

Table 1 Effects of N topdressing on rice grain biochemical compositions

Year	Treatment	L/W	AC (%)	Albumin (%)	Globulin (%)	Prolamin (%)	Glutelin (%)	PC (%)	1000-grain weight (g)
2016	N0	2.66a	22.60a	0.53a	0.43a	0.57b	7.24b	8.77b	28.20a
	N+	2.63a	22.05b	0.52a	0.45a	0.63a	8.67a	10.27a	27.81b
2017	N0	2.70a	21.92a	0.56a	0.42a	0.63a	7.34b	8.95b	27.77a
	N+	2.67a	21.36b	0.54a	0.44a	0.60a	8.75a	10.33a	27.35b

L/W, the ratio of grain length to grain width; AC, amylose content; PC, protein content. Means within a column followed by the same letter do not differ significantly at $P < 0.05$

Table 2 Functional classification of up-regulated proteins in N+/N0

ProteinID	UniProt Entry	Protein name	Mass (kDa)	Cov.(%)	Unique peptide	Fold-Change (N+/N0)
Protein metabolism						
Storage protein						
40718	A2WVB9	glutelin	56.30	39	92	1.53
40720	A2X399	glutelin precursor	56.8	40	72	1.58
40716	B8AEZ5	glutelin	54.06	8	14	1.61
40717	A2X301	glutelin	43.55	5	3	1.63
40983	B8A9T8	glutelin	21.93	11	3	1.88
Stress and defense						
40963	A2YJG5	allergenic	17.28	59	33	1.72
40907	B8B8F2	allergenic	17.27	69	31	1.67
40962	A2YJG2	allergenic	16.98	65	25	1.62
40843	A2YRY3	germin 8-5-like	23.71	64	17	1.94

Values are means of three replications. The screening criteria for differentially expressed proteins was a fold change >1.5 or <0.67 and a p-value <0.05

Table 3 Functional classification of down-regulated proteins in N+/N0

Protein ID	UniProt Entry	Protein name	Mass (kDa)	Cov. (%)	Unique peptide	Fold-Change (N+/N0)
Protein metabolism						
Storage protein						
40724	A2XKC1	cupin family expressed	58.85	67	81	-1.70
40733	B8AL97	globulin-1 S allele-like	52.06	63	42	-2.28
Protein synthesis, folding and degradation						
41453	A2YVI4	extracellular ribonuclease LE-like	24.83	20	4	-2.34
41882	B8BEF4	mitochondrial amidoxime reducing component 2-like	36.40	8	2	-1.56
41197	B8AI71	40S ribosomal S14	16.36	55	10	-1.54
41106	A2YJM2	40S ribosomal S12	14.75	25	2	-1.83
41111	B8B7B6	40S ribosomal S12	14.81	25	2	-1.55
41262	A2Y8Y0	40S ribosomal S20-1-like	14.05	15	2	-1.72
41480	A2XIT7	40S ribosomal S3-3	25.44	21	4	-1.71
40966	B8AS12	60S ribosomal L14-1	15.42	49	8	-1.69
41243	A2YSN9	60S ribosomal L7-2	28.45	15	4	-1.68
41254	A2Y5F8	60S ribosomal L36-3-like	12.74	32	4	-1.50
41289	A2XCC4	60S ribosomal L21	18.70	9	2	-1.77
41247	B8AK76	translation initiation factor 5A (eIF-5A)	56.74	4	2	-1.65
41116	A2XP46	mitochondrial translation elongation factor Tu	48.42	13	5	-1.55
41133	A2YPM1	elongation factor 1-beta	23.80	34	5	-1.50
41141	B8AYR2	60S acidic ribosomal P2B	20.12	43	5	-1.99
41393	A2WMF3	60S acidic ribosomal P3	11.88	42	4	-1.83
41523	A2WLK9	60S acidic ribosomal P2A	11.61	18	2	-1.77
41385	A2YQN3	60S acidic ribosomal P1	11.08	51	3	-2.99
40743	A2ZCE6	disulfide isomerase	56.84	77	46	-2.24
40814	B8AGU2	disulfide isomerase-like 1-4	62.25	26	14	-1.78
40730	B8BP25	stromal 70 kDa heat shock-related chloroplastic-like	76.22	33	21	-2.28
40739	A2Y2Y4	stromal 70 kDa heat shock-related chloroplastic	69.28	14	9	-1.82
40809	A2XF47	heat shock cognate 70 kDa -like	45.25	15	5	-1.76
40812	B8B3P0	20 kDa chloroplastic-like	29.00	44	10	-1.74
40845	A2Z1N0	20 kDa chloroplastic	25.51	42	8	-1.64
40736	A2X036	luminal-binding 2 precursor	73.39	47	30	-2.04
40828	B8AGV6	Rularge subunit-binding subunit chloroplastic-like	63.80	23	12	-1.59
42052	B8AA60	signal recognition particle 54 kDa 2	54.77	4	2	-1.55
40961	B8AY77	importin subunit alpha-1b-like	54.71	15	6	-1.59
41173	A2WRD4	ras-related RIC1	22.48	8	2	-1.62
41611	A2XDW4	transport Sec61 subunit alpha-like	52.26	6	3	-1.81
41471	B8B4J5	E3 ubiquitin- ligase RGLG2-like	49.83	7	3	-1.76
41347	P0C8Y9	proteasome subunit alpha type	27.03	16	4	-1.68
42062	A2XKY8	proteasome subunit beta type-2	23.48	13	2	-1.70
41354	A2YXU2	proteasome subunit alpha type-7-A-like	27.30	14	3	-1.64
41454	A2X7K2	ATP-dependent Clp protease proteolytic subunit	34.07	15	5	-1.58
41305	A2WLL2	mitochondrial-processing peptidase subunit alpha-like	53.93	7	4	-1.56
41569	A2WXA2	urate oxidase	34.50	9	3	-1.53
Amino acid metabolism						
40958	B8AK88	aspartate-semialdehyde dehydrogenase	40.18	35	8	-1.61
41154	B8AEH4	Aspartate aminotransferase	50.35	15	6	-1.70

