} Aspartate aminotransferase	1/1	55	3	46038	*Zea mays*
159/EXPA1_ARATH/SwissProt	^{C} Expansin-A1	1/1	51	3	26957	*Arabidopsis thaliana*
160/NSF_ORYSJ/SwissProt	^{Z} Vesicle-fusing ATPase	1/1	49	1	81591	*Oryza sativa* subsp. *japonica*
161/AOC_ORYSI/SwissProt	^{D} Allene oxide cyclase, chloroplastic	1/1	57	3	26206	*Oryza sativa* subsp. *indica*
162/B4FN19/UP7305_Z_mays	^{D} 60S ribosomal protein L12-3	3/3	114	22	17925	*Zea mays*
163/K7TWV7/UP7305_Z_mays	^{D} Peptidyl-prolyl cis-trans isomerase	2/1	89	15	18502	*Zea mays*
164/K7VFF7/UP7305_Z_mays	^{C} Glutaredoxin-dependent peroxiredoxin	1/1	73	7	23860	*Zea mays*
165/A0A1D6EL67/UP7305_Z_mays	^{D} ADP-ribosylation factor A1F	1/1	65	7	21298	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
166/A0A1D6F0E2/UP7305_Z_mays	^{D} Eukaryotic translation initiation factor 5A	1/1	77	8	15487	*Zea mays*
167/B4G227/UP7305_Z_mays	^{C} Peptide-N4-(N-acetyl-beta-glucosaminyl) asparagine amidase A protein	1/1	55	2	67783	*Zea mays*
168/A0A1D6QSC9/UP7305_Z_mays	^{C} Glycine cleavage system H protein	1/1	52	8	19817	*Zea mays*
169/A0A1D6M9Z1/UP7305_Z_mays	^{C} Ras-related protein RABG3f	1/1	43	5	20757	*Zea mays*
170/B6TN41/UP7305_Z_mays	^{Z} 4-hydroxy-4-methyl-2-oxoglutarate aldolase	1/1	40	6	18390	*Zea mays*
171/B4FMB1/UP7305_Z_mays	^{C} DUF538 family protein	1/1	55	4	17499	*Zea mays*
172/RABD1_ARATH/SwissProt	^{D} Ras-related protein RABD1	1/1	38	7	22995	*Arabidopsis thaliana*
173/RIC1_ORYSJ/SwissProt	^{D} Ras-related protein RIC1	2/2	63	13	22690	*Oryza sativa* subsp. *japonica*
174/Q19VG6/UP7305_Z_mays	^{Z} Major latex protein 22	1/1	42	7	17101	*Zea mays*
175/A0A1D6I867/UP7305_Z_mays	^{Z} Clathrin heavy chain 2	3/1	84	8	50622	*Zea mays*
176/B4F8S9/UP7305_Z_mays	^{C} Uncharacterized protein (Fasciclin-like arabinogalactan protein 15 – UniProtKB)	1/1	49	3	50125	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
177/A0A1D6PBS4/UP7305_Z_mays	[Z] pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH3	1/1	40	3	40873	*Zea mays*
178/A0A096UGL9/UP7305_Z_mays	[Z] Exportin-2	1/1	29	1	109050	*Zea mays*
179/A0A1D6F5B9/UP7305_Z_mays	[D] Protein disulfide-isomerase	2/2	55	5	61141	*Zea mays*
180/A0A1D6L977/UP7305_Z_mays	[Z] Methylenetetrahydrofolate reductase	1/1	49	2	64872	*Zea mays*
181/C0HHH9/UP7305_Z_mays	[A] Stress-response A/B barrel domain-containing protein UP3	1/1	71	4	26448	*Zea mays*
182/B6UAK0/UP7305_Z_mays	[C] Probable 6-phosphogluconolactonase	1/1	65	5	34874	*Zea mays*
183/TCPQ_ARATH/UP7305_Z_mays	[A] T-complex protein 1 subunit theta	1/1	43	2	59472	*Zea mays*
184/A0A1D6LJS9/UP7305_Z_mays	[D] Chaperonin 60 subunit beta 2 chloroplastic	2/1	86	4	62041	*Zea mays*
185/B6TQC0/UP7305_Z_mays	[D] 3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase	1/1	67	2	46584	*Zea mays*
186/A0A1D6ER22/UP7305_Z_mays	[D] Aldehyde dehydrogenase family 7 member B4	2/2	64	4	55365	*Zea mays*
187/A0A1D6IIX9/UP7305_Z_mays	[Z] Pentatricopeptide repeat-containing protein mitochondrial	1/1	57	2	69042	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
188/GAPN_MAIZE/UP7305_Z_mays	[C] NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	1/1	56	3	53740	*Zea mays*
189/A0A1D6HP32/UP7305_Z_mays	[D] Glutathione reductase cytosolic	1/1	69	3	57389	*Zea mays*
190/A0A096PQR7/UP7305_Z_mays	[D] Cytochrome P450 CYP74A19	1/1	50	3	53248	*Zea mays*
191/A0A1D6FMC1/UP7305_Z_mays	[D] Importin subunit alpha	1/1	37	3	40019	*Zea mays*
192/A0A1D6L6N3/UP7305_Z_mays	[Z] Inosine-5'-monophosphate dehydrogenase	1/1	44	2	48769	*Zea mays*
193/B6T484/UP7305_Z_mays	[Z] Mitogen-activated protein kinase	1/1	43	4	42649	*Zea mays*
194/A0A1D6JQK4/UP7305_Z_mays	[Z] Topless-related protein 2	1/1	39	5	34475	*Zea mays*
195/A0A1D6HJJ4/UP7305_Z_mays	[D] Glutamine synthetase	2/2	82	7	40876	*Zea mays*
196/B4FIV0/UP7305_Z_mays	[Z] Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial	1/1	65	9	34600	*Zea mays*
197/B6TEK2/UP7305_Z_mays	[A] GroES-like zinc-binding alcohol dehydrogenase family protein	2/2	61	6	39052	*Zea mays*
198/A0A1D6DUW9/UP7305_Z_mays	[D] 26S proteasome non-ATPase regulatory subunit 7 homolog A	1/1	52	3	35966	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
199/K7TK74/UP7305_Z_mays	^{D} Putative alcohol dehydrogenase superfamily protein	1/1	50	6	38476	*Zea mays*
200/A0A1D6GLS4/UP7305_Z_mays	^{Z} Serpin-Z1	1/1	36	2	44359	*Zea mays*
201/A0A1D6NZT3/UP7305_Z_mays	^{A} Uncharacterized conserved protein (UCP030210)	1/1	29	5	45907	*Zea mays*
202/B6TQ06/UP7305_Z_mays	^{D} Aminomethyltransferase	1/1	27	4	44406	*Zea mays*
203/A0A1D6G0Z9/UP7305_Z_mays	^{D} Ribokinase	2/2	91	6	37978	*Zea mays*
204/KDSA2_ARATH/SwissProt	^{D} 2-dehydro-3-deoxyphosphooctonate aldolase 2	2/2	79	7	31998	*Arabidopsis thaliana*
205/B4F7V1/UP7305_Z_mays	^{D} 3-deoxy-8-phosphooctulonate synthase	2/1	79	7	32126	*Zea mays*
206/A0A1D6JG12/UP7305_Z_mays	^{Z} Cysteine protease 1	1/1	53	3	53108	*Zea mays*
207/A0A1D6M5S1/UP7305_Z_mays	^{D} Aldo-keto reductase family 4 member C9	1/1	44	2	39115	*Zea mays*
208/A0A1D6HW85/UP7305_Z_mays	^{C} Nitrile-specifier protein 1	1/1	40	3	40635	*Zea mays*
209/C4J5P0/UP7305_Z_mays	^{D} Aspartyl protease AED1	1/1	40	2	51276	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
210/A0A1D6Q3E1/UP7305_Z_mays	^{Z} 2-hydroxy-3-oxopropionate reductase	1/1	49	8	26974	*Zea mays*
211/A0A1D6PA07/UP7305_Z_mays	^{C} Beta-adaptin-like protein C	1/1	42	1	95514	*Zea mays*
212/A0A1D6GPP6/UP7305_Z_mays	^{C} Heterogeneous nuclear ribonucleoprotein 1	1/1	36	3	48323	*Zea mays*
213/B4FWD0/UP7305_Z_mays	^{D} NAD(P)H dehydrogenase	2/2	98	20	21603	*Zea mays*
214/B4FB55/UP7305_Z_mays	^{C} Ras-related protein ARA-3	3/1	87	16	24038	*Zea mays*
215/A0A1D6FLR1/UP7305_Z_mays	^{D} Spliceosome RNA helicase BAT1 isoform 1	2/2	76	6	52857	*Zea mays*
216/A0A1D6JQM9/UP7305_Z_mays	^{A} 40S ribosomal protein Sa-1	1/1	50	4	28786	*Zea mays*
217/A0A1D6GAY3/UP7305_Z_mays	^{Z} Glutathione transferase	1/1	49	6	13576	*Zea mays*
218/A0A1X7YIJ7/UP7305_Z_mays	^{Z} Chitinase	1/1	47	5	31374	*Zea mays*
219/A0A1D6GQ45/UP7305_Z_mays	^{D} Cell division cycle protein 48	1/1	74	1	69832	*Zea mays*
220/A0A1D6EW83/UP7305_Z_mays	^{C} Ras-related protein RABH1b	1/1	43	7	15909	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
221/B7ZY32/UP7305_Z_mays	^{D} DUF642 domain-containing protein	1/1	68	6	14960	*Zea mays*
222/A0A1D6HBU2/UP7305_Z_mays	^{C} Glycerophosphodiester phosphodiesterase	1/1	58	1	81765	*Zea mays*
223/A0A1D6P3B9/UP7305_Z_mays	^{Z} 110 kDa U5 small nuclear ribonucleoprotein component CLO	1/1	43	1	109001	*Zea mays*
224/A0A1D6GYM1/UP7305_Z_mays	^{D} Luminal-binding protein 2	3/2	97	8	60635	*Zea mays*
225/A0A096S0J0/UP7305_Z_mays	^{D} Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha	1/1	65	2	68229	*Zea mays*
226/A0A1D6E267/UP7305_Z_mays	^{C} Fasciclin-like arabinogalactan protein 10	1/1	50	4	44168	*Zea mays*
227/A0A1D6GY62/UP7305_Z_mays	^{Z} Uncharacterized protein	1/1	36	1	44904	*Zea mays*
228/BGL31_ORYSJ/SwissProt	^{Z} Beta-glucosidase 31	1/1	35	1	58696	*Oryza sativa* subsp. *japonica*
229/C0P6C5/UP7305_Z_mays	^{C} Threonine synthase	1/1	35	3	57919	*Zea mays*
230/A0A1D6L056/UP7305_Z_mays	^{Z} BGGP Beta-1-3-galactosyl-O-glycosyl-glycoprotein	1/1	34	2	50083	*Zea mays*
231/A0A1D6ETB0/ UP7305_Z_mays	^{D} p-loop containing nucleoside triphosphate hydrolase superfamily protein (ATPase 100193266)	1/1	66	11	14273	*Zea mays*

Table S3 – Cont.

N°/Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
232/A0A1D6KEG7/UP7305_Z_mays	[Z] Heparanase-like protein 1	1/1	53	3	50610	*Zea mays*
233/AT9_ORYSJ/SwissProt	[A] Acyl transferase 9	1/1	46	2	46535	*Oryza sativa* subsp. *japonica*
234/A0A1D6L117/UP7305_Z_mays	[C] Tryptophanyl-tRNA synthetase	1/1	44	4	28162	*Zea mays*
235/A0A1D6G3W9/UP7305_Z_mays	[A] UDP-D-apiose/UDP-D-xylose synthase 2	1/1	35	2	45261	*Zea mays*
236/A0A1D6HIW8/UP7305_Z_mays	[Z] Enhancer of mRNA-decapping protein 4	1/1	32	2	38475	*Zea mays*
237/MDHM2_ARATH/SwissProt	[C] Malate dehydrogenase 2, mitochondrial	2/1	115	8	36024	*Arabidopsis thaliana*
238/A0A1D6ESW5/UP7305_Z_mays	[D] Pyruvate dehydrogenase E1 component subunit beta	1/1	38	4	37682	*Zea mays*
239/A0A1D6F487/UP7305_Z_mays	[Z] Ubiquitin-like-specific protease ESD4	1/1	37	1	51520	*Zea mays*
240/PER2_ORYSI/SwissProt	[Z] Peroxidase 2	1/1	74	5	33070	*Oryza sativa* subsp. *indica*
241/B8A2X5/UP7305_Z_mays	[D] Pectinesterase	1/1	54	1	60684	*Zea mays*
242/LGUL_ORYSJ/SwissProt	[C] Lactoylglutathione lyase	1/1	40	3	32875	*Oryza sativa* subsp. *japonica*

Z: Detected proteins only at fifth cut; D: Detected proteins at all cuts; C: Detected proteins only at third and fifth cuts; **A**: Detected proteins only at first and fifth cuts.

