Table S1. Primers used for quantitative real-time PCR

Primer description	Primer sequences 5' - 3'
qEF1-α fw	TGAGCACGCTCTTCTTGCTTTCA
qEF1-α rev	GGTGGTGGCATCCATCTTGTTACA
qPCR_TUB4_for	GCGGTCAATGTGGAAACCAG
qPCR_TUB4_rev	TTTCCACCGCTAGCTTCGTT
qPCR_TSN1_for	AGAGCAAGTGCGTGATGGAA
qPCR_TSN1_rev	TTGTGGTTCGCCTTCCCATT
qPCR_TSN2_for	TTCGGCTCAGTGTTCCTTCC
qPCR_TSN2_rev	ACGATGTCGAACCACAGTCC
qPCR_PCAP1_for	TCAAGCAGGCTTTGGTGAGA
qPCR_PCAP1_rev	CTCCGAAGCTAGACGAAGCC
qPCR_PRF1_for	TCGAAGGCAACCATCTCACC
qPCR_PRF1_rev	CGGGCTCCTCAAAGTCCTTC
qPCR_ADF3_for	AACCCATGAGGACCTTGCTG
qPCR_ADF3_rev	AGTTCTCTTCTTGCTGTGTCCG
qPCR_ACT7_for	CCATCGCTCATCGGAATGGA
qPCR_ACT7_rev	TGGAACCACCACTGAGAACG
qPCR_VAB1_for	GAAGAGTGCTATCGGCGAGG
qPCR_VAB1_rev	CCAACAACAGCTTTCATCGCT
qPCR_PATL2_for	TCGTTCCAGTAGAAACCACACC
qPCR_PATL2_rev	AGGCGGTTGCTTTCTCTTCTTT
qPCR_WPP2_for	AGCAGCCTCAAAAGACACAGA
qPCR_WPP2_rev	GGTCTCGATCAGGCGATTCA
qPCR_ANNAT1_for	GCACAAGGACATCAACGCAG
qPCR_ANNAT1_rev	AAGTCACCGGTAGTGTGGTG

Table S2. Quantification details of proteins identified in roots of Arabidopsis *fra2* and *ktn1-2* mutant seedlings. Proteins with significantly changed abundance in the mutants compared to wild type (Col-0) are highlighted in green. n.e.v. = not enough values; n.a. = not applicable

								Fold change		*P* value	
Accession	Description	Coverage Average	# Peptides Average	Score Average	intensity average Col-0	intensity average *fra2*	intensity average *ktn1-2*	*fra2* vs Col-0	*ktn1-2* vs Col-0	*fra2* vs Col-0	*ktn1-2* vs Col-0
gi15241472	tubulin beta-4 chain	11.49	8	71.49	240128.62	47077.51	186521.94	0.20	0.78	0.01	0.69
gi22326646	TUDOR-SN protein 1	6.26	5	82.27	95564.72	143115.98	n.e.v.	1.50	n.e.v.	0.03	n.e.v.
gi15240352	TUDOR-SN protein 2	2.84	3	65.71	38936.46	174370.46	121379.87	4.48	3.12	0.02	0.26
gi79325183	plasma-membrane associated cation-binding protein 1 (MDP25)	22.22	12	88	215393.92	347248.10	494622.54	1.61	2.30	0.01	0.15
gi15224838	profilin 1	43.51	11	57.82	322859.36	351118.86	476648.98	1.09	1.50	0.79	0.02
gi15219901	patellin 2	4.98	4	62.71	313719.17	n.e.v.	69599.32	n.e.v.	0.22	n.e.v.	0.05
gi15221692	pyruvate dehydrogenase E1 component subunit alpha-2	17.56	11	57.29	253127.82	55389.52	66337.07	0.22	0.26	0.01	0.02
gi334187077	aspartate aminotransferase	9.15	6	82.13	121708.75	32934.98	116714.08	0.27	0.96	0.03	0.91
gi30678219	aconitate hydratase 3	13.23	18	166.58	323778.47	109380.02	n.e.v.	0.34	n.e.v.	0.01	n.e.v.
gi334185828	Clp ATPase	3.26	2	35.74	107823.61	37454.35	48712.02	0.35	0.45	0.02	0.03
gi79324564	40S ribosomal protein S5-1	13.53	7	47.38	219962.29	82575.80	94830.59	0.38	0.43	0.01	0.01
gi15225353	Succinyl-CoA ligase [GDP-forming] subunit beta	18.53	10	80.15	263495.39	111292.66	174312.91	0.42	0.66	0.03	0.08
gi15239146	NADP-dependent malic enzyme 2	30.44	38	187.86	1003320.78	441619.72	935877.16	0.44	0.93	0.00	0.69
gi186509731	methionine synthase 2	18.56	33	207.59	962657.34	434796.09	939037.61	0.45	0.98	0.02	0.92
gi18404748	GDSL esterase/lipase	13.99	5	65.13	267720.15	121028.16	158559.70	0.45	0.59	0.03	0.18
gi18401618	WPP domain-containing protein 2	12.22	1	12.05	57976.36	26540.86	n.e.v.	0.46	n.e.v.	0.04	n.e.v.
gi15228895	40S ribosomal protein S26-3	11.54	6	27.3	240410.89	116984.90	329962.43	0.49	1.37	0.00	0.11
gi145334507	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	24.18	57	347.83	1667078.84	815465.26	1473279.95	0.49	0.88	0.01	0.45
gi334187695	voltage dependent anion channel 3	21.17	11	67.7	317107.17	168096.32	164290.15	0.53	0.52	0.03	0.20
gi79313261	PYK10-binding protein 1	39.26	25	148.67	1166764.61	630062.78	644475.44	0.54	0.55	0.01	0.01
gi79313263	jacalin-related lectin	12.67	5	57.36	197278.44	124270.53	170624.66	0.63	0.86	0.03	0.28
gi334187577	40S ribosomal protein S6-2	16.24	8	43.67	228169.71	149712.38	239319.90	0.66	1.05	0.04	0.75
gi15218740	aspartyl protease-like protein	12.7	10	69.22	345642.04	227866.91	389789.99	0.66	1.13	0.05	0.59
gi30681554	mitochondrial F1F0-ATP synthase subunit	23.18	14	101.49	274230.25	181283.09	221030.28	0.66	0.81	0.04	0.20

	Fad										
gi15238217	sulfite reductase	9.03	7	48.75	162345.48	108951.42	70398.53	0.66	0.43	0.15	0.00
gi15225120	Stress responsive alpha-beta barrel domain protein	6.46	4	17.72	238471.81	166266.40	196401.63	0.66	0.82	0.05	0.15
gi15235213	putative caffeoyl-CoA O-methyltransferase	34.36	12	83.45	297355.15	210995.81	59388.23	0.71	0.20	0.07	0.01
gi15237069	phosphoserine aminotransferase	17.67	11	69.68	396111.97	356296.83	263792.36	0.90	0.67	0.33	0.03
gi79313265	JA-responsive protein 1	29.27	15	116.9	439830.08	465524.20	780848.43	1.06	1.78	0.32	0.05
gi18379240	MLP-like protein 328	23.84	9	86.32	237937.93	251919.29	486694.26	1.06	2.05	0.79	0.01
gi15234263	osmotin-like protein OSM34	6.56	1	19.56	195744.35	210699.81	585130.95	1.08	2.99	0.85	0.05
gi15219200	curculin-like (mannose-binding) lectin family protein	19.05	11	84.07	291204.27	325774.36	561134.27	1.12	1.93	0.73	0.01
gi15227259	cyclophilin ROC3	47.4	15	108.15	888249.94	1028777.50	382179.25	1.16	0.43	0.56	0.03
gi30695409	acetoacetyl-CoA thiolase 2	11.06	6	45.72	164420.32	196171.01	62697.70	1.19	0.38	0.66	0.02
gi18406229	TRAF-like protein	10.86	10	47.33	314828.44	376025.56	456418.28	1.19	1.50	0.31	0.02
gi15231137	endoribonuclease L-PSP family protein	25.13	10	82.93	204849.00	265371.55	78599.01	1.30	0.38	0.09	0.01
gi15229559	heat shock protein 60	13.86	18	155.8	398046.67	531190.64	601597.63	1.33	1.51	0.41	0.01
gi15228498	UDP-GLUCOSE PYROPHOSPHORYLASE 1	20.26	15	107.67	429397.39	614619.63	506492.94	1.50	1.18	0.01	0.24
gi15235282	D-3-phosphoglycerate dehydrogenase	19.73	18	119.46	490117.51	721429.62	425614.23	1.50	0.87	0.03	0.28
gi15242451	AIG2-like protein	13.37	3	21.23	49929.87	74003.83	135910.94	1.50	2.72	0.24	0.05
gi15233272	triosephosphate isomerase	48.43	39	217.85	1888300.02	2821310.28	2256180.12	1.50	1.19	0.01	0.31
gi15239019	FK506- and rapamycin-binding protein 15-2	23.93	6	33.42	136788.89	205017.27	229492.03	1.50	1.68	0.03	0.16
gi15241849	heat shock cognate protein 70-1	32.57	58	351.8	2335111.93	3539564.81	3074931.18	1.52	1.32	0.02	0.07
gi15230382	cinnamyl alcohol dehydrogenase 4	13.15	7	61.29	182824.12	280063.58	47992.34	1.53	0.26	0.46	0.05
gi15242753	adenylate kinase 1	11.79	6	44.34	171132.55	264137.25	211883.01	1.54	1.24	0.02	0.17
gi15234648	peroxidase 45	35.69	17	103.39	447213.47	690524.52	951861.94	1.54	2.13	0.05	0.02
gi15221798	60S ribosomal protein L6-1	5.15	3	25.18	123564.32	196333.48	383764.34	1.59	3.11	0.00	0.01
gi15221913	high mobility group A5	6.05	3	18.16	44255.56	70349.10	n.e.v.	1.59	n.e.v.	0.01	n.e.v.
gi15240288	glutamine synthetase 1;1	25	13	81.3	298680.74	482880.39	697291.84	1.62	2.33	0.21	0.00
gi15241316	40S ribosomal protein S8-1	33.78	23	119.99	577782.54	945834.49	1084878.94	1.64	1.88	0.01	0.05
gi15242459	mitochondrial HSO70 2	6.74	10	121.78	229554.60	382186.76	289759.50	1.66	1.26	0.01	0.43
gi18413214	nucleoside diphosphate kinase 1	14.79	6	37.37	226388.99	380425.14	393491.58	1.68	1.74	0.02	0.39
gi145324909	putative mitochondrial-processing peptidase subunit alpha-1	8.87	4	60.09	242648.10	410943.54	372890.28	1.69	1.54	0.01	0.68