Table 3 Functional classification of down-regulated proteins in N+/N0 (*Continued*)

40731	A2WVA6	Aspartate aminotransferase	44.51	62	27	-1.61
40728	B8BGM4	alanine aminotransferase 2	52.59	56	30	-1.64
41364	B8AU84	arginase mitochondrial	36.97	12	4	-2.05
41045	B8AH93	ornithine chloroplastic	39.99	29	8	-1.86
40783	A2ZJA1	argininosuccinate chloroplastic	52.22	41	20	-1.73
41131	B8AQE3	glutamine synthetase	40.74	16	5	-1.65
41491	B8AI28	glutamine synthetase	40.21	5	2	-1.80
40936	A2XYC2	D-3-phosphoglycerate dehydrogenase chloroplastic-like	63.97	13	7	-1.58
41639	A2YY43	dihydroxy-acid chloroplastic	63.65	4	2	-2.76
41121	B8ADR9	fumarylacetoacetase	47.12	18	7	-1.81
41546	A2XNL0	fumarylacetoacetate hydrolase domain-containing 1	24.21	14	3	-1.80
40860	B8AWH3	threonine chloroplastic-like	44.92	13	3	-1.59
41210	A2XK82	3-isopropylmalate dehydrogenase chloroplastic-like	41.75	17	5	-1.76
41716	B8ADM7	3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase	46.17	5	2	-1.51
41407	A2WSL8	3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase-like	40.85	11	4	-1.53
Carbon metabolism						
Glycolysis						
40746	B8AF09	glyceraldehyde-3-phosphate dehydrogenase	38.55	33	10	-2.58
40763	A2XUU7	glyceraldehyde-3-phosphate dehydrogenase	42.05	20	6	-2.06
40769	A2YQT7	glyceraldehyde-3-phosphate dehydrogenase	36.41	35	12	-1.69
40747	B8BFV2	enolase	48.04	26	8	-1.84
41092	A2Z0L8	enolase chloroplastic	50.75	16	5	-1.70
40745	B8AIH2	phosphoglycerate cytosolic	42.11	37	11	-1.63
40749	A2YG06	Phosphoglycerate cytosolic	42.28	34	12	-1.67
40832	B8AD93	triosephosphate cytosolic	27.06	52	15	-2.49
40942	A2WWV4	triosephosphate cytosolic-like	27.20	34	7	-1.71
40760	B8ABA7	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	60.76	23	9	-1.83
40779	B8AQE1	cytoplasmic 2	62.27	38	18	-1.60
40819	A2YQL4	fructokinase-2	35.52	45	12	-1.61
40915	A2YB91	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit beta	61.26	17	9	-1.50
41410	B8B1A6	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit alpha-like	67.57	5	2	-1.55
41429	A2XYZ3	pyruvate kinase	55.23	5	2	-1.51
TCA cycle						
40778	B8BHG9	malate dehydrogenase	34.55	45	12	-1.65
41098	A2WWL6	malate chloroplastic	41.76	11	3	-1.81
40974	A2WUY6	NADP-dependent malic enzyme	63.22	10	6	-1.53
41775	B8AR20	A Chain Dihydrolipoamide Dehydrogenase Of Glycine Decarboxylase From Pisum Sativum	434.52	1	2	-1.58
40852	B8AYE1	dihydrolipoyl mitochondrial-like	52.78	9	3	-1.54
40947	B8BBF4	aconitate cytoplasmic	42.48	22	7	-1.63
41282	A2X7X9	3-isopropylmalate dehydratase small subunit 3-like	21.57	30	5	-1.51