Table S4. Differentially expressed protein (down-regulated) in axillary buds of the RB867515 sugarcane cultivar at the first cut compared to third cutting stage.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
REF_HEVBR/SwissProt	Rubber elongation factor protein	1/1	57	11	14713	*Hevea brasiliensis*
A0A1D6N717/UP7305_Z_mays	Alpha-1,4 glucan phosphorylase	1/1	53	1	77875	*Zea mays*
A0A1D6JSM9/UP7305_Z_mays	T-complex protein 1 subunit gamma	1/1	62	1	58500	*Zea mays*
A0A1D6L4F0/UP7305_Z_mays	Exhydrolase II	1/1	56	2	73960	*Zea mays*
C0P905/UP7305_Z_mays	Glucan endo-1,3-beta-D-glucosidase	1/1	55	2	53994	*Zea mays*
A0A1D6FSJ2/UP7305_Z_mays	60S ribosomal protein L24	1/1	46	6	21113	*Zea mays*
A0A1D6JFG2/UP7305_Z_mays	Beta-D-xylosidase	1/1	52	1	82773	*Zea mays*
ILVB1_MAIZE/SwissProt	Acetolactate synthase 1, chloroplastic	1/1	48	2	69172	*Zea mays*
VATB2_HORVU/SwissProt	V-type proton ATPase subunit B 2	4/4	224	13	53806	*Hordeum vulgare*
A0A1D6NMU3/UP7305_Z_mays	Ubiquitin carboxyl-terminal hydrolase	1/1	144	6	41416	*Zea mays*
A0A1D6HR41/UP7305_Z_mays	Pyridoxal 5'-phosphate synthase-like subunit PDX1.2	1/1	27	1	44219	*Zea mays*

Table S4 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6KMC8/UP7305_Z_mays	Dihydroxy-acid dehydratase chloroplastic	1/1	113	3	66497	*Zea mays*
A0A1D6FI07/UP7305_Z_mays	Dihydrolipoyl dehydrogenase	2/2	70	5	44851	*Zea mays*
A0A1D6FAH0/UP7305_Z_mays	T-complex protein 1 subunit epsilon	2/2	60	7	61109	*Zea mays*
A0A1D6GPS2/UP7305_Z_mays	Pre-mRNA-processing factor 19	1/1	41	2	60914	*Zea mays*
ATPA_SACHY/SwissProt	ATP synthase subunit alpha, chloroplastic	1/1	40	2	55773	*Saccharum* hybrid
A0A1D6IX59/UP7305_Z_mays	Beta-glucosidase, chloroplastic	1/1	39	1	52535	*Zea mays*
TCPZA_ARATH/SwissProt	T-complex protein 1 subunit zeta	1/1	38	2	59426	*Arabidopsis thaliana*
FB250_ARATH/SwissProt	F-box protein At5g03100	1/1	37	2	35271	*Arabidopsis thaliana*
A0A1D6F1W9/UP7305_Z_mays	Phospho-2-dehydro-3-deoxyheptonate aldolase	1/1	45	3	41118	*Zea mays*

Table S4 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6IXG3/UP7305_Z_mays	Citrulline--aspartate ligase	1/1	38	2	46015	*Zea mays*
A0A1D6H3Y9/UP7305_Z_mays	Proteasome component4	1/1	80	7	31580	*Zea mays*
A0A1D6L4P1/UP7305_Z_mays	Protein STRICTOSIDINE SYNTHASE-LIKE 3	1/1	33	3	59693	*Zea mays*
SCRK7_ARATH/SwissProt	Probable fructokinase-7	2/1	76	5	37233	*Arabidopsis thaliana*
C0PNU9/UP7305_Z_mays	Protein binding protein	1/1	34	2	31083	*Zea mays*
B4FMW6/UP7305_Z_mays	Aspartyl protease AED3	1/1	45	1	45280	*Zea mays*
A0A1Q0ZFB6/UP7305_Z_mays	Alba DNA/RNA-binding protein	1/1	43	3	36593	*Zea mays*
GSA_BRANA/UP7305_Z_mays	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic	1/1	42	2	50562	*Brassica napus*
B4G195/UP7305_Z_mays	Glutamate-oxaloacetate transaminase5	1/1	39	2	49619	*Zea mays*
A0A1D6FBT4/UP7305_Z_mays	Transcription factor Pur-alpha 1	1/1	35	2	43177	*Zea mays*
Q6TM44/UP7305_Z_mays	Germin-like protein	1/1	41	10	22101	*Zea mays*

Table S4 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6PVR8/UP7305_Z_mays	40S ribosomal protein S3-1	4/4	114	18	28696	*Zea mays*
A0A1D6NHH6/UP7305_Z_mays	GTP-binding nuclear protein	2/2	83	11	25440	*Zea mays*
A0A1D6GF42/UP7305_Z_mays	40S ribosomal protein S2-1	1/1	53	5	30027	*Zea mays*
B6TPA4/UP7305_Z_mays	Carnitine racemase/catalytic	1/1	46	5	25869	*Zea mays*
A0A1D6FVM4/UP7305_Z_mays	ULP_PROTEASE domain-containing protein	1/1	45	1	117912	*Zea mays*
B4F848/UP7305_Z_mays	20 kDa chaperonin chloroplastic	1/1	40	7	25796	*Zea mays*
A0A1D6PI62/UP7305_Z_mays	40S ribosomal protein S3a	2/2	61	7	34634	*Zea mays*
A0A1D6KEX3/UP7305_Z_mays	Adenine phosphoribosyltransferase	1/1	39	9	16873	*Zea mays*
A0A1D6KQ94/UP7305_Z_mays	Co-chaperone protein SBA1	1/1	35	8	15736	*Zea mays*
COP52_ORYSJ/SwissProt	Putative copper transporter 5.2	1/1	31	5	17936	*Oryza sativa* subsp. *japonica*
B4FB66/UP7305_Z_mays	40S ribosomal protein S5-2	1/1	57	6	22297	*Zea mays*

Table S4 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6IV93/UP7305_Z_mays	Agamous-like MADS-box protein AGL8	1/1	29	3	29077	*Zea mays*
A0A1D6J4Q3/UP7305_Z_mays	Translation elongation factor EF1A/initiation factor IF2gamma family protein	1/1	54	2	46081	*Zea mays*
A0A1D6KNM8/UP7305_Z_mays	Phosphoglycerate dehydrogenase	1/1	43	1	69667	*Zea mays*
C4J4W3/UP7305_Z_mays	Hsp70-Hsp90 organizing protein 3	1/1	40	1	65563	*Zea mays*
A0A1D6F4V8/UP7305_Z_mays	26S proteasome regulatory subunit 4 homolog A	1/1	58	3	41048	*Zea mays*
A0A1D6FL86/UP7305_Z_mays	Putative calcium-dependent protein kinase family protein	1/1	57	4	44614	*Zea mays*
A0A1D6NUR0/UP7305_Z_mays	Carotenoid 910(9'10')-cleavage dioxygenase 1	1/1	34	1	69195	*Zea mays*
A0A1D6M1D4/UP7305_Z_mays	Eukaryotic peptide chain release factor subunit 1-1	1/1	48	2	49026	*Zea mays*
GME1_ORYSI/SwissProt	GDP-mannose 3,5-epimerase 1	2/2	86	7	43180	*Oryza sativa* subsp. *indica*
ACT_MESVI/SwissProt	Actin	3/2	123	8	41791	*Mesostigma viride*
K7V9P7/UP7305_Z_mays	Beta-ketoacyl-[acyl-carrier-protein] synthase I	1/1	63	2	51721	*Zea mays*

Table S4 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6H7L0/UP7305_Z_mays	26S protease regulatory subunit 8 homolog B	1/1	50	3	41699	*Zea mays*
A0A1D6GVM3/UP7305_Z_mays	Delta-aminolevulinic acid dehydratase	2/2	58	5	46434	*Zea mays*
ACT4_SOLLC/SwissProt	Actin-105 (Fragment)	1/1	35	4	37362	*Solanum lycopersicum*
A0A1D6HI32/UP7305_Z_mays	Thioredoxin reductase	1/1	52	4	37630	*Zea mays*
FBRL2_ARATH/SwissProt	rRNA 2'-O-methyltransferase fibrillarin 2	1/1	51	3	33803	*Arabidopsis thaliana*
A0A1D6FR00/UP7305_Z_mays	Elongation factor 1-beta	1/1	55	3	27466	*Zea mays*
TPIC_SPIOL/SwissProt	Triosephosphate isomerase, chloroplastic	1/1	46	4	34787	*Spinacia oleracea*
A0A1D6G511/UP7305_Z_mays	40S ribosomal protein S6-1	1/1	45	7	13533	*Zea mays*
CAMT1_MAIZE/SwissProt	Caffeoyl-CoA O-methyltransferase 1	1/1	36	6	29016	*Zea mays*
P45633/UP7305_Z_mays	60S ribosomal protein L10	1/1	78	5	25359	*Zea mays*
DOT2_ARATH/SwissProt	SART-1 family protein DOT2	1/1	54	1	94086	*Arabidopsis thaliana*

Table S4 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
SKM1_ARATH/SwissProt	Leucine-rich repeat receptor-like serine/threonine-protein kinase SKM1	1/1	38	1	107464	*Arabidopsis thaliana*
A0A1D6HNE6/UP7305_Z_mays	DNA helicase	1/1	39	2	82318	*Zea mays*
A0A1D6GZE7/UP7305_Z_mays	RuvB-like helicase	1/1	62	3	50233	*Zea mays*
PRS6B_ARATH/SwissProt	26S proteasome regulatory subunit 6B homolog	1/1	74	4	45894	*Arabidopsis thaliana*
A0A1D6M0K3/UP7305_Z_mays	GOLD domain-containing protein	1/1	26	3	49812	*Zea mays*
LDHA_HORVU/SwissProt	L-lactate dehydrogenase A	1/1	72	3	37840	*Hordeum vulgare*
A0A1D6KNS0/UP7305_Z_mays	Cinnamoyl CoA reductase1	1/1	32	3	45016	*Zea mays*
A0A1D6EGZ7/UP7305_Z_mays	ARM repeat superfamily protein	1/1	32	3	47837	*Zea mays*
A0A1D6DT56/UP7305_Z_mays	NADPH-protochlorophyllide oxidoreductase	1/1	54	3	41525	*Zea mays*
KCAB_ARATH/SwissProt	Probable voltage-gated potassium channel subunit beta	1/1	40	3	36744	*Arabidopsis thaliana*
B4FVD5/UP7305_Z_mays	V-type proton ATPase subunit E3	1/1	39	4	26727	*Zea mays*

Table S4 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6MQ90/UP7305_Z_mays	26S proteasome regulatory subunit RPN11	1/1	35	2	31682	*Zea mays*
RS8_MAIZE/SwissProt	40S ribosomal protein S8	2/2	134	13	25155	*Zea mays*
A0A1D6EC19/UP7305_Z_mays	Diadenosine tetraphosphate synthetase	1/1	55	2	63383	*Zea mays*
A0A1D6QHK0/UP7305_Z_mays	Pyruvate kinase	3/3	119	10	52618	*Zea mays*
A0A1D6F6Z2/UP7305_Z_mays	T-complex protein 1 subunit theta	1/1	43	4	29684	*Zea mays*
A0A1D6HTM2/UP7305_Z_mays	60S ribosomal protein L4-1	4/3	153	14	36321	*Zea mays*
A0A1D6IYG5/UP7305_Z_mays	Obg-like ATPase 1	1/1	62	4	46058	*Zea mays*
A0A1D6MDY 4/UP7305_Z_mays	V-type proton ATPase subunit C	1/1	77	4	39756	*Zea mays*
A0A1D6JQM9/UP7305_Z_mays	40S ribosomal protein Sa-1	2/2	65	7	28786	*Zea mays*
B6TEK2/UP7305_Z_mays	GroES-like zinc-binding alcohol dehydrogenase family protein	1/1	43	3	39052	*Zea mays*
B4F7W6/UP7305_Z_mays	GDSL esterase/lipase	1/1	46	3	42051	*Zea mays*

Table S4 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
PMM_ORYSI/SwissProt	Phosphomannomutase	1/1	42	7	28403	*Oryza sativa* subsp. *indica*
C0HHH9/UP7305_Z_mays	Stress-response A/B barrel domain-containing protein UP3	1/1	39	4	26448	*Zea mays*
LOX2_ORYSJ/SwissProt	Linoleate 9S-lipoxygenase 2	1/1	47	1	97294	*Oryza sativa* subsp. *japonica*
TAD3_ARATH/SwissProt	tRNA-specific adenosine deaminase TAD3	1/1	32	2	45697	*Zea mays*
A0A1D6NZT3/UP7305_Z_mays	Uncharacterized conserved protein (UCP030210)	1/1	32	5	45907	*Zea mays*
A0A1D6QTN1/UP7305_Z_mays	NAD(P)-linked oxidoreductase superfamily protein	1/1	48	7	18913	*Zea mays*
A0A1D6EYG6/UP7305_Z_mays	HOPM interactor 7	1/1	52	1	122829	*Zea mays*
A0A1D6HN05/UP7305_Z_mays	T-complex protein 1 subunit alpha	1/1	41	2	42446	*Zea mays*
A0A1D6G3W9/UP7305_Z_mays	UDP-D-apiose/UDP-D-xylose synthase 2	1/1	71	2	45261	*Zea mays*
AT9_ORYSJ/SwissProt	Acyl transferase 9	1/1	49	2	46535	*Oryza sativa* subsp. *japonica*

Table S5. Differentially expressed protein (up-regulated) in axillary buds of the RB867515 sugarcane cultivar at the third cut compared to first cutting stage.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6KZB9/UP7305_Z_mays	Tetratricopeptide repeat (TPR)-like superfamily protein	1/1	33	1	73005	*Zea mays*
B4FM07/UP7305_Z_mays	Thioredoxin-dependent peroxiredoxin	1/1	37	5	28318	*Zea mays*
A0A1D6FU93/UP7305_Z_mays	Arginyl-tRNA synthetase	1/1	38	1	67511	*Zea mays*
A0A1D6HYS3/UP7305_Z_mays	Phosphoglucosamine mutase family protein	1/1	63	5	20237	*Zea mays*
A0A1D6DTX6 /UP7305_Z_mays	Protein DJ-1 homolog D	1/1	39	3	35815	*Zea mays*
GLYM_PEA/SwissProt	Serine hydroxymethyltransferase, mitochondrial	1/1	41	2	57371	*Pisum sativum*
A0A1D6PNA2/UP7305_Z_mays	U2 snRNP auxiliary factor large subunit	1/1	30	4	38886	*Zea mays*
SPL8_ARATH/UP7305_Z_mays	Squamosa promoter-binding-like protein 8	1/1	41	2	37261	*Zea mays*
A0A1D6H5M9/UP7305_Z_mays	ATP-dependent DNA helicase	1/1	68	24	8239	*Zea mays*
A0A1D6KDZ6/UP7305_Z_mays	Translocon-associated protein beta (TRAPB) family protein	1/1	40	5	22107	*Zea mays*
A0A1D6KE00/UP7305_Z_mays	Thaumatin-like protein	1/1	42	1	118090	*Zea mays*

