Supplemental materials

Insights into the Response of Soybean Mitochondrial Proteins to Various Sizes of Aluminum Oxide Nanoparticles under Flooding Stress

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Table S1. Primer sequences of genes selected for qRT-PCR
Table S2. List of commonly identified proteins in soybean root including hypocotyl exposed to 5, 30-60, and 135 nm of Al_2O_3 NPs under flooding stress.
Table S3. List of commonly identified mitochondrial proteins in soybean root tip exposed to 5, 30-60, and 135 nm of Al_2O_3 NPs under flooding stress.
Figure S1. Purity of mitochondrial fractions from the soybean root tip.
Figure S2. Agarose gel electrophoresis of qRT-PCR products.

Table S1. Primer sequences of genes selected for qRT-PCR.

Protein ID[a)]	Description	Sequence of primers
Glyma09g37570.1	Voltage dependent anion channel 1	F: 5'-ATGCTGGACTGAGCTTCACC-3'
		R: 5'-ATCAGAGCACTTGTCCTGCC-3'
Glyma13g31520.1	Alpha helical ferredoxin	F: 5'-ATGGCCTTCGGTTAAGTGCA-3'
		R: 5'-CTCCCCTGTTGGATATCGCC-3'
Glyma02g38160.3	Serine hydroxymethyltransferase 2	F: 5'-TCTTCGCAGACTCTCCTCCA-3'
		R: 5'-TCGAACCCCTTCCATTGACG-3'
Glyma13g18950.1	NAD(P) binding Rossmann fold superfamily protein	F: 5'-GACGTCGCTCAAGTCCATCT-3'
		R: 5'-ACGAACGAGGTGACCAACTC-3'
Glyma15g37200.1	LYR family of Fe/S cluster biogenesis protein	F: 5'-TCTGTCTCCTCCCAGATCCG-3'
		R: 5'-CCACGACGTTCTTCAGCTCT-3'
Glyma10g03440.1	Methylcrotonyl CoA carboxylase alpha chain mitochondrial	F: 5'-TAATGGGAGCTGCAGGTGTG-3'
		R: 5'-CCGTTGTGCTGCTAAGAACG-3'
Glyma04g06610.1	Casein lytic proteinase B4	F: 5'-GGCAACCAGAAGAACTCCGA-3'
		R: 5'-ATCTGTGAAGTCCGTCTGCG-3'
Glyma14g00500.1	Isocitrate dehydrogenase 1	F: 5'-ATGGTGGAGCAGAAGAAGGC-3'
		R: 5'-CGAGATTGGCAATGACAGCG-3'
18S rRNA	X02623.1[b)]	F: 5'-TGATTAACAGGGACAGTCGG-3'
		R: 5'-ACGGTATCTGATCGTCTTCG-3'

[a)] Protein ID according to the Phytozome database; [b)] according to Genebank.

Table S2. List of commonly identified proteins in soybean root including hypocotyl exposed to 5, 30-60, and 135 nm of Al_2O_3 NPs under flooding stress.

					Ratio[d]												
					Flooding				Flooding+Al_2O_3 5nm			Flooding+$Al_2O_3$30-60nm			Flooding+Al_2O_3 135nm		
No.	Protein ID[a]	Description	M.P.[b]	*p*-value[c]	2(0)	3(1)	4(2)	5(3)	3(1)	4(2)	5(3)	3(1)	4(2)	5(3)	3(1)	4(2)	5(3)
1.	Glyma05g25360.1	polygalacturonase inhibiting protein 1	8	0.00	1	90.53	169.37	265.10	10.68	80.71	194.55	608.75	962.35	1170.09	95.46	262.05	7.72
2.	Glyma05g25370.1	polygalacturonase inhibiting protein 1	7	0.00	1	21.31	30.20	52.49	19.82	107.09	159.16	407.52	734.56	818.17	68.20	114.99	116.41
3.	Glyma09g38010.2	Aldolase type TIM barrel	3	0.00	1	5.53	19.18	18.52	2.60	16.66	35.05	0.09	0.21	0.79	1.49	0.63	0.72
4.	Glyma18g48370.1	Aldolase type TIM barrel	3	0.00	1	5.53	19.18	18.52	2.60	16.66	35.05	0.09	0.21	0.79	1.49	0.63	0.72
5.	Glyma14g27940.1	alcohol dehydrogenase 1	10	0.00	1	9.26	18.39	19.57	8.18	32.55	55.11	14.18	56.27	28.34	3.54	2.01	2.51
6.	Glyma13g33590.1	glyoxalase II 3	8	0.00	1	12.06	13.27	7.90	5.17	23.39	28.32	16.87	14.04	21.12	7.26	8.80	6.52
7.	Glyma07g18570.1	Thiamine pyrophosphate dependent pyruvate decarboxylase	7	0.00	1	6.36	10.96	13.38	6.89	8.67	22.13	71.97	73.38	50.37	9.77	1.29	2.03
8.	Glyma18g43460.1	pyruvate decarboxylase 2	6	0.00	1	4.92	9.02	10.45	4.51	7.32	20.41	55.20	62.21	39.52	7.28	0.99	1.79
9.	Glyma09g28100.1	Enolase	10	0.00	1	5.87	8.13	9.08	5.99	13.47	16.13	1.03	2.32	1.89	3.81	3.08	1.32
10.	Glyma16g32960.1	Enolase	11	0.00	1	5.11	7.54	8.43	4.67	13.89	16.31	4.50	7.35	2.49	4.15	3.45	1.80
11.	Glyma01g18780.1	basic transcription factor 3	2	0.00	1	2.31	6.16	5.62	0.92	8.82	22.12	4.40	5.25	13.28	2.35	7.60	4.69
12.	Glyma02g02560.1	ND	3	0.00	1	5.77	5.32	6.07	2.40	9.79	15.39	6.41	3.32	8.28	2.33	2.07	1.39
13.	Glyma03g40490.2	O acetylserine (thiol) lyase (OAS TL) isoform A1	6	0.00	1	3.25	4.92	4.14	2.62	2.54	4.44	1.69	2.99	3.97	2.35	2.45	0.82
14.	Glyma04g41990.1	alcohol dehydrogenase 1	13	0.00	1	3.95	4.91	6.22	3.29	8.75	12.26	12.05	17.29	12.34	4.61	5.20	1.71
15.	Glyma06g12780.1	alcohol dehydrogenase 1	13	0.00	1	3.95	4.91	6.22	3.29	8.75	12.26	12.05	17.29	12.34	4.61	5.20	1.71
16.	Glyma20g28631.1	O acetylserine (thiol) lyase (OAS TL) isoform A1	3	0.00	1	3.76	4.89	3.69	2.94	2.10	2.31	1.80	2.76	3.66	2.52	2.33	0.79
17.	Glyma13g30490.1	pyruvate decarboxylase 2	7	0.00	1	3.47	4.80	4.92	3.75	7.83	19.61	13.85	14.36	21.44	3.81	2.19	2.42
18.	Glyma15g12100.1	fumarylacetoacetase putative	4	0.00	1	4.18	4.70	9.47	5.69	13.43	16.12	0.07	0.08	0.42	0.50	0.17	0.05
19.	Glyma13g36780.1	late embryogenesis	4	0.00	1	3.49	4.43	2.71	3.07	2.00	2.76	4.53	3.53	2.61	3.33	4.38	2.09
20.	Glyma15g36180.1	cystatin B	7	0.00	1	6.70	4.39	3.66	5.29	7.41	7.28	4.70	1.78	5.20	0.41	0.08	0.02
21.	Glyma13g29400.1	Protein of unknown function (DUF1000)	2	0.00	1	2.15	4.29	2.65	4.11	8.14	11.49	6.94	6.79	4.31	8.12	4.46	3.34
22.	Glyma10g07710.1	Aldolase	4	0.00	1	2.51	4.16	3.53	2.75	4.29	6.00	18.41	52.32	107.73	2.15	0.03	0.86
23.	Glyma13g21540.1	Aldolase	4	0.00	1	2.51	4.16	3.53	2.30	4.15	5.58	18.41	52.32	107.73	2.15	0.03	0.86
24.	Glyma10g23790.1	uricase	7	0.00	1	3.92	3.94	3.79	4.32	4.38	4.67	5.83	12.42	8.90	5.12	3.87	4.60
25.	Glyma13g25870.1	cystatin B	8	0.00	1	5.59	3.78	3.19	3.82	6.08	5.62	2.76	1.62	4.37	0.82	0.57	0.03
26.	Glyma14g13480.1	aspartate aminotransferase 5	10	0.00	1	2.31	3.75	4.56	1.34	4.06	20.53	0.34	0.29	0.98	1.04	0.76	0.70
27.	Glyma09g01270.1	fumarylacetoacetase putative	6	0.00	1	3.09	3.64	7.19	4.88	12.90	14.80	0.07	0.12	0.57	0.67	0.22	0.08