Table 3 Functional classification of down-regulated proteins in N+/N0 (*Continued*)

41642	A2XTC1	succinate dehydrogenase subunit mitochondrial	27.48	11	3	-1.67
41434	B8B7R8	probable succinyl- ligase [ADP-forming] subunit mitochondrial	45.29	9	4	-1.73
40732	B8AYC1	cytosolic orthophosphate dikinase	93.64	42	32	-1.68
40793	A2XIA2	cytosolic orthophosphate dikinase	96.58	18	11	-1.53
Pentose phosphate pathway and fermentation						
40824	A2Y087	glucose and ribitol dehydrogenase homolog 1	32.28	49	16	-2.36
40787	A2YBK1	aldehyde dehydrogenase family 2 member mitochondrial-like	59.32	43	21	-1.62
40930	Q75ZX4	alcohol dehydrogenase family-1	40.98	16	5	-1.68
41177	A2XFI3	pyruvate decarboxylase 2	64.85	9	5	-1.62
Starch synthesis and amylolysis						
40757	A3QQQ3	UDP-glucose pyrophosphorylase	51.65	42	17	-2.58
40744	P93430	ADP-glucose pyrophosphorylase large subunit	57.58	55	25	-1.87
40750	A2YU91	ADP-glucose pyrophosphorylase small subunit	56.10	34	15	-1.85
40817	B8BE16	ADP-glucose pyrophosphorylase small subunit	55.00	6	2	-1.53
40866	B8AR31	glucose-1-phosphate adenylyltransferase large subunit	55.15	22	9	-1.72
40726	A2Y8X2	granule-bound starch synthase I	66.48	66	53	-2.79
41194	A2Y9M4	soluble starch synthase I	70.95	10	5	-1.85
40738	B8AV01	pullulanase	113.62	43	40	-1.65
41458	B8BBE6	glucose-6-phosphate translocator	43.06	7	3	-1.86
41696	B8AD38	Plastidic glucose transporter 4	51.51	3	2	-1.60
40762	A2X256	adenine nucleotide transporter chloroplastic amyloplastic mitochondrial-like	44.25	47	17	-1.55
40970	A2WYY5	lichenase-2 precursor	34.19	33	9	-1.97
40752	B8B1F4	alpha-glucosidase	97.84	16	15	-1.50
Photosynthesis and electron transport						
40946	A2Z8U8	chloroplastic	99.38	12	9	-1.62
41763	B8BGJ5	chloroplastic-like isoform X1	18.78	10	2	-1.73
42500	B8AB91	Reticulata-Related chloroplastic-like	34.92	9	2	-1.50
41732	A2Z1Z6	alpha carbonic anhydrase 7-like	32.03	7	2	-1.54
41501	P0C511	ribulose-1,5-bisphosphate carboxylase oxygenase large subunit (chloroplast)	52.88	6	3	-1.63
41085	A2Z2Q9	probable sarcosine oxidase	44.32	14	5	-1.65
41594	A2ZBG3	plant T22K18-16	15.86	19	2	-1.52
41622	A2WLZ0	heme-binding 2	23.60	29	3	-1.61
42137	B8AZT0	NADH dehydrogenase [ubiquinone] flavo mitochondrial-like	30.04	8	2	-2.08
Lipid metabolism						
41353	A2YAA3	3-oxoacyl-[acyl-carrier-] synthase chloroplastic-like	33.86	15	4	-1.69
41440	A2YSI3	beta-hydroxyacyl-ACP dehydratase	38.50	8	3	-1.65
40829	B8B9S9	enoyl-[acyl-carrier-] reductase [NADH] chloroplastic	48.91	18	7	-1.86
41014	B8BDP7	Enoyl-[acyl-carrier-] reductase [NADH] chloroplastic	39.04	4	2	-1.83
41724	A2YIF2	probable carboxylesterase 15	36.01	6	2	-1.79