Table S5 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
HS704_ARATH/SwissProt	Heat shock 70 kDa protein 4	6/5	203	12	71456	*Arabidopsis thaliana*
C0P5E7/UP7305_Z_mays	Leukotriene A-4 hydrolase-like protein	1/1	49	2	68240	*Zea mays*
A0A1D6ICM8/UP7305_Z_mays	SKU5 similar 4	1/1	51	2	61378	*Zea mays*
A0A1D6FSA7/UP7305_Z_mays	Protein RETICULATA-RELATED 6 chloroplastic	1/1	38	1	61907	*Zea mays*
A0A1D6JE05/UP7305_Z_mays	Coproporphyrinogen oxidase	1/1	52	3	38083	*Zea mays*
A0A1D6NU66/UP7305_Z_mays	Telomere-associated protein RIF1	1/1	41	1	69208	*Zea mays*
OBP1A_ARATH/SwissProt	Oil body-associated protein 1A	1/1	41	2	27447	*Arabidopsis thaliana*
A0A1D6L8I1/UP7305_Z_mays	Uncharacterized protein (Putative Galactose-binding domain-containing protein - UniProtKB)	1/1	38	4	41166	*Zea mays*
B4FT32/UP7305_Z_mays	Diaminopimelate decarboxylase 2 chloroplastic	1/1	32	1	53771	*Zea mays*
FABI2_ORYSJ/SwissProt	Enoyl-[acyl-carrier-protein] reductase [NADH] 2, chloroplastic	1/1	54	3	39167	*Oryza sativa* subsp. *japonica*
A0A1D6IT39/UP7305_Z_mays	Aluminum-induced protein homolog1	1/1	60	16	12359	*Zea mays*

Table S5 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6NMI8/UP7305_Z_mays	Thioredoxin family Trp26	2/2	65	12	24902	*Zea mays*
K7TFG6/UP7305_Z_mays	Cyclin superfamily protein, putative	1/1	36	1	44803	*Zea mays*
A0A1D6KTZ2/UP7305_Z_mays	Chaperonin2	3/3	75	5	60983	*Zea mays*
A0A1D6M7L9/UP7305_Z_mays	Assimilatory sulfite reductase	1/1	40	1	70336	*Zea mays*
A0A1D6FF26/UP7305_Z_mays	2-hydroxyacyl-CoA lyase	1/1	39	1	71527	*Zea mays*
K7VX77/UP7305_Z_mays	Phosphotransferase	1/1	57	3	55001	*Zea mays*
A0A1D6PIQ7/UP7305_Z_mays	Eukaryotic translation initiation factor 3 subunit K	1/1	42	4	27923	*Zea mays*
API5_ORYSJ/SwissProt	Apoptosis inhibitor 5-like protein API5	1/1	38	1	60176	*Oryza sativa* subsp. *japonica*
SODC_ANACO/SwissProt	Superoxide dismutase [Cu-Zn]	3/3	115	16	15280	*Ananas comosus*
A8WER4/UP7305_Z_mays	ZCN2	1/1	34	5	19501	*Zea mays*
TPS7_PHYDL/SwissProt	Trans-alpha-bergamotene synthase	1/1	33	2	63908	*Phyla dulcis*

Table S5 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
IAAT_MAIZE/SwissProt	Alpha-amylase/trypsin inhibitor	1/1	46	5	22973	*Zea mays*
A0A1D6H284/UP7305_Z_mays	4-coumarate--CoA ligase 1	1/1	37	2	62506	*Zea mays*
GCSP_PEA/SwissProt	Glycine dehydrogenase (decarboxylating), mitochondrial	1/1	34	1	115411	*Pisum sativum*
A0A1D6EGS0/UP7305_Z_mays	Protein transport protein Sec24-like CEF	1/1	23	1	117330	*Zea mays*
A0A1D6JKV2/UP7305_Z_mays	Actin-related protein 4	1/1	39	3	38583	*Zea mays*
PUB25_ARATH/SwissProt	U-box domain-containing protein 25	1/1	35	1	46654	*Arabidopsis thaliana*
C0P790/UP7305_Z_mays	Eukaryotic translation initiation factor 3 subunit B	1/1	67	1	83062	*Zea mays*
PDC2_ORYSI/SwissProt	Pyruvate decarboxylase 2	3/3	145	6	65889	*Oryza sativa* subsp. *indica*
A0A1D6GN16/UP7305_Z_mays	Putative serine protease EDA2	1/1	57	2	55538	*Zea mays*
A0A1D6PRL0/UP7305_Z_mays	Apyrase 1	1/1	44	2	52164	*Zea mays*
C0P6C5/UP7305_Z_mays	Threonine synthase	1/1	40	3	57919	*Zea mays*

Table S5 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6L117/UP7305_Z_mays	Tryptophanyl-tRNA synthetase	1/1	61	4	28162	*Zea mays*
MDHM2_ARATH/SwissProt	Malate dehydrogenase 2, mitochondrial	2/1	89	8	36024	*Arabidopsis thaliana*
A0A1D6FQM0/UP7305_Z_mays	Alpha/beta-Hydrolases superfamily protein	1/1	80	16	11663	*Zea mays*
B6UAK0/UP7305_Z_mays	Probable 6-phosphogluconolactonase	1/1	77	5	34874	*Zea mays*
B4FB55/UP7305_Z_mays	Ras-related protein ARA-3	3/3	120	16	24038	*Zea mays*
A0A1D6FNG1/UP7305_Z_mays	Superoxide dismutase	3/3	118	11	26419	*Zea mays*
EXPA1_ARATH/SwissProt	Expansin-A1	1/1	46	3	26957	*Arabidopsis thaliana*
A0A1D6QSC9/UP7305_Z_mays	Glycine cleavage system H protein	1/1	45	8	19817	*Zea mays*
B4FMB1/UP7305_Z_mays	DUF538 family protein	1/1	60	4	17499	*Zea mays*
A0A1D6E267/UP7305_Z_mays	Fasciclin-like arabinogalactan protein 10	1/1	39	3	44168	*Zea mays*
A0A1D6NDJ4/UP7305_Z_mays	Malic enzyme	1/1	41	3	65868	*Zea mays*

Table S5 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6IYD6/UP7305_Z_mays	Glyoxalase I	2/2	79	6	36506	*Zea mays*
LGUL_ORYSJ/SwissProt	Lactoylglutathione lyase	1/1	41	3	32875	*Oryza sativa* subsp. *japonica*
A0A1D6HW85/UP7305_Z_mays	Nitrile-specifier protein 1	1/1	46	3	40635	*Zea mays*
E1AFV5/UP7305_Z_mays	Beta-1,3-glucanase	2/2	92	10	36068	*Zea mays*
K7VFF7/UP7305_Z_mays	Glutaredoxin-dependent peroxiredoxin	1/1	80	7	23860	*Zea mays*
B4F8S9/UP7305_Z_mays	Uncharacterized protein (Fasciclin-like arabinogalactan protein 15 – UniProtKB)	2/2	65	7	50125	*Zea mays*
A0A1D6PA07/UP7305_Z_mays	Beta-adaptin-like protein C	1/1	32	1	95514	*Zea mays*
A0A1D6FTA3/UP7305_Z_mays	Ras-related protein RABG3f	1/1	43	5	22374	*Zea mays*
A0A1D6JIH1/UP7305_Z_mays	Pre-mRNA cleavage factor Im 25 kDa subunit	1/1	35	6	23457	*Zea mays*
A0A1D6E5L0/UP7305_Z_mays	Ras-related protein18A1	1/1	56	5	21581	*Zea mays*
B4G227/UP7305_Z_mays	Peptide-N4-(N-acetyl-beta-glucosaminyl) asparagine amidase A protein	1/1	48	2	67783	*Zea mays*

Table S5 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
GAPN_ARATH/SwissProt	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	1/1	26	4	53710	*Arabidopsis thaliana*
A0A1D6QRC6/UP7305_Z_mays	Fumarylacetoacetase	1/1	26	5	41938	*Zea mays*
A0A1D6EW83/UP7305_Z_mays	Ras-related protein RABH1b	1/1	43	7	15909	*Zea mays*
LOX1_HORVU/SwissProt	Linoleate 9S-lipoxygenase 1	1/1	30	1	96447	*Zea mays*
A0A1D6P2Q0/UP7305_Z_mays	Transducin/WD40 repeat-like superfamily protein	1/1	45	4	28752	*Zea mays*
A0A1D6LVE5/UP7305_Z_may	Gibberellin receptor GID1L2	1/1	38	4	34811	*Zea mays*
A0A1D6GPP6/UP7305_Z_mays	Heterogeneous nuclear ribonucleoprotein 1	1/1	92	3	48323	*Zea mays*
A0A1D6HBU2/UP7305_Z_mays	Glycerophosphodiester phosphodiesterase	1/1	59	1	81765	Zea mays

Table S6. Differentially expressed protein (down-regulated) in axillary buds of the RB867515 sugarcane cultivar at the first cut compared to fifth cutting stage.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
REF_HEVBR/SwissProt	Rubber elongation factor protein	1/1	57	11	14713	*Hevea brasiliensis*
A0A1D6N717/UP7305_Z_mays	Alpha-1,4 glucan phosphorylase	1/1	53	1	77875	*Zea mays*
A0A1D6JSM9/UP7305_Z_mays	T-complex protein 1 subunit gamma	1/1	62	1	58500	*Zea mays*
A0A1D6L4F0/UP7305_Z_mays	Exhydrolase II	1/1	56	2	73960	*Zea mays*
C0P905/UP7305_Z_mays	Glucan endo-1,3-beta-D-glucosidase	1/1	55	2	53994	*Zea mays*
A0A1D6FSJ2/UP7305_Z_mays	60S ribosomal protein L24	1/1	46	6	21113	*Zea mays*
A0A1D6JFG2/UP7305_Z_mays	Beta-D-xylosidase	1/1	52	1	82773	*Zea mays*
ILVB1_MAIZE/SwissProt	Acetolactate synthase 1, chloroplastic	1/1	48	2	69172	*Zea mays*
VATB2_HORVU/SwissProt	V-type proton ATPase subunit B 2	4/4	224	13	53806	*Hordeum vulgare*
A0A1D6NMU3/UP7305_Z_mays	Ubiquitin carboxyl-terminal hydrolase	1/1	144	6	41416	*Zea mays*
A0A1D6HR41/UP7305_Z_mays	Pyridoxal 5'-phosphate synthase-like subunit PDX1.2	1/1	27	1	44219	*Zea mays*

Table S6 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6KMC8/UP7305_Z_mays	Dihydroxy-acid dehydratase chloroplastic	1/1	113	3	66497	*Zea mays*
A0A1D6FI07/UP7305_Z_mays	Dihydrolipoyl dehydrogenase	2/2	70	5	44851	*Zea mays*
A0A1D6FAH0/UP7305_Z_mays	T-complex protein 1 subunit epsilon	2/2	60	7	61109	*Zea mays*
A0A1D6GPS2/UP7305_Z_mays	Pre-mRNA-processing factor 19	1/1	41	2	60914	*Zea mays*
ATPA_SACHY/SwissProt	ATP synthase subunit alpha, chloroplastic	1/1	40	2	55773	*Saccharum* hybrid
A0A1D6IX59/UP7305_Z_mays	Beta-glucosidase, chloroplastic	1/1	39	1	52535	*Zea mays*
TCPZA_ARATH/SwissProt	T-complex protein 1 subunit zeta	1/1	38	2	59426	*Arabidopsis thaliana*
FB250_ARATH/SwissProt	F-box protein At5g03100	1/1	37	2	35271	*Arabidopsis thaliana*
A0A1D6F1W9/UP7305_Z_mays	Phospho-2-dehydro-3-deoxyheptonate aldolase	1/1	45	3	41118	*Zea mays*

Table S6 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6IXG3/UP7305_Z_mays	Citrulline--aspartate ligase	1/1	38	2	46015	*Zea mays*
A0A1D6H3Y9/UP7305_Z_mays	Proteasome component4	1/1	80	7	31580	*Zea mays*
A0A1D6L4P1/UP7305_Z_mays	Protein STRICTOSIDINE SYNTHASE-LIKE 3	1/1	33	3	59693	*Zea mays*
SCRK7_ARATH/SwissProt	Probable fructokinase-7	2/1	76	5	37233	*Arabidopsis thaliana*
C0PNU9/UP7305_Z_mays	Protein binding protein	1/1	34	2	31083	*Zea mays*
B4FMW6/UP7305_Z_mays	Aspartyl protease AED3	1/1	45	1	45280	*Zea mays*
A0A1Q0ZFB6/UP7305_Z_mays	Alba DNA/RNA-binding protein	1/1	43	3	36593	*Zea mays*
GSA_BRANA/UP7305_Z_mays	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic	1/1	42	2	50562	*Brassica napus*
B4G195/UP7305_Z_mays	Glutamate-oxaloacetate transaminase5	1/1	39	2	49619	*Zea mays*
A0A1D6FBT4/UP7305_Z_mays	Transcription factor Pur-alpha 1	1/1	35	2	43177	*Zea mays*
Q6TM44/UP7305_Z_mays	Germin-like protein	1/1	41	10	22101	*Zea mays*

Table S6 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6PVR8/UP7305_Z_mays	40S ribosomal protein S3-1	4/4	114	18	28696	*Zea mays*
A0A1D6NHH6/UP7305_Z_mays	GTP-binding nuclear protein	2/2	83	11	25440	*Zea mays*
A0A1D6GF42/UP7305_Z_mays	40S ribosomal protein S2-1	1/1	53	5	30027	*Zea mays*
B6TPA4/UP7305_Z_mays	Carnitine racemase/catalytic	1/1	46	5	25869	*Zea mays*
A0A1D6FVM4/UP7305_Z_mays	ULP_PROTEASE domain-containing protein	1/1	45	1	117912	*Zea mays*
B4F848/UP7305_Z_mays	20 kDa chaperonin chloroplastic	1/1	40	7	25796	*Zea mays*
A0A1D6PI62/UP7305_Z_mays	40S ribosomal protein S3a	2/2	61	7	34634	*Zea mays*
A0A1D6KEX3/UP7305_Z_mays	Adenine phosphoribosyltransferase	1/1	39	9	16873	*Zea mays*
A0A1D6KQ94/UP7305_Z_mays	Co-chaperone protein SBA1	1/1	35	8	15736	*Zea mays*
COP52_ORYSJ/SwissProt	Putative copper transporter 5.2	1/1	31	5	17936	*Oryza sativa* subsp. *japonica*
B4FB66/UP7305_Z_mays	40S ribosomal protein S5-2	1/1	57	6	22297	*Zea mays*