28.	Glyma16g06850.1	glucose 6 phosphate dehydrogenase 6	7	0.00	1	2.39	3.53	3.13	1.79	1.97	2.03	10.51	6.94	5.94	2.35	1.38	0.98
29.	Glyma19g24250.4	glucose 6 phosphate dehydrogenase 6	7	0.00	1	2.44	3.53	3.14	1.79	1.98	2.04	10.32	9.73	6.31	2.43	1.25	0.94
30.	Glyma02g38730.1	Aldolase	12	0.00	1	2.99	3.33	5.77	5.09	8.61	10.62	13.76	16.11	18.85	1.68	0.06	0.66
31.	Glyma13g42310.1	lipoxygenase 1	26	0.00	1	3.10	3.22	1.72	0.75	0.92	0.42	9.95	4.05	8.05	0.79	0.64	0.48
32.	Glyma17g33050.1	aspartate aminotransferase 5	11	0.00	1	2.08	3.16	3.97	1.33	4.01	20.11	0.31	0.33	0.95	1.03	0.78	0.63
33.	Glyma07g14090.1	peroxisomal NAD malate dehydrogenase 1	2	0.00	1	1.63	3.10	2.08	2.74	3.95	3.21	3.78	1.55	1.55	3.68	3.16	2.40
34.	Glyma02g00810.1	Lactate	11	0.00	1	1.97	3.09	2.33	1.30	2.02	1.95	3.55	4.92	1.08	0.92	0.58	1.12
35.	Glyma12g02790.2	rotamase CYP 3	5	0.00	1	2.96	3.03	3.18	1.69	6.02	5.65	7.26	6.72	5.53	3.81	2.00	2.18
36.	Glyma10g00920.1	Lactate	10	0.00	1	1.97	3.02	2.25	1.30	2.03	1.64	3.57	5.32	1.08	0.91	0.37	0.43
37.	Glyma13g44170.3	phospholipase D alpha 1	5	0.00	1	3.54	2.98	5.06	4.59	5.31	7.29	3.29	3.47	3.59	4.98	4.72	5.51
38.	Glyma04g42700.1	PDI like 1 1	2	0.00	1	2.64	2.96	4.47	2.40	19.49	30.60	17.47	13.89	8.46	4.06	6.36	9.86
39.	Glyma06g12080.2	PDI like 1 1	2	0.00	1	2.64	2.96	4.47	2.40	19.49	30.60	17.47	13.89	8.46	4.06	6.36	9.86
40.	Glyma09g29360.2	Kunitz family trypsin	2	0.00	1	3.89	2.88	4.70	1.49	2.66	3.07	7.89	9.23	3.41	0.78	0.12	0.04
41.	Glyma18g01330.1	glyceraldehyde 3 phosphate dehydrogenase C1	9	0.00	1	2.11	2.85	2.50	24.32	27.95	29.51	6.33	7.93	6.98	4.11	3.03	3.36
42.	Glyma09g01050.1	Phosphofructokinase	7	0.00	1	1.69	2.69	1.65	1.82	2.90	2.51	1.53	3.96	2.20	1.50	1.75	0.82
43.	Glyma18g26190.1	Ribosomal protein S6e	2	0.02	1	2.75	2.69	1.99	2.53	2.39	2.18	2.18	1.82	1.90	1.53	1.30	1.29
44.	Glyma13g29700.1	Aldolase type TIM barrel	4	0.00	1	2.29	2.65	2.28	1.06	1.46	1.24	0.82	0.60	0.73	2.28	1.09	1.05
45.	Glyma08g31890.1	alpha xylosidase 1	7	0.00	1	4.35	2.59	2.13	1.17	1.05	2.10	9.26	12.27	21.01	0.61	0.16	0.13
46.	Glyma11g37360.1	glyceraldehyde 3 phosphate dehydrogenase C1	10	0.00	1	1.89	2.57	1.98	17.04	20.19	11.42	2.68	9.29	6.18	1.97	1.13	0.78
47.	Glyma15g42301.1	Citrate synthase	7	0.00	1	3.39	2.55	3.15	1.79	2.29	2.45	4.49	2.65	2.61	2.52	2.42	1.81
48.	Glyma15g19670.1	aldehyde dehydrogenase 7B4	11	0.00	1	1.64	2.50	2.00	1.21	2.52	2.57	0.58	1.02	0.82	2.44	0.66	0.71
49.	Glyma20g38320.3	importin alpha isoform 1	4	0.00	1	1.68	2.50	1.90	1.80	2.46	2.72	0.23	0.34	1.06	0.44	0.09	0.01
50.	Glyma09g04430.1	importin alpha isoform 2	6	0.00	1	2.00	2.47	2.04	1.61	2.22	2.60	0.79	0.68	1.17	1.31	0.79	0.92
51.	Glyma17g10710.1	Ribosomal protein S4	6	0.00	1	2.05	2.46	2.14	1.74	0.73	0.81	0.69	1.51	1.60	1.11	0.72	0.28
52.	Glyma19g43150.1	O acetylserine (thiol) lyase (OAS TL) isoform A1	7	0.00	1	1.89	2.43	2.19	1.29	1.33	4.32	0.02	0.53	1.12	1.34	0.98	0.43
53.	Glyma05g06420.1	glyceraldehyde 3 phosphate dehydrogenase C2	4	0.00	1	1.81	2.41	1.99	1.81	3.26	7.32	0.31	0.52	1.06	1.94	1.01	0.72
54.	Glyma19g22780.1	glyceraldehyde 3 phosphate dehydrogenase C2	4	0.00	1	1.81	2.41	1.99	1.81	3.26	7.32	0.31	0.52	1.06	1.94	1.01	0.72
55.	Glyma01g31360.1	20S proteasome alpha subunit C1	2	0.00	1	2.17	2.40	2.10	2.88	2.97	3.38	180.99	113.79	99.56	2.29	0.99	1.36
56.	Glyma14g39810.1	catalase 2	8	0.00	1	2.39	2.40	1.31	0.90	1.13	0.95	4.90	2.68	1.42	1.35	0.45	0.19
57.	Glyma17g38140.1	catalase 2	9	0.00	1	2.32	2.33	1.30	0.87	0.78	0.22	3.17	0.30	1.34	1.27	0.34	0.15
58.	Glyma15g11890.1	Phosphofructokinase	8	0.00	1	1.64	2.29	1.40	1.50	2.76	2.38	1.42	2.35	2.07	1.13	1.42	0.61
59.	Glyma10g29000.1	importin alpha isoform 1	6	0.00	1	1.48	2.27	1.72	1.33	1.91	1.61	0.30	0.52	0.94	0.44	0.58	0.02
60.	Glyma07g03890.1	Coatomer beta	3	0.00	1	4.49	2.26	6.66	10.43	14.15	11.34	5.70	18.94	2.32	6.91	8.93	9.79

61.	Glyma08g22140.1	Coatomer beta	3	0.00	1	4.49	2.26	6.66	10.43	14.15	11.34	5.70	18.94	2.32	6.91	8.93	9.79
62.	Glyma13g43680.1	Coatomer beta	3	0.00	1	4.49	2.26	6.66	10.43	14.15	11.34	5.70	18.94	2.32	6.91	8.93	9.79
63.	Glyma05g35340.1	aldehyde dehydrogenase 2C4	4	0.00	1	1.66	2.23	1.63	2.30	2.79	2.50	3.11	1.99	6.16	3.61	3.10	5.59
64.	Glyma06g18120.1	glyceraldehyde 3 phosphate dehydrogenase C1	9	0.00	1	1.68	2.19	1.63	25.47	27.37	28.63	0.33	0.44	0.93	1.79	0.96	0.67
65.	Glyma08g16770.2	Citrate synthase	8	0.00	1	2.78	2.18	2.51	1.75	2.18	2.38	4.13	2.60	2.61	2.37	2.32	1.16
66.	Glyma01g24650.1	Metal dependent protein hydrolase	2	0.00	1	2.09	2.17	1.91	1.72	3.11	2.48	0.40	0.49	0.65	0.93	0.41	0.66
67.	Glyma03g12130.1	Metal dependent protein hydrolase	2	0.00	1	2.09	2.17	1.91	1.72	3.11	2.48	0.40	0.49	0.65	0.93	0.41	0.66
68.	Glyma04g09180.1	phosphofructokinase 3	7	0.00	1	2.20	2.17	2.17	1.30	2.00	2.54	0.23	0.24	0.64	1.02	0.14	0.19
69.	Glyma11g36620.1	S adenosyl L homocysteine hydrolase	3	0.00	1	1.41	2.16	1.86	1.96	1.99	1.36	22.66	0.98	2.10	0.70	0.14	0.13
70.	Glyma20g17440.1	uricase	6	0.00	1	1.93	2.16	1.86	3.25	4.02	4.59	5.66	10.96	8.62	5.12	2.35	3.85
71.	Glyma15g15480.1	importin alpha isoform 2	8	0.00	1	1.78	2.15	1.80	1.57	2.00	2.39	0.67	0.46	1.14	1.24	0.67	0.80
72.	Glyma11g08020.1	GDP D mannose 4 6 dehydratase 1	2	0.00	1	2.90	2.11	1.69	2.61	2.64	3.07	0.87	1.47	1.51	0.94	2.30	1.88
73.	Glyma01g45110.1	methylesterase PCR A	3	0.00	1	1.73	2.09	1.87	4.51	4.78	9.44	0.37	0.56	0.95	1.19	1.01	0.86
74.	Glyma05g22180.1	root hair specific 19	8	0.00	1	2.06	2.09	2.45	2.56	3.60	4.22	1.19	1.24	2.19	1.22	1.26	1.16
75.	Glyma16g00410.1	chloroplast heat shock protein 70 2	10	0.00	1	1.77	2.07	2.69	1.29	2.37	1.58	0.79	2.35	1.57	3.24	0.91	0.86
76.	Glyma11g25650.1	Eukaryotic aspartyl protease	3	0.00	1	2.14	2.06	1.63	3.71	5.02	4.34	2.24	1.16	3.34	2.51	1.88	1.92
77.	Glyma17g17730.1	root hair specific 19	9	0.00	1	1.99	2.05	2.37	2.77	3.64	4.20	1.13	1.15	1.96	1.19	1.28	1.00
78.	Glyma16g04420.1	tubulin alpha 5	7	0.00	1	1.89	2.04	1.48	1.76	1.99	1.92	0.37	0.84	1.50	1.10	0.56	0.08
79.	Glyma19g28990.1	tubulin alpha 3	7	0.00	1	1.89	2.04	1.48	1.76	1.99	1.92	0.37	0.84	1.50	1.10	0.56	0.08
80.	Glyma11g33160.1	UDP glucose pyrophosphorylase 2	13	0.00	1	1.51	2.03	2.13	1.80	4.75	4.25	3.62	2.79	4.54	2.07	1.46	0.47
81.	Glyma18g42280.1	acetyl Co enzyme carboxyltransferase alpha subunit	2	0.00	1	2.84	2.02	0.36	1.24	1.34	1.70	1.07	0.88	1.78	0.93	0.68	1.96
82.	Glyma18g42300.1	acetyl Co enzyme a carboxylase carboxyltransferase	2	0.00	1	2.84	2.02	0.36	1.24	1.34	1.70	1.07	0.88	1.78	0.93	0.68	1.96
83.	Glyma18g42325.1	acetyl Co enzyme a carboxylase carboxyltransferase	2	0.00	1	2.84	2.02	0.36	1.24	1.34	1.70	1.07	0.88	1.78	0.93	0.68	1.96
84.	Glyma05g31490.1	aspartate aminotransferase	3	0.00	1	2.07	2.01	2.14	2.39	1.79	2.02	1.79	1.48	0.63	0.84	0.68	1.85
85.	Glyma08g14720.1	aspartate aminotransferase	3	0.00	1	2.07	2.01	2.14	2.39	1.79	2.02	1.79	1.48	0.63	0.84	0.68	1.85
86.	Glyma09g08150.1	aldehyde dehydrogenase 7B4	10	0.00	1	1.64	2.01	1.14	1.32	2.77	3.06	1.23	1.66	1.06	2.09	0.46	0.87
87.	Glyma08g18110.1	Ribosomal protein S5	15	0.00	1	1.35	2.00	2.08	4.47	9.13	8.88	3.01	1.76	0.79	2.81	1.60	0.82
88.	Glyma15g40860.1	Ribosomal protein S5	15	0.00	1	1.35	2.00	2.08	4.47	9.13	8.88	3.01	1.76	0.79	2.81	1.60	0.82
89.	Glyma09g28440.1	Ribosomal protein S3	5	0.00	1	0.74	0.50	0.97	1.14	1.28	0.77	0.30	0.21	0.21	0.85	0.40	0.20
90.	Glyma16g33230.1	Ribosomal protein S3	5	0.00	1	0.74	0.50	0.97	1.14	1.28	0.77	0.30	0.21	0.21	0.85	0.40	0.20
91.	Glyma16g33240.1	Ribosomal protein S3	5	0.00	1	0.74	0.50	0.97	1.14	1.28	0.77	0.30	0.21	0.21	0.85	0.40	0.20
92.	Glyma19g37750.1	starch branching enzyme 2.1	3	0.05	1	0.53	0.49	0.44	0.71	0.55	0.32	0.81	0.77	0.65	0.56	0.88	0.90
93.	Glyma03g35020.1	starch branching enzyme 2.2	4	0.00	1	0.52	0.48	0.44	0.68	0.54	0.27	0.69	0.72	0.63	1.77	0.97	1.28