Table 3 Functional classification of down-regulated proteins in N+/N0 (*Continued*)

41667	A2Y6S0	enoyl-CoA delta isomerase	25.45	9	2	-1.59
		peroxisomal-like				
Cell growth /division						
41791	B8B5T6	xylose isomerase	53.36	5	2	-1.76
41967	A2WZI6	UDP-D-apiose UDP-D-xylose synthase 2	45.20	7	2	-1.63
41760	A2ZK00	beta-galactosidase 15 isoform X1	78.10	4	2	-1.50
41436	A2Y2C4	xylanase inhibitor 2-like	32.54	7	2	-2.16
40863	B8B8B1	UDP-arabinopyranose mutase 3	41.25	10	4	-1.57
40856	B8AM48	UDP-arabinopyranose mutase 1	35.34	8	2	-1.60
40876	A2Y534	Actin-7	41.61	9	3	-1.77
40883	A2XMI9	tubulin beta chain	49.82	6	2	-1.94
41135	B8BLP4	translationally-controlled tumor homolog	55.62	14	7	-2.06
41691	B8AEU3	tubulin-folding cofactor A-like	24.75	8	2	-1.86
41102	A2XAI5	formin 7	61.82	13	6	-1.62
41365	B8BD95	nitrile-specifier 5	34.48	17	4	-1.52
42158	B8AWT3	embryo-specific Ose731	9.82	32	2	-1.56
41284	B8BH45	cell division cycle 48 homolog	84.17	9	5	-1.64
40951	A2YAT3	annexin D1-like	35.70	22	6	-1.55
41428	B8B2R4	nucleosome assembly 1 1	42.60	13	4	-1.72
40782	A2YYH2	polyadenylate-binding 2-like	71.63	33	18	-1.54
Stress and defense						
40773	A2YS08	Lactoylglutathione lyase	32.55	54	17	-2.42
41543	B8ANY4	hydroxyacylglutathione hydrolase	28.56	15	3	-1.90
		cytoplasmic				
40790	B8B7Y3	methylmalonate-semialdehyde dehydrogenase [acylating] mitochondrial	57.18	34	14	-1.86
41244	B8AEF1	quinone oxidoreductase PIG3	34.30	24	5	-1.70
40910	A2YF78	peroxiredoxin-2E-chloroplasmic-like	23.69	59	10	-1.73
41400	B8AJ36	2-Cys peroxiredoxin chloroplasmic	28.27	21	5	-1.53
41581	A2YWB1	probable 2-oxoglutarate Fe(II)-dependent dioxygenase	37.00	10	3	-1.61
40830	Q6WSC2	tau class GST 3	25.33	42	10	-1.54
41149	A2WVD3	glutathione s-transferase	23.98	21	4	-2.17
41237	A2YL42	glutathione transferase	26.35	20	6	-1.58
41511	B8B5S6	gamma-glutamylcysteine synthetase	74.92	5	3	-2.15
40975	A2WYB3	selenium-binding 1-like	53.14	21	8	-1.78
41338	A2WQY7	carboxymethylenebutenolidase homolog	30.50	12	4	-2.23
40816	A2XT28	desiccation-related PCC13-62-like	33.70	50	17	-2.09
40846	A2YCK6	late embryogenesis abundant D-34-like	27.88	70	13	-2.06
41360	A2XLZ1	late embryogenesis abundant D-34-like	21.21	30	4	-1.58
41026	A2XF50	dessication-induced 1VOC superfamily	15.02	17	2	-1.68
41031	B8BPJ0	11-beta-hydroxysteroid dehydrogenase 1B-like	39.91	24	9	-1.68
41053	A2XSU3	11-beta-hydroxysteroid dehydrogenase 1B-like	39.65	22	6	-1.51
41317	B8AJW5	universal stress A	18.25	39	4	-1.74
41521	A2Z7R2	universal stress A	18.84	12	2	-2.00
40939	A2XNF0	chalcone-flavanone isomerase	23.89	45	8	-1.60
41557	B8BC40	tricin synthase 1-like	32.03	9	2	-2.01
41705	B3VMC0	betaine aldehyde dehydrogenase	54.68	4	2	-1.57