Table S6 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6IV93/UP7305_Z_mays	Agamous-like MADS-box protein AGL8	1/1	29	3	29077	*Zea mays*
A0A1D6J4Q3/UP7305_Z_mays	Translation elongation factor EF1A/initiation factor IF2gamma family protein	1/1	54	2	46081	*Zea mays*
A0A1D6KNM8/UP7305_Z_mays	Phosphoglycerate dehydrogenase	1/1	43	1	69667	*Zea mays*
C4J4W3/UP7305_Z_mays	Hsp70-Hsp90 organizing protein 3	1/1	40	1	65563	*Zea mays*
A0A1D6F4V8/UP7305_Z_mays	26S proteasome regulatory subunit 4 homolog A	1/1	58	3	41048	*Zea mays*
A0A1D6FL86/UP7305_Z_mays	Putative calcium-dependent protein kinase family protein	1/1	57	4	44614	*Zea mays*
A0A1D6NUR0/UP7305_Z_mays	Carotenoid 910(9'10')-cleavage dioxygenase 1	1/1	34	1	69195	*Zea mays*
A0A1D6M1D4/UP7305_Z_mays	Eukaryotic peptide chain release factor subunit 1-1	1/1	48	2	49026	*Zea mays*
GME1_ORYSI/SwissProt	GDP-mannose 3,5-epimerase 1	2/2	86	7	43180	*Oryza sativa* subsp. *indica*
ACT_MESVI/SwissProt	Actin	3/2	123	8	41791	*Mesostigma viride*
K7V9P7/UP7305_Z_mays	Beta-ketoacyl-[acyl-carrier-protein] synthase I	1/1	63	2	51721	*Zea mays*

Table S6 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6H7L0/UP7305_Z_mays	26S protease regulatory subunit 8 homolog B	1/1	50	3	41699	*Zea mays*
A0A1D6GVM3/UP7305_Z_mays	Delta-aminolevulinic acid dehydratase	2/2	58	5	46434	*Zea mays*
ACT4_SOLLC/SwissProt	Actin-105 (Fragment)	1/1	35	4	37362	*Solanum lycopersicum*
A0A1D6HI32/UP7305_Z_mays	Thioredoxin reductase	1/1	52	4	37630	*Zea mays*
FBRL2_ARATH/SwissProt	rRNA 2'-O-methyltransferase fibrillarin 2	1/1	51	3	33803	*Arabidopsis thaliana*
A0A1D6FR00/UP7305_Z_mays	Elongation factor 1-beta	1/1	55	3	27466	*Zea mays*
TPIC_SPIOL/SwissProt	Triosephosphate isomerase, chloroplastic	1/1	46	4	34787	*Spinacia oleracea*
A0A1D6G511/UP7305_Z_mays	40S ribosomal protein S6-1	1/1	45	7	13533	*Zea mays*
CAMT1_MAIZE/SwissProt	Caffeoyl-CoA O-methyltransferase 1	1/1	36	6	29016	*Zea mays*
P45633/UP7305_Z_mays	60S ribosomal protein L10	1/1	78	5	25359	*Zea mays*
DOT2_ARATH/SwissProt	SART-1 family protein DOT2	1/1	54	1	94086	*Arabidopsis thaliana*

Table S6 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
SKM1_ARATH/SwissProt	Leucine-rich repeat receptor-like serine/threonine-protein kinase SKM1	1/1	38	1	107464	*Arabidopsis thaliana*
A0A1D6HNE6/UP7305_Z_mays	DNA helicase	1/1	39	2	82318	*Zea mays*
A0A1D6GZE7/UP7305_Z_mays	RuvB-like helicase	1/1	62	3	50233	*Zea mays*
PRS6B_ARATH/SwissProt	26S proteasome regulatory subunit 6B homolog	1/1	74	4	45894	*Arabidopsis thaliana*
A0A1D6M0K3/UP7305_Z_mays	GOLD domain-containing protein	1/1	26	3	49812	*Zea mays*
LDHA_HORVU/SwissProt	L-lactate dehydrogenase A	1/1	72	3	37840	*Hordeum vulgare*
A0A1D6KNS0/UP7305_Z_mays	Cinnamoyl CoA reductase1	1/1	32	3	45016	*Zea mays*
A0A1D6EGZ7/UP7305_Z_mays	ARM repeat superfamily protein	1/1	32	3	47837	*Zea mays*
A0A1D6DT56/UP7305_Z_mays	NADPH-protochlorophyllide oxidoreductase	1/1	54	3	41525	*Zea mays*
KCAB_ARATH/SwissProt	Probable voltage-gated potassium channel subunit beta	1/1	40	3	36744	*Arabidopsis thaliana*
B4FVD5/UP7305_Z_mays	V-type proton ATPase subunit E3	1/1	39	4	26727	*Zea mays*

Table S6 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6MQ90/UP7305 _Z_mays	26S proteasome regulatory subunit RPN11	1/1	35	2	31682	*Zea mays*
RS8_MAIZE/SwissProt	40S ribosomal protein S8	2/2	134	13	25155	*Zea mays*
A0A1D6H9F2/UP7305_ Z_mays	TUDOR-SN protein 1	1/1	73	2	49468	*Zea mays*
A0A1D6JVQ5/UP7305_ Z_mays	Peptidylprolyl isomerase	1/1	51	2	47904	*Zea mays*
A0A1D6FV26/UP7305_ Z_mays	Glutamate--cysteine ligase	1/1	39	5	38071	*Zea mays*
A0A1D6FUX8/UP7305_ Z_mays	S-adenosylmethionine synthase	3/3	93	7	51644	*Zea mays*
CHS5_SORBI/SwissProt	Chalcone synthase 5	1/1	41	3	44070	*Sorghum bicolor*
A0A1D6EZI3/UP7305_Z _mays	Succinyl-CoA ligase alpha-chain 2	1/1	66	23	5271	*Zea mays*
A0A1D6K1B9/UP7305_ Z_mays	Hydroxyproline-rich glycoprotein family protein	1/1	47	3	41036	*Zea mays*
A0A1D6K371/UP7305_ Z_mays	Nascent polypeptide-associated complex alpha subunit-like protein	2/2	81	17	19099	*Zea mays*
A0A1D6LMW9/UP7305 _Z_mays	Endoplasmin-like protein	2/2	69	2	92572	*Zea mays*

Table S6 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
PILR4_THUPL/SwissProt	Bifunctional pinoresinol-lariciresinol reductase	1/1	47	3	34834	*Thuja plicata*
A0A1D6DVE8/UP7305_Z_mays	Protein-serine/threonine phosphatase	1/1	45	2	34798	*Zea mays*
A0A1D6JMR6/UP7305_Z_mays	60S ribosomal protein L5-1	1/1	55	3	33179	*Zea mays*
A0A1D6FQA7/UP7305_Z_mays	Gibberellin receptor GID1A	1/1	29	2	35017	*Zea mays*
A0A1D6NQP7/UP7305_Z_mays	Chalcone-flavonone isomerase family protein	1/1	50	5	25446	*Zea mays*
A0A1D6DZS2/UP7305_Z_mays	UDP-N-acetylglucosamine diphosphorylase 2	1/1	59	2	49205	*Zea mays*
C0HDR0/UP7305_Z_mays	Histidinol dehydrogenase, chloroplastic	1/1	43	3	51496	*Zea mays*
A0A1D6HNF6/UP7305_Z_mays	Aspartate transaminase	1/1	41	2	46492	*Zea mays*
A0A1D6HDG0/UP7305_Z_mays	Succinate-CoA ligase subunit beta	1/1	39	1	40725	*Zea mays*
A0A1D6H1H5/UP7305_Z_mays	Hydroxymethylbilane synthase	1/1	42	3	46158	*Zea mays*
B6SHT0/UP7305_Z_mays	OB-fold nucleic acid binding domain containing protein	1/1	62	6	15544	*Zea mays*

Table S6 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
RL11_ORYSI/SwissProt	60S ribosomal protein L11	1/1	53	7	20994	*Zea mays*
B4F922/UP7305_Z_mays	Acyltransferase	1/1	60	3	47893	*Zea mays*
A0A1D6MQV8/UP7305_Z_mays	Glycine hydroxymethyltransferase	1/1	80	11	10741	*Zea mays*
A0A1D6HJS1/UP7305_Z_mays	Pyruvate dehydrogenase E1 component subunit alpha	1/1	67	3	43016	*Zea mays*
A0A1D6G8L3/UP7305_Z_mays	Triose phosphate isomerase5	1/1	41	6	24871	*Zea mays*

Table S7. Differentially expressed protein (up-regulated) in axillary buds of the RB867515 sugarcane cultivar at the fifth cut compared to first cutting stage.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6JY65/UP7305_Z_mays	Heat shock cognate 70 kDa protein 2	1/1	43	2	65343	*Zea mays*
C0PDC7/UP7305_Z_mays	Chaperone protein ClpB1	1/1	53	2	101284	*Zea mays*
A0A1D6GCT9/UP7305_Z_mays	Protein EXPORTIN 1A	1/1	44	1	123719	*Zea mays*
B6T3V0/UP7305_Z_mays	Ferredoxin-related	1/1	34	3	24446	*Zea mays*
CGEP_ORYSJ /SwissProt	Probable glutamyl endopeptidase, chloroplastic	1/1	32	2	104400	*Oryza sativa* subsp. *japonica*
A0A1D6E312/UP7305_Z_mays	Argonaute1c	1/1	31	1	58007	*Zea mays*
A0A1D6I3K9/UP7305_Z_mays	Endo-1,3(4)-beta-glucanase	1/1	41	3	82719	*Zea mays*
CATA3_MAIZE/UP7305_Z_mays	Catalase isozyme 3	4/1	127	14	57159	*Zea mays*
CATA2_HORVU/SwissProt	Catalase isozyme 2	3/2	110	7	57390	*Hordeum vulgare*
A0A1D6IWN4/UP7305_Z_mays	Shikimate dehydrogenase	1/1	38	1	62956	*Zea mays*
K7V938/UP7305_Z_mays	Putative carboxylesterase 2	1/1	51	3	31561	*Zea mays*

Table S7 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6DZK5/UP7305_Z_mays	Adenosylmethionine aminotransferase1	1/1	68	2	56004	*Zea mays*
B4FTN5/UP7305_Z_mays	Metal-dependent protein hydrolase	1/1	49	3	43011	*Zea mays*
PGIP1_ORYSJ/SwissProt	Polygalacturonase inhibitor 1	1/1	36	4	36012	*Oryza sativa* subsp. *japonica*
A0A1D6HKP7/UP7305_Z_mays	Annexin	1/1	47	2	45684	*Zea mays*
ACLB1_ARATH/SwissProt	ATP-citrate synthase beta chain protein 1	1/1	57	2	66342	*Arabidopsis thaliana*
A0A1D6L8E8/UP7305_Z_mays	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex	1/1	44	2	53355	*Zea mays*
A0A1D6NY34/UP7305_Z_mays	Putative threonine aldolase family protein	1/1	38	2	46800	*Zea mays*
A0A1D6NB04/UP7305_Z_mays	Aspartate aminotransferase	1/1	55	3	46038	*Zea mays*
NSF_ORYSJ/SwissProt	Vesicle-fusing ATPase	1/1	49	1	81591	*Oryza sativa* subsp. *japonica*
B6TN41/UP7305_Z_mays	4-hydroxy-4-methyl-2-oxoglutarate aldolase	1/1	40	6	18390	*Zea mays*
Q19VG6/UP7305_Z_mays	Major latex protein 22	1/1	42	7	17101	*Zea mays*

Table S7 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6I867/UP7305_Z_mays	Clathrin heavy chain 2	3/1	84	8	50622	*Zea mays*
A0A1D6PBS4/UP7305_Z_mays	pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH3	1/1	40	3	40873	*Zea mays*
A0A096UGL9/UP7305_Z_mays	Exportin-2	1/1	29	1	109050	*Zea mays*
A0A1D6L977/UP7305_Z_mays	Methylenetetrahydrofolate reductase	1/1	49	2	64872	*Zea mays*
A0A1D6IIX9/UP7305_Z_mays	Pentatricopeptide repeat-containing protein mitochondrial	1/1	57	2	69042	*Zea mays*
A0A1D6L6N3/UP7305_Z_mays	Inosine-5'-monophosphate dehydrogenase	1/1	44	2	48769	*Zea mays*
B6T484/UP7305_Z_mays	Mitogen-activated protein kinase	1/1	43	4	42649	*Zea mays*
A0A1D6JQK4/UP7305_Z_mays	Topless-related protein 2	1/1	39	5	34475	*Zea mays*
B4FIV0/UP7305_Z_mays	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial	1/1	65	9	34600	*Zea mays*
A0A1D6GLS4/UP7305_Z_mays	Serpin-Z1	1/1	36	2	44359	*Zea mays*
A0A1D6JG12/UP7305_Z_mays	Cysteine protease 1	1/1	53	3	53108	*Zea mays*