94.	Glyma12g35840.2	phosphoenolpyruvate carboxylase 3	10	0.01	1	0.62	0.47	0.44	0.64	0.42	0.17	0.31	0.43	0.44	0.45	0.34	0.16
95.	Glyma13g34560.2	phosphoenolpyruvate carboxylase 3	10	0.01	1	0.62	0.47	0.44	0.64	0.42	0.17	0.31	0.43	0.44	0.45	0.34	0.16
96.	Glyma12g33820.1	phosphoenolpyruvate carboxylase 2	8	0.00	1	0.45	0.47	0.49	0.67	0.43	0.16	0.35	0.53	0.71	0.43	0.27	0.05
97.	Glyma13g36670.1	phosphoenolpyruvate carboxylase 1	8	0.00	1	0.45	0.47	0.49	0.67	0.43	0.16	0.35	0.53	0.71	0.43	0.27	0.05
98.	Glyma05g37190.1	vacuolar H ATPase subunit E isoform 3	2	0.00	1	0.84	0.46	0.57	0.71	0.51	0.33	1.85	2.12	0.87	0.69	0.44	0.27
99.	Glyma08g02390.1	vacuolar ATP synthase subunit E1	2	0.00	1	0.84	0.46	0.57	0.71	0.51	0.33	1.85	2.12	0.87	0.69	0.44	0.27
100.	Glyma08g39110.1	Pyruvate phosphate dikinase PEP	5	0.00	1	0.74	0.46	0.72	1.16	0.89	0.32	0.32	0.32	0.70	0.20	0.28	0.09
101.	Glyma18g20600.2	Pyruvate phosphate dikinase PEP	5	0.00	1	0.74	0.46	0.72	1.16	0.89	0.32	0.32	0.32	0.70	0.20	0.28	0.09
102.	Glyma17g37820.1	Chaperone protein htpG	12	0.00	1	1.21	0.46	0.72	1.41	1.28	0.69	1.11	1.24	0.69	1.00	0.58	0.68
103.	Glyma14g40320.1	Chaperone protein htpG	13	0.00	1	1.19	0.46	0.71	1.40	1.28	0.62	1.11	1.20	0.68	0.99	0.58	0.68
104.	Glyma12g09390.1	NAD ADP ribosyltransferases	14	0.00	1	0.49	0.43	0.33	0.71	0.51	0.73	0.36	0.55	0.39	0.78	0.63	0.90
105.	Glyma10g28500.1	S adenosylmethionine synthetase 2	4	0.00	1	0.45	0.43	0.67	0.60	0.29	0.56	0.29	0.18	0.31	0.72	0.87	0.29
106.	Glyma18g02820.1	Eukaryotic translation initiation factor 2 subunit 1	3	0.03	1	0.57	0.43	0.72	0.60	0.45	0.37	0.33	0.31	0.37	0.83	0.49	0.45
107.	Glyma10g35700.2	GTP binding Elongation factor Tu family protein	8	0.00	1	0.80	0.42	0.49	0.62	0.20	0.08	0.03	0.04	0.25	0.62	0.13	0.05
108.	Glyma15g13830.1	GTP binding	4	0.05	1	0.67	0.41	0.54	0.73	0.39	0.20	0.45	0.33	0.32	0.45	0.78	0.35
109.	Glyma07g00420.1	regulatory particle triple A ATPase 6A	5	0.00	1	0.47	0.41	0.22	0.66	0.30	0.18	7.86	3.34	0.50	0.71	0.55	0.54
110.	Glyma08g24000.1	regulatory particle triple A ATPase 6A	5	0.00	1	0.47	0.41	0.22	0.66	0.30	0.18	7.86	3.34	0.50	0.71	0.55	0.54
111.	Glyma08g36700.1	ARF GAP domain 8	5	0.00	1	0.38	0.38	0.37	1.12	0.34	0.32	0.64	1.36	0.66	0.33	0.30	0.70
112.	Glyma11g37320.1	NAD(P) binding Rossmann fold	3	0.00	1	0.86	0.38	1.40	0.73	1.84	1.72	1.33	0.28	0.47	1.14	0.17	0.27
113.	Glyma18g01280.1	NAD(P) binding Rossmann fold	3	0.00	1	0.86	0.38	1.40	0.73	1.84	1.72	1.33	0.28	0.47	1.14	0.17	0.27
114.	Glyma16g05530.1	translocon associated protein beta (TRAPB)	3	0.02	1	0.51	0.38	0.41	0.68	0.47	0.21	0.29	0.23	0.56	0.50	0.24	0.60
115.	Glyma02g47210.1	HEAT SHOCK PROTEIN 81.4	10	0.02	1	0.45	0.37	0.44	0.49	0.43	0.34	0.14	0.34	0.37	0.42	0.19	0.10
116.	Glyma12g31620.1	DNAJ homologue 2	5	0.00	1	0.50	0.36	0.38	0.42	0.37	0.16	0.27	0.25	0.26	0.51	0.21	0.08
117.	Glyma01g42010.1	stress inducible protein putative	12	0.00	1	0.86	0.36	0.58	0.57	0.29	0.27	0.19	0.11	0.19	0.69	0.25	0.09
118.	Glyma17g05067.1	sucrose synthase 4	23	0.01	1	0.27	0.35	0.41	0.38	0.20	0.12	0.40	0.32	0.72	0.60	0.18	0.19
119.	Glyma13g31130.1	Ribosomal protein S6e	3	0.02	1	0.59	0.35	0.57	0.46	0.37	0.61	0.31	0.28	0.46	0.47	0.32	0.21
120.	Glyma13g17421.1	sucrose synthase 4	23	0.00	1	0.27	0.34	0.38	0.39	0.20	0.13	0.42	0.34	0.70	0.58	0.18	0.20
121.	Glyma02g42210.1	eukaryotic translation initiation factor 2	2	0.00	1	0.93	0.33	0.50	0.52	0.27	0.20	1.43	0.96	0.48	0.54	0.70	0.46
122.	Glyma19g07240.3	GTP binding Elongation factor Tu family protein	8	0.00	1	0.85	0.33	0.47	0.59	0.24	0.17	0.03	0.04	0.23	0.51	0.12	0.04
123.	Glyma05g24110.1	GTP binding Elongation factor Tu family protein	10	0.00	1	0.83	0.33	0.46	0.60	0.24	0.17	0.05	0.04	0.22	0.52	0.13	0.04
124.	Glyma05g25810.1	chlorophyll A/B binding protein 1	3	0.00	1	0.29	0.32	0.39	2.10	2.02	0.82	0.16	0.33	0.50	0.51	0.25	0.56
125.	Glyma17g09280.2	Ribosomal protein L18e/L15 superfamily protein	4	0.00	1	0.37	0.32	0.20	0.30	0.27	0.31	0.39	0.23	0.45	0.41	0.44	0.29
126.	Glyma11g19070.1	NAD ADP ribosyltransferases	15	0.03	1	0.52	0.31	0.35	0.48	0.33	0.14	0.11	0.22	0.23	0.34	0.17	0.16

127.	Glyma16g07350.1	GTP binding Elongation factor Tu family protein	9	0.00	1	0.76	0.30	0.43	0.58	0.19	0.08	0.03	0.04	0.23	0.52	0.13	0.04
128.	Glyma05g22060.1	Subtilase family protein	5	0.00	1	0.28	0.30	0.19	0.26	0.29	0.65	0.27	0.15	0.08	0.34	0.11	0.07
129.	Glyma18g12090.1	tryptophan synthase beta subunit 2	2	0.00	1	0.42	0.30	0.23	0.25	0.32	0.21	0.07	0.25	0.25	0.16	0.08	0.01
130.	Glyma11g03330.2	stress inducible protein putative	11	0.00	1	0.52	0.30	0.30	0.29	0.15	0.10	0.14	0.11	0.17	0.42	0.22	0.09
131.	Glyma08g01140.1	CLPC homologue 1	3	0.00	1	0.57	0.30	0.28	0.62	0.18	0.08	0.13	0.13	0.19	0.41	0.30	0.10
132.	Glyma05g11630.2	GTP binding Elongation factor Tu family protein	8	0.00	1	0.75	0.30	0.40	0.57	0.19	0.07	0.03	0.04	0.20	0.51	0.12	0.04
133.	Glyma17g17850.1	Subtilase family protein	7	0.00	1	0.27	0.28	0.18	0.23	0.27	0.61	0.25	0.12	0.08	0.37	0.12	0.07
134.	Glyma17g23900.1	GTP binding Elongation factor Tu family protein	9	0.00	1	0.73	0.28	0.35	0.52	0.18	0.06	0.07	0.10	0.27	0.47	0.12	0.04
135.	Glyma07g11560.1	homolog of nucleolar protein NOP56	3	0.00	1	0.34	0.28	0.13	0.35	0.10	0.26	0.10	0.13	0.25	0.29	0.26	0.16
136.	Glyma12g30600.1	histone deacetylase 2C	2	0.00	1	0.49	0.28	0.33	0.34	0.15	0.16	0.01	0.05	0.11	0.42	0.04	0.01
137.	Glyma03g21710.1	Ribosomal protein S8e family protein	5	0.00	1	0.35	0.28	0.22	0.27	0.11	0.10	0.92	1.82	3.54	0.29	0.19	0.14
138.	Glyma16g10700.1	Ribosomal protein S8e family protein	6	0.00	1	0.37	0.28	0.25	0.28	0.06	0.08	0.85	2.15	3.03	0.26	0.18	0.04
139.	Glyma08g46070.1	Ribosomal protein S8e family protein	5	0.00	1	0.36	0.28	0.25	0.23	0.09	0.09	0.13	0.16	0.29	0.30	0.17	0.06
140.	Glyma18g09430.1	Ribosomal protein S8e family protein	4	0.00	1	0.43	0.26	0.23	0.37	0.14	0.05	1.00	3.79	5.39	0.29	0.11	0.11
141.	Glyma13g28840.1	Ribosomal protein S11 family protein	5	0.00	1	0.54	0.25	0.23	0.43	0.18	0.15	0.09	0.10	0.11	0.66	0.23	0.07
142.	Glyma13g16040.2	ubiquitin specific protease 13	2	0.00	1	0.45	0.24	0.27	0.46	0.21	0.12	0.07	0.11	0.27	0.24	0.15	0.11
143.	Glyma10g31590.1	methionine gamma lyase	2	0.00	1	0.19	0.24	0.19	0.22	0.05	0.10	0.08	0.06	0.12	0.09	0.06	0.08
144.	Glyma11g11020.3	cell elongation protein	4	0.00	1	0.36	0.23	0.25	0.30	0.21	0.14	0.12	0.15	0.21	0.33	0.09	0.04
145.	Glyma10g12760.1	heat shock protein 81 2	2	0.00	1	0.37	0.22	0.30	0.30	0.08	0.08	0.01	0.02	0.23	0.21	0.02	0.01
146.	Glyma11g08050.1	Ribosomal protein L2 family	2	0.00	1	0.44	0.22	0.15	0.19	0.14	0.15	0.13	0.20	0.34	0.27	0.35	0.18
147.	Glyma13g24200.1	cytochrome P450 family 93	4	0.00	1	0.42	0.22	0.25	0.39	0.30	0.10	0.34	0.32	0.38	0.31	0.31	0.32
148.	Glyma11g12200.1	NOP56 like pre RNA processing ribonucleoprotein	3	0.00	1	0.32	0.21	0.11	0.29	0.16	0.17	0.22	0.21	0.32	0.25	0.10	0.03
149.	Glyma12g04400.1	NOP56 like pre RNA processing ribonucleoprotein	3	0.00	1	0.32	0.21	0.11	0.29	0.16	0.17	0.23	0.22	0.33	0.26	0.11	0.29
150.	Glyma10g36780.1	ribosomal protein 1	9	0.00	1	0.30	0.21	0.30	0.32	0.13	0.15	0.07	0.09	0.32	0.38	0.12	0.06
151.	Glyma05g02570.1	Ribosomal protein L18e/L15	3	0.02	1	0.20	0.21	0.16	0.25	0.13	0.13	0.05	0.11	0.37	0.31	0.06	0.20
152.	Glyma05g38510.1	CLPC homologue 1	4	0.02	1	0.46	0.20	0.25	0.55	0.15	0.07	0.12	0.10	0.18	0.48	0.33	0.12
153.	Glyma05g06050.3	*S* adenosyl L methionine dependent methyltransferases	2	0.02	1	0.43	0.20	0.10	0.26	0.19	0.48	0.13	0.29	0.39	0.42	0.15	0.09
154.	Glyma10g02290.1	NAD(P) binding Rossmann fold	4	0.02	1	0.30	0.19	0.20	0.32	0.16	0.09	0.09	0.21	0.22	0.27	0.12	0.11
155.	Glyma08g43690.1	Ribosomal protein S8e family protein	4	0.02	1	0.35	0.18	0.16	0.26	0.05	0.01	1.03	3.85	6.25	0.23	0.03	0.06
156.	Glyma06g46350.1	SKU5 similar 5	2	0.02	1	0.24	0.18	0.12	0.18	0.06	0.09	0.23	0.14	0.07	0.12	0.04	0.02
157.	Glyma12g10420.1	SKU5 similar 5	2	0.02	1	0.24	0.18	0.12	0.18	0.06	0.09	0.23	0.14	0.07	0.12	0.04	0.02
158.	Glyma06g20540.1	Ribosomal protein S4	6	0.02	1	0.44	0.17	0.18	0.60	0.57	0.59	0.09	0.15	0.38	0.13	0.03	0.03