gi42572347	adenosine kinase 1	32.45	26	188.85	800267.16	1372076.81	n.e.v.	1.71	n.e.v.	0.04	n.e.v.
gi15230922	dihydrolipoamide S-acetyltransferase	9.79	11	49.86	180992.18	316567.24	392827.01	1.75	2.17	0.09	0.05
gi15229033	S-adenosylmethionine synthase 4	16.79	10	76.2	420397.84	747635.70	183269.66	1.78	0.44	0.00	0.05
gi18391066	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1	6.46	9	119.98	277089.35	494797.65	399212.91	1.79	1.44	0.02	0.16
gi145334765	60S acidic ribosomal protein P1-3	49.56	8	38.75	161868.97	289181.64	168375.04	1.79	1.04	0.03	0.32
gi18407594	vacuolar calcium-binding protein-like protein	18.42	4	22.5	103165.04	187351.14	201343.38	1.82	1.95	0.29	0.04
gi15224648	membrane-associated progesterone binding protein 2	30	5	43.83	203330.29	371469.14	439583.49	1.83	2.16	0.03	0.02
gi15227443	40S ribosomal protein S2-3	10.53	8	33.78	136552.55	250379.15	111717.93	1.83	0.82	0.05	0.36
gi145334587	glutamine synthetase	5.12	3	30.66	46791.31	88530.95	106136.58	1.89	2.27	0.01	0.09
gi18415982	tetratricopeptide repeat protein	15.42	14	80.39	222702.14	427357.63	486498.43	1.92	2.18	0.03	0.02
gi18399100	40S ribosomal protein S18	13.16	6	46.7	113741.22	227944.46	394848.67	2.00	3.47	0.00	0.00
gi18411901	14-3-3-like protein GF14 omega	16.99	15	112.66	296525.00	596614.35	490908.54	2.01	1.66	0.10	0.05
gi30683366	calmodulin 5	29.2	8	49.72	534139.91	1135953.50	162121.80	2.13	0.30	0.05	0.11
gi186513977	aconitase 2	5.53	3	83.56	53681.62	117622.48	57680.04	2.19	1.07	0.03	0.81
gi15229529	putative dihydropyrimidine dehydrogenase	15.49	6	36.61	75887.92	179154.41	189102.54	2.36	2.49	0.05	0.26
gi15235401	glutathione S-transferase F2	22.17	12	83.3	644121.71	1578139.78	2106336.43	2.45	3.27	0.00	0.01
gi145329204	triosephosphate isomerase	13.07	6	43.94	148158.00	366354.23	305748.27	2.47	2.06	0.00	0.00
gi15226755	60S ribosomal protein L18a-2	10.11	1	14.24	16044.61	40464.01	109596.73	2.52	6.83	0.01	0.09
gi18401719	succinate dehydrogenase 5	6.23	3	21.64	72328.48	183138.94	53708.23	2.53	0.74	0.01	0.53
gi15224960	uclacyanin 2	5.94	1	36.84	22191.00	62684.20	44995.58	2.82	2.03	0.05	0.60
gi15220770	1-aminocyclopropane-1-carboxylate oxidase 2	5.31	3	18.34	67502.45	215775.65	75197.41	3.20	1.11	0.02	0.82
gi145323888	60S ribosomal protein L10-1	7.36	3	13.03	68685.02	219605.46	45737.34	3.20	0.67	0.03	0.45
gi15220930	26S proteasome AAA-ATPase subunit RPT1a	6.1	3	28.29	77453.43	261863.02	261909.23	3.38	3.38	0.00	0.21
gi15239772	aspartate aminotransferase	5.19	1	21.24	29222.23	101792.69	103084.18	3.48	3.53	0.00	0.14
gi15231536	cytochrome P450 71B4	2.98	2	24.75	74432.31	264185.16	135042.09	3.55	1.81	0.02	0.13
gi15233111	cysteine synthase C1	3.26	3	23.97	52115.82	185447.46	136112.56	3.56	2.61	0.05	0.01
gi15223910	aspartate semialdehyde dehydrogenase	10.4	4	49.17	55508.12	230059.47	125986.93	4.14	2.27	0.05	0.05
gi30682601	vacuolar calcium-binding protein-like protein	18.84	1	10.37	57633.53	242968.33	103128.61	4.22	1.79	0.01	0.05
gi18402225	Granulin repeat cysteine protease family protein	12.39	5	30.53	75658.44	343248.11	448897.32	4.54	5.93	0.01	0.00

gi30678607	40S ribosomal protein S7-2	14.66	2	27.07	27700.14	127495.13	n.e.v.	4.60	n.e.v.	0.02	n.e.v.
gi15235002	glycine-rich RNA-binding protein 8	31.95	12	94.88	355850.01	n.e.v.	670428.41	n.e.v.	1.88	n.e.v.	0.00
gi15230358	adenylosuccinate synthetase	7.35	3	21.96	61378.48	0	0	unique in Col0		n.a.	n.a.
gi15236014	Lipase/lipooxygenase, PLAT/LH2 family protein	9.94	2	22.5	38041.31	0	0	unique in Col0		n.a.	n.a.
gi18397991	MD-2-related lipid recognition domain-containing protein	8.75	1	9.53	102011.46	0	0	unique in Col0		n.a.	n.a.
gi18413181	14-3-3-like protein GF14 chi	29.21	22	158.43	797937.21	0	0	unique in Col0		n.a.	n.a.
gi42570831	S-alkyl-thiohydroximate lyase SUR1	5.28	1	10.32	6362.74	0	0	unique in Col0		n.a.	n.a.
gi79313434	gamma-hydroxybutyrate dehydrogenase	8.63	1	28.24	14385.25	0	0	unique in Col0		n.a.	n.a.
gi15227825	ankyrin repeat-containing 2B	8.72	3	28.73	60614.28	106301.7	68474.64	1.75	1.13	0.20	0.51
gi334187059	20S proteasome subunit PBA1	5.15	1	17.04	123007.4	211269.2	186257.8	1.72	1.51	0.241144559	0.16
gi30699430	phosphoglycerate kinase	34.66	32	217.23	1071051	1426708	1117471	1.33	1.04	0.02	0.72
gi334182565	salt tolerance-related protein	30.97	4	38.44	370103.4	246086.9	317337.1	0.66	0.86	0.44	0.55
gi15224582	glutathione S-transferase PHI 10	12.56	7	66.12	265852.9	189714	204613.4	0.71	0.77	0.03	0.13
gi18411929	glutathione S-transferase TAU 19	5.48	6	35.69	227662.9	125293.2	85204.78	0.55	0.37	0.40	0.16
gi15233740	HSP90-like protein GRP94	13.73	17	109.76	532936	686679.5	460754.2	1.29	0.86	0.51	0.75
gi15236375	serine hydroxymethyltransferase 4	16.35	18	103.77	652113.1	1045704	983510.9	1.60	1.51	0.11	0.16
gi15226314	chaperonin-60 alpha	20.99	19	125.7	334610.8	455697.4	385873.6	1.36	1.15	0.32	0.54
gi15236220	putative elongation factor Tu	24.45	9	61.29	383886.1	431545.9	416486.4	1.12	1.08	0.77	0.87
gi15237303	plastidial pyruvate kinase 2	6.04	2	39.58	35424.46	24692.28	n.e.v.	0.70	n.e.v.	0.06	n.e.v.
gi26557005	ATPase subunit 1	19.72	23	208.15	821656	865850.3	505762.8	1.05	0.62	0.89	0.16
gi30690396	Peroxidase family protein	21.59	23	157.24	943373.3	670760	727175.2	0.71	0.77	0.06	0.28
gi42572663	Adenine nucleotide alpha hydrolases-like superfamily protein	21.43	7	37.52	228025.2	132442.5	38634.42	0.58	0.17	0.15	0.08
gi334186539	O-acetylserine (thiol) lyase (OAS-TL) isoform A1	18.63	8	77.44	364273.3	169538.3	320063.4	0.47	0.88	0.06	0.59
gi15228869	copper chaperone	43.8	18	88.41	491435.1	1058727	832819.4	2.15	1.69	0.06	0.18
gi79321468	V-type proton ATPase catalytic subunit A	25.68	28	184.93	922538.3	609994	1050542	0.66	1.14	0.06	0.44
gi145323700	60S acidic ribosomal protein P1-1	49.11	9	40.16	263484	524790.1	269684.6	1.99	1.02	0.06	0.95
gi79607896	jacalin-like lectin domain-containing protein	32.91	52	287.78	1672903	2084962	1937789	1.25	1.16	0.06	0.55
gi15232626	beta-glucosidase 23	31.87	34	316.73	1659867	511820.5	1076137	0.31	0.65	0.07	0.37
gi30680156	fructose-bisphosphate aldolase 4	16.43	18	85.77	1525785	922811.3	1445175	0.60	0.95	0.07	0.73
gi30683070	tubulin alpha-6 chain	28.81	17	107.08	594989.8	312812.7	421923.1	0.53	0.71	0.07	0.30

gi79329956	beta-ketoacyl-[acyl carrier protein] synthase I	11.96	7	36.83	176865.2	54172.24	166929.6	0.31	0.94	0.07	0.90
gi15226212	60S ribosomal protein L7-2	6.2	1	16.54	52260.27	111169.4	52038.55	2.13	1.00	0.08	0.99
gi79315306	alpha-soluble NSF attachment protein 2	5.42	1	18.14	34115.82	85732.52	123493.2	2.51	3.62	0.08	0.08
gi15225232	myrosinase-binding protein-like protein	3.79	1	40.22	73486.83	35284.07	44856.13	0.48	0.61	0.08	0.22
gi79315846	proteasome subunit beta type-1	13.45	4	36.55	135330.6	239261.7	199524.7	1.77	1.47	0.08	0.38
gi186502696	aminopeptidase family protein	23.27	31	197.74	699849.6	588234.6	547988.6	0.84	0.78	0.09	0.05
gi18379072	aspartyl protease-like protein	9.45	4	41.6	132442.1	51730.51	n.e.v.	0.39	n.e.v.	0.09	n.e.v.
gi18423437	probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	26.04	7	42.49	183652.7	301487	255523.9	1.64	1.39	0.09	0.25
gi15229522	adenosylhomocysteinase 2	18.14	14	128.1	323730.3	542894.2	n.e.v.	1.68	n.e.v.	0.10	n.e.v.
gi15220424	methylesterase PCR A	12.39	13	90.3	394656.1	962139.7	520390.6	2.44	1.32	0.10	0.65
gi15241125	40S ribosomal protein S24-2	11.28	9	36.59	81865.11	142543.9	100467.1	1.74	1.23	0.10	0.21
gi15241051	60S ribosomal protein L22-3	10.48	1	21.24	136593.8	364631	223416.9	2.67	1.64	0.10	0.34
gi30685069	actin 2	15.63	14	108.61	82023.85	482384.7	144480	5.88	1.76	0.10	0.20
gi334186158	transketolase	5.81	8	64.14	225482.9	367178.1	325339.5	1.63	1.44	0.10	0.30
gi18414298	monodehydroascorbate reductase (NADH)	29.66	17	113.76	519666.5	358611.6	331488.5	0.69	0.64	0.10	0.14
gi15226906	glycine decarboxylase complex protein H2	24.36	5	29.82	105867.2	283194.6	166261.2	2.67	1.57	0.11	0.07
gi15236606	putative apoplastic peroxidase Prx37	19.94	7	69.72	76723.02	144336.8	n.e.v.	1.88	n.e.v.	0.11	n.e.v.
gi15221156	pyrophosphate--fructose-6-phosphate 1-phosphotransferase	16.61	13	91.21	233085.5	529836.5	230435	2.27	0.99	0.11	0.98
gi186510200	transcription factor TCP18	2.8	1	25.86	2971.544	31959.05	23027.12	10.76	7.75	0.11	0.11
gi30684428	dihydrolipoyl dehydrogenase 2	13.02	9	78.08	83174.05	435584.4	n.e.v.	5.24	n.e.v.	0.12	n.e.v.
gi30687521	protein disulfide isomerase-like 1-1	17.04	17	129.45	593145.6	890299.1	667233.6	1.50	1.12	0.12	0.37
gi15233268	20S proteasome alpha-3 subunit	24.4	8	55.89	189118.6	300046.8	199879.4	1.59	1.06	0.12	0.85
gi18395103	14-3-3-like protein GF14 epsilon	17.72	12	110.9	407906.9	229008.6	371855.2	0.56	0.91	0.13	0.67
gi145328282	Methylmalonate-semialdehyde dehydrogenase [acylating]	6.22	1	17.26	27934.12	53320.42	42865.21	1.91	1.53	0.13	0.47
gi79313181	Superoxide dismutase [Mn]	6.52	3	15.36	134552.9	192707.6	193478	1.43	1.44	0.13	0.11
gi30694819	60S ribosomal protein L11-2	8.14	1	26.89	35442.36	154771.9	24248.15	4.37	0.68	0.13	0.50
gi15238030	peroxidase 57	4.47	3	26.56	136596.5	41044.43	n.e.v.	0.30	n.e.v.	0.13	n.e.v.
gi15242674	glutaredoxin-C2	34.23	8	41.69	212851.1	148184.5	244587.7	0.70	1.15	0.14	0.58
gi15224669	probable fructokinase-1	17.85	7	59.04	353801.4	617127.9	418762.7	1.74	1.18	0.14	0.75
gi15238284	CBS domain-containing protein	26.7	8	73.39	207136.4	309751.4	333288.1	1.50	1.61	0.14	0.21