Table S7 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6Q3E1/UP7305_Z_mays	2-hydroxy-3-oxopropionate reductase	1/1	49	8	26974	*Zea mays*
A0A1D6GAY3/UP7305_Z_mays	Glutathione transferase	1/1	49	6	13576	*Zea mays*
A0A1X7YIJ7/UP7305_Z_mays	Chitinase	1/1	47	5	31374	*Zea mays*
A0A1D6P3B9/UP7305_Z_mays	110 kDa U5 small nuclear ribonucleoprotein component CLO	1/1	43	1	109001	*Zea mays*
A0A1D6GY62/UP7305_Z_mays	Uncharacterized protein	1/1	36	1	44904	*Zea mays*
BGL31_ORYSJ/SwissProt	Beta-glucosidase 31	1/1	35	1	58696	*Oryza sativa* subsp. *japonica*
A0A1D6L056/UP7305_Z_mays	BGGP Beta-1-3-galactosyl-O-glycosyl-glycoprotein	1/1	34	2	50083	*Zea mays*
A0A1D6KEG7/UP7305_Z_mays	Heparanase-like protein 1	1/1	53	3	50610	*Zea mays*
A0A1D6HIW8/UP7305_Z_mays	Enhancer of mRNA-decapping protein 4	1/1	32	2	38475	*Zea mays*
A0A1D6F487/UP7305_Z_mays	Ubiquitin-like-specific protease ESD4	1/1	37	1	51520	*Zea mays*
PER2_ORYSI/SwissProt	Peroxidase 2	1/1	74	5	33070	*Oryza sativa* subsp. *indica*

Table S7 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
LOX1_HORVU/UP7305_Z_mays	Linoleate 9S-lipoxygenase 1	2/2	51	3	96447	*Hordeum vulgare*
A0A1D6NDJ3/UP7305_Z_mays	Malic enzyme	2/2	89	4	67301	*Zea mays*
C0P790/UP7305_Z_mays	Eukaryotic translation initiation factor 3 subunit B	1/1	62	1	83062	*Zea mays*
Q8S4W9/UP7305_Z_mays	Pyruvate decarboxylase	4/4	175	10	65990	*Zea mays*
A0A1D6PRL0/UP7305_Z_mays	Apyrase 1	1/1	52	2	52164	*Zea mays*
A0A1D6GN16/UP7305_Z_mays	Putative serine protease EDA2	1/1	36	2	55538	*Zea mays*
A0A1D6QRC6/UP7305_Z_mays	Fumarylacetoacetase	1/1	30	5	41938	*Zea mays*
A0A1D6LVE5/UP7305_Z_mays	Gibberellin receptor GID1L2	1/1	54	4	34811	*Zea mays*
A0A1D6IYD6/UP7305_Z_mays	Glyoxalase I	1/1	59	3	36506	*Zea mays*
A0A1D6P2Q0/UP7305_Z_mays	Transducin/WD40 repeat-like superfamily protein	1/1	42	4	28752	*Zea mays*
E1AFV5/UP7305_Z_mays	Beta-1,3-glucanase	2/2	136	10	36068	*Zea mays*

Table S7 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6FQM0/UP7305_Z_mays	Alpha/beta-Hydrolases superfamily protein	2/2	102	25	11663	*Zea mays*
A0A1D6FNG1/UP7305_Z_mays	Superoxide dismutase	4/4	124	18	26419	*Zea mays*
CFIS2_ARATH/SwissProt	Pre-mRNA cleavage factor Im 25 kDa subunit 2	1/1	78	7	23043	*Arabidopsis thaliana*
A0A1D6E5L0/UP7305_Z_mays	Ras-related protein18A1	1/1	56	5	21581	*Zea mays*
EXPA1_ARATH/SwissProt	Expansin-A1	1/1	51	3	26957	*Arabidopsis thaliana*
K7VFF7/UP7305_Z_mays	Glutaredoxin-dependent peroxiredoxin	1/1	73	7	23860	*Zea mays*
B4G227/UP7305_Z_mays	Peptide-N4-(N-acetyl-beta-glucosaminyl) asparagine amidase A protein	1/1	55	2	67783	*Zea mays*
A0A1D6QSC9/UP7305_Z_mays	Glycine cleavage system H protein	1/1	52	8	19817	*Zea mays*
A0A1D6M9Z1/UP7305_Z_mays	Ras-related protein RABG3f	1/1	43	5	20757	*Zea mays*
B4FMB1/UP7305_Z_mays	DUF538 family protein	1/1	55	4	17499	*Zea mays*
B4F8S9/UP7305_Z_mays	Uncharacterized protein (Fasciclin-like arabinogalactan protein 15 – UniProtKB)	1/1	49	3	50125	*Zea mays*
LGUL_ORYSJ/SwissProt	Lactoylglutathione lyase	1/1	40	3	32875	*Oryza sativa* subsp. *japonica*

Table S7 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
B6UAK0/UP7305_Z_mays	[i]Probable 6-phosphogluconolactonase	1/1	65	5	34874	*Zea mays*
GAPN_MAIZE/UP7305_Z_mays	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	1/1	56	3	53740	*Zea mays*
A0A1D6HW85/UP7305_Z_mays	Nitrile-specifier protein 1	1/1	40	3	40635	*Zea mays*
A0A1D6PA07/UP7305_Z_mays	Beta-adaptin-like protein C	1/1	42	1	95514	*Zea mays*
A0A1D6GPP6/UP7305_Z_mays	Heterogeneous nuclear ribonucleoprotein 1	1/1	36	3	48323	*Zea mays*
B4FB55/UP7305_Z_mays	Ras-related protein ARA-3	3/1	87	16	24038	*Zea mays*
A0A1D6EW83/UP7305_Z_mays	Ras-related protein RABH1b	1/1	43	7	15909	*Zea mays*
A0A1D6HBU2/UP7305_Z_mays	Glycerophosphodiester phosphodiesterase	1/1	58	1	81765	*Zea mays*
A0A1D6E267/UP7305_Z_mays	Fasciclin-like arabinogalactan protein 10	1/1	50	4	44168	*Zea mays*
C0P6C5/UP7305_Z_mays	Threonine synthase	1/1	35	3	57919	*Zea mays*
A0A1D6L117/UP7305_Z_mays	Tryptophanyl-tRNA synthetase	1/1	44	4	28162	*Zea mays*
MDHM2_ARATH/Swiss Prot	Malate dehydrogenase 2, mitochondrial	2/1	115	8	36024	*Arabidopsis thaliana*

Table S8. Differentially expressed protein (down-regulated) in axillary buds of the RB867515 sugarcane cultivar at the third cut compared to fifth cutting stage.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6KZB9/UP7305_Z_mays	Tetratricopeptide repeat (TPR)-like superfamily protein	1/1	33	1	73005	*Zea mays*
B4FM07/UP7305_Z_mays	Thioredoxin-dependent peroxiredoxin	1/1	37	5	28318	*Zea mays*
A0A1D6FU93/UP7305_Z_mays	Arginyl-tRNA synthetase	1/1	38	1	67511	*Zea mays*
A0A1D6HYS3/UP7305_Z_mays	Phosphoglucosamine mutase family protein	1/1	63	5	20237	*Zea mays*
A0A1D6DTX6 /UP7305_Z_mays	Protein DJ-1 homolog D	1/1	39	3	35815	*Zea mays*
GLYM_PEA/SwissProt	Serine hydroxymethyltransferase, mitochondrial	1/1	41	2	57371	*Pisum sativum*
A0A1D6PNA2/UP7305_Z_mays	U2 snRNP auxiliary factor large subunit	1/1	30	4	38886	*Zea mays*
SPL8_ARATH/UP7305_Z_mays	Squamosa promoter-binding-like protein 8	1/1	41	2	37261	*Zea mays*
A0A1D6H5M9/UP7305_Z_mays	ATP-dependent DNA helicase	1/1	68	24	8239	*Zea mays*
A0A1D6KDZ6/UP7305_Z_mays	Translocon-associated protein beta (TRAPB) family protein	1/1	40	5	22107	*Zea mays*
A0A1D6KE00/UP7305_Z_mays	Thaumatin-like protein	1/1	42	1	118090	*Zea mays*

Table S8 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
HS704_ARATH/SwissProt	Heat shock 70 kDa protein 4	6/5	203	12	71456	*Arabidopsis thaliana*
C0P5E7/UP7305_Z_mays	Leukotriene A-4 hydrolase-like protein	1/1	49	2	68240	*Zea mays*
A0A1D6ICM8/UP7305_Z_mays	SKU5 similar 4	1/1	51	2	61378	*Zea mays*
A0A1D6FSA7/UP7305_Z_mays	Protein RETICULATA-RELATED 6 chloroplastic	1/1	38	1	61907	*Zea mays*
A0A1D6JE05/UP7305_Z_mays	Coproporphyrinogen oxidase	1/1	52	3	38083	*Zea mays*
A0A1D6NU66/UP7305_Z_mays	Telomere-associated protein RIF1	1/1	41	1	69208	*Zea mays*
OBP1A_ARATH/SwissProt	Oil body-associated protein 1A	1/1	41	2	27447	*Arabidopsis thaliana*
A0A1D6L8I1/UP7305_Z_mays	Uncharacterized protein (Putative Galactose-binding domain-containing protein - UniProtKB)	1/1	38	4	41166	*Zea mays*
B4FT32/UP7305_Z_mays	Diaminopimelate decarboxylase 2 chloroplastic	1/1	32	1	53771	*Zea mays*
FABI2_ORYSJ/SwissProt	Enoyl-[acyl-carrier-protein] reductase [NADH] 2, chloroplastic	1/1	54	3	39167	*Oryza sativa* subsp. *japonica*
A0A1D6IT39/UP7305_Z_mays	Aluminum-induced protein homolog1	1/1	60	16	12359	*Zea mays*

Table S8 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6NMI8/UP7305_Z_mays	Thioredoxin family Trp26	2/2	65	12	24902	*Zea mays*
K7TFG6/UP7305_Z_mays	Cyclin superfamily protein, putative	1/1	36	1	44803	*Zea mays*
A0A1D6KTZ2/UP7305_Z_mays	Chaperonin2	3/3	75	5	60983	*Zea mays*
A0A1D6M7L9/UP7305_Z_mays	Assimilatory sulfite reductase	1/1	40	1	70336	*Zea mays*
A0A1D6FF26/UP7305_Z_mays	2-hydroxyacyl-CoA lyase	1/1	39	1	71527	*Zea mays*
K7VX77/UP7305_Z_mays	Phosphotransferase	1/1	57	3	55001	*Zea mays*
A0A1D6PIQ7/UP7305_Z_mays	Eukaryotic translation initiation factor 3 subunit K	1/1	42	4	27923	*Zea mays*
API5_ORYSJ/SwissProt	Apoptosis inhibitor 5-like protein API5	1/1	38	1	60176	*Oryza sativa* subsp. *japonica*
SODC_ANACO/SwissProt	Superoxide dismutase [Cu-Zn]	3/3	115	16	15280	*Ananas comosus*
A8WER4/UP7305_Z_mays	ZCN2	1/1	34	5	19501	*Zea mays*
TPS7_PHYDL/SwissProt	Trans-alpha-bergamotene synthase	1/1	33	2	63908	*Phyla dulcis*

Table S8 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
IAAT_MAIZE/SwissProt	Alpha-amylase/trypsin inhibitor	1/1	46	5	22973	*Zea mays*
A0A1D6H284/UP7305_Z_mays	4-coumarate--CoA ligase 1	1/1	37	2	62506	*Zea mays*
GCSP_PEA/SwissProt	Glycine dehydrogenase (decarboxylating), mitochondrial	1/1	34	1	115411	*Pisum sativum*
A0A1D6EGS0/UP7305_Z_mays	Protein transport protein Sec24-like CEF	1/1	23	1	117330	*Zea mays*
A0A1D6JKV2/UP7305_Z_mays	Actin-related protein 4	1/1	39	3	38583	*Zea mays*
PUB25_ARATH/SwissProt	U-box domain-containing protein 25	1/1	35	1	46654	*Arabidopsis thaliana*
C0P790/UP7305_Z_mays	Eukaryotic translation initiation factor 3 subunit B	1/1	67	1	83062	*Zea mays*
PDC2_ORYSI/SwissProt	Pyruvate decarboxylase 2	3/3	145	6	65889	*Oryza sativa* subsp. *indica*
A0A1D6GN16/UP7305_Z_mays	Putative serine protease EDA2	1/1	57	2	55538	*Zea mays*
A0A1D6PRL0/UP7305_Z_mays	Apyrase 1	1/1	44	2	52164	*Zea mays*
C0P6C5/UP7305_Z_mays	Threonine synthase	1/1	40	3	57919	*Zea mays*

Table S8 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6L117/UP7305_Z_mays	Tryptophanyl-tRNA synthetase	1/1	61	4	28162	*Zea mays*
MDHM2_ARATH/Swiss Prot	Malate dehydrogenase 2, mitochondrial	2/1	89	8	36024	*Arabidopsis thaliana*
A0A1D6FQM0/UP7305_Z_mays	Alpha/beta-Hydrolases superfamily protein	1/1	80	16	11663	*Zea mays*
B6UAK0/UP7305_Z_mays	Probable 6-phosphogluconolactonase	1/1	77	5	34874	*Zea mays*
B4FB55/UP7305_Z_mays	Ras-related protein ARA-3	3/3	120	16	24038	*Zea mays*
A0A1D6FNG1/UP7305_Z_mays	Superoxide dismutase	3/3	118	11	26419	*Zea mays*
EXPA1_ARATH/SwissProt	Expansin-A1	1/1	46	3	26957	*Arabidopsis thaliana*
A0A1D6QSC9/UP7305_Z_mays	Glycine cleavage system H protein	1/1	45	8	19817	*Zea mays*
B4FMB1/UP7305_*Z_mays*	DUF538 family protein	1/1	60	4	17499	*Zea mays*
A0A1D6HBU2/UP7305_*Z_mays*	Glycerophosphodiester phosphodiesterase	1/1	59	1	81765	*Zea mays*
A0A1D6E267/UP7305_*Z_mays*	Fasciclin-like arabinogalactan protein 10	1/1	39	3	44168	*Zea mays*