Table 3 Functional classification of down-regulated proteins in N+/N0 (*Continued*)

41080	B8AI32	dihydropyrimidine dehydrogenase [NADP(+)]	45.31	23	8	-1.68
41608	A2XCT8	1,2-dihydroxy-3-keto-5-methylthiopentane dioxygenase 2	23.50	14	3	-1.60
41832	B8AN79	salt tolerance	34.80	7	2	-1.72
40766	B8BCI1	formate-tetrahydrofolate ligase	68.11	41	21	-1.57
41800	A2YCT4	caleosin related	23.85	12	2	-1.85
40723	B8B9C5	sorbitol dehydrogenase	39.23	74	29	-2.84
40777	B8AZC3	aldose reductase	35.59	53	19	-1.65
Energy production						
41082	A2YFL3	ATP synthase subunit mitochondrial-like	25.07	32	7	-1.55
40993	A2X0J1	probable ATP synthase 24 kDa mitochondrial	27.34	35	9	-1.61
40759	B8A7M8	ATP synthase subunit mitochondrial-like	65.92	6	2	inf
40842	B8BBN7	obg-like ATPase 1	44.35	29	10	-1.66
40935	A2X7E9	adenosine kinase 2	34.24	34	9	-1.67
Material transport						
40857	A2Z0D1	mitochondrial outer membrane porin 1-like	29.17	45	10	-1.89
41145	B8A6Q5	outer envelope pore 16- chloroplastic	17.86	36	6	-1.85
41064	A2XFS7	outer envelope pore 16- chloroplastic	19.19	41	7	-1.68
40873	B8AQH5	mitochondrial outer membrane porin 5-like	29.48	42	11	-1.56
41630	A2Y7T3	oleosin 1-like	18.10	16	2	-1.54
41330	A2WRY9	Outer plastidial membrane porin	29.89	15	3	-1.50
41487	A2YKV4	aquaporin	30.29	12	3	-1.77
41252	A2Z4X9	Ankyrin repeat domain-containing 2	35.55	18	5	-1.98
Signal transduction						
41012	A2WN93	calmodulin-7	16.83	16	4	-1.76
41551	A2XHW8	EF hand family	16.53	23	3	-1.56
41836	A2WQ18	cullin 1	83.11	2	2	-1.56
40811	A2WTW6	guanine nucleotide-binding subunit beta A	36.23	36	9	-2.74
41473	B8ABU1	GTP-binding SAR1A-like	21.94	24	4	-1.75
Phosphorus metabolism						
41128	A2XAM4	probable phosphatase 2C 27	39.29	20	7	-1.59
41164	A2YE26	acid phosphatase 1-like	28.37	31	8	-1.88
41478	A2Y925	acid phosphatase 1-like	32.30	13	3	-1.53
41350	A2ZI40	probable purple acid phosphatase 20	48.18	15	5	-1.89
Unknown						
41009	A2WSI6	hypothetical protein OsI_02826	38.64	17	5	-1.60
41095	B8BHC3	hypothetical protein OsI_33929	39.96	21	6	-1.67
41052	A2ZI12	stem-specific TSJT1	25.20	21	4	-1.67
41285	B8AD25	Predicted: uncharacterized protein LOC102722617	63.32	6	4	-1.67

Values are means of three replications. The screening criteria for differentially expressed proteins was a fold change >1.5 or <0.67 and a p-value <0.05