gi15218869	isocitrate dehydrogenase	30.98	34	236.4	1189832	1741557	1004663	1.46	0.84	0.14	0.65
gi15221019	GDSL esterase/lipase	42.46	26	176.55	1000005	565640.9	1074455	0.57	1.07	0.15	0.79
gi15227376	S-formylglutathione hydrolase	4.58	2	17.57	56487.42	32323.48	56323.47	0.57	1.00	0.15	0.99
gi30697327	beta-glucosidase 21	6.13	9	134.82	331499.9	182980.3	226582.3	0.55	0.68	0.16	0.25
gi79314806	ATP synthase subunit d	9.84	3	24.91	232170.3	386089.1	214557.7	1.66	0.92	0.16	0.84
gi145332383	translational initiation factor 4A-1	10.95	8	59.4	399775.2	1084615	312686.4	2.71	0.78	0.16	0.69
gi15219721	malate dehydrogenase	35.84	33	278.82	1198445	597346.1	814478.6	0.50	0.68	0.16	0.28
gi15220216	annexin 1	19.24	10	112.36	594053.9	482464.8	399719.4	0.81	0.67	0.16	0.20
gi15237488	prohibitin 3	11.55	4	24.78	113197.3	155499.8	87873.02	1.37	0.78	0.16	0.68
gi18404382	malate dehydrogenase 1	39.3	33	167.15	1015713	780770.1	923296.7	0.77	0.91	0.16	0.84
gi186513287	argininosuccinate synthase	3.78	3	33.98	44407.28	155850.8	51412.36	3.51	1.16	0.17	0.75
gi79557518	NADPH-dependent thioredoxin reductase A	15.61	11	66.47	287342.6	183857.5	n.e.v.	0.64	n.e.v.	0.17	n.e.v.
gi18394249	transducin/WD40 repeat-like superfamily protein	3.9	1	3.75	12181.55	110242.1	53317.78	9.05	4.38	0.17	0.12
gi15232865	reversibly glycosylated polypeptide 1	7.56	5	53.08	212790.2	81049.55	n.e.v.	0.38	n.e.v.	0.17	n.e.v.
gi145331433	fumarate hydratase 1	4.88	5	31.35	149029.1	249892.9	222139.1	1.68	1.49	0.17	0.40
gi15241286	pyruvate dehydrogenase E1 beta	21.49	13	84.97	436970.5	522400.5	552052.9	1.20	1.26	0.19	0.05
gi30691988	chaperone protein dnaJ 3	3.5	1	7.27	35153.51	74732.45	53895.21	2.13	1.53	0.19	0.23
gi15227987	bifunctional enolase 2/transcriptional activator	55.41	57	348.22	2065402	3408545	2036043	1.65	0.99	0.19	0.91
gi42571329	prohibitin 2	15.84	7	38.35	108785.6	170489.9	n.e.v.	1.57	n.e.v.	0.19	n.e.v.
gi15219413	nascent polypeptide-associated complex subunit beta	24.24	7	37.02	63927.13	118736.8	n.e.v.	1.86	n.e.v.	0.19	n.e.v.
gi30691626	heat shock protein 70-1	8.36	11	127.07	231959.5	356487	317863.8	1.54	1.37	0.20	0.35
gi334186408	L-ascorbate peroxidase S	7.23	4	36.91	58671.7	114218.2	58162.26	1.95	0.99	0.21	0.95
gi15234357	tolB-related protein	2.3	1	24.89	46619.94	91283.19	n.e.v.	1.96	n.e.v.	0.21	n.e.v.
gi15231255	TCP-1/cpn60 chaperonin family protein	16.11	18	96.06	392465.4	494515.8	402418	1.26	1.03	0.22	0.90
gi15233538	profilin 2	29.01	8	46.09	224872.5	350126.8	288355.6	1.56	1.28	0.23	0.40
gi15229095	peroxidase 34	23.8	13	117.14	371096.3	496393.3	372518.7	1.34	1.00	0.23	0.98
gi15241844	Luminal-binding protein 1	15.25	28	182.32	787075.7	589865.9	n.e.v.	0.75	n.e.v.	0.23	n.e.v.
gi15237278	40S ribosomal protein S7-3	20	5	53.4	140769.5	204226.8	247043.4	1.45	1.75	0.25	0.07
gi15222848	glyceraldehyde 3-phosphate dehydrogenase	44.97	40	282.94	2871802	4791030	908515	1.67	0.32	0.25	0.16
gi15218877	thioredoxin-dependent peroxidase 1	24.07	2	19.35	34522.62	77674.66	n.e.v.	2.25	n.e.v.	0.25	n.e.v.
gi18405982	AIG2-like protein	13.61	1	17.88	115209	79376.46	110613.3	0.69	0.96	0.25	0.88

gi15224221	Aconitase/3-isopropylmalate dehydratase protein	12.75	6	52.45	143631.2	168321.2	n.e.v.	1.17	n.e.v.	0.26	n.e.v.
gi18418498	NADH-ubiquinone oxidoreductase complex 1B22	17.09	2	7.41	208558.5	151687.6	223466.8	0.73	1.07	0.27	0.83
gi30681492	glycine-rich RNA-binding protein 7	28.93	18	88.98	815631.8	1274428	736228.7	1.56	0.90	0.28	0.80
gi15237613	peroxidase 69	12.99	2	22.18	178051.3	311319	477299.3	1.75	2.68	0.29	0.10
gi30697102	Ran-binding protein 1	9.13	1	6.42	34335.47	157514.8	n.e.v.	4.59	n.e.v.	0.30	n.e.v.
gi15231705	60S ribosomal protein L38	17.39	1	8.35	28664.91	131144	n.e.v.	4.58	n.e.v.	0.30	n.e.v.
gi18397457	peroxiredoxin-2F	14.93	4	29.85	238292.1	273962.7	178243	1.15	0.75	0.31	0.24
gi145329995	glutathione S-transferase PHI 9	21.08	10	76.73	220587.4	123652.7	164151.7	0.56	0.74	0.31	0.55
gi15241847	heat shock protein 70	16.23	17	165.97	1232496	1704128	n.e.v.	1.38	n.e.v.	0.32	n.e.v.
gi15221141	aspartic proteinase A1	24.31	15	95.99	250559.9	192369.6	175216.4	0.77	0.70	0.32	0.68
gi15232215	methylenetetrahydrofolate reductase 1	5.91	3	37.43	114191	48802.48	46025.46	0.43	0.40	0.33	0.32
gi334185265	TCP-1/cpn60 chaperonin family protein	7.93	4	35.74	132987.2	75716.54	44749.87	0.57	0.34	0.33	0.07
gi15229806	2-Cys peroxiredoxin BAS1	6.39	2	13.54	28723.55	50748.03	50031.86	1.77	1.74	0.33	0.19
gi15236211	rotamase cyclophilin 5	40.7	13	129.46	707180	1142772	498407.8	1.62	0.70	0.34	0.47
gi238478984	homolog of anti-oxidant 1	21.21	1	21.82	107749.7	227350.8	n.e.v.	2.11	n.e.v.	0.34	n.e.v.
gi15218420	UDP-L-rhamnose synthase	3.44	2	60.17	70868	106850	n.e.v.	1.51	n.e.v.	0.34	n.e.v.
gi15220874	kunitz type trypsin and protease inhibitor domain-containing protein	11.22	1	12.05	55033.99	237865.8	103154.3	4.32	1.87	0.34	0.29
gi240254562	uncharacterized protein	2.1	2	64.81	80571.09	128972.2	156163.7	1.60	1.94	0.34	0.44
gi18411985	NADH dehydrogenase (ubiquinone) flavoprotein 2	11.37	5	33.19	45401.28	68203.36	n.e.v.	1.50	n.e.v.	0.34	n.e.v.
gi30684617	40S ribosomal protein S12-1	9.72	4	22.33	649675.8	420826.1	499174.4	0.65	0.77	0.35	0.52
gi18394184	chaperonin 10	27.55	5	28.18	105365.3	173316.4	176061.5	1.64	1.67	0.35	0.14
gi15230595	phosphoglycerate kinase 1	24.95	14	95.96	316787.9	508526.5	n.e.v.	1.61	n.e.v.	0.36	n.e.v.
gi18410311	kunitz trypsin inhibitor 1	6.51	1	10.24	34829.83	74958.64	95067.91	2.15	2.73	0.36	0.06
gi15232981	Isopentenyl-diphosphate Delta-isomerase II	12.32	4	39.14	91241.37	117459.4	n.e.v.	1.29	n.e.v.	0.37	n.e.v.
gi30694420	40S ribosomal protein S7-1	19.37	5	32.93	43038.55	71669.22	43347.75	1.67	1.01	0.37	0.97
gi79329200	ribulose bisphosphate carboxylase small chain 3B	8.05	5	33.31	109932.4	158305	158777.2	1.44	1.44	0.37	0.31
gi15222338	60S ribosomal protein L35a-2	22.52	1	7.42	40265.84	68910.13	n.e.v.	1.71	n.e.v.	0.37	n.e.v.
gi30692256	glycine-rich RNA-binding protein 8	42.39	7	52.11	183101	342973.4	n.e.v.	1.87	n.e.v.	0.37	n.e.v.
gi79313237	protein DJ-1-like A	26.02	13	88.48	492270.7	350595.9	485305.1	0.71	0.99	0.37	0.94
gi15238533	40S ribosomal protein S3-3	5.24	3	19.1	243344.6	164318.8	287570.3	0.68	1.18	0.38	0.63

gi15220372	putative 60S ribosomal protein L30-1	34.82	7	32.8	206322.3	287417.9	n.e.v.	1.39	n.e.v.	0.38	n.e.v.
gi18422289	Granulin repeat cysteine protease family protein	11.02	5	47.08	143695.5	402403.7	255139.1	2.80	1.78	0.38	0.08
gi15232603	60S acidic ribosomal protein P0-2	44.69	16	110.25	498277	349160.8	189787.9	0.70	0.38	0.39	0.14
gi334185190	heat shock protein 70-3	25.42	40	255.43	1392172	1762013	2459512	1.27	1.77	0.39	0.07
gi15237054	V-type proton ATPase subunit E1	10.43	5	60.69	123264.4	216234.7	121186.2	1.75	0.98	0.39	0.97
gi186521400	ATP synthase subunit beta-1	37.95	69	415.2	2907771	2506249	2083053	0.86	0.72	0.40	0.40
gi30687350	Elongation factor 1-beta 2	16.96	11	50.5	191020	93444.83	137135.3	0.49	0.72	0.40	0.19
gi79313167	60S ribosomal protein L4-1	2.72	1	22.78	170799.3	242917.2	81244.15	1.42	0.48	0.40	0.20
gi15234781	peptidyl-prolyl cis-trans isomerase CYP1	39.53	12	105.95	577885.3	746948.6	767629	1.29	1.33	0.41	0.30
gi15231024	T-complex protein 1 subunit alpha	7.34	4	40.89	135802.8	51421.25	n.e.v.	0.38	n.e.v.	0.41	n.e.v.
gi30686836	dehydrin ERD10	25.1	9	52.87	349229.8	525961.6	243301.7	1.51	0.70	0.41	0.34
gi15229809	uncharacterized protein	5.88	3	11.57	113424.6	170400.4	199748.1	1.50	1.76	0.41	0.62
gi15235944	uncharacterized protein	4.49	1	23.02	97156.15	57556.29	n.e.v.	0.59	n.e.v.	0.43	n.e.v.
gi79327017	clathrin adaptor complexes medium subunit family protein	2.09	2	9.87	133907.1	346761.6	95557.14	2.59	0.71	0.43	0.32
gi79325175	Glutathione S-transferase family protein	14.38	6	26.05	209693	151900.8	53030.94	0.72	0.25	0.44	0.16
gi15239136	thioredoxin H3	11.86	1	5.96	68507.55	123920.5	106366.6	1.81	1.55	0.44	0.71
gi79314469	UDP-XYL synthase 5	12.32	8	52.27	89032.04	136128.9	88169.24	1.53	0.99	0.44	0.99
gi22331875	cysteine synthase C	8.37	4	54.96	87683.57	117906	n.e.v.	1.34	n.e.v.	0.45	n.e.v.
gi334187803	chaperonin 20	11.86	3	21.64	47278.56	101828	n.e.v.	2.15	n.e.v.	0.46	n.e.v.
gi18398761	60S ribosomal protein L9-1	8.76	3	53.49	172740	111122.6	208685.7	0.64	1.21	0.47	0.69
gi18411224	40S ribosomal protein S13-2	7.95	1	10.76	58949.64	42017.33	36569.27	0.71	0.62	0.48	0.41
gi15240080	MATE efflux family protein	4.89	1	23.82	43947.61	123290.5	n.e.v.	2.81	n.e.v.	0.48	n.e.v.
gi30685167	40S ribosomal protein S12-2	9.03	4	21.89	222250.7	348313.8	114499	1.57	0.52	0.48	0.29
gi334186086	ketol-acid reductoisomerase	8.8	9	69.08	154381	96835.4	106170.7	0.63	0.69	0.48	0.59
gi7525040	ATP synthase CF1 beta subunit	6.22	2	26.01	49981.98	41045.72	n.e.v.	0.82	n.e.v.	0.49	n.e.v.
gi15226185	fructose-bisphosphate aldolase 3	20.46	13	83.97	703673.9	419880.6	642582.9	0.60	0.91	0.49	0.88
gi15230534	heat shock protein 70-4	17.85	27	196.33	1176706	1406763	1493865	1.20	1.27	0.50	0.26
gi79314572	40S ribosomal protein S20-2	9.84	1	10.98	78697.45	200038.5	108057.5	2.54	1.37	0.51	0.78
gi15226231	60S acidic ribosomal protein P2-1	54.78	9	49.21	262379.2	370785.5	207903.2	1.41	0.79	0.51	0.63
gi334185072	60S ribosomal protein L23	28	10	41.17	101857.1	76797.7	136349.5	0.75	1.34	0.53	0.42
gi15225798	3-ketoacyl-CoA thiolase 2	24.68	14	83.38	356263.9	387675.9	511825.1	1.09	1.44	0.53	0.15
gi79321519	heat shock protein 91	14.7	19	135.59	164377	226335.7	151683.4	1.38	0.92	0.55	0.87