Table S8 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6NDJ4/UP7305_*Z_mays*	Malic enzyme	1/1	41	3	65868	*Zea mays*
A0A1D6IYD6/UP7305_*Z_mays*	Glyoxalase I	2/2	79	6	36506	*Zea mays*
LGUL_ORYSJ/SwissProt	Lactoylglutathione lyase	1/1	41	3	32875	*Oryza sativa* subsp. *japonica*
A0A1D6HW85/UP7305_*Z_mays*	Nitrile-specifier protein 1	1/1	46	3	40635	*Zea mays*
E1AFV5/UP7305_*Z_mays*	Beta-1,3-glucanase	2/2	92	10	36068	*Zea mays*
/K7VFF7/UP7305_*Z_mays*	Glutaredoxin-dependent peroxiredoxin	1/1	80	7	23860	*Zea mays*
B4F8S9/UP7305_*Z_mays*	Uncharacterized protein (Fasciclin-like arabinogalactan protein 15 – UniProtKB)	2/2	65	7	50125	*Zea mays*
A0A1D6PA07/UP7305_*Z_mays*	Beta-adaptin-like protein C	1/1	32	1	95514	*Zea mays*
A0A1D6FTA3/UP7305_*Z_mays*	Ras-related protein RABG3f	1/1	43	5	22374	*Zea mays*
A0A1D6JIH1/UP7305_*Z_mays*	Pre-mRNA cleavage factor Im 25 kDa subunit	1/1	35	6	23457	*Zea mays*
A0A1D6E5L0/UP7305_Z_mays	Ras-related protein18A1	1/1	56	5	21581	*Zea mays*
B4G227/UP7305_*Z_mays*	Peptide-N4-(N-acetyl-beta-glucosaminyl) asparagine amidase A protein	1/1	48	2	67783	*Zea mays*

Table S8 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
GAPN_ARATH/SwissProt	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	1/1	26	4	53710	*Arabidopsis thaliana*
A0A1D6QRC6/UP7305_ *Z_mays*	Fumarylacetoacetase	1/1	26	5	41938	*Zea mays*
A0A1D6EW83/UP7305_ *Z_mays*	Ras-related protein RABH1b	1/1	43	7	15909	*Zea mays*
LOX1_HORVU/SwissProt	Linoleate 9S-lipoxygenase 1	1/1	30	1	96447	*Zea mays*
A0A1D6P2Q0/UP7305_ *Z_mays*	Transducin/WD40 repeat-like superfamily protein	1/1	45	4	28752	*Zea mays*
A0A1D6LVE5/UP7305_ *Z_may*	Gibberellin receptor GID1L2	1/1	38	4	34811	*Zea mays*
A0A1D6GPP6/UP7305_ *Z_mays*	Heterogeneous nuclear ribonucleoprotein 1	1/1	92	3	48323	*Zea mays*

Table S9. Differentially expressed protein (up-regulated) in axillary buds of the RB867515 sugarcane cultivar at the fifth cut compared to third cutting stage.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6JY65/UP7305_Z_mays	Heat shock cognate 70 kDa protein 2	1/1	43	2	65343	*Zea mays*
C0PDC7/UP7305_Z_mays	Chaperone protein ClpB1	1/1	53	2	101284	*Zea mays*
A0A1D6GCT9/UP7305_Z_mays	Protein EXPORTIN 1A	1/1	44	1	123719	*Zea mays*
B6T3V0/UP7305_Z_mays	Ferredoxin-related	1/1	34	3	24446	*Zea mays*
CGEP_ORYSJ /SwissProt	Probable glutamyl endopeptidase, chloroplastic	1/1	32	2	104400	*Oryza sativa* subsp. *japonica*
A0A1D6E312/UP7305_Z_mays	Argonaute1c	1/1	31	1	58007	*Zea mays*
A0A1D6I3K9/UP7305_Z_mays	Endo-1,3(4)-beta-glucanase	1/1	41	3	82719	*Zea mays*
CATA3_MAIZE/UP7305_Z_mays	Catalase isozyme 3	4/1	127	14	57159	*Zea mays*
CATA2_HORVU/SwissProt	Catalase isozyme 2	3/2	110	7	57390	*Hordeum vulgare*
A0A1D6IWN4/UP7305_Z_mays	Shikimate dehydrogenase	1/1	38	1	62956	*Zea mays*
K7V938/UP7305_Z_mays	Putative carboxylesterase 2	1/1	51	3	31561	*Zea mays*

Table S9 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6DZK5/UP7305_Z_mays	Adenosylmethionine aminotransferase1	1/1	68	2	56004	*Zea mays*
B4FTN5/UP7305_Z_mays	Metal-dependent protein hydrolase	1/1	49	3	43011	*Zea mays*
PGIP1_ORYSJ/SwissProt	Polygalacturonase inhibitor 1	1/1	36	4	36012	*Oryza sativa* subsp. *japonica*
A0A1D6HKP7/UP7305_Z_mays	Annexin	1/1	47	2	45684	*Zea mays*
ACLB1_ARATH/SwissProt	ATP-citrate synthase beta chain protein 1	1/1	57	2	66342	*Arabidopsis thaliana*
A0A1D6L8E8/UP7305_Z_mays	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex	1/1	44	2	53355	*Zea mays*
A0A1D6NY34/UP7305_Z_mays	Putative threonine aldolase family protein	1/1	38	2	46800	*Zea mays*
A0A1D6NB04/UP7305_Z_mays	Aspartate aminotransferase	1/1	55	3	46038	*Zea mays*
NSF_ORYSJ/SwissProt	Vesicle-fusing ATPase	1/1	49	1	81591	*Oryza sativa* subsp. *japonica*
B6TN41/UP7305_Z_mays	4-hydroxy-4-methyl-2-oxoglutarate aldolase	1/1	40	6	18390	*Zea mays*
Q19VG6/UP7305_Z_mays	Major latex protein 22	1/1	42	7	17101	*Zea mays*

Table S9 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6I867/UP7305_Z_mays	Clathrin heavy chain 2	3/1	84	8	50622	*Zea mays*
A0A1D6PBS4/UP7305_Z_mays	pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH3	1/1	40	3	40873	*Zea mays*
A0A096UGL9/UP7305_Z_mays	Exportin-2	1/1	29	1	109050	*Zea mays*
A0A1D6L977/UP7305_Z_mays	Methylenetetrahydrofolate reductase	1/1	49	2	64872	*Zea mays*
A0A1D6IIX9/UP7305_Z_mays	Pentatricopeptide repeat-containing protein mitochondrial	1/1	57	2	69042	*Zea mays*
A0A1D6L6N3/UP7305_Z_mays	Inosine-5'-monophosphate dehydrogenase	1/1	44	2	48769	*Zea mays*
B6T484/UP7305_Z_mays	Mitogen-activated protein kinase	1/1	43	4	42649	*Zea mays*
A0A1D6JQK4/UP7305_Z_mays	Topless-related protein 2	1/1	39	5	34475	*Zea mays*
B4FIV0/UP7305_Z_mays	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial	1/1	65	9	34600	*Zea mays*
A0A1D6GLS4/UP7305_Z_mays	Serpin-Z1	1/1	36	2	44359	*Zea mays*
A0A1D6JG12/UP7305_Z_mays	Cysteine protease 1	1/1	53	3	53108	*Zea mays*

Table S9 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6Q3E1/UP7305_Z_mays	2-hydroxy-3-oxopropionate reductase	1/1	49	8	26974	*Zea mays*
A0A1D6GAY3/UP7305_Z_mays	Glutathione transferase	1/1	49	6	13576	*Zea mays*
A0A1X7YIJ7/UP7305_Z_mays	Chitinase	1/1	47	5	31374	*Zea mays*
A0A1D6P3B9/UP7305_Z_mays	110 kDa U5 small nuclear ribonucleoprotein component CLO	1/1	43	1	109001	*Zea mays*
A0A1D6GY62/UP7305_Z_mays	Uncharacterized protein	1/1	36	1	44904	*Zea mays*
BGL31_ORYSJ/SwissProt	Beta-glucosidase 31	1/1	35	1	58696	*Oryza sativa* subsp. *japonica*
A0A1D6L056/UP7305_Z_mays	BGGP Beta-1-3-galactosyl-O-glycosyl-glycoprotein	1/1	34	2	50083	*Zea mays*
A0A1D6KEG7/UP7305_Z_mays	Heparanase-like protein 1	1/1	53	3	50610	*Zea mays*
A0A1D6HIW8/UP7305_Z_mays	Enhancer of mRNA-decapping protein 4	1/1	32	2	38475	*Zea mays*
A0A1D6F487/UP7305_Z_mays	Ubiquitin-like-specific protease ESD4	1/1	37	1	51520	*Zea mays*
PER2_ORYSI/SwissProt	Peroxidase 2	1/1	74	5	33070	*Oryza sativa* subsp. *indica*

Table S9 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6EYZ1/UP7305_Z_mays	HOPM interactor 7	1/1	58	1	104180	*Zea mays*
TAD3_ARATH/UP7305_Z_mays	tRNA-specific adenosine deaminase TAD3	1/1	50	2	45697	*Zea mays*
LOX2_ORYSJ/SwissProt	Linoleate 9S-lipoxygenase 2	2/1	49	3	97294	*Oryza sativa* subsp. *japonica*
A0A1D6HTM2/UP7305_Z_mays	60S ribosomal protein L4-1	1/1	34	2	36321	*Zea mays*
A0A1D6EC20/UP7305_Z_mays	Glycine--tRNA ligase mitochondrial 1	1/1	67	5	30725	*Zea mays*
A0A1D6HN04/UP7305_Z_mays	T-complex protein 1 subunit alpha	1/1	55	7	45938	*Zea mays*
A0A1D6QHK0/UP7305_Z_mays	Pyruvate kinase	1/1	53	5	52618	*Zea mays*
A0A1D6MDY2/UP7305_Z_mays	V-type proton ATPase subunit C	1/1	42	6	29124	*Zea mays*
A0A1D6IYG5/UP7305_Z_mays	Obg-like ATPase 1	1/1	77	4	46058	*Zea mays*
PMM_ORYSI/SwissProt	Phosphomannomutase	1/1	55	7	28403	*Oryza sativa* subsp. *indica*
A0A1D6QTN1/UP7305_Z_mays	NAD(P)-linked oxidoreductase superfamily protein	1/1	47	7	18913	*Zea mays*

Table S9 – Cont.

Accession/ Database	Description	N° of match/ unique	Mascot Score	Protein sequence coverage (%)	Monoisotopic mass (Mr)	Species
A0A1D6LLB2/UP7305_Z_mays	GDSL esterase/lipase	1/1	41	2	37713	*Zea mays*
C0HHH9/UP7305_Z_mays	Stress-response A/B barrel domain-containing protein UP3	1/1	71	4	26448	*Zea mays*
TCPQ_ARATH/UP7305_Z_mays	T-complex protein 1 subunit theta	1/1	43	2	59472	*Zea mays*
B6TEK2/UP7305_Z_mays	GroES-like zinc-binding alcohol dehydrogenase family protein	2/2	61	6	39052	*Zea mays*
A0A1D6NZT3/UP7305_Z_mays	Uncharacterized conserved protein (UCP030210)	1/1	29	5	45907	*Zea mays*
A0A1D6JQM9/UP7305_Z_mays	40S ribosomal protein Sa-1	1/1	50	4	28786	*Zea mays*
AT9_ORYSJ/SwissProt	Acyl transferase 9	1/1	46	2	46535	*Oryza sativa* subsp. *japonica*
A0A1D6G3W9/UP7305_Z_mays	UDP-D-apiose/UDP-D-xylose synthase 2	1/1	35	2	45261	*Zea mays*

Table S10. The 77 proteins detected only in the axillary buds of the RB867515 sugarcane at first cutting stage within functional categories based on their biological process and subcellular localization.

N°/Accession/ Database	Description	Biological process	Subcelullar location
REF_HEVBR/SwissProt	Rubber elongation factor protein	Other functional categories	Cytoplasm
A0A1D6N717/UP7305_Z_mays	Alpha-1,4 glucan phosphorylase	Carbohydrate metabolic process	Uncharacterized
A0A1D6JSM9/UP7305_Z_mays	T-complex protein 1 subunit gamma	Protein folding	Cytoplasm
A0A1D6L4F0/UP7305_Z_mays	Exhydrolase II	Glucan catabolic process (carbohydrate metabolic process)	Extracellular region or secreted
C0P905/UP7305_Z_mays	Glucan endo-1,3-beta-D-glucosidase	Carbohydrate metabolic process	Plasma membrane
A0A1D6FSJ2/UP7305_Z_mays	60S ribosomal protein L24	Translation	Cytosol
A0A1D6JFG2/UP7305_Z_mays	Beta-D-xylosidase	Arabinan catabolic process; Xylan catabolic process	Cell wall; Extracellular region or secreted
ILVB1_MAIZE/SwissProt	Acetolactate synthase 1, chloroplastic	Amino acid biosynthesis; Herbicide resistance	Chloroplast
VATB2_HORVU/SwissProt	V-type proton ATPase subunit B 2	Hydrogen ion transport; Ion transport; ATP metabolic process	Other locations

Table S10 – Cont.

N°/Accession/ Database	Description	Biological process	Subcelullar location
A0A1D6NMU3/UP7305_Z_mays	Ubiquitin carboxyl-terminal hydrolase	Ubl conjugation pathway	Uncharacterized
A0A1D6HR41/UP7305_Z_mays	Pyridoxal 5'-phosphate synthase-like subunit PDX1.2	Amino acid metabolic process; Pyridoxine biosynthetic process	Uncharacterized
A0A1D6J4Q3/UP7305_Z_mays	Translation elongation factor EF1A/initiation factor IF2gamma family protein	Protein biosynthesis	Uncharacterized
A0A1D6KMC8/UP7305_Z_mays	Dihydroxy-acid dehydratase chloroplastic	Amino acid metabolic process; Branched-chain amino acid biosynthetic process	Chloroplast
A0A1D6FI07/UP7305_Z_mays	Dihydrolipoyl dehydrogenase	Cell redox homeostasis	Uncharacterized
A0A1D6FAH0/UP7305_Z_mays	T-complex protein 1 subunit epsilon	Protein folding	Cytoplasm and Cytosol
A0A1D6GPS2/UP7305_Z_mays	Pre-mRNA-processing factor 19	DNA repair; Generation of catalytic spliceosome for first transesterification step; Protein ubiquitination	Nucleus

ATPA_SACHY/SwissProt	ATP synthase subunit alpha, chloroplastic	Hydrogen ion transport; Ion transport; ATP metabolic process	Chloroplast
A0A1D6IX59/UP7305_Z_mays	Beta-glucosidase, chloroplastic	Carbohydrate metabolic process	Chloroplast
TCPZA_ARATH/SwissProt	T-complex protein 1 subunit zeta	Protein folding; Response to cadmium ion; Response to zinc ion	Cytoplasm and cytosol
FB250_ARATH/SwissProt	F-box protein At5g03100	Other functional categories	Peroxisome

Table S10 – Cont.