159.	Glyma14g37440.1	glutamine dependent asparagine synthase 1	8	0.02	1	0.25	0.17	0.12	0.18	0.12	0.08	0.13	0.14	0.08	0.19	0.15	0.05
160.	Glyma12g03210.3	cell elongation protein	3	0.02	1	0.18	0.17	0.17	0.18	0.08	0.06	0.08	0.08	0.15	0.16	0.07	0.01
161.	Glyma15g08210.1	Ribosomal protein S6e	2	0.01	1	0.34	0.16	0.18	0.23	0.09	0.03	0.03	0.03	0.39	0.13	0.03	0.02
162.	Glyma10g43770.2	Ribosomal L29 family protein	3	0.00	1	0.27	0.16	0.11	0.19	0.10	0.09	0.07	0.12	0.24	0.13	0.02	0.04
163.	Glyma10g39170.1	cupin family protein	6	0.00	1	0.28	0.16	0.12	0.16	0.12	0.16	0.06	0.13	0.18	0.28	0.08	0.10
164.	Glyma13g40780.2	ribosomal protein L23AB	2	0.00	1	0.42	0.16	0.15	0.16	0.26	0.13	0.30	0.32	0.13	0.07	0.05	1.08
165.	Glyma18g52310.2	ribosomal protein L23AB	2	0.00	1	0.42	0.16	0.15	0.16	0.26	0.13	0.30	0.32	0.13	0.07	0.05	1.08
166.	Glyma09g00280.1	ribosomal protein 1	2	0.00	1	0.31	0.16	0.16	0.24	0.08	0.03	0.01	0.02	0.16	0.29	0.04	0.01
167.	Glyma03g21680.1	FK506 and rapamycin binding protein 15 kD 2	2	0.05	1	0.39	0.16	0.13	0.25	0.84	0.86	0.74	1.15	0.48	0.08	0.03	0.01
168.	Glyma16g10750.1	FK506 and rapamycin binding protein 15 kD 2	2	0.05	1	0.39	0.16	0.13	0.25	0.84	0.86	0.74	1.15	0.48	0.08	0.03	0.01
169.	Glyma09g25830.2	CAP160 protein	8	0.00	1	0.35	0.15	0.25	0.52	0.35	0.22	0.37	0.38	0.23	0.68	0.73	0.33
170.	Glyma10g38450.1	valyl tRNA synthetase	3	0.00	1	0.35	0.15	0.31	0.48	0.37	0.24	0.22	0.25	0.23	0.46	0.28	0.73
171.	Glyma12g36940.2	R protein L3 B	3	0.00	1	0.28	0.15	0.12	0.22	0.07	0.02	0.02	0.02	0.16	0.24	0.03	0.01
172.	Glyma20g38480.1	Ribosomal L29 family protein	4	0.00	1	0.25	0.15	0.11	0.17	0.09	0.07	0.05	0.09	0.17	0.11	0.02	0.04
173.	Glyma04g40470.1	Ribosomal protein L6 family	5	0.00	1	0.30	0.15	0.16	0.27	0.17	0.14	0.23	0.16	0.15	0.25	0.18	0.13
174.	Glyma10g20880.1	heat shock protein 81 2	2	0.00	1	0.28	0.15	0.18	0.27	0.06	0.04	0.01	0.01	0.16	0.17	0.02	0.00
175.	Glyma19g40080.1	Ribosomal protein L19e family protein	2	0.00	1	0.25	0.14	0.16	0.21	0.14	0.04	0.08	0.13	0.28	0.25	0.05	0.53
176.	Glyma20g30810.1	ribosomal protein 1	8	0.00	1	0.27	0.14	0.25	0.30	0.12	0.15	0.08	0.10	0.27	0.37	0.10	0.08
177.	Glyma14g38950.2	Ribosomal protein S26e family protein	2	0.00	1	0.24	0.13	0.12	0.23	0.12	0.03	0.22	0.31	0.20	0.47	0.32	0.50
178.	Glyma08g04990.3	Ribosomal protein S7e family protein	3	0.00	1	0.24	0.09	0.11	0.32	0.09	0.05	0.11	0.12	0.12	0.31	0.10	0.08
179.	Glyma05g34680.2	Ribosomal protein S7e family protein	2	0.00	1	0.21	0.08	0.08	0.27	0.05	0.04	0.07	0.09	0.11	0.28	0.10	0.07
180.	Glyma06g18800.1	Ribosomal protein L18e/L15 superfamily protein	4	0.00	1	0.24	0.06	0.04	0.18	0.04	0.04	3.61	2.77	2.95	0.65	0.06	0.28
181.	Glyma09g02790.1	Ribosomal protein L13 family protein	2	0.00	1	0.08	0.05	0.05	0.07	0.04	0.05	0.03	0.05	0.06	0.07	0.04	0.03

[a] Protein ID, according to the Phytozome database; [b] M.P., matched peptide;[c] *p*-value, calculated with 2-way ANOVA; [d] Ratio, relative abundance of protein; ND, no description; *p*-value<0.05.

Table S3. List of commonly identified mitochondrial proteins in soybean root tip exposed to 5, 30-60, and 135 nm of Al_2O_3 NPs under flooding stress.

No.	Protein ID[a]	Description	M.P.[b]	Ratio[c]					Subcellular Localization			
				2(0)	4(2)F	4(2)F Al_2O_3 5 nm	4(2)F Al_2O_3 30-60 nm	4(2)F Al_2O_3 135 nm	SUBA3	MitoProt	MitoPred	TargetP
1.	Glyma04g39930.1	manganese superoxide dismutase 1	2	1	0.95	1.23	0.85	1.39	+	+	+	+
2.	Glyma06g14960.1	manganese superoxide dismutase 1	2	1	0.80	1.20	0.86	1.44	+	+	+	+
3.	Glyma05g09970.1	Ribosomal protein L25/Gln tRNA synthetase anti codon binding	3	1	0.77	0.22	0.32	0.52	+	+	+	+
4.	Glyma15g02390.1	mitochondrial processing peptidase alpha subunit	4	1	0.57	0.60	0.68	0.57	+	+	+	+
5.	Glyma13g43000.1	mitochondrial processing peptidase alpha subunit	5	1	0.57	0.60	0.67	0.57	+	+	+	+
6.	Glyma14g08040.1	pentatricopeptide (PPR) repeat containing protein	2	1	0.57	0.56	0.53	0.47	+	+	+	+
7.	Glyma10g17370.1	L galactono 1 4 lactone dehydrogenase	5	1	0.56	0.99	1.07	0.84	+	+	-	+
8.	Glyma02g27260.1	L galactono 1 4 lactone dehydrogenase	6	1	0.53	0.97	1.14	0.77	+	+	-	+
9.	Glyma12g06770.1	Tim10/DDP family zinc finger protein	5	1	0.51	0.26	0.34	0.45	+	-	-	-
10.	Glyma14g38840.5	Cystathionine beta synthase (CBS) family protein	6	1	0.47	0.80	0.47	0.36	+	+	+	+
11.	Glyma15g02030.1	Tetratricopeptide repeat (TPR) like superfamily protein	2	1	0.46	0.29	0.37	0.37	+	+	-	-
12.	Glyma02g47580.1	HEAT SHOCK PROTEIN 89.1	11	1	0.44	0.80	0.47	0.56	+	+	+	+
13.	Glyma05g38160.1	gamma carbonic anhydrase like 1	4	1	0.44	0.59	0.61	0.47	+	+	+	+
14.	Glyma14g01100.1	Heat shock protein 89.1	13	1	0.44	0.77	0.47	0.54	+	+	+	+
15.	Glyma01g33761.1	arginase	4	1	0.44	0.30	0.29	0.35	+	+	-	+
16.	Glyma17g14040.1	arginase	4	1	0.44	0.30	0.29	0.35	+	+	-	+
17.	Glyma18g49070.1	voltage dependent anion channel 1	10	1	0.44	0.49	0.58	4.83	+	-	-	-
18.	Glyma05g04510.1	ND	2	1	0.43	0.56	0.55	0.42	+	+	-	+
19.	Glyma17g14940.1	ND	2	1	0.43	0.56	0.55	0.42	+	+	-	+
20.	Glyma11g10190.1	Pyridoxal phosphate (PLP) dependent transferases	5	1	0.43	0.80	0.29	0.43	+	+	+	+
21.	Glyma13g41540.2	ADP/ATP carrier 2	4	1	0.42	0.18	0.23	0.32	+	-	-	-
22.	Glyma08g21380.1	Insulinase (Peptidase family M16) protein	6	1	0.42	0.55	0.57	0.56	+	+	+	+
23.	Glyma07g01720.1	Insulinase (Peptidase family M16) protein	6	1	0.42	0.54	0.57	0.55	+	+	+	+
24.	Glyma12g19520.1	Lactate/malate dehydrogenase family protein	6	1	0.41	0.39	0.42	0.59	+	+	+	+
25.	Glyma01g40140.1	voltage dependent anion channel 2	6	1	0.40	0.44	0.52	0.28	+	-	-	-
26.	Glyma11g05170.1	voltage dependent anion channel 2	6	1	0.40	0.44	0.52	0.28	+	-	-	-
27.	Glyma06g14340.1	SPFH/Band 7/PHB domain containing membrane protein	4	1	0.40	0.55	0.58	0.48	+	+	-	+