gi15231702	monodehydroascorbate reductase (NADH)	11.29	5	45.13	128455.5	93598.86	97754.87	0.73	0.76	0.55	0.32
gi79327837	isopropylmalate dehydrogenase 1	19.33	12	71.98	188766.5	123342.6	291064	0.65	1.54	0.56	0.49
gi15231814	60S ribosomal protein L12-2	35.54	12	63.43	331698.6	549980.6	n.e.v.	1.66	n.e.v.	0.56	n.e.v.
gi15240765	voltage dependent anion channel 2	11.96	5	51.94	148394.6	130197.9	110167	0.88	0.74	0.58	0.01
gi15221770	T-complex protein 1 subunit epsilon	11.03	4	34.4	38947.6	73784.2	n.e.v.	1.89	n.e.v.	0.60	n.e.v.
gi15222639	6-phosphogluconate dehydrogenase, decarboxylating 1	24.85	26	123.06	378339.7	488448	n.e.v.	1.29	n.e.v.	0.61	n.e.v.
gi15223138	12-oxophytodienoate reductase 1	15.59	6	66.67	180334.3	160825.7	n.e.v.	0.89	n.e.v.	0.61	n.e.v.
gi15232845	probable mitochondrial-processing peptidase subunit beta	15.25	16	137.88	497740.7	420516.8	424944.6	0.84	0.85	0.62	0.58
gi79313339	alpha/beta-Hydrolases superfamily protein	14.83	6	38.09	119444.4	171868.8	n.e.v.	1.44	n.e.v.	0.63	n.e.v.
gi15220463	peroxidase 3	4.6	4	30.02	175978	223155.6	212490.2	1.27	1.21	0.63	0.67
gi15239571	caffeic acid/5-hydroxyferulic acid O-methyltransferase	22.31	12	78.91	258577.8	243015.9	289862.9	0.94	1.12	0.64	0.70
gi15232776	cell division control protein 48-A	10.51	9	86.29	339664.5	418279.5	200181.2	1.23	0.59	0.64	0.36
gi18423628	universal stress protein (USP) family protein	9.92	1	6.6	60304.91	101342.8	n.e.v.	1.68	n.e.v.	0.65	n.e.v.
gi30697913	Histidinol dehydrogenase	2.88	1	14.2	44488.05	65246.91	n.e.v.	1.47	n.e.v.	0.66	n.e.v.
gi297834302	ATPME3 [Arabidopsis lyrata subsp. lyrata]	4.58	5	51.65	306291.3	244552	427709.9	0.80	1.40	0.66	0.44
gi7525041	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	12.73	7	62.69	198359.1	242585.4	n.e.v.	1.22	n.e.v.	0.67	n.e.v.
gi15228276	translationally-controlled tumor protein-like protein	26.19	9	50	137549.9	94528.87	n.e.v.	0.69	n.e.v.	0.69	n.e.v.
gi18400762	chloroplast inner membrane localized protein	9.52	7	29.23	73150.74	76366.95	177561.8	1.04	2.43	0.69	0.21
gi15222929	V-type proton ATPase subunit B1	35.39	25	162.76	483320.7	538461.2	581760.4	1.11	1.20	0.71	0.57
gi186509939	monodehydroascorbate reductase (NADH)	4.39	1	14.9	81578.19	102903.9	142710.1	1.26	1.75	0.71	0.32
gi15242516	actin 7	20.95	13	105.99	533993.4	498986	666088.8	0.93	1.25	0.72	0.18
gi30687359	phosphoenolpyruvate carboxylase family protein	9.52	2	18.38	593145.6	683454.6	552464.4	1.15	0.93	0.73	0.77
gi30693966	Luminal-binding protein 2	16.64	28	193.03	757719.4	702395.8	308540.6	0.93	0.41	0.73	0.06
gi18391442	V-type proton ATPase subunit C	7.73	3	28.07	113566.5	84752.94	n.e.v.	0.75	n.e.v.	0.74	n.e.v.
gi18399899	PLAT-plant-stress domain-containing protein	23.5	6	43.3	74246.38	87612.09	n.e.v.	1.18	n.e.v.	0.76	n.e.v.
gi79320145	elongation factor EF-1 gamma subunit	12.83	8	47.89	187487.8	173485.7	123947	0.93	0.66	0.77	0.38
gi18403295	gamma-aminobutyrate transaminase POP2	11.31	7	40.5	135639.3	140865.3	144494.3	1.04	1.07	0.81	0.69
gi18407630	beta-fructofuranosidase	9.26	13	84.92	322865.7	295665.8	388350.4	0.92	1.20	0.82	0.65

gi30696930	Monodehydroascorbate reductase	19.09	19	121.05	867706.9	931626.1	994118.5	1.07	1.15	0.85	0.72
gi18425082	gamma carbonic anhydrase 3	5.04	1	15.24	120511	110314.7	n.e.v.	0.92	n.e.v.	0.85	n.e.v.
gi18398038	galactose oxidase/kelch repeat-containing protein	3.65	3	12.87	36533.75	38950.96	53018.84	1.07	1.45	0.85	0.40
gi30696056	elongation factor EF-2	28	43	312.56	878604.3	833860.6	764487.1	0.95	0.87	0.86	0.63
gi15240075	succinate dehydrogenase [ubiquinone] flavoprotein subunit 1	14.51	10	52.64	139569.6	122781.1	n.e.v.	0.88	n.e.v.	0.87	n.e.v.
gi22331076	Subtilase family protein	1.67	2	13.71	139299.1	155701.9	45854.63	1.12	0.33	0.87	0.17
gi145333007	Nascent polypeptide-associated complex subunit alpha-like protein 4	7.11	5	40.4	299610.7	275094.5	106772.6	0.92	0.36	0.87	0.25
gi15229530	glutamine synthetase cytosolic isozyme 1-3	4.52	4	43.01	82226.7	77084.28	70161.39	0.94	0.85	0.90	0.72
gi15220941	WD-40 repeat ArcA-like protein	17.43	7	90.15	221660	213089.7	171585.7	0.96	0.77	0.91	0.47
gi15237853	UDP-glucuronic acid decarboxylase 3	12.28	7	52.42	86856.38	92710.75	52710.17	1.07	0.61	0.91	0.53
gi15227257	ATP synthase subunit gamma	22.46	10	64.24	149112.8	158408.4	n.e.v.	1.06	n.e.v.	0.91	n.e.v.
gi15232820	malate dehydrogenase	34	20	125.56	581272.8	598337.7	631753.1	1.03	1.09	0.92	0.72
gi240255920	putative beta-1,3-endoglucanase that interacts with the 30C02 cyst nematode effector. May play a role in host defense.	9.59	2	30.23	126910.8	138988.2	n.e.v.	1.10	n.e.v.	0.92	n.e.v.
gi15239652	flavodoxin-like quinone reductase 1	16.18	4	27.74	191462.7	179291.8	215537.3	0.94	1.13	0.93	0.85
gi15237548	40S ribosomal protein S28-1	18.75	2	9.98	72985.71	77092.71	132498	1.06	1.82	0.93	0.50
gi15236566	polyketide cyclase/dehydrase and lipid transport superfamily protein	7.28	1	43.49	181644.9	173051.3	185643.5	0.95	1.02	0.94	0.94
gi145323784	L-ascorbate peroxidase 1	12.05	7	95.46	131688.2	127523.7	66033.87	0.97	0.50	0.94	0.22
gi15225103	glutathione peroxidase GPx	7.69	4	30.94	166707.6	171230.7	126960.7	1.03	0.76	0.95	0.40
gi334183935	dehydrin ERD14	7.03	5	26.69	78409.02	76113.45	35279.99	0.97	0.45	0.96	0.19
gi15231715	fructose-bisphosphate aldolase	43.58	34	229.3	2494621	2478479	2067356	0.99	0.83	0.96	0.31
gi15242465	soluble inorganic pyrophosphatase 1	8	2	35	93259.8	94329.73	244143.1	1.01	2.62	0.97	0.12
gi334188531	protein disulfide isomerase-like 1-4	2.63	1	16.05	118331.9	121752.5	180427	1.03	1.52	0.98	0.63
gi145323706	Rossmann-fold NAD(P)-binding domain-containing protein	5.38	2	13.49	119203.8	165346.8	122228.6	1.39	1.03	0.98	0.23
gi79320796	glutamine synthetase	35.66	12	73.52	351937.2	349584.1	545855.2	0.99	1.55	0.98	0.34
gi15221284	putative calcium-binding protein CML13	10.81	2	21.04	233085.5	230435	n.e.v.	0.99	n.e.v.	0.98	n.e.v.
gi15219406	glyceraldehyde-3-phosphate dehydrogenase of plastid	22.51	14	70.62	450783.7	447730.4	429739.2	0.99	0.95	0.99	0.88
gi79326317	catalase 2	6.54	4	63.72	141989.2	86071.98	341622.3	0.61	2.41	0.56	0.11
gi145334543	26S proteasome non-ATPase regulatory subunit 14	5.79	1	16.82	36019.95	n.e.v.	43408.75	n.e.v.	1.21	n.e.v.	0.82