N°/Accession/ Database	Description	Biological process	Subcelullar location
A0A1D6F1W9/UP7305_Z_mays	Phospho-2-dehydro-3-deoxyheptonate aldolase	Amino-acid biosynthesis; Aromatic amino acid biosynthesis	Chloroplast
A0A1D6IXG3/UP7305_Z_mays	Citrulline--aspartate ligase	Amino-acid biosynthesis; Arginine biosynthesis	Other locations
A0A1D6KNM8/UP7305_Z_mays	Phosphoglycerate dehydrogenase	Amino-acid biosynthesis	Chloroplast
A0A1D6H3Y9/UP7305_Z_mays	Proteasome component4	Protein catabolic process	Other locations
A0A1D6L4P1/UP7305_Z_mays	Protein STRICTOSIDINE SYNTHASE-LIKE 3	Biosynthetic process	Vacuole
SCRK7_ARATH/SwissProt	Probable fructokinase-7	Carbohydrate metabolism; Response to cadmium ion	Cytosol
C0PNU9/UP7305_Z_mays	Protein binding protein	Protein ubiquitination; Response to abscisic acid	Cytosol; Nucleus; Other locations
B4FMW6/UP7305_Z_mays	Aspartyl protease AED3	Regulation of programmed cell death; Systemic acquired resistance	Cell wall; Extracellular region or secreted
A0A1Q0ZFB6/UP7305_Z_mays	Alba DNA/RNA-binding protein	rRNA processing	Cytosol; Nucleus; Plasma membrane
GSA_BRANA/UP7305_Z_mays	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic	Chlorophyll biosynthesis; Porphyrin biosynthesis	Chloroplast
B4G195/UP7305_Z_mays	Glutamate-oxaloacetate transaminase5	Biosynthetic process	Uncharacterized
A0A1D6FBT4/UP7305_Z_mays	Transcription factor Pur-alpha 1	Gluconeogenesis; Glucose biosynthetic process	Nucleus
Q6TM44/UP7305_Z_mays	Germin-like protein	Other functional categories	Extracellular region or secreted
A0A1D6IV93/UP7305_Z_mays	Agamous-like MADS-box protein AGL8	Transcription; transcription regulation	Nucleus
C4J4W3/UP7305_Z_mays	Hsp70-Hsp90 organizing protein 3	Stress response; Heat acclimation	Other locations; Plastid; Thylakoid

Table S10 – Cont.

N°/Accession/ Database	Description	Biological process	Subcelullar location
A0A1D6PVR8/UP7305_Z_mays	40S ribosomal protein S3-1	Translation	Chloroplast; Cytosol; Nucleus
A0A1D6NHH6/UP7305_Z_mays	GTP-binding nuclear protein	Protein transport; Protein import into nucleus; Ribosomal subunit export from nucleus	Nucleus
A0A1D6GF42/UP7305_Z_mays	40S ribosomal protein S2-1	Translation	Cytosol
B6TPA4/UP7305_Z_mays	Carnitine racemase/catalytic	Fatty acid beta-oxidation	Peroxisome
A0A1D6FVM4/UP7305_Z_mays	ULP_PROTEASE domain-containing protein	mRNA splicing, via spliceosome	Nucleus
B4F848/UP7305_Z_mays	20 kDa chaperonin chloroplastic	Chaperone cofactor-dependent protein refolding; Positive regulation of superoxide dismutase activity	Chloroplast; Mitochondrion; Other locations
A0A1D6PI62/UP7305_Z_mays	40S ribosomal protein S3a	Translation	Cytoplasm and Cytosol
A0A1D6KEX3/UP7305_Z_mays	Adenine phosphoribosyltransferase	Purine salvage; Adenine salvage; AMP salvage	Cytoplasm and Cytosol
A0A1D6KQ94/UP7305_Z_mays	Co-chaperone protein SBA1	Chaperone-mediated protein complex assembly; Protein folding	Cytosol; Nucleus
COP52_ORYSJ/SwissProt	Putative copper transporter 5.2	Copper transport, Ion transport, Transport	Other locations
B4FB66/UP7305_Z_mays	40S ribosomal protein S5-2	Ribosomal small subunit assembly; Translation	Cytosol; Ribosome
A0A1D6F4V8/UP7305_Z_mays	26S proteasome regulatory subunit 4 homolog A	Protein catabolic process	Cytoplasm and Cytosol; Nucleus
A0A1D6FL86/UP7305_Z_mays	Putative calcium-dependent protein kinase family protein	Intracellular signal transduction; Peptidyl-serine phosphorylation; Protein autophosphorylation	Nucleus; Cytoplasm
A0A1D6NUR0/UP7305_Z_mays	Carotenoid 910(9'10')-cleavage dioxygenase 1	Carotene catabolic process	Chloroplast
A0A1D6M1D4/UP7305_Z_mays	Eukaryotic peptide chain release factor subunit 1-1	Growth regulation; Protein biosynthesis	Cytoplasm and Cytosol

Table S10 – Cont.

N°/Accession/ Database	Description	Biological process	Subcelullar location
GME1_ORYSI/SwissProt	GDP-mannose 3,5-epimerase 1	Ascorbate biosynthesis	Uncharacterized
ACT_MESVI/SwissProt	Actin	Protein transport, Transport; Cell division; Other functional categories	Cytoskeleton

K7V9P7/UP7305_Z_mays	Beta-ketoacyl-[acyl-carrier-protein] synthase I	Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism	Chloroplast; Other locations
A0A1D6H7L0/UP7305_Z_mays	26S protease regulatory subunit 8 homolog B	Protein catabolic process	Cytoplasm and Cytosol
A0A1D6GVM3/UP7305_Z_mays	Delta-aminolevulinic acid dehydratase	Chlorophyll biosynthetic; Heme biosynthetic; Protoporphyrinogen IX biosynthetic	Cytosol
ACT4_SOLLC/SwissProt	Actin-105 (Fragment)	Protein transport, Transport; Cell division; Other functional categories	Cytoskeleton
A0A1D6HI32/UP7305_Z_mays	Thioredoxin reductase	Removal of superoxide radicals	Cytoplasm
FBRL2_ARATH/SwissProt	rRNA 2'-O-methyltransferase fibrillarin 2	Plant defense, rRNA processing	Nucleus
A0A1D6FR00/UP7305_Z_mays	Elongation factor 1-beta	Protein biosynthesis; Translational elongation	Cytosol; Other locations
TPIC_SPIOL/SwissProt	Triosephosphate isomerase, chloroplastic	Calvin cycle; Glycolytic process; Reductive pentose-phosphate cycle	Chloroplast
A0A1D6G511/UP7305_Z_mays	40S ribosomal protein S6-1	Translation	Ribosome
CAMT1_MAIZE/SwissProt	Caffeoyl-CoA O-methyltransferase 1	Lignin biosynthesis; Methylation	Cytosol; Plasma Membrane
P45633/UP7305_Z_mays	60S ribosomal protein L10	Translation	Cytosol; Cytosolic large ribosomal subunit
DOT2_ARATH/SwissProt	SART-1 family protein DOT2	Meristem structural organization; Root development; Shoot system development; Other functional categories	Nucleus
SKM1_ARATH/SwissProt	Leucine-rich repeat receptor-like serine/threonine-protein kinase SKM1	Response to temperature stimulus	Plasma membrane
A0A1D6HNE6/UP7305_Z_mays	DNA helicase	DNA replication	Nucleus

Table S10 – Cont.

N°/Accession/ Database	Description	Biological process	Subcelullar location
A0A1D6GZE7/UP7305_Z_mays	RuvB-like helicase	Transcription; Transcription regulation	Nucleus; Other locations
PRS6B_ARATH/SwissProt	26S proteasome regulatory subunit 6B homolog	Protein catabolic process; Positive regulation of RNA polymerase II transcription preinitiation complex assembly	Cytoplasm and Cytosol; Nucleus
A0A1D6M0K3/UP7305_Z_mays	GOLD domain-containing protein	Transport; Golgi organization	Membrane
LDHA_HORVU/SwissProt	L-lactate dehydrogenase A	Stress response; Carbohydrate metabolic process; Carboxylic acid metabolic process	Cytoplasm

A0A1D6KNS0/UP7305_Z_mays	Cinnamoyl CoA reductase1	Lignin biosynthetic process; Response to cold	Cytosol
A0A1D6EGZ7/UP7305_Z_mays	ARM repeat superfamily protein	Cell division; Mitotic chromosome condensation	Cytoplasm; Chromosome
A0A1D6DT56/UP7305_Z_mays	NADPH-protochlorophyllide oxidoreductase	Chlorophyll biosynthesis; Photosynthesis	Chloroplast
KCAB_ARATH/SwissProt	Probable voltage-gated potassium channel subunit beta	Ion transport; Potassium transport; Transport	Extracellular region or secreted; Plasma Membrane; Plasmodesma
B4FVD5/UP7305_Z_mays	V-type proton ATPase subunit E3	Ion transport; Transport	Other locations
A0A1D6MQ90/UP7305_Z_mays	26S proteasome regulatory subunit RPN11	Ubl conjugation pathway; Protein catabolic process	Cytosol; Nucleus; Proteasome complex
RS8_MAIZE/SwissProt	40S ribosomal protein S8	Translation	Chloroplast; Cytosol; Ribosome

Table S11. The 39 proteins detected only in the axillary buds of the RB867515 sugarcane at third cutting stage within functional categories based on their biological process and subcellular localization.

N°/Accession/ Database	Description	Biological process	Subcelular location
A0A1D6KZB9/UP7305_Z_mays	Tetratricopeptide repeat (TPR)-like superfamily protein	RNA modification	Intracellular membrane-bounded organelle
B4FM07/UP7305_Z_mays	Thioredoxin-dependent peroxiredoxin	Cell redox homeostasis	Uncharacterized
A0A1D6FU93/UP7305_Z_mays	Arginyl-tRNA synthetase	Arginyl-tRNA aminoacylation	Cytoplasm
A0A1D6HYS3/UP7305_Z_mays	Phosphoglucosamine mutase family protein	Carbohydrate metabolic process	Chloroplast
A0A1D6DTX6 /UP7305_Z_mays	Protein DJ-1 homolog D	Stress response	Cytosol
GLYM_PEA/SwissProt	Serine hydroxymethyltransferase, mitochondrial	One-carbon metabolism	Mitochondrion
A0A1D6PNA2/UP7305_Z_mays	U2 snRNP auxiliary factor large subunit	mRNA processing; mRNA splicing	Nucleus
SPL8_ARATH/UP7305_Z_m	Squamosa promoter-binding-like protein	Differentiation; Flowering; Transcription; Transcription	Cytoplasm and Cytosol; Nucleus

ays	8	regulation	
A0A1D6H5M9/UP7305_Z_mays	ATP-dependent DNA helicase	Proteolysis involved in cellular protein catabolic process	Proteasome core complex, alpha-subunit complex
A0A1D6KDZ6/UP7305_Z_mays	Translocon-associated protein beta (TRAPB) family protein	Uncharacterized	Other locations
A0A1D6KE00/UP7305_Z_mays	Thaumatin-like protein	Protein import into nucleus	Cytoplasm and Cytosol
HS704_ARATH/SwissProt	Heat shock 70 kDa protein 4	Stress response; Transcription; Transcription regulation; Ubl conjugation pathway	Cytoplasm and Cytosol; Nucleus
C0P5E7/UP7305_Z_mays	Leukotriene A-4 hydrolase-like protein	Uncharacterized	Cytosol
A0A1D6ICM8/UP7305_Z_mays	SKU5 similar 4	Cell tip growth	Plasma membrane; Cell wall

Table S11 – Cont.

N°/Accession/ Database	Description	Biological process	Subcelular location
A0A1D6FSA7/UP7305_Z_mays	Protein RETICULATA-RELATED 6 chloroplastic	Multicellular organism development	Chloroplast
A0A1D6JE05/UP7305_Z_mays	Coproporphyrinogen oxidase	Porphyrin biosynthesis	Chloroplast; Cytoplasm
A0A1D6NU66/UP7305_Z_mays	Telomere-associated protein RIF1	Cell cycle; Telomere maintenance	Nucleus
OBP1A_ARATH/SwissProt	Oil body-associated protein 1A	Seed oilbody biogenesis; Response to abscisic acid; Lipid storage; Embryo development ending in seed dormancy	Other locations
A0A1D6L8I1/UP7305_Z_mays	Uncharacterized protein (Putative Galactose-binding domain-containing protein - UniProtKB)	Carbohydrate metabolic process	Uncharacterized
B4FT32/UP7305_Z_mays	Diaminopimelate decarboxylase 2 chloroplastic	Lysine biosynthetic process via diaminopimelate	Chloroplast
FABI2_ORYSJ/SwissProt	Enoyl-[acyl-carrier-protein] reductase [NADH] 2, chloroplastic	Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism	Chloroplast
A0A1D6IT39/UP7305_Z_mays	Aluminum-induced protein homolog1	Uncharacterized	Uncharacterized
A0A1D6NMI8/UP7305_Z_mays	Thioredoxin family Trp26	Uncharacterized	Uncharacterized

K7TFG6/UP7305_Z_mays	Cyclin superfamily protein, putative	Cell cycle; Cell division	Nucleus; Other localizations
A0A1D6KTZ2/UP7305_Z_mays	Chaperonin2	Stress response; Protein folding; Protein refolding.	Mitochondrion
A0A1D6M7L9/UP7305_Z_mays	Assimilatory sulfite reductase	Sulfate assimilation	Chloroplast
A0A1D6FF26/UP7305_Z_mays	2-hydroxyacyl-CoA lyase	Fatty acid alpha-oxidation	Peroxisome
K7VX77/UP7305_Z_mays	Phosphotransferase	Glycolysis	Cytosol; Mitochondrion
A0A1D6PIQ7/UP7305_Z_mays	Eukaryotic translation initiation factor 3 subunit K	Protein biosynthesis	Cytoplasm and Cytosol

Table S11 – Cont.