28.	Glyma17g36210.2	succinate dehydrogenase 5	3	1	0.39	0.60	0.60	0.48	+	-	+	+
29.	Glyma05g31830.1	copper ion binding;cobalt ion binding;zinc ion binding	6	1	0.38	0.81	0.67	0.59	+	+	+	+
30.	Glyma08g15100.1	copper ion binding;cobalt ion binding;zinc ion binding	6	1	0.38	0.81	0.67	0.59	+	+	+	+
31.	Glyma09g37570.1	voltage dependent anion channel 1	10	1	0.38	0.49	0.57	5.77	+	-	-	-
32.	Glyma09g27910.1	Ribosomal L18p/L5e family protein	2	1	0.37	1.19	0.81	0.69	+	+	+	+
33.	Glyma15g42900.1	ADP/ATP carrier 2	10	1	0.37	0.25	0.26	0.31	+	-	-	-
34.	Glyma17g31280.1	Cytochrome bd ubiquinol oxidase 14kDa subunit	4	1	0.37	0.36	0.50	0.58	+	+	+	+
35.	Glyma08g40800.1	voltage dependent anion channel 1	8	1	0.36	0.45	0.43	0.29	+	-	-	-
36.	Glyma18g16260.1	voltage dependent anion channel 1	8	1	0.36	0.46	0.40	0.28	+	-	-	-
37.	Glyma14g36540.1	Transketolase family protein	6	1	0.36	0.47	0.46	0.53	+	+	-	+
38.	Glyma17g36970.1	pentatricopeptide (PPR) repeat containing protein	4	1	0.36	0.49	0.70	0.42	+	+	+	+
39.	Glyma10g43220.1	pyrimidine d	4	1	0.36	0.74	0.76	0.60	+	+	+	+
40.	Glyma20g23670.1	pyrimidine d	4	1	0.36	0.74	0.76	0.60	+	+	+	+
41.	Glyma05g22510.1	NADH ubiquinone oxidoreductase related	2	1	0.36	0.39	0.53	0.41	+	+	+	+
42.	Glyma13g27340.2	ADP/ATP carrier 2	6	1	0.35	0.17	0.19	0.30	+	-	-	-
43.	Glyma16g32760.1	Ribosomal L18p/L5e family protein	2	1	0.35	0.83	0.80	0.33	+	+	+	+
44.	Glyma07g08110.1	NAD dependent malic enzyme 2	7	1	0.35	0.31	0.32	0.34	+	+	+	+
45.	Glyma20g23010.1	lon protease 1	7	1	0.34	0.60	0.55	0.52	+	+	+	-
46.	Glyma19g01200.1	formate dehydrogenase	7	1	0.34	0.53	0.32	0.42	+	+	+	+
47.	Glyma02g46380.1	Transketolase family protein	5	1	0.34	0.49	0.47	0.57	+	+	-	+
48.	Glyma14g02380.3	Transketolase family protein	5	1	0.34	0.49	0.47	0.57	+	+	-	+
49.	Glyma10g28840.1	lon protease 1	9	1	0.34	0.54	0.48	0.49	+	+	+	-
50.	Glyma03g01680.1	NAD dependent malic enzyme 2	6	1	0.34	0.35	0.33	0.47	+	+	+	+
51.	Glyma14g08960.1	succinate dehydrogenase 5	3	1	0.33	0.47	0.40	0.45	+	-	+	+
52.	Glyma11g11670.3	prohibitin 2	2	1	0.33	0.42	0.36	0.34	+	+	-	-
53.	Glyma12g01850.1	prohibitin 6	2	1	0.33	0.42	0.36	0.34	+	-	-	-
54.	Glyma19g02380.1	voltage dependent anion channel 1	7	1	0.33	0.43	0.41	0.34	+	-	-	-
55.	Glyma13g33410.1	Complex I subunit NDUFS6	3	1	0.33	1.20	1.05	1.02	+	-	-	-
56.	Glyma09g01210.1	Uncharacterised protein family (UPF0041)	3	1	0.33	0.27	0.44	0.33	+	-	+	-
57.	Glyma08g43430.2	Co chaperone GrpE family protein	7	1	0.33	0.71	0.42	0.72	+	+	+	+
58.	Glyma16g01630.1	alanine aminotransferase 2	5	1	0.32	0.37	0.51	0.35	+	+	+	+
59.	Glyma05g07020.1	Cytochrome C1 family	9	1	0.32	0.29	0.28	0.30	+	+	+	+

60.	Glyma19g22530.1	Cytochrome C1 family	9	1	0.32	0.29	0.28	0.30	+	+	+	+
61.	Glyma17g10610.1	aldehyde dehydrogenase 12A1	10	1	0.32	0.61	0.44	0.67	+	+	+	+
62.	Glyma19g24620.3	Cytochrome C1 family	9	1	0.32	0.30	0.28	0.30	+	+	+	+
63.	Glyma07g05130.1	alanine aminotransferase 2	7	1	0.32	0.40	0.50	0.52	+	+	+	+
64.	Glyma05g14300.1	translocase outer membrane 20 2	4	1	0.32	0.28	0.30	0.30	+	-	-	-
65.	Glyma16g06700.3	Cytochrome C1 family	10	1	0.32	0.29	0.28	0.29	+	+	+	+
66.	Glyma06g35981.1	lon protease 1	2	1	0.32	0.41	0.38	0.37	+	+	+	-
67.	Glyma06g05470.1	glycine decarboxylase P protein 2	7	1	0.32	0.41	0.30	0.31	+	+	+	+
68.	Glyma13g05130.1	voltage dependent anion channel 1	4	1	0.31	0.48	0.50	0.31	+	-	-	-
69.	Glyma18g31550.3	Insulinase (Peptidase family M16) protein	9	1	0.31	0.54	0.41	0.69	+	+	+	+
70.	Glyma13g32030.1	NAD(P)H dehydrogenase B2	2	1	0.31	0.33	0.82	0.27	+	-	+	-
71.	Glyma15g07290.1	NAD(P)H dehydrogenase B2	2	1	0.31	0.33	0.82	0.27	+	-	+	-
72.	Glyma10g03440.1	methylcrotonyl CoA carboxylase alpha chain mitochondrial	5	1	0.31	0.42	2.26	1.10	+	+	+	+
73.	Glyma04g05420.1	glycine decarboxylase P protein 1	7	1	0.31	0.39	0.30	0.41	+	+	+	+
74.	Glyma14g10950.1	FTSH protease 4	5	1	0.31	0.28	0.24	0.21	+	+	-	+
75.	Glyma14g10960.2	FTSH protease 4	5	1	0.31	0.28	0.24	0.21	+	+	-	+
76.	Glyma13g37140.1	ADP/ATP carrier 3	7	1	0.31	0.20	0.28	0.30	+	+	+	-
77.	Glyma16g10360.1	Insulinase (Peptidase family M16) protein	7	1	0.31	0.51	0.41	0.66	+	+	+	+
78.	Glyma14g11860.2	ATP dependent caseinolytic (Clp) protease/crotonase	2	1	0.30	0.44	0.53	0.36	+	+	-	+
79.	Glyma18g10120.1	Co chaperone GrpE family protein	7	1	0.30	0.34	0.32	0.43	+	+	+	+
80.	Glyma08g46020.1	Insulinase (Peptidase family M16) protein	8	1	0.30	0.51	0.39	0.63	+	+	+	+
81.	Glyma11g15900.1	isovaleryl CoA dehydrogenase	2	1	0.30	0.36	0.28	0.26	+	+	-	+
82.	Glyma12g07570.2	isovaleryl CoA dehydrogenase	2	1	0.30	0.36	0.28	0.24	+	+	-	+
83.	Glyma13g36940.1	prohibitin 1	2	1	0.30	0.36	0.34	0.43	+	+	-	-
84.	Glyma01g43850.1	NADH:ubiquinone oxidoreductase 17.2kDa subunit	3	1	0.30	0.25	0.25	0.32	+	-	-	-
85.	Glyma20g33910.1	heat shock protein 60	19	1	0.30	0.51	0.47	0.46	+	+	-	+
86.	Glyma10g33680.1	heat shock protein 60	18	1	0.30	0.51	0.48	0.43	+	+	-	+
87.	Glyma13g18730.1	ATP citrate lyase (ACL) family protein	11	1	0.30	0.50	0.47	0.43	+	+	+	+
88.	Glyma10g06590.1	isocitrate dehydrogenase V	3	1	0.30	0.39	0.32	0.29	+	+	-	+
89.	Glyma13g20790.1	isocitrate dehydrogenase V	3	1	0.30	0.39	0.32	0.29	+	+	-	+
90.	Glyma15g11590.1	Glycine cleavage T protein family	6	1	0.29	0.52	0.39	0.46	+	+	+	+
91.	Glyma04g16350.1	prohibitin 4	5	1	0.29	0.60	0.53	0.84	+	-	-	-

92.	Glyma18g04730.1	NADH ubiquinone dehydrogenase mitochondrial putative	16	1	0.29	0.53	0.48	0.47	+	+	-	+
93.	Glyma10g04480.1	ATP citrate lyase (ACL) family protein	10	1	0.29	0.42	0.34	0.46	+	+	+	+
94.	Glyma12g33520.1	prohibitin 2	3	1	0.29	0.35	0.33	0.38	+	+	-	-
95.	Glyma14g10820.1	glycine decarboxylase P protein 2	5	1	0.29	0.33	0.23	0.41	+	+	+	+
96.	Glyma17g34690.1	glycine decarboxylase P protein 2	5	1	0.29	0.33	0.23	0.41	+	+	+	+
97.	Glyma13g27710.1	peroxiredoxin IIF	4	1	0.29	0.29	0.30	0.37	+	+	+	+
98.	Glyma02g46200.1	Dihydrolipoamide succinyltransferase	6	1	0.29	0.39	0.40	0.45	+	+	-	+
99.	Glyma11g01320.1	NADH:ubiquinone oxidoreductase 17.2kDa subunit	4	1	0.29	0.24	0.25	0.32	+	-	-	-
100.	Glyma07g39190.1	Glycine cleavage T protein family	4	1	0.29	0.46	0.37	0.43	+	+	+	+
101.	Glyma17g01550.4	Glycine cleavage T protein family	4	1	0.29	0.46	0.37	0.43	+	+	+	+
102.	Glyma02g41840.1	Mitochondrial glycoprotein family protein	5	1	0.28	0.39	0.39	0.46	+	+	-	+
103.	Glyma08g24950.1	prohibitin 3	4	1	0.28	0.54	0.40	0.43	+	+	-	-
104.	Glyma08g06376.1	NAD(P)H dehydrogenase B2	5	1	0.28	0.32	0.58	0.30	+	-	+	-
105.	Glyma13g26270.1	LYR family of Fe/S cluster biogenesis protein	3	1	0.28	0.31	2.14	1.18	+	-	+	+
106.	Glyma08g40380.1	Thiamin diphosphate binding fold (THDP binding)	4	1	0.28	0.31	0.35	0.31	+	+	+	+
107.	Glyma18g17240.1	Thiamin diphosphate binding fold (THDP binding)	4	1	0.28	0.31	0.35	0.31	+	+	+	+
108.	Glyma06g46190.2	aconitase 3	10	1	0.28	0.31	0.24	0.29	+	+	-	-
109.	Glyma12g10580.1	aconitase 3	10	1	0.28	0.31	0.24	0.29	+	+	-	-
110.	Glyma05g08480.1	FAD/NAD(P) binding oxidoreductase	4	1	0.28	0.66	0.68	0.44	+	+	-	+
111.	Glyma04g06610.1	casein lytic proteinase B4	5	1	0.28	1.48	0.94	0.90	+	+	-	+
112.	Glyma13g44000.1	glutaredoxin 4	2	1	0.28	0.17	0.26	0.29	+	+	+	+
113.	Glyma02g40530.5	Cystathionine beta synthase (CBS) family protein	6	1	0.28	0.31	0.20	0.44	+	+	+	+
114.	Glyma02g03080.1	pyruvate dehydrogenase complex E1 alpha subunit	3	1	0.28	0.29	0.33	0.28	+	+	+	-
115.	Glyma06g47520.1	prohibitin 3	3	1	0.28	0.48	0.39	1.01	+	+	-	-
116.	Glyma14g02530.1	Dihydrolipoamide succinyltransferase	5	1	0.28	0.39	0.41	0.40	+	+	-	+
117.	Glyma12g13240.1	ADP/ATP carrier 3	7	1	0.28	0.15	0.18	0.25	+	+	+	-
118.	Glyma01g07091.1	Tetratricopeptide repeat (TPR) like superfamily protein	4	1	0.28	0.37	0.38	0.36	+	+	+	+
119.	Glyma10g00820.1	51 kDa subunit of complex I	5	1	0.27	0.43	0.36	0.31	+	+	+	+
120.	Glyma08g17760.1	mercaptopyruvate sulfurtransferase 1	4	1	0.27	0.23	0.26	0.28	+	+	+	-
121.	Glyma15g41370.1	mercaptopyruvate sulfurtransferase 1	4	1	0.27	0.23	0.26	0.28	+	+	+	-
122.	Glyma11g33480.1	NADH ubiquinone dehydrogenase mitochondrial putative	16	1	0.27	0.46	0.43	0.44	+	+	+	+
123.	Glyma05g36900.1	Nucleoside diphosphate kinase family protein	3	1	0.27	0.19	0.16	0.11	+	+	+	+