gi145362282	spermidine synthase 1	13.15	5	39.49	115616.4	n.e.v.	103808	n.e.v.	0.90	n.e.v.	0.89
gi15220668	putative phosphoglucomutase	2.4	1	28.2	40091.76	n.e.v.	10533.42	n.e.v.	0.26	n.e.v.	0.24
gi15222163	glutathione S-transferase DHAR2	5.16	1	5.53	54461.99	n.e.v.	63786.79	n.e.v.	1.17	n.e.v.	0.75
gi15229062	4-coumarate--CoA ligase-like 10	2.53	2	30.71	67040.88	n.e.v.	80302.71	n.e.v.	1.20	n.e.v.	0.74
gi15229231	glyceraldehyde-3-phosphate dehydrogenase C subunit 1	54.14	67	408.73	2139642	n.e.v.	2594521	n.e.v.	1.21	n.e.v.	0.18
gi15229595	TCP-1/cpn60 chaperonin family protein	6.72	4	42.74	100980.1	n.e.v.	92050.24	n.e.v.	0.91	n.e.v.	0.73
gi15232058	peroxidase 27	9.66	3	24	54508.31	n.e.v.	37508.78	n.e.v.	0.69	n.e.v.	0.31
gi15232074	voltage dependent anion channel 1	11.23	6	46.72	273267.4	n.e.v.	78210.07	n.e.v.	0.29	n.e.v.	0.08
gi15235280	ADP/ATP carrier 3 protein	2.9	2	31.95	71026.49	n.e.v.	200950.3	n.e.v.	2.83	n.e.v.	0.08
gi15236376	adenosylhomocysteinase	28.45	23	166.19	662582.2	n.e.v.	726896.3	n.e.v.	1.10	n.e.v.	0.72
gi15236932	Isocitrate dehydrogenase [NAD] regulatory subunit 1	7.08	3	33.72	66444.4	n.e.v.	108913.1	n.e.v.	1.64	n.e.v.	0.13
gi15238025	NADH--cytochrome B5 reductase 1	6.76	3	13.06	34881.67	n.e.v.	63898.6	n.e.v.	1.83	n.e.v.	0.56
gi15238104	TIR-NBS-LRR class disease resistance protein	1.35	1	25.67	14663.69	n.e.v.	13795.55	n.e.v.	0.94	n.e.v.	0.93
gi15238776	cytochrome B5 isoform E	11.19	5	22.74	75165.04	n.e.v.	121170.5	n.e.v.	1.61	n.e.v.	0.59
gi15242351	reversibly glycosylated polypeptide 2	11.94	8	47.85	158284	n.e.v.	142398.4	n.e.v.	0.90	n.e.v.	0.84
gi18379244	MLP-like protein 329	15.23	7	71.73	210160	n.e.v.	255337.5	n.e.v.	1.21	n.e.v.	0.20
gi18401345	Adenine nucleotide alpha hydrolases-like superfamily protein	11.04	2	16.24	38976.06	n.e.v.	30912.31	n.e.v.	0.79	n.e.v.	0.23
gi18406515	citrate synthase 4	11.63	3	24.56	56884.96	n.e.v.	74330.12	n.e.v.	1.31	n.e.v.	0.57
gi18410982	S-phase kinase-associated protein 1	9.38	6	30.72	79933.94	n.e.v.	41013.33	n.e.v.	0.51	n.e.v.	0.10
gi186504418	aspartate aminotransferase	7.21	5	48.47	118972.7	n.e.v..	107089.3	n.e.v..	0.90	n.e.v..	0.70
gi186510565	short-chain dehydrogenase reductase 4	4.62	1	3.27	70809.8	n.e.v.	92597.47	n.e.v.	1.31	n.e.v.	0.48
gi186532608	elongation factor 1-alpha 4	18.71	13	166.82	851893.7	n.e.v.	646468.9	n.e.v.	0.76	n.e.v.	0.70
gi238479752	ribosomal protein S5/Elongation factor G/III/V family protein	12.07	12	120.95	330763.5	n.e.v.	389038.9	n.e.v.	1.18	n.e.v.	0.64
gi238480186	HSP20-like chaperone	5.83	4	31.09	140796.2	n.e.v.	131995.7	n.e.v.	0.94	n.e.v.	0.27
gi30678090	Chaperone protein htpG family protein	8.11	5	74.15	46704.59	n.e.v.	117455.9	n.e.v.	2.51	n.e.v.	0.09
gi30678559	6-phosphogluconate dehydrogenase, decarboxylating 3	16.46	21	100.22	168067.9	n.e.v.	399081.3	n.e.v.	2.37	n.e.v.	0.10
gi30680575	phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	7.68	6	81.7	312741.8	n.e.v.	290315.7	n.e.v.	0.93	n.e.v.	0.84
gi30689398	Cytochrome bd ubiquinol oxidase	23.76	2	17.95	98895.74	n.e.v.	35175.03	n.e.v.	0.36	n.e.v.	0.37
gi30697298	actin depolymerizing factor 3	39.52	4	29.55	298772.3	n.e.v.	120221.8	n.e.v.	0.40	n.e.v.	0.13

gi334185304	DNA damage-inducible protein 1	6.54	1	16.31	49348.04	n.e.v.	38277.77	n.e.v.	0.78	n.e.v.	0.67
gi334185905	putative nuclear DNA-binding protein G2p	2.6	1	35.08	38657.68	n.e.v.	41094.57	n.e.v.	1.06	n.e.v.	0.93
gi79313259	Nitrile-specifier protein 1	19.15	14	117.46	522573.8	n.e.v.	709536.5	n.e.v.	1.36	n.e.v.	0.14
gi79313984	putative UDP-glucose 6-dehydrogenase 1	13.13	10	52.98	193145.2	n.e.v.	176687.1	n.e.v.	0.91	n.e.v.	0.82
gi79314743	20S proteasome alpha subunit PAD1	10.29	4	24.71	121630.3	n.e.v.	86787.95	n.e.v.	0.71	n.e.v.	0.50
gi79317690	glyoxalase I homolog	5.17	2	20.81	186687.6	n.e.v.	203659.3	n.e.v.	1.09	n.e.v.	0.91
gi79329220	14-3-3-like protein GF14 psi	12.99	14	111.3	218467.6	n.e.v.	198983	n.e.v.	0.91	n.e.v.	0.88
gi79587736	glyoxalase I homolog	14.49	7	47.52	240875.1	n.e.v.	406470.3	n.e.v.	1.69	n.e.v.	0.71

Table S3. Quantification details of proteins identified in aerial parts of Arabidopsis *fra2* and *ktn1-2* mutant seedlings. Proteins with significantly changed abundance in the mutants compared to wild type (Col-0) are highlighted in green. n.e.v. = not enough values; n.a. = not applicable

								Fold change		*P* value	
Accession	Description	Coverage Average	# Peptides Average	Score Average	intensity average Col-0	intensity average *fra2*	intensity average *ktn1-2*	*fra2* vs Col-0	*ktn1-2* vs Col-0	*fra2* vs Col-0	*ktn1-2* vs Col-0
gi18421172	F-box protein	2.8	3	22.92	1525934.87	1496285.72	458709.01	0.98	0.30	0.962	0.001
gi18422548	ATP-dependent Clp protease proteolytic subunit 4	29.79	14	92.62	4296557.72	2994015.35	2780555.61	0.70	0.65	0.236	0.002
gi30699430	phosphoglycerate kinase	29.18	15	104.21	13776048.64	15493346.42	7708960.73	1.12	0.56	0.215	0.003
gi15222551	phosphoribulokinase	49.37	34	253.28	29224342.73	21370677.20	15460624.58	0.73	0.53	0.061	0.003
gi79317147	50S ribosomal protein L4	14.39	12	86.58	7808895.67	1985714.83	2279779.83	0.25	0.29	0.005	0.003
gi15230595	phosphoglycerate kinase 1	67.78	107	689.86	99022520.01	73663523.69	28363047.45	0.74	0.29	0.026	0.003
gi15230544	50S ribosomal protein L9	17.77	8	44.65	4315620.38	3353938.95	2213732.12	0.78	0.51	0.139	0.003
gi15218708	photosystem I reaction center subunit D-2	35.78	18	147.36	29928939.40	20989637.76	45286749.26	0.70	1.51	0.108	0.004
gi15237739	cyclophilin ROC7	5.88	4	30.68	10957142.37	3657898.57	3546535.06	0.33	0.32	0.002	0.004
gi15220620	hydroxypyruvate reductase	33.94	18	109.34	7611724.98	7507159.98	11718680.82	0.99	1.54	0.953	0.004
gi30697298	actin depolymerizing factor 3	29.84	4	26.88	2798163.88	3931799.27	844293.53	1.41	0.30	0.256	0.005
gi15230982	peroxiredoxin Q	28.24	12	95.05	9363992.23	5543512.31	3980676.95	0.59	0.43	0.042	0.005
gi30692346	small subunit ribosomal protein S1	23.56	16	103.48	8943813.19	5884181.99	5048811.79	0.66	0.56	0.055	0.005

gi18404496	NAD(P)-binding Rossmann-fold-containing protein	26.15	11	82.92	8607872.32	5447058.47	5603099.42	0.63	0.65	0.008	0.007
gi15231715	fructose-bisphosphate aldolase	26.26	14	107.52	11694893.04	14913979.01	5815125.12	1.28	0.50	0.042	0.007
gi15217918	DNA-damage resistance protein DRT112	38.92	11	66.51	13493270.03	2986221.23	4416446.13	0.22	0.33	0.011	0.007
gi42573724	lactate/malate dehydrogenase family protein	25.45	11	56.46	6669811.14	6626916.60	3797117.68	0.99	0.57	0.960	0.007
gi15232603	60S acidic ribosomal protein P0-2	21.56	11	82.08	9543945.84	4587130.63	4871300.09	0.48	0.51	0.001	0.009
gi15229349	ribose 5-phosphate isomerase A	23.19	12	63.28	10874344.78	9538380.22	6773457.57	0.88	0.62	0.190	0.009
gi18417239	photosystem II reaction center PSB28 protein	6.01	2	9.41	801932.90	1470543.52	2235577.13	1.83	2.79	0.062	0.010
gi18417320	elongation factor Ts family protein	3.15	2	140.37	2240299.62	2437842.21	4520013.96	1.09	2.02	0.804	0.014
gi15220216	annexin 1	3.79	3	29.09	2805234.71	4684400.46	1554300.17	1.67	0.55	0.000	0.014
gi15236531	microfibrillar-associated protein-like protein	3.45	3	21.26	680626.00	n.e.v.	1477020.25	n.e.v.	2.17	n.e.v.	0.015
gi30696056	elongation factor EF-2	15.42	21	153.47	8767528.43	14268445.56	6254971.93	1.63	0.66	0.065	0.018
gi7525041	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	49.27	185	1453.91	411927407.76	294914235.63	277266195.81	0.72	0.66	0.019	0.019
gi238479213	ribulose bisphosphate carboxylase large chain, catalytic domain	25	13	95.85	15069515.17	10777815.24	9451326.29	0.72	0.63	0.021	0.021
gi79314769	RNA recognition motif-containing protein	11.86	3	52.67	3096627.62	4322926.07	1443801.71	1.40	0.47	0.305	0.021
gi15231137	endoribonuclease L-PSP family protein	25.13	6	37.64	3014346.53	2626481.52	1390369.98	0.87	0.46	0.472	0.022
gi18410833	50S ribosomal protein L31	9.72	3	18.37	6417292.09	2295801.19	4254452.45	0.36	0.66	0.007	0.023
gi145323698	60S acidic ribosomal protein P1-1	16.67	3	11.72	1361039.66	1734301.84	370706.66	1.27	0.27	0.362	0.023
gi18420758	uncharacterized protein	42.67	5	24	71493.56	31188.08	408371.85	0.44	5.71	0.003	0.024
gi15224648	membrane-associated progesterone binding protein 2	30	4	19.5	1728692.29	1892273.62	959780.25	1.09	0.56	0.623	0.025
gi15232820	malate dehydrogenase	16.38	9	64.98	6601561.31	5052235.71	2813838.31	0.77	0.43	0.464	0.026
gi15242465	soluble inorganic pyrophosphatase 1	21.67	10	76.03	11022571.57	5807403.25	5763606.13	0.53	0.52	0.044	0.027
gi26557005	ATPase subunit 1	4.54	3	50.6	2793480.24	7217395.44	5089236.13	2.58	1.82	0.007	0.030
gi30681492	glycine-rich RNA-binding protein 7	18.87	8	53.05	9935985.08	8804814.06	4317353.95	0.89	0.43	0.545	0.030
gi18412632	ATP synthase gamma chain 1	39.14	25	154.86	24872995.56	16236642.88	17444031.98	0.65	0.70	0.022	0.030
gi15235745	serine transhydroxymethyltransferase 1	25.53	27	215.92	19247529.43	18987719.17	15749313.32	0.99	0.82	0.911	0.031
gi15235029	chlorophyll a-b binding protein CP26	31.43	9	64.98	4581201.95	9236218.52	6837980.22	2.02	1.49	0.056	0.033
gi15241286	pyruvate dehydrogenase E1 beta	4.41	3	16.33	1206930.24	1328676.98	548799.25	1.10	0.45	0.665	0.037
gi15228194	Sedoheptulose-1,7-bisphosphatase	17.3	11	120.86	8304146.35	13526281.91	13754753.35	1.63	1.66	0.010	0.045
gi15234637	photosystem II subunit Q-2	32.61	14	105.66	9345172.06	11457444.74	13596700.72	1.23	1.50	0.279	0.051
gi30684767	ATP-dependent zinc metalloprotease FTSH 2	22.73	15	111.71	10406900.99	5403906.75	6122905.04	0.52	0.59	0.027	0.052