N°/Accession/Database	Description	Biological process	Subcelullar location
API5_ORYSJ/SwissProt	Apoptosis inhibitor 5-like protein API5	Apoptosis	Nucleus
SODC_ANACO/SwissProt	Superoxide dismutase [Cu-Zn]	Removal of superoxide radicals	Cytoplasm and Cytosol
A8WER4/UP7305_Z_mays	ZCN2	Inflorescence development; Regulation of timing of transition from vegetative to reproductive phase	Uncharacterized
TPS7_PHYDL/SwissProt	Trans-alpha-bergamotene synthase	Terpenoid biosynthetic process	Uncharacterized
IAAT_MAIZE/SwissProt	Alpha-amylase/trypsin inhibitor	Plant defense	Extracellular region or secreted
A0A1D6H284/UP7305_Z_mays	4-coumarate--CoA ligase 1	Phenylpropanoid metabolic process	Cytoplasm
GCSP_PEA/SwissProt	Glycine dehydrogenase (decarboxylating), mitochondrial	Glycine catabolic process	Mitochondrion
A0A1D6EGS0/UP7305_Z_mays	Protein transport protein Sec24-like CEF	Protein transport	Cytoskeleton
A0A1D6JKV2/UP7305_Z_mays	Actin-related protein 4	Chromatin organization; Regulation of transcription by RNA polymerase II; Other functional categories	Cytoplasm and Cytosol; Nucleus
PUB25_ARATH/SwissProt	U-box domain-containing protein 25	Ubl conjugation pathway; Defense response to other organism; Response to chitin	Plasma membrane

Table S12. The 44 proteins detected only in the axillary buds of the RB867515 sugarcane at fifth cutting stage within functional categories based on their biological process and subcellular localization.

N°/Accession/ Database	Description	Biological process	Subcelullar location
A0A1D6JY65/UP7305_Z_mays	Heat shock cognate 70 kDa protein 2	Stress response	Cytoplasm
C0PDC7/UP7305_Z_mays	Chaperone protein ClpB1	Cellular response to heat	Cytoplasm
A0A1D6GCT9/UP7305_Z_mays	Protein EXPORTIN 1A	Protein transport	Nucleus
B6T3V0/UP7305_Z_mays	Ferredoxin-related	Electron transport; Transport; Response to Karrikin	Chloroplast
A0A1D6E312/UP7305_Z_mays	Argonaute1c	RNA-mediated gene silencing	Cytoplasm
A0A1D6I3K9/UP7305_Z_mays	Endo-1,3(4)-beta-glucanase	Metabolic process	Uncharacterized
CATA3_MAIZE/UP7305_Z_mays	Catalase isozyme 3	Hydrogen peroxide catabolic process; Response to oxidative stress; Cold acclimation	Mitochondrion
CATA2_HORVU/SwissProt	Catalase isozyme 2	Hydrogen peroxide catabolic process; Response to oxidative stress	Peroxisome; Glyoxysome
A0A1D6IWN4/UP7305_Z_mays	Shikimate dehydrogenase	Amino-acid biosynthesis; Aromatic amino acid biosynthesis	Chloroplast
K7V938/UP7305_Z_mays	Putative carboxylesterase 2	Uncharacterized	Uncharacterized
A0A1D6DZK5/UP7305_Z_mays	Adenosylmethionine aminotransferase1	Uncharacterized	Uncharacterized
B4FTN5/UP7305_Z_mays	Metal-dependent protein hydrolase	Uncharacterized	Nucleus; Cytoplasm
PGIP1_ORYSJ/SwissProt	Polygalacturonase inhibitor 1	Cell differentiation	Cell wall
A0A1D6HKP7/UP7305_Z_mays	Annexin	Uncharacterized	Cytoplasm

Table S12 – Cont.

N°/Accession/	Description	Biological process	Subcelullar location

Database			
ACLB1_ARATH/SwissProt	ATP-citrate synthase beta chain protein 1	Lipid biosynthesis; Lipid metabolism	Cytoplasm and Cytosol
A0A1D6L8E8/UP7305_Z_mays	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex	Acetyl-CoA biosynthetic process from pyruvate	Mitochondrion; Other locations
A0A1D6NY34/UP7305_Z_mays	Putative threonine aldolase family protein	Glycine biosynthetic process; Threonine catabolic process	Cytosol
A0A1D6NB04/UP7305_Z_mays	Aspartate aminotransferase	Cellular amino acid metabolic process	Peroxisome; Plastid
NSF_ORYSJ/SwissProt	Vesicle-fusing ATPase	ER-Golgi transport, Protein transport, Transport	Cytoplasm and Cytosol
B6TN41/UP7305_Z_mays	4-hydroxy-4-methyl-2-oxoglutarate aldolase	Regulation of RNA metabolic process	Plastid
Q19VG6/UP7305_Z_mays	Major latex protein 22	Defense response; Abscisic acid-activated signaling pathway	Nucleus
A0A1D6I867/UP7305_Z_mays	Clathrin heavy chain 2	Protein transport	Chloroplast; Cytosol; Golgi apparatus; Plasma Membrane; Other locations
A0A1D6PBS4/UP7305_Z_mays	pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH3	mRNA processing, mRNA splicing	Nucleus
A0A096UGL9/UP7305_Z_mays	Exportin-2	Intracellular protein transport	Cytosol; Nucleus
A0A1D6L977/UP7305_Z_mays	Methylenetetrahydrofolate reductase	Methionine metabolic process. Tetrahydrofolate interconversion	Cytosol
A0A1D6IIX9/UP7305_Z_mays	Pentatricopeptide repeat-containing protein mitochondrial	mRNA processing	Mitochondrion
A0A1D6L6N3/UP7305_Z_mays	Inosine-5'-monophosphate dehydrogenase	Purine nucleotide biosynthetic process	Cytoplasm and Cytosol
B6T484/UP7305_Z_mays	Mitogen-activated protein kinase	Intracellular signal transduction	Nucleus; Cytosol
A0A1D6JQK4/UP7305_Z_mays	Topless-related protein 2	Regulation of transcription, DNA-templated	Uncharacterized
B4FIV0/UP7305_Z_mays	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial	Tricarboxylic acid cycle	Mitochondrion

Table S12 – Cont.

N°/Accession/ Database	Description	Biological process	Subcelullar location
B4FIV0/UP7305_Z_mays	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial	Tricarboxylic acid cycle	Mitochondrion
A0A1D6GLS4/UP7305_Z_m	Serpin-Z1	Negative regulation of endopeptidase activity	Extracellular region or secreted

ays			
A0A1D6JG12/UP7305_Z_mays	Cysteine protease 1	Proteolysis involved in cellular protein catabolic process	Extracellular region or secreted; Lysosome
A0A1D6Q3E1/UP7305_Z_mays	2-hydroxy-3-oxopropionate reductase	Uncharacterized	Uncharacterized
A0A1D6GAY3/UP7305_Z_mays	Glutathione transferase	Glutathione metabolic process; Response to herbicide; Response to reactive oxygen species; Response to salicylic acid	Cytoplasm
A0A1X7YIJ7/UP7305_Z_mays	Chitinase	Carbohydrate metabolism; Polysaccharide degradation	Extracellular region or secreted
A0A1D6P3B9/UP7305_Z_mays	110 kDa U5 small nuclear ribonucleoprotein component CLO	mRNA processing, mRNA splicing	Nucleus
A0A1D6GY62/UP7305_Z_mays	Uncharacterized protein	Uncharacterized	Uncharacterized
BGL31_ORYSJ/SwissProt	Beta-glucosidase 31	Carbohydrate metabolic process	Chloroplast
A0A1D6L056/UP7305_Z_mays	BGGP Beta-1-3-galactosyl-O-glycosyl-glycoprotein	Uncharacterized	Membrane
A0A1D6KEG7/UP7305_Z_mays	Heparanase-like protein 1	Unidimensional cell growth	Membrane
A0A1D6HIW8/UP7305_Z_mays	Enhancer of mRNA-decapping protein 4	Deadenylation-independent decapping of nuclear-transcribed mRNA	Other locations
A0A1D6F487/UP7305_Z_mays	Ubiquitin-like-specific protease ESD4	Ubl conjugation pathway	Nucleus
PER2_ORYSI/SwissProt	Peroxidase 2	Hydrogen peroxide catabolic process; Response to oxidative stress	Extracellular region or secreted

Table S13. The 34 proteins detected only in the axillary buds of the RB867515 sugarcane at fifth and third cutting stages within functional categories based on their biological process and subcellular localization.

N°/Accession/ Database	Description	Biological process	Subcelullar location
LOX1_HORVU/UP7305_Z_mays	Linoleate 9S-lipoxygenase 1	Fatty acid biosynthesis, Fatty acid metabolism, Lipid biosynthesis, Lipid metabolism, Oxylipin biosynthesis	Cytoplasm and Cytosol
A0A1D6NDJ3/UP7305_Z_mays	Malic enzyme	Malate metabolic process	Chloroplast
C0P790/UP7305_Z_mays	Eukaryotic translation initiation factor 3 subunit B	Protein biosynthesis	Cytoplasm and Cytosol

A0A1D6PRL0/UP7305_Z_mays	Apyrase 1	Nucleoside diphosphate catabolic process	Membrane
A0A1D6GN16/UP7305_Z_mays	Putative serine protease EDA2	Proteolysis	Vacuole
A0A1D6QRC6/UP7305_Z_mays	Fumarylacetoacetase	Phenylalanine catabolism; L-phenylalanine catabolic process; Tyrosine catabolic process	Cytosol
A0A1D6LVE5/UP7305_Z_mays	Gibberellin receptor GID1L2	Gibberellin signaling pathway	Nucleus
A0A1D6IYD6/UP7305_Z_mays	Glyoxalase I	Methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione	Cytoplasm
A0A1D6P2Q0/UP7305_Z_mays	Transducin/WD40 repeat-like superfamily protein	Spliceosomal snRNP assembly	Other locations
E1AFV5/UP7305_Z_mays	Beta-1,3-glucanase	Carbohydrate metabolic process	Plasma Membrane
A0A1D6FQM0/UP7305_Z_mays	Alpha/beta-Hydrolases superfamily protein	Cutin biosynthetic process	Cytosol
A0A1D6FNG1/UP7305_Z_mays	Superoxide dismutase	Response to abscisic acid; Superoxide dismutase activity	Mitochondrion
CFIS2_ARATH/SwissProt	Pre-mRNA cleavage factor Im 25 kDa subunit 2	mRNA processing	Nucleus
A0A1D6E5L0/UP7305_Z_mays	Ras-related protein18A1	Intracellular protein transport	Golgi apparatus; Endomembrane system
EXPA1_ARATH/SwissProt	Expansin-A1	Cell wall biogenesis/degradation	Cell wall; Membrane

Table S13- Cont.

N°/Accession/ Database	Description	Biological process	Subcelullar location
K7VFF7/UP7305_Z_mays	Glutaredoxin-dependent peroxiredoxin	cellular response to oxidative stress; Hydrogen peroxide catabolic process;	Cytoplasm
B4G227/UP7305_Z_mays	Peptide-N4-(N-acetyl-beta-glucosaminyl) asparagine amidase A protein	Glycoprotein catabolic process; Response to microbial phytotoxin; Response to salicylic acid	Cytoplasm and Cytosol; Vacuole
A0A1D6QSC9/UP7305_Z_mays	Glycine cleavage system H protein	Glycine decarboxylation via glycine cleavage system; Protein lipoylation	Mitochondrion
A0A1D6M9Z1/UP7305_Z_mays	Ras-related protein RABG3f	Uncharacterized	Uncharacterized
B4FMB1/UP7305_Z_mays	DUF538 family protein	Uncharacterized	Uncharacterized

B4F8S9/UP7305_Z_mays	Uncharacterized protein (Fasciclin-like arabinogalactan protein 15 – UniProtKB)	Plant-type secondary cell wall biogenesis	Extracellular region or secreted
B6UAK0/UP7305_Z_mays	Probable 6-phosphogluconolactonase	Carbohydrate metabolic process	Cytoplasm
GAPN_MAIZE/UP7305_Z_mays	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	Stress response	Cytoplasm and Cytosol
A0A1D6HW85/UP7305_Z_mays	Nitrile-specifier protein 1	Nitrile biosynthetic process	Cytosol; Nucleus
A0A1D6PA07/UP7305_Z_mays	Beta-adaptin-like protein C	Protein transport	Other locations: clathrin adaptor complex
A0A1D6GPP6/UP7305_Z_mays	Heterogeneous nuclear ribonucleoprotein 1	mRNA processing, mRNA splicing, mRNA transport, Transport	Cytoplasm and Cytosol; Nucleus
B4FB55/UP7305_Z_mays	Ras-related protein ARA-3	Protein secretion	Plasma Membrane
A0A1D6EW83/UP7305_Z_mays	Ras-related protein RABH1b	ER-Golgi transport, Protein transport, Transport	Golgi apparatus; Cytoplasm and Cytosol
A0A1D6HBU2/UP7305_Z_mays	Glycerophosphodiester phosphodiesterase	Glycerol metabolism; Cell wall biogenesis/degradation	Plasma membrane

Table S13- Cont.

N°/Accession/ Database	Description	Biological process	Subcelullar location
A0A1D6E267/UP7305_Z_mays	Fasciclin-like arabinogalactan protein 10	Plant-type secondary cell wall biogenesis	Plasma Membrane
C0P6C5/UP7305_Z_mays	Threonine synthase	Amino-acid biosynthesis, Threonine biosynthesis	Cytoplasm
A0A1D6L117/UP7305_Z_mays	Tryptophanyl-tRNA synthetase	Protein biosynthesis	Cytoplasm
MDHM2_ARATH/SwissProt	Malate dehydrogenase 2, mitochondrial	Carbohydrate metabolic process; Tricarboxylic acid cycle; Defense response to bacterium	Mitochondrion
LGUL_ORYSJ/SwissProt	Lactoylglutathione lyase	Response to salt stress; Response to oxidative stress; Response to osmotic stress	Cytoplasm