124.	Glyma08g02630.1	Nucleoside diphosphate kinase family protein	3	1	0.27	0.19	0.16	0.11	+	+	+	+
125.	Glyma12g32000.1	aconitase 3	12	1	0.27	0.32	0.31	0.29	+	+	-	-
126.	Glyma04g05340.1	NADH ubiquinone oxidoreductase 20 kDa subunit	2	1	0.27	0.24	0.25	0.28	+	+	+	+
127.	Glyma06g05410.1	NADH ubiquinone oxidoreductase 20 kDa subunit	2	1	0.27	0.24	0.25	0.28	+	+	+	+
128.	Glyma12g33280.1	ADP/ATP carrier 3	8	1	0.27	0.20	0.26	0.28	+	+	+	-
129.	Glyma08g20560.1	heat shock protein 60 3A	8	1	0.27	0.38	0.32	0.33	+	+	-	+
130.	Glyma13g38480.1	aconitase 3	12	1	0.27	0.31	0.31	0.29	+	+	-	-
131.	Glyma08g16420.1	ADP/ATP carrier 2	10	1	0.27	0.17	0.25	0.30	+	-	-	-
132.	Glyma1246s00210.1	NADH dehydrogenase subunit 9	3	1	0.27	0.31	0.33	0.29	+	-	-	-
133.	Glyma17g12530.1	FAD/NAD(P) binding oxidoreductase	4	1	0.27	0.67	0.75	0.42	+	+	-	+
134.	Glyma13g44380.1	NADH ubiquinone oxidoreductase 24 kDa subunit putative	4	1	0.27	0.38	0.41	0.65	+	+	-	+
135.	Glyma15g00900.1	NADH ubiquinone oxidoreductase 24 kDa subunit putative	4	1	0.27	0.38	0.41	0.65	+	+	-	+
136.	Glyma15g12040.1	Uncharacterised protein family (UPF0041)	2	1	0.27	0.25	0.40	0.33	+	-	+	-
137.	Glyma17g09860.1	aldehyde dehydrogenase 2B4	4	1	0.27	0.76	0.52	0.78	+	+	-	+
138.	Glyma20g19980.1	heat shock protein 60	20	1	0.27	0.48	0.43	0.49	+	+	-	+
139.	Glyma07g30290.1	mitochondrial HSO70 2	12	1	0.26	0.33	0.35	0.35	+	+	-	+
140.	Glyma01g03820.1	aldehyde dehydrogenase 2B7	6	1	0.26	0.66	0.43	0.39	+	+	-	+
141.	Glyma04g03310.3	gamma carbonic anhydrase 1	6	1	0.26	0.34	0.31	0.33	+	+	+	+
142.	Glyma10g01600.1	Cytochrome c oxidase subunit Vc family protein	2	1	0.26	0.24	0.64	0.42	+	-	+	-
143.	Glyma02g07340.1	Ubiquinol cytochrome C reductase iron sulfur subunit	6	1	0.26	0.29	0.30	0.19	+	+	+	+
144.	Glyma08g06950.1	mitochondrial HSO70 2	14	1	0.26	0.32	0.35	0.35	+	+	-	+
145.	Glyma16g07150.1	succinate dehydrogenase 2 2	3	1	0.26	0.39	0.40	0.25	+	+	+	+
146.	Glyma02g46390.1	Co chaperone GrpE family protein	3	1	0.26	0.30	0.29	0.34	+	+	+	+
147.	Glyma06g03380.1	gamma carbonic anhydrase 2	8	1	0.26	0.36	0.33	0.32	+	+	-	+
148.	Glyma07g03930.1	Dihydrolipoamide acetyltransferase long form protein	10	1	0.26	0.46	0.31	0.41	+	-	-	+
149.	Glyma07g30920.2	NAD(P)H dehydrogenase B2	2	1	0.26	0.32	0.18	0.45	+	-	+	-
150.	Glyma02g06400.1	succinate dehydrogenase 1 1	6	1	0.26	0.44	0.37	0.35	+	+	+	+
151.	Glyma03g24630.1	NAD dependent malic enzyme 1	5	1	0.26	0.30	0.30	0.37	+	+	+	+
152.	Glyma17g34610.2	FTSH protease 4	5	1	0.25	0.27	0.24	0.21	+	+	-	+
153.	Glyma01g45650.2	presequence protease 2	3	1	0.25	0.57	0.67	0.56	+	+	+	-
154.	Glyma13g03410.1	ATP synthase alpha/beta family protein	2	1	0.25	0.44	0.31	0.22	+	+	+	+
155.	Glyma16g04560.1	glutamate dehydrogenase 1	3	1	0.25	0.31	0.25	0.15	+	+	+	+

156.	Glyma19g28770.2	glutamate dehydrogenase 1	3	1	0.25	0.31	0.25	0.15	+	+	+	+
157.	Glyma16g24320.2	Protein of unknown function (DUF1640)	2	1	0.25	0.26	0.32	0.24	+	-	+	+
158.	Glyma17g17170.1	Protein of unknown function (DUF1640)	2	1	0.25	0.26	0.32	0.24	+	-	+	+
159.	Glyma11g12630.1	RAB GTPase homolog G3F	3	1	0.25	0.17	0.25	0.18	+	+	-	+
160.	Glyma12g04830.1	RAB GTPase homolog G3F	3	1	0.25	0.17	0.25	0.18	+	+	-	+
161.	Glyma09g30410.1	prohibitin 2	3	1	0.25	0.32	0.30	0.60	+	+	-	-
162.	Glyma02g14860.1	3 methylcrotonyl CoA carboxylase	4	1	0.25	0.38	0.69	0.42	+	+	+	+
163.	Glyma07g33620.2	3 methylcrotonyl CoA carboxylase	4	1	0.25	0.38	0.69	0.42	+	+	+	+
164.	Glyma16g00590.1	Dihydrolipoamide acetyltransferase long form protein	11	1	0.25	0.39	0.31	0.33	+	-	-	+
165.	Glyma11g07250.1	succinate dehydrogenase 1 1	9	1	0.25	0.36	0.34	0.29	+	+	+	+
166.	Glyma19g23570.1	succinate dehydrogenase 2 2	5	1	0.25	0.38	0.37	0.31	+	+	+	+
167.	Glyma06g44510.1	ADP/ATP carrier 3	8	1	0.25	0.15	0.17	0.24	+	+	+	-
168.	Glyma10g41330.1	ATP synthase alpha/beta family protein	17	1	0.25	0.46	0.39	0.44	+	+	+	+
169.	Glyma16g26330.1	Ubiquinol cytochrome C reductase iron sulfur subunit	5	1	0.25	0.30	0.30	0.22	+	+	+	+
170.	Glyma01g38200.1	succinate dehydrogenase 1 1	8	1	0.25	0.38	0.33	0.29	+	+	+	+
171.	Glyma10g25630.1	heat shock protein 60	22	1	0.25	0.49	0.45	0.42	+	+	-	+
172.	Glyma08g01460.1	gamma carbonic anhydrase like 2	4	1	0.25	0.54	0.42	0.33	+	+	+	+
173.	Glyma20g25920.1	ATP synthase alpha/beta family protein	18	1	0.25	0.46	0.36	0.42	+	+	+	+
174.	Glyma15g37200.1	LYR family of Fe/S cluster biogenesis protein	2	1	0.25	0.27	3.12	1.45	+	-	+	+
175.	Glyma02g03870.1	aldehyde dehydrogenase 2B7	5	1	0.25	0.39	0.29	0.18	+	+	-	+
176.	Glyma08g10020.2	Ribosomal protein S24/S35 mitochondrial	2	1	0.24	0.35	0.27	0.29	+	+	-	+
177.	Glyma11g08920.1	isocitrate dehydrogenase 1	3	1	0.24	1.30	0.29	0.25	+	+	-	+
178.	Glyma06g42140.1	electron transfer flavoprotein alpha	4	1	0.24	0.26	0.36	0.52	+	+	+	+
179.	Glyma14g00500.1	isocitrate dehydrogenase 1	3	1	0.24	1.36	0.31	0.26	+	+	-	+
180.	Glyma07g01190.1	heat shock protein 60 3A	13	1	0.24	0.69	0.36	0.52	+	+	-	+
181.	Glyma12g02510.1	Pyridoxal phosphate (PLP) dependent transferases	5	1	0.24	0.31	0.24	0.18	+	+	+	+
182.	Glyma01g14800.1	Translation elongation factor EFG/EF2 protein	3	1	0.24	0.25	0.27	0.23	+	+	+	+
183.	Glyma02g35864.1	NADH ubiquinone oxidoreductase B8 subunit putative	2	1	0.24	0.29	0.26	0.31	+	+	+	-
184.	Glyma04g34960.2	NADH ubiquinone oxidoreductase B8 subunit putative	2	1	0.24	0.29	0.26	0.31	+	+	+	-
185.	Glyma06g19750.1	NADH ubiquinone oxidoreductase B8 subunit putative	2	1	0.24	0.29	0.26	0.31	+	+	+	-
186.	Glyma11g16460.2	Translation elongation factor EFG/EF2 protein	4	1	0.24	0.25	0.27	0.24	+	+	+	+
187.	Glyma13g01040.4	voltage dependent anion channel 4	2	1	0.24	0.31	0.35	0.22	+	-	-	-