gi18415805	ferredoxin/thioredoxin reductase subunit A (variable subunit) 2	7.61	3	16.73	2441812.37	895399.11	1305568.55	0.37	0.53	0.011	0.053
gi30680156	fructose-bisphosphate aldolase 4	12.53	9	44.56	8102332.78	10388963.45	5429628.64	1.28	0.66	0.097	0.053
gi334183935	dehydrin ERD14	7.03	3	12.57	730208.39	164264.57	378435.34	0.22	0.52	0.035	0.058
gi15232626	beta-glucosidase 23	14.69	13	105.67	7464398.90	19013285.63	5980946.45	2.55	0.80	0.008	0.070
gi79327392	peroxisomal NAD-malate dehydrogenase 2	3.95	4	103.97	11969792.64	9599227.40	16061351.34	0.66	1.34	0.031	0.085
gi334186086	ketol-acid reductoisomerase	27.03	17	23.26	1227147.94	3621264.18	2036112.73	2.95	1.66	0.003	0.122
gi334186238	Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein	4.91	2	14.21	1347917.29	289130.91	610818.85	0.21	0.45	0.050	0.137
gi79325271	fructose-bisphosphate aldolase 5	25.17	3	101.57	12439885.88	6433657.19	16000008.98	0.52	1.29	0.001	0.184
gi42565672	protein plastid transcriptionally active 16	31.84	18	78.95	6826913.64	5112829.33	5328989.85	0.66	0.78	0.035	0.210
gi334182565	salt tolerance-related protein	18.63	11	43.01	12896727.52	7426301.93	9497316.55	0.58	0.74	0.029	0.227
gi145334507	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	25.81	9	285.83	27889762.70	40686866.93	23371175.75	1.50	0.84	0.026	0.258
gi15217555	glyceraldehyde-3-phosphate dehydrogenase B	31.24	46	340.25	50628432.48	37530141.97	43822030.20	0.66	0.87	0.002	0.286
gi15242028	germin-like protein subfamily 3 member 3	47.65	50	57.79	9455857.95	6684537.10	11816491.98	0.66	1.25	0.021	0.305
gi15231805	epithiospecifier modifier 1	7.65	5	34.31	3651106.425	1111352.035	3345424.546	0.30	0.91	0.03	0.78
gi15234136	50S ribosomal protein L5	10.31	5	52.82	2743302.09	717615.93	2248307.48	0.26	0.82	0.001	0.564
gi15237593	photosystem I reaction center subunit N	22.81	9	81.26	10513483.92	7633678.30	9283239.98	0.66	0.88	0.000	0.566
gi30678347	carbonic anhydrase 1	52.59	42	265.87	41385244.68	30783020.27	45824341.17	0.66	1.11	0.029	0.570
gi30690396	Peroxidase family protein	7.1	3	13.8	471022.25	893673.94	524371.27	1.90	1.11	0.034	0.622
gi15232123	peptidyl-prolyl cis-trans isomerase CYP38	13.5	6	61.35	2219547.38	1106414.69	2645436.31	0.50	1.19	0.019	0.708
gi15222929	V-type proton ATPase subunit B1	21.4	14	96.4	6520949.41	8049057.24	6213597.77	1.50	0.95	0.008	0.738
gi42573371	carbonic anhydrase 2	47.1	38	238.54	37905917.75	22108355.35	39647420.40	0.58	1.05	0.017	0.778
gi15230922	dihydrolipoamide S-acetyltransferase	10	6	28.81	1997795.85	533972.92	1896046.64	0.27	0.95	0.040	0.826
gi15219721	malate dehydrogenase	14.46	14	108.7	14045684.04	21985576.80	13733268.12	1.57	0.98	0.016	0.884
gi15220854	alkenal/one oxidoreductase	23.58	10	72.58	5527126.12	2881873.56	5532446.97	0.52	1.00	0.007	0.995
gi30687411	Dihydrolipoamide succinyltransferase	6.58	1	28.43	0	464466.70	0	*fra2* unique	n.a.	n.a.	n.a.
gi30681437	SMAD/FHA domain-containing protein	6.7	5	37.62	0	0	7871772.71	*ktn1-2* unique	n.a.	n.a.	n.a.
gi15219623	beta-glucosidase 22	3.63	3	44.19	1885333.25	4339221.91	n.e.v.	2.30	n.e.v.	0.010	n.e.v.
gi15242516	actin 7	16.45	5	46.24	2167456.23	4527353.81	n.e.v.	2.09	n.e.v.	0.020	n.e.v.
gi79326500	putative cinnamyl alcohol dehydrogenase 9	15.76	4	22.94	244304.39	721482.69	n.e.v.	2.95	n.e.v.	0.046	n.e.v.

gi334187997	uncharacterized protein	5.58	1	44.1	739698.22	0	0	Col0 unique	n.a.	n.a.	n.a.
gi15236386	selenium-binding protein 2	3.29	1	9.5	1289730.38	0	0	Col0 unique	n.a.	n.a.	n.a.
gi30689934	adenine phosphoribosyl transferase 1	21.86	2	14.32	0	846412.85	0	*fra2* unique	n.a.	n.a.	n.a.
gi42569601	Calcium-binding EF-hand family protein	4.42	1	24.71	0	1090114.84	0	*fra2* unique	n.a.	n.a.	n.a.
gi145323784	L-ascorbate peroxidase 1	45.78	16	105.28	8389649.71	9816665.12	2402686.50	1.17	0.29	0.68	0.07
gi145323868	Pentapeptide repeat-containing protein	7.77	1	13.01	625649.34	1048222.92	150160.10	1.68	0.24	0.36	0.10
gi145323950	dehydroascorbate reductase	15.09	3	12.6	1900755.29	1832340.86	2340819.09	0.96	1.23	0.95	0.44
gi145327197	putative delta-aminolevulinic acid dehydratase	3.49	1	15.31	536170.17	589583.21	429183.59	1.10	0.80	0.58	0.42
gi145328732	cyclophilin ROC3	21.85	3	29.79	8484373.88	7098976.29	4088843.82	0.84	0.48	0.54	0.06
gi145329204	triosephosphate isomerase	25.16	10	65.48	5297393.67	8483975.07	8401121.91	1.60	1.59	0.28	0.17
gi145331980	60S ribosomal protein L22-2	9.68	2	11.55	1141072.21	717630.13	1823848.78	0.63	1.60	0.51	0.20
gi145332383	translational initiation factor 4A-1	10.95	5	25.34	2429443.12	2537153.02	2998051.76	1.04	1.23	0.58	0.16
gi145332737	nitrilase 1	10.69	5	26.46	1370521.76	1197717.62	n.e.v.	0.87	n.e.v.	0.68	n.e.v.
gi145332989	RNA recognition motif-containing protein	7.38	1	8.7	261250.25	n.e.v.	230520.32	n.e.v.	0.88	n.e.v.	0.78
gi145333041	glycine-rich RNA-binding protein 2	12.4	3	12	2823629.34	n.e.v.	1455543.25	n.e.v.	0.52	n.e.v.	0.06
gi145333043	adenosylhomocysteinase	16	3	35.39	1662490.41	n.e.v.	2473463.22	n.e.v.	1.49	n.e.v.	0.67
gi145334189	40S ribosomal protein S6-1	9.04	1	21.56	384882.59	659162.48	n.e.v.	1.71	n.e.v.	0.40	n.e.v.
gi145334587	glutamine synthetase	43.02	48	379.52	35802464.65	n.e.v.	25929217.12	n.e.v.	0.72	n.e.v.	0.08
gi145334919	ferredoxin-NADP(+)-oxidoreductase 1	46.95	14	109.63	7933062.86	n.e.v.	12329565.36	n.e.v.	1.55	n.e.v.	0.08
gi15217431	26S proteasome AAA-ATPase subunit RPT5B	3.78	1	14.77	815272.83	n.e.v.	445719.22	n.e.v.	0.55	n.e.v.	0.32
gi15217485	chloroplast stem-loop binding protein	32.28	21	165.55	19993629.01	n.e.v.	20152294.47	n.e.v.	1.01	n.e.v.	0.96
gi15217549	Gcn5-interacting protein EML	9.04	2	11.56	207301.17	n.e.v.	116590.34	n.e.v.	0.56	n.e.v.	0.36
gi15218311	glutathione S-transferase TAU 20	5.53	3	12.89	2185367.28	n.e.v.	2015546.58	n.e.v.	0.92	n.e.v.	0.46
gi15218330	light harvesting complex photosystem II subunit 6	13.18	4	25.1	1383594.56	n.e.v.	1221279.37	n.e.v.	0.88	n.e.v.	0.86
gi15218869	isocitrate dehydrogenase	30.49	27	155.41	14418450.87	16088600.48	n.e.v.	1.12	n.e.v.	0.44	n.e.v.
gi15219078	histone H2A protein 9	21.64	1	7.51	97092.31	923912.82	n.e.v.	9.52	n.e.v.	0.25	n.e.v.
gi15219206	glyceraldehyde 3-phosphate dehydrogenase	5.48	3	31.17	2163260.99	n.e.v.	1717005.67	n.e.v.	0.79	n.e.v.	0.23
gi15219413	nascent polypeptide-associated complex subunit beta	12.73	1	14.22	449671.55	328703.78	n.e.v.	0.73	n.e.v.	0.23	n.e.v.

gi15219822	ADP-ribosylation factor GTPase-activating protein AGD2	2.19	1	18.04	995788.74	n.e.v.	575033.96	n.e.v.	0.58	n.e.v.	0.18
gi15219826	ribulose bisphosphate carboxylase small chain 1A	40.56	63	494.97	75189685.77	n.e.v.	71141164.50	n.e.v.	0.95	n.e.v.	0.72
gi15220003	30S ribosomal protein S17	13.42	3	13.28	1452732.86	n.e.v.	1427263.44	n.e.v.	0.98	n.e.v.	0.98
gi15220382	putative plastid developmental protein DAG	16.81	2	25.84	1369796.64	n.e.v.	369990.79	n.e.v.	0.27	n.e.v.	0.01
gi15220770	1-aminocyclopropane-1-carboxylate oxidase 2	6.25	5	34.45	776171.93	n.e.v.	439977.22	n.e.v.	0.57	n.e.v.	0.31
gi15220941	WD-40 repeat ArcA-like protein	3.36	1	15.91	702498.72	1014588.21	n.e.v.	1.44	n.e.v.	0.59	n.e.v.
gi15221102	phosphoribulokinase/uridine kinase-like protein	2.02	4	59.1	2248649.95	n.e.v.	1304434.79	n.e.v.	0.58	n.e.v.	0.44
gi15221187	glycine-rich RNA-binding protein 5	5.54	3	10.24	1413457.55	n.e.v.	503907.12	n.e.v.	0.36	n.e.v.	0.16
gi15221198	glutamine synthetase cytosolic isozyme 1-5	4.53	5	24	2225225.16	2595701.15	n.e.v.	1.17	n.e.v.	0.34	n.e.v.
gi15221261	geranylgeranyl diphosphate reductase	2.78	2	28.61	2086826.00	n.e.v.	955857.29	n.e.v.	0.46	n.e.v.	0.33
gi15221851	acyl carrier protein 2	15.44	6	28.05	1213546.13	1126512.90	811139.33	0.93	0.67	0.87	0.54
gi15222660	phosphoribulokinase/uridine kinase-like protein	1.93	2	41.41	824530.40	n.e.v.	1009471.83	n.e.v.	1.22	n.e.v.	0.69
gi15222848	glyceraldehyde 3-phosphate dehydrogenase	57.1	47	332.02	41606970.22	64780118.13	53247393.36	1.56	1.28	0.07	0.11
gi15222954	thioredoxin-like protein CDSP32	4.64	3	30.12	1527492.72	1120619.24	2216975.68	0.73	1.45	0.57	0.31
gi15222956	plastocyanin 1	14.04	2	13	2407268.80	1497555.65	1921567.96	0.62	0.80	0.06	0.16
gi15223217	probable glycine cleavage system H protein 2	21.69	12	77.4	12506580.42	8157287.82	9796585.81	0.65	0.78	0.02	0.04
gi15223294	pyruvate dehydrogenase E1 component subunit alpha	4.67	3	22.16	681937.79	821464.54	n.e.v.	1.20	n.e.v.	0.13	n.e.v.
gi15223354	plastid ribosomal protein l11	13.06	5	24.51	3817828.25	2267850.40	1052464.48	0.59	0.28	0.34	0.13
gi15223975	protein disulfide-isomerase 2	2.95	1	14.92	1115419.82	745653.15	n.e.v.	0.67	n.e.v.	0.58	n.e.v.
gi15224205	50S ribosomal protein L3-1	17.34	4	43.48	3943068.57	2270580.88	2375984.51	0.58	0.60	0.14	0.27
gi15224451	plastid-specific ribosomal protein 4	10.17	2	10.29	892279.30	n.e.v.	321391.70	n.e.v.	0.36	n.e.v.	0.13
gi15224581	glutathione S-transferase PHI 9	22.79	3	38.08	594687.51	n.e.v.	7794161.45	n.e.v.	13.11	n.e.v.	0.21
gi15224582	glutathione S-transferase PHI 10	20	4	35.85	4208634.26	3850078.10	4268153.15	0.91	1.01	0.79	0.95
gi15225333	monothiol glutaredoxin-S12	15.08	2	17.22	582982.83	609717.64	734198.28	1.05	1.26	0.90	0.51
gi15225798	3-ketoacyl-CoA thiolase 2	8.66	3	27.13	1630031.73	2063097.55	2807386.89	1.27	1.72	0.39	0.18
gi15226185	fructose-bisphosphate aldolase 3	7.16	1	27.56	537573.36	1905572.37	n.e.v.	3.54	n.e.v.	0.08	n.e.v.
gi15226231	60S acidic ribosomal protein P2-1	25.22	3	32.64	2798711.94	3949916.26	584232.94	1.41	0.21	0.58	0.19
gi15226314	chaperonin-60 alpha	34.13	60	404.16	30046199.13	30819695.46	23607334.36	1.03	0.79	0.86	0.24
gi15226690	Uroporphyrinogen decarboxylase	7.11	3	27.16	839792.59	746377.07	481519.92	0.89	0.57	0.82	0.15

gi15226998	outer plastid envelope protein 16-1	18.92	4	23.73	826961.01	599014.18	1102991.17	0.72	1.33	0.36	0.23
gi15227257	ATP synthase subunit gamma	4.62	1	11.28	1420663.46	1094676.92	1485627.01	0.77	1.05	0.36	0.85
gi15227428	putative plastid-lipid-associated protein 3	12.5	4	20.64	1774576.82	1488160.50	2315577.01	0.84	1.30	0.66	0.56
gi15227623	pentatricopeptide repeat-containing protein	3.63	1	22.22	1524409.77	703436.01	n.e.v.	0.46	n.e.v.	0.41	n.e.v.
gi15227987	bifunctional enolase 2/transcriptional activator	26.58	20	124.31	20587853.33	23967917.01	17984998.25	1.16	0.87	0.29	0.38
gi15228098	ribosomal protein L11 family protein	16.87	4	35.71	3353509.37	4542193.76	n.e.v.	1.35	n.e.v.	0.45	n.e.v.
gi15228102	chloroplast RNA binding protein	33.22	17	99.76	9859968.76	9410031.25	9772550.28	0.95	0.99	0.86	0.97
gi15228229	legume lectin-like protein	20.65	8	53.69	6504801.68	1446267.22	n.e.v.	0.22	n.e.v.	0.14	n.e.v.
gi15228276	translationally-controlled tumor protein-like protein	26.79	9	55.47	7786016.48	7504242.16	6765961.74	0.96	0.87	0.89	0.49
gi15228752	calvin cycle protein CP12-2	25.19	1	12.4	923272.94	1805031.88	1565473.18	1.96	1.70	0.14	0.36
gi15228869	copper chaperone	11.57	3	20.54	2287006.35	2442265.80	3383232.86	1.07	1.48	0.87	0.39
gi15228889	ATP sulfurylase 1	4.75	4	25.49	2026411.44	1486967.13	1519748.70	0.73	0.75	0.13	0.14
gi15229018	glutamate-1-semialdehyde 2,1-aminomutase 2	21.61	10	68.11	8159722.39	6401101.75	7340691.94	0.78	0.90	0.52	0.63
gi15229033	S-adenosylmethionine synthase 4	9.67	5	57.1	6888719.74	5431510.63	5215082.74	0.79	0.76	0.65	0.61
gi15229084	peroxidase 33	7.06	1	7.29	178535.65	509696.11	n.e.v.	2.85	n.e.v.	0.08	n.e.v.
gi15229095	peroxidase 34	7.08	3	14.22	786140.95	964035.01	267921.06	1.23	0.34	0.58	0.22
gi15229231	glyceraldehyde-3-phosphate dehydrogenase C subunit 1	57.1	55	314.73	44071052.00	n.e.v.	6308583.89	n.e.v.	0.14	n.e.v.	0.18
gi15229384	chloroplast stem-loop binding protein-41	3.2	1	31.8	912066.98	958608.00	2205603.64	1.05	2.42	0.94	0.41
gi15229443	50S ribosomal protein L1	9.83	9	61.22	5665634.60	3798146.40	3761491.98	0.67	0.66	0.13	0.28
gi15229559	heat shock protein 60	2.25	1	69.22	1122101.04	2346075.15	1845352.21	2.09	1.64	0.42	0.53
gi15229806	2-Cys peroxiredoxin BAS1	35.71	19	100.05	14183743.56	10492212.32	10960332.57	0.74	0.77	0.09	0.13
gi15229809	uncharacterized protein	5.88	5	17.09	3184347.88	3321639.58	3386126.43	1.04	1.06	0.84	0.69
gi15230324	oxygen-evolving enhancer protein 1-2	46.22	44	357.9	52548331.87	64026796.19	58479312.51	1.22	1.11	0.25	0.60
gi15230358	adenylosuccinate synthetase	3.88	1	13.24	745924.57	n.e.v.	450550.46	n.e.v.	0.60	n.e.v.	0.57
gi15231200	chloroplast RNA-binding protein 33	8.81	4	32.43	2167758.52	1982975.82	570755.20	0.91	0.26	0.86	0.06
gi15231255	TCP-1/cpn60 chaperonin family protein	38.26	52	310.3	36960876.00	39805152.40	27147995.90	1.08	0.73	0.58	0.14
gi15232074	voltage dependent anion channel 1	11.23	3	19.21	2436702.86	2386435.22	1206865.43	0.98	0.50	0.97	0.15
gi15232313	mitochondrial transcription termination factor family protein	3.41	2	41.12	1314689.13	664480.74	720255.96	0.51	0.55	0.08	0.20
gi15232503	aspartyl protease family protein	3.76	2	21.13	1517707.97	603808.01	1970272.17	0.40	1.30	0.24	0.56
gi15232567	thioredoxin M4	10.88	5	27.84	1908579.76	1681327.76	2962619.72	0.88	1.55	0.78	0.51

gi15232724	uncharacterized protein	34	11	59.28	6377011.35	4020306.03	4524593.83	0.63	0.71	0.30	0.48
gi15232776	cell division control protein 48-A	4.94	4	38.31	648488.99	923703.46	n.e.v.	1.42	n.e.v.	0.45	n.e.v.
gi15233111	cysteine synthase C1	6.79	4	31.45	2286497.23	1513919.04	1066310.65	0.66	0.47	0.37	0.15
gi15233272	triosephosphate isomerase	48.43	34	193.77	22725284.41	26720416.55	20393172.78	1.18	0.90	0.52	0.59
gi15233291	photosystem I subunit H-1	7.59	4	52.61	4254678.31	5524514.19	2330351.74	1.30	0.55	0.46	0.25
gi15233357	fibrillin	17.61	10	46.53	5298060.34	1608786.68	5161025.09	0.30	0.97	0.15	0.94
gi15233538	profilin 2	9.92	1	15.12	662552.06	n.e.v.	471700.45	n.e.v.	0.71	n.e.v.	0.56
gi15233587	oxygen evolving complex of photosystem II subunit PsbQ	32.29	23	188.34	41468643.49	36764085.21	35378584.63	0.89	0.85	0.64	0.50
gi15233740	HSP90-like protein GRP94	1.58	1	23.57	640436.27	1118889.77	530008.41	1.75	0.83	0.14	0.66
gi15233779	chloroplast heat shock protein 70-1	10.86	10	118.06	13753470.19	n.e.v.	2429839.91	n.e.v.	0.18	n.e.v.	0.08
gi15233985	F-type H+-transporting ATPase subunit delta	20.51	10	85.74	7285028.80	5782385.53	4223932.48	0.79	0.58	0.37	0.24
gi15234781	peptidyl-prolyl cis-trans isomerase CYP1	15.7	1	19.06	732410.87	1646497.84	1646497.84	2.25	2.25	0.47	0.47
gi15234875	acyl carrier protein 4	32.85	10	45.57	6910168.92	4601051.96	6199524.31	0.67	0.90	0.10	0.68
gi15234942	peptide methionine sulfoxide reductase A4	5.43	4	31.71	1414578.04	743974.58	n.e.v.	0.53	n.e.v.	0.07	n.e.v.
gi15235282	D-3-phosphoglycerate dehydrogenase	6.14	4	48.04	2098063.03	3582173.58	1960872.74	1.71	0.93	0.19	0.61
gi15235431	V-type proton ATPase subunit F	13.28	1	9.04	545884.00	397091.27	n.e.v.	0.73	n.e.v.	0.78	n.e.v.
gi15235575	plastid-lipid associated protein PAP / fibrillin family protein	9.68	5	28.07	3099796.08	n.e.v.	4989601.72	n.e.v.	1.61	n.e.v.	0.18
gi15236166	small subunit ribosomal protein 16	42.48	6	33.74	2036087.11	1338713.13	464407.86	0.66	0.23	0.30	0.16
gi15236211	rotamase cyclophilin 5	10.47	2	50.16	4712851.68	5349831.26	766075.48	1.14	0.16	0.81	0.33
gi15236264	catalase 2	23.17	14	137.29	10652982.56	8328679.81	n.e.v.	0.78	n.e.v.	0.61	n.e.v.
gi15236327	thioredoxin M2	18.28	6	31.27	4493676.20	4028145.24	3513330.92	0.90	0.78	0.55	0.08
gi15236375	serine hydroxymethyltransferase 4	6.16	7	41.22	7488640.38	5268927.62	4276233.32	0.70	0.57	0.48	0.24
gi15236566	polyketide cyclase/dehydrase and lipid transport superfamily protein	23.84	7	55.72	5946195.44	5405847.21	4959098.19	0.91	0.83	0.67	0.70
gi15237054	V-type proton ATPase subunit E1	4.35	1	11.69	1054875.19	n.e.v.	2443269.32	n.e.v.	2.32	n.e.v.	0.11
gi15237059	putative elongation factor Tu	38.45	58	354.19	39366121.42	40106532.10	38883309.85	1.02	0.99	0.55	0.93
gi15237069	phosphoserine aminotransferase	7.44	3	17.1	1669656.42	1233058.30	1398139.33	0.74	0.84	0.57	0.66
gi15237084	putative translation initiation factor IF-1	11.35	2	7.97	1415457.07	1061795.59	207116.68	0.75	0.15	0.67	0.19
gi15237225	photosystem II stability/assembly factor HCF136	20.6	13	70.97	8037180.05	7257591.05	7434766.92	0.90	0.93	0.80	0.81
gi15237488	prohibitin 3	5.42	2	13.8	2166378.28	1225060.79	n.e.v.	0.57	n.e.v.	0.48	n.e.v.
gi15237548	40S ribosomal protein S28-1	18.75	3	11.5	2888609.12	1996194.52	1633673.92	0.69	0.57	0.43	0.25