188.	Glyma17g07140.1	voltage dependent anion channel 4	2	1	0.24	0.31	0.35	0.22	+	-	-	-
189.	Glyma0776s50.1	NADH dehydrogenase subunit 7	5	1	0.24	0.65	0.20	0.33	+	+	+	+
190.	Glyma15g11250.1	peroxiredoxin IIF	4	1	0.24	0.25	0.27	0.34	+	+	+	+
191.	Glyma08g16770.2	Citrate synthase family protein	5	1	0.23	0.36	0.28	0.31	+	+	+	+
192.	Glyma02g28000.1	FAD dependent oxidoreductase family protein	2	1	0.23	0.17	0.31	0.22	+	+	-	-
193.	Glyma08g16470.1	delta subunit of Mt ATP synthase	7	1	0.23	0.32	0.29	0.19	+	+	+	+
194.	Glyma15g42940.1	delta subunit of Mt ATP synthase	7	1	0.23	0.32	0.29	0.19	+	+	+	+
195.	Glyma07g36040.1	lipoamide dehydrogenase 2	10	1	0.23	0.26	0.28	0.26	+	+	-	+
196.	Glyma09g29460.1	Succinyl CoA ligase alpha subunit	4	1	0.23	0.29	0.23	0.27	+	+	+	+
197.	Glyma05g01300.1	aldehyde dehydrogenase 12A1	7	1	0.23	0.46	0.35	0.36	+	+	+	+
198.	Glyma05g34360.1	translocase of the outer mitochondrial membrane 40	2	1	0.23	0.24	0.32	0.23	+	-	-	-
199.	Glyma08g05280.1	translocase of the outer mitochondrial membrane 40	2	1	0.23	0.24	0.32	0.23	+	-	-	-
200.	Glyma13g32790.1	mitochondrial HSO70 2	16	1	0.23	0.28	0.31	0.31	+	+	-	+
201.	Glyma02g01920.1	fumarase 1	8	1	0.23	1.01	0.32	0.31	+	+	-	+
202.	Glyma02g00590.1	51 kDa subunit of complex I	6	1	0.23	0.43	0.35	0.31	+	+	+	+
203.	Glyma02g04780.1	isocitrate dehydrogenase 1	4	1	0.23	1.14	0.23	0.25	+	+	-	+
204.	Glyma16g22640.1	isocitrate dehydrogenase 1	4	1	0.23	1.14	0.23	0.25	+	+	-	+
205.	Glyma10g36420.1	RAB GTPase homolog G3A	2	1	0.22	0.20	0.20	0.21	+	+	+	+
206.	Glyma20g31150.1	RAB GTPase homolog G3A	2	1	0.22	0.20	0.20	0.21	+	+	+	+
207.	Glyma16g33870.1	Succinyl CoA ligase alpha subunit	3	1	0.22	0.29	0.23	0.26	+	+	+	+
208.	Glyma09g04480.1	cytochrome oxidase 2	2	1	0.22	0.17	0.13	0.13	+	-	+	-
209.	Glyma08g39770.1	aldehyde dehydrogenase 2B4	9	1	0.22	0.34	0.34	0.52	+	+	-	+
210.	Glyma14g36280.1	serine hydroxymethyltransferase 2	10	1	0.22	0.62	0.35	2.43	+	+	+	+
211.	Glyma15g06400.2	aldehyde dehydrogenase 6B2	4	1	0.22	0.37	0.30	0.30	+	+	-	+
212.	Glyma02g06340.1	FAD/NAD(P) binding oxidoreductase family protein	4	1	0.22	0.28	0.26	0.25	+	+	+	+
213.	Glyma16g25390.1	FAD/NAD(P) binding oxidoreductase family protein	4	1	0.22	0.28	0.26	0.25	+	+	+	+
214.	Glyma17g04210.1	lipoamide dehydrogenase 2	9	1	0.22	0.26	0.27	0.24	+	+	-	+
215.	Glyma07g30210.1	aldehyde dehydrogenase 6B2	4	1	0.22	0.38	0.30	0.30	+	+	-	+
216.	Glyma08g07110.2	aldehyde dehydrogenase 6B2	4	1	0.22	0.38	0.30	0.30	+	+	-	+
217.	Glyma05g31630.1	alanine:glyoxylate aminotransferase 2	2	1	0.22	0.19	0.86	0.85	+	+	+	+
218.	Glyma08g14850.1	alanine:glyoxylate aminotransferase 2	2	1	0.22	0.19	0.86	0.85	+	+	+	+
219.	Glyma02g12940.2	Tetratricopeptide repeat (TPR) like superfamily protein	3	1	0.22	0.32	0.22	0.25	+	+	+	+

220.	Glyma02g38160.3	serine hydroxymethyltransferase 2	9	1	0.22	0.62	0.35	2.53	+	+	+	+
221.	Glyma05g01305.1	aldehyde dehydrogenase 12A1	4	1	0.22	0.39	0.32	0.36	+	+	+	+
222.	Glyma02g01570.1	Cytochrome c oxidase subunit Vc family protein	2	1	0.22	0.20	0.64	0.34	+	-	+	-
223.	Glyma10g28690.1	Metallopeptidase M24 family protein	2	1	0.22	0.36	0.25	0.25	+	+	-	+
224.	Glyma20g22820.1	Metallopeptidase M24 family protein	2	1	0.22	0.36	0.25	0.25	+	+	-	+
225.	Glyma15g06530.1	mitochondrial HSO70 2	17	1	0.22	0.27	0.24	0.30	+	+	-	+
226.	Glyma18g27710.2	serine transhydroxymethyltransferase 1	3	1	0.22	0.36	0.32	0.33	+	+	+	+
227.	Glyma08g37270.1	serine transhydroxymethyltransferase 1	4	1	0.22	0.36	0.31	0.33	+	+	+	+
228.	Glyma10g02040.3	fumarase 1	5	1	0.21	0.26	0.22	0.24	+	+	-	+
229.	Glyma08g42330.1	Ribosomal protein L14p/L23e family protein	2	1	0.21	0.21	0.24	0.22	+	+	+	+
230.	Glyma15g42301.1	Citrate synthase family protein	4	1	0.21	0.35	0.28	0.28	+	+	+	+
231.	Glyma12g16291.1	electron transfer flavoprotein alpha	2	1	0.21	0.25	0.29	0.61	+	+	+	+
232.	Glyma07g14761.1	ATP synthase alpha/beta family protein	2	1	0.21	0.40	0.38	1.20	+	+	+	+
233.	Glyma03g30720.1	GTP binding Elongation factor Tu family protein	9	1	0.21	0.40	0.35	0.39	+	+	+	-
234.	Glyma05g33140.1	GroES like zinc binding alcohol dehydrogenase family protein	5	1	0.21	0.25	0.26	0.23	+	+	-	+
235.	Glyma08g00740.1	GroES like zinc binding alcohol dehydrogenase family protein	5	1	0.21	0.25	0.26	0.23	+	+	-	+
236.	Glyma02g16390.1	methylcrotonyl CoA carboxylase alpha chain mitochondrial	4	1	0.21	0.24	0.22	0.28	+	+	+	+
237.	Glyma04g06210.1	NAD(P) binding Rossmann fold superfamily protein	5	1	0.21	0.29	0.22	0.30	+	+	+	+
238.	Glyma19g33570.1	GTP binding Elongation factor Tu family protein	8	1	0.21	0.37	0.32	0.35	+	+	+	-
239.	Glyma04g32460.1	gamma subunit of Mt ATP synthase	5	1	0.20	0.29	0.27	0.39	+	+	-	+
240.	Glyma10g25670.1	GRIM 19 protein	2	1	0.20	0.24	0.32	0.27	+	-	-	-
241.	Glyma11g07540.1	gamma carbonic anhydrase 1	4	1	0.20	0.31	0.32	0.23	+	+	+	+
242.	Glyma01g37780.1	gamma carbonic anhydrase 1	5	1	0.20	0.30	0.30	0.22	+	+	+	+
243.	Glyma18g52430.2	2 oxoglutarate dehydrogenase E1 component	20	1	0.20	0.38	0.22	0.31	+	+	+	+
244.	Glyma12g02340.1	Ribosomal protein S5 domain 2 like superfamily protein	3	1	0.20	0.26	0.29	0.31	+	+	-	+
245.	Glyma05g27040.1	Ribosomal protein S24/S35 mitochondrial	4	1	0.20	0.35	0.28	0.32	+	+	-	+
246.	Glyma06g14620.1		2	1	0.20	0.11	0.08	0.16	+	+	+	+
247.	Glyma13g31520.1	Alpha helical ferredoxin	3	1	0.20	0.31	0.27	2.91	+	+	+	+
248.	Glyma15g07790.1	Alpha helical ferredoxin	3	1	0.20	0.31	0.27	2.91	+	+	+	+
249.	Glyma18g43300.2	electron transport SCO1/SenC family protein	3	1	0.20	0.18	0.21	0.18	+	+	+	+
250.	Glyma06g22050.1	gamma subunit of Mt ATP synthase	5	1	0.20	0.28	0.27	0.31	+	+	-	+
251.	Glyma02g10470.1	2 oxoglutarate dehydrogenase E1 component	19	1	0.20	0.38	0.23	0.28	+	+	+	+

252.	Glyma19g00800.1	translation elongation factor Ts (EF Ts) putative	3	1	0.20	0.29	0.20	0.18	+	+	-	+
253.	Glyma18g18910.1	aldehyde dehydrogenase 2B4	10	1	0.19	0.33	0.33	0.39	+	+	-	+
254.	Glyma04g08460.1	Ribosomal protein S5 family protein	2	1	0.19	0.39	0.54	0.25	+	+	+	+
255.	Glyma05g27360.1	ornithine delta aminotransferase	2	1	0.19	0.65	0.54	0.27	+	+	+	+
256.	Glyma08g10340.1	ornithine delta aminotransferase	2	1	0.19	0.65	0.54	0.27	+	+	+	+
257.	Glyma10g43610.2	2 oxoglutarate dehydrogenase E1 component	2	1	0.19	0.29	0.27	0.22	+	+	+	+
258.	Glyma11g10000.1	Ribosomal protein S5 domain 2 like superfamily protein	3	1	0.19	0.19	0.25	0.30	+	+	-	+
259.	Glyma05g30090.3	LETM1 like protein	6	1	0.19	0.19	0.23	0.20	+	+	+	+
260.	Glyma02g00270.1	PENTATRICOPEPTIDE REPEAT 596	6	1	0.19	0.38	0.31	0.31	+	+	+	+
261.	Glyma08g45710.1	2Fe 2S ferredoxin like superfamily protein	4	1	0.19	0.32	0.28	0.24	+	+	+	-
262.	Glyma01g42120.2	Glycine cleavage T protein family	2	1	0.18	0.19	0.18	0.22	+	+	+	+
263.	Glyma10g29580.1	MIRO related GTP ase 1	9	1	0.18	0.24	0.21	0.19	+	-	-	-
264.	Glyma20g37730.1	MIRO related GTP ase 1	9	1	0.18	0.24	0.21	0.19	+	-	-	-
265.	Glyma08g13240.1	LETM1 like protein	5	1	0.18	0.20	0.15	0.29	+	+	+	+
266.	Glyma13g18950.1	NAD(P) binding Rossmann fold superfamily protein	6	1	0.18	0.22	0.27	1.82	+	+	-	+
267.	Glyma03g14780.1	plant uncoupling mitochondrial protein 1	2	1	0.18	0.16	0.13	0.18	+	-	-	-
268.	Glyma09g33480.1	serine transhydroxymethyltransferase 1	2	1	0.18	0.35	0.31	0.29	+	+	+	+
269.	Glyma08g17450.1	aldehyde dehydrogenase 5F1	6	1	0.18	0.37	0.43	0.33	+	+	-	+
270.	Glyma15g41690.1	aldehyde dehydrogenase 5F1	7	1	0.18	0.36	0.30	0.33	+	+	-	+
271.	Glyma13g23790.1	formate dehydrogenase	7	1	0.17	0.21	0.24	0.18	+	+	+	+
272.	Glyma19g01210.1	formate dehydrogenase	7	1	0.17	0.21	0.24	0.18	+	+	+	+
273.	Glyma04g40420.1	SPFH/Band 7/PHB domain containing membrane protein	3	1	0.17	0.32	0.41	0.30	+	+	-	+
274.	Glyma03g04990.1	PYRIMIDINE 4	2	1	0.17	0.07	0.18	0.14	+	+	+	+
275.	Glyma18g40240.1	Tetratricopeptide repeat (TPR) like	4	1	0.17	0.20	0.20	0.24	+	+	-	+
276.	Glyma02g46900.1	Haloacid dehalogenase like hydrolase (HAD)	4	1	0.16	0.37	0.36	0.24	+	+	+	+
277.	Glyma07g18460.1	electron transport SCO1/SenC family protein	2	1	0.16	0.14	0.20	0.16	+	+	+	+
278.	Glyma14g01810.1	Haloacid dehalogenase like hydrolase (HAD)	3	1	0.16	0.37	0.36	0.24	+	+	+	+
279.	Glyma20g23200.1	2 oxoglutarate dehydrogenase E1 component	6	1	0.16	0.33	0.18	0.19	+	+	+	+
280.	Glyma04g41420.1	Pentatricopeptide repeat (PPR) superfamily protein	4	1	0.16	0.24	0.28	0.29	+	+	+	+
281.	Glyma13g34810.1	GroES like zinc binding alcohol dehydrogenase family protein	2	1	0.16	0.18	0.18	0.21	+	+	-	+
282.	Glyma12g29060.1	ND	2	1	0.15	0.32	0.43	0.33	+	+	+	+
283.	Glyma11g30090.1	P loop containing nucleoside triphosphate hydrolases	4	1	0.15	0.26	0.24	0.37	+	+	+	+

284.	Glyma02g08540.4	Ribosomal protein S13/S18 family	2	1	0.14	0.12	0.12	0.08	+	+	+	+
285.	Glyma12g35620.1	GroES like zinc binding alcohol dehydrogenase family protein	4	1	0.14	0.17	0.14	0.17	+	+	-	+
286.	Glyma06g13430.1	Pentatricopeptide repeat (PPR) superfamily protein	5	1	0.14	0.27	0.27	0.37	+	+	+	+
287.	Glyma07g03000.1	S15/NS1 RNA binding protein	3	1	0.14	0.16	0.17	0.27	+	+	-	+
288.	Glyma14g03760.1	putative mitochondrial RNA helicase 2	6	1	0.13	0.22	0.20	0.35	+	+	+	+
289.	Glyma01g40510.1	nitrogen fixation S (NIFS) like 1	3	1	0.13	0.07	0.15	0.15	+	+	-	+
290.	Glyma11g04800.1	nitrogen fixation S (NIFS) like 1	3	1	0.13	0.07	0.15	0.15	+	+	-	+
291.	Glyma17g05570.1	ND	4	1	0.12	0.14	0.15	0.14	+	+	+	+
292.	Glyma19g24670.1	Ribosomal protein L9/RNase H1	2	1	0.11	0.13	0.15	0.23	+	+	-	+
293.	Glyma02g45030.1	putative mitochondrial RNA helicase 2	4	1	0.11	0.20	0.16	0.18	+	+	+	+
294.	Glyma09g40030.2	Ribosomal protein L22p/L17e family protein	2	1	0.11	0.10	0.07	0.12	+	+	-	+
295.	Glyma09g39390.1	cysteine synthase C1	9	1	0.11	0.19	0.16	0.10	+	+	-	+
296.	Glyma18g46170.1	Ribosomal protein L22p/L17e family protein	3	1	0.10	0.10	0.07	0.12	+	+	-	+
297.	Glyma12g28610.2	glutamine rich protein 23	3	1	0.10	0.18	0.22	0.22	+	+	-	+
298.	Glyma18g46920.1	cysteine synthase C1	9	1	0.10	0.25	0.16	0.09	+	+	-	+
299.	Glyma07g10170.1	Complex I subunit NDUFS6	3	1	0.10	0.10	0.28	0.28	+	-	-	-
300.	Glyma06g42830.1	aspartate aminotransferase 1	2	1	0.10	0.12	0.12	0.13	+	+	+	+
301.	Glyma11g10800.1	P loop containing nucleoside triphosphate hydrolases	3	1	0.10	0.05	0.11	0.07	+	+	+	+
302.	Glyma12g03080.2	P loop containing nucleoside triphosphate hydrolases	3	1	0.10	0.05	0.11	0.07	+	+	+	+
303.	Glyma08g48050.2	Nucleic acid binding OB fold like protein	3	1	0.09	0.09	0.11	0.27	+	+	+	+
304.	Glyma19g31020.1	PENTATRICOPEPTIDE REPEAT 596	2	1	0.09	0.21	0.22	0.34	+	+	+	+
305.	Glyma10g00280.1	PENTATRICOPEPTIDE REPEAT 596	4	1	0.09	0.32	0.31	0.22	+	+	+	+
306.	Glyma13g17150.1	ND	5	1	0.09	0.13	0.15	0.19	+	+	+	+
307.	Glyma11g29760.1	mitochondrial 28S ribosomal protein S29 related	2	1	0.09	0.21	0.17	0.34	+	+	+	+
308.	Glyma12g06530.1	FTSH protease 10	3	1	0.09	0.15	0.06	0.06	+	+	-	+
309.	Glyma01g41310.1	glutamate dehydrogenase 2	3	1	0.08	0.09	0.15	0.27	+	+	+	+
310.	Glyma11g15210.1	ND	2	1	0.08	0.18	0.14	0.21	+	-	+	+
311.	Glyma17g15740.1	glutamate dehydrogenase 2	3	1	0.08	0.11	0.16	0.25	+	+	+	+
312.	Glyma11g09590.1	SWIB/MDM2 domain superfamily protein	2	1	0.07	0.06	0.02	0.02	+	+	-	+
313.	Glyma01g37910.1	Regulator of chromosome condensation (RCC1) family protein	3	1	0.07	0.20	0.10	0.16	+	+	+	+
314.	Glyma19g22670.1	Mitochondrial ribosomal protein L37	2	1	0.06	0.06	0.04	0.19	+	+	+	-
315.	Glyma19g22420.3	Ribosomal protein L13 family protein	2	1	0.06	0.09	0.12	0.06	+	+	+	-

316.	Glyma19g36450.1	Ribosomal protein L13 family protein	2	1	0.06	0.09	0.12	0.06	+	+	+	-
317.	Glyma20g07443.1	Ribosomal protein L13 family protein	2	1	0.06	0.09	0.12	0.06	+	+	+	-
318.	Glyma05g05460.1	glutamate dehydrogenase 2	3	1	0.06	0.13	0.14	0.22	+	+	+	+
319.	Glyma12g06580.2	FTSH protease 10	2	1	0.05	0.03	0.06	0.06	+	+	-	+

[a] Protein ID, according to the Phytozome database; [b] M.P., matched peptide; [c] Ratio, relative abundance of protein; ND, no description; *p*-value<0.05. (+) sign indicates the proteins predicted to be localized in mitochondria while (-) sign indicates not predicted to be mitochondrial protiens.

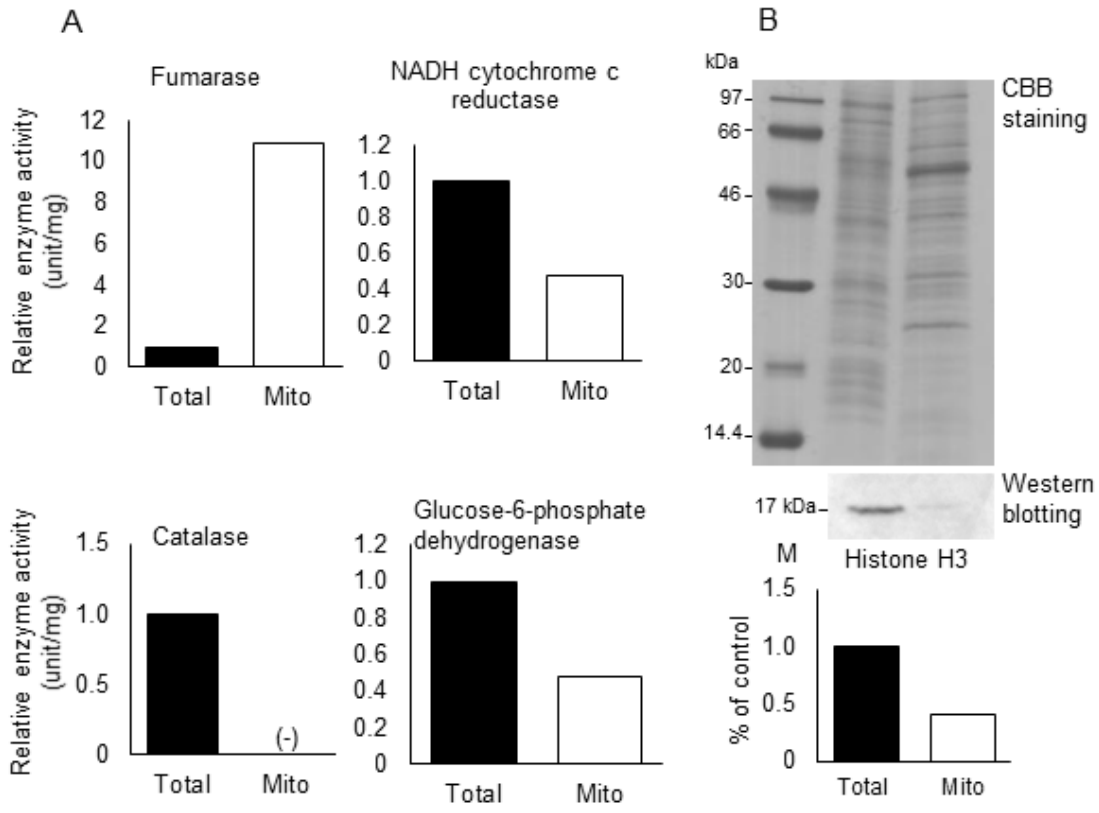
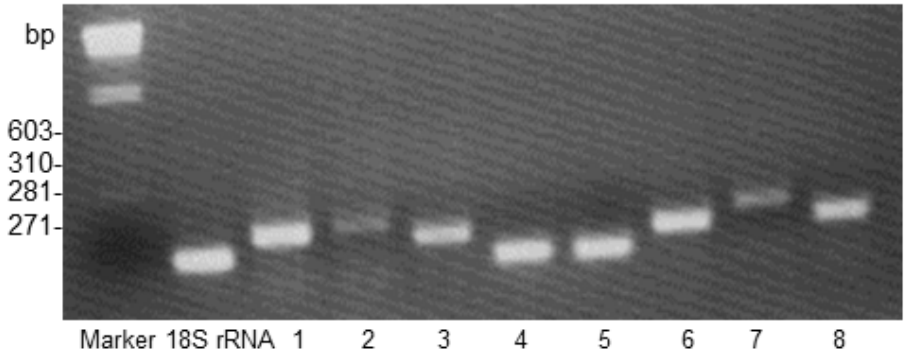


Figure S1. Purity of mitochondrial fractions from the soybean root tip. A) Assessment of purity of the mitochondrial fractions by enzyme activities. Fumarase, glucose-6-phosphate dehydrogenase, NADH cytochrome c reductase, and catalase were used as marker enzymes of mitochondria, cytosol, endoplasmic reticulum, and peroxisomes, respectively. B) Purity assessment of mitochondrial proteins through Western blotting for histone H3. Relative intensities of bands were calculated using image J software.



1. Voltage dependent anion channel
2. Alpha helical ferredoxin
3. Serine hydoxymethyltaransferase 2
4. NAD(P) binding Rossaman fold superfamily protein
5. LYR family of Fe/S cluster biogenesis protein
6. Methylcrotonyl CoA carboxylase alpha chain mitochondrial
7. Casein lytic proteinase B4
8. Isocitrate dehydrogenase 1

Figure S2. Agarose gel electrophoresis of qRT-PCR products. qRT-PCR products of the primers listed in Supplemental Table 1 were separated on an agarose gel, stained with ethidium bromide, and visualized under UV illumination.