gi15238554	proteasome alpha subunit A1	10.98	4	24.6	240176.27	195264.51	n.e.v.	0.81	n.e.v.	0.58	n.e.v.
gi15239146	NADP-dependent malic enzyme 2	3.57	1	17.68	1645515.54	2992046.19	1900543.40	1.82	1.15	0.40	0.84
gi15239282	ferredoxin-NADP(+)-oxidoreductase 1	36.11	18	126.34	16064927.61	13910673.70	11760369.91	0.87	0.73	0.61	0.35
gi15239602	light-harvesting chlorophyll B-binding protein 3	22.26	10	66.8	5424404.67	3860222.64	5422017.91	0.71	1.00	0.34	1.00
gi15239697	histone H2A	17.69	3	13.56	1720688.01	1924711.31	n.e.v.	1.12	n.e.v.	0.42	n.e.v.
gi15239735	thiazole biosynthetic enzyme	17.48	18	80.84	9570474.80	6831340.26	9357404.06	0.71	0.98	0.20	0.91
gi15239755	tryptophan synthase beta chain	3.19	2	12.53	722988.44	823921.26	n.e.v.	1.14	n.e.v.	0.67	n.e.v.
gi15240013	PS II oxygen-evolving complex 1	50.6	48	355.28	49139499.45	63565393.61	68494194.30	1.29	1.39	0.22	0.17
gi15240578	heat shock protein 70-2	14.21	20	149.02	14981509.58	11983942.10	n.e.v.	0.80	n.e.v.	0.54	n.e.v.
gi15240641	chloroplast RNA-binding protein 31B	4.84	1	10.92	543601.09	699430.78	n.e.v.	1.29	n.e.v.	0.09	n.e.v.
gi15240644	ribosomal protein L10	19.09	3	36.67	1652218.76	1771529.94	635999.92	1.07	0.38	0.75	0.09
gi15240901	ribulose bisphosphate carboxylase small chain 3B	40.88	58	432.81	69865146.94	76445170.22	n.e.v.	1.09	n.e.v.	0.67	n.e.v.
gi15240903	ribulose bisphosphate carboxylase small chain 2B	40.88	47	382.18	106326725.31	n.e.v.	85126451.75	n.e.v.	0.80	n.e.v.	0.66
gi15240912	ribulose bisphosphate carboxylase small chain 1B	37.02	48	351.28	60584998.04	57941091.80	53444008.13	0.96	0.88	0.75	0.38
gi15241005	chlorophyll a-b binding protein CP29.1	13.1	7	41.42	6287517.06	6279226.36	8500807.73	1.00	1.35	1.00	0.41
gi15241125	40S ribosomal protein S24-2	11.28	2	12.3	434863.67	n.e.v.	186477.15	n.e.v.	0.43	n.e.v.	0.32
gi15241316	40S ribosomal protein S8-1	27.03	8	43.53	2212564.47	1995105.56	n.e.v.	0.90	n.e.v.	0.73	n.e.v.
gi15241472	tubulin beta-4 chain	5.63	5	41.15	2019649.12	3686107.64	3268645.66	1.83	1.62	0.53	0.39
gi15241492	formate dehydrogenase	3.39	1	23.07	1380013.30	940917.95	3122327.29	0.68	2.26	0.67	0.22
gi15241573	Porphobilinogen deaminase	18.06	6	43.16	4596332.19	3758132.30	3665689.92	0.82	0.80	0.60	0.59
gi15241849	heat shock cognate protein 70-1	39.48	33	310.03	36342011.08	26093159.11	26806051.58	0.72	0.74	0.54	0.44
gi15242674	glutaredoxin-C2	12.61	1	10.15	217470.89	530880.32	n.e.v.	2.44	n.e.v.	0.10	n.e.v.
gi15242717	adenosine kinase 2	22.9	11	71.86	3106404.00	6387782.00	n.e.v.	2.06	n.e.v.	0.36	n.e.v.
gi15242753	adenylate kinase 1	11.79	3	21.42	1466029.61	1154213.27	1920562.05	0.79	1.31	0.66	0.26
gi18379115	photosystem II Psb27 protein	27.59	7	41.65	6010595.56	6330353.64	6088861.60	1.05	1.01	0.86	0.96
gi18391062	aspartyl protease-like protein	4.23	2	25.92	1579427.85	1511715.40	1251818.99	0.96	0.79	0.92	0.52
gi18391066	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1	7	2	12.83	696281.61	1626194.99	846459.45	2.34	1.22	0.11	0.68
gi18394322	uncharacterized protein	4.15	1	15.84	429544.95	535812.40	n.e.v.	1.25	n.e.v.	0.61	n.e.v.
gi18394414	ACT domain-containing protein	16.9	7	66.88	3972682.53	2987153.68	2707535.06	0.75	0.68	0.57	0.52
gi18398333	NAD(P)-binding Rossmann-fold-containing	9.12	2	17.06	195958.28	362056.87	1633285.92	1.85	8.33	0.07	0.19

	protein										
gi18398761	60S ribosomal protein L9-1	34.02	8	61.75	7776894.13	5124939.74	2757375.51	0.66	0.35	0.20	0.07
gi18399100	40S ribosomal protein S18	13.16	1	19.12	891858.91	2159337.15	1384238.47	2.42	1.55	0.08	0.43
gi18401614	cysteine proteinase RD21a	3.46	3	21.07	2526781.30	2223812.94	n.e.v.	0.88	n.e.v.	0.71	n.e.v.
gi18402859	photosystem II subunit T	11.65	1	5.19	694480.45	n.e.v.	526638.38	n.e.v.	0.76	n.e.v.	0.57
gi18403751	FIBRILLIN 4	17.96	6	41.85	2963167.71	2897005.18	3003547.50	0.98	1.01	0.95	0.90
gi18404382	malate dehydrogenase 1	34.6	26	139.06	27560311.53	21037857.94	19679066.19	0.76	0.71	0.31	0.30
gi18405008	acyl carrier protein 3	15.44	7	36.63	1361922.46	1998625.13	1022143.96	1.47	0.75	0.19	0.51
gi18405061	thylakoid lumen protein 18.3	5.96	2	29.07	1352259.16	1183735.47	2976729.86	0.88	2.20	0.67	0.31
gi18405145	ribulose bisphosphate carboxylase/oxygenase activase	66.24	141	839.69	140657575.13	129685181.23	175178313.90	0.92	1.25	0.44	0.37
gi18405391	ZKT protein containing PDZ, K-box and a TPR region	9.55	6	38.29	5078877.89	4868790.97	4190408.64	0.96	0.83	0.88	0.49
gi18407594	vacuolar calcium-binding protein-like protein	11.18	5	19.79	3423729.59	2207189.44	1552592.30	0.64	0.45	0.35	0.14
gi18408627	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	3.45	1	21.18	521299.88	n.e.v.	1928968.30	n.e.v.	3.70	n.e.v.	0.33
gi18410104	tryptophan synthase alpha chain	4.17	1	10.49	582825.05	1182229.65	n.e.v.	2.03	n.e.v.	0.09	n.e.v.
gi18410661	alpha/beta-Hydrolases superfamily protein	2.97	2	41.34	3093476.49	1948938.14	947940.74	0.63	0.31	0.15	0.14
gi18411523	thylakoid rhodanese-like protein	5.58	4	34.91	2727404.34	2057499.30	2228359.91	0.75	0.82	0.38	0.58
gi18411929	glutathione S-transferase TAU 19	5.48	3	21.72	1684971.34	1858317.21	2078616.33	1.10	1.23	0.54	0.21
gi18412406	E-Z type HEAT repeat-containing protein	5.88	3	13.29	605494.14	733487.78	n.e.v.	1.21	n.e.v.	0.03	0.14
gi18412657	ribosome-recycling factor	14.18	5	31.22	2548345.18	4106636.93	n.e.v.	1.61	n.e.v.	0.30	n.e.v.
gi18413214	nucleoside diphosphate kinase 1	41.42	11	75.35	5423175.11	4379196.93	3611846.16	0.81	0.67	0.33	0.12
gi18415378	proline-rich family protein	13.62	7	32.43	3170309.41	1873481.84	3517759.84	0.59	1.11	0.15	0.77
gi18415911	ATP synthase subunit beta-2	30.22	38	283.85	52082926.64	80457398.67	23312214.05	1.54	0.45	0.38	0.12
gi18415982	tetratricopeptide repeat protein	3.4	2	13.74	1808018.74	1690772.40	1346363.81	0.94	0.74	0.90	0.56
gi18416264	histone H3	23.53	2	15.76	288889.94	245923.23	n.e.v.	0.85	n.e.v.	0.82	n.e.v.
gi18417512	heavy metal transport/detoxification domain-containing protein	27.53	6	40.17	4333986.17	3924513.46	3338151.60	0.91	0.77	0.72	0.37
gi18418410	embryo defective 1241	11.11	2	21.19	1078930.79	817225.39	1126690.63	0.76	1.04	0.65	0.96
gi18420348	fructose-bisphosphate aldolase 2	39.95	44	278.29	43505101.82	56121757.85	41622980.56	1.29	0.96	0.17	0.46
gi18420800	putative 30S ribosomal protein	5.19	1	13.56	1201030.05	n.e.v.	576090.89	n.e.v.	0.48	n.e.v.	0.26
gi18422918	lactoylglutathione lyase / glyoxalase I-like protein	8.43	1	18.6	1017430.10	949666.79	n.e.v.	0.93	n.e.v.	0.87	n.e.v.
gi186478207	photosystem II subunit P-1	55.25	31	223.87	32365290.11	23419089.58	28133387.10	0.72	0.87	0.03	0.48

gi186491325	phosphoglycerate kinase	50.12	60	373.13	45940184.09	34815640.49	29639272.07	0.76	0.65	0.20	0.16
gi186509731	methionine synthase 2	21.57	26	163.37	15729796.76	n.e.v.	12521697.93	n.e.v.	0.80	n.e.v.	0.17
gi186515763	glycine dehydrogenase [decarboxylating] 2	8.2	14	137.35	5756764.64	8096644.36	4890798.61	1.41	0.85	0.08	0.16
gi186521400	ATP synthase subunit beta-1	33.27	41	316.64	34909557.41	29223552.21	23032318.08	0.84	0.66	0.66	0.36
gi186524998	Succinyl-CoA ligase [GDP-forming] subunit alpha-2	9.76	3	13.9	571861.97	630863.51	554793.16	1.10	0.97	0.69	0.94
gi186526990	2-phosphoglycolate phosphatase 1	11.75	4	38.8	3292871.33	1849367.98	2122528.65	0.56	0.64	0.23	0.41
gi22327852	trigger factor type chaperone family protein	2.19	2	38.31	1230435.89	845906.86	353925.56	0.69	0.29	0.65	0.15
gi22328910	argininosuccinate synthase	8.5	4	30.45	1118964.18	1253970.64	n.e.v.	1.12	n.e.v.	0.31	n.e.v.
gi22331102	lectin-like protein	7.01	1	14.15	1070070.24	3105707.74	544425.44	2.90	0.51	0.10	0.27
gi238479568	thiocyanate methyltransferase 1	8.59	1	6.33	535858.21	528403.11	749635.18	0.99	1.40	0.96	0.46
gi238479752	ribosomal protein S5/Elongation factor G/III/V family protein	9.15	12	82.38	5546768.62	6448165.69	n.e.v.	1.16	n.e.v.	0.09	n.e.v.
gi238480186	HSP20-like chaperone	5.83	3	21.96	2574690.11	1842353.08	1489732.49	0.72	0.58	0.25	0.19
gi30678090	Chaperone protein htpG family protein	15.19	12	88.92	5783297.66	3688398.94	5624539.26	0.64	0.97	0.12	0.86
gi30678219	aconitate hydratase 3	3.13	5	22.06	1533836.46	381846.34	0.00	0.25	0.00	0.42	0.06
gi30678634	thioredoxin M1	8.94	3	34.22	3140471.26	1387651.08	1975533.34	0.44	0.63	0.19	0.34
gi30678951	protoporphyrinogen oxidase	3.56	1	20.78	1165623.30	n.e.v.	530772.55	n.e.v.	0.46	n.e.v.	0.53
gi30679426	cytochrome b6-f complex iron-sulfur subunit	27.14	10	73.48	10495171.19	6505979.32	7777874.09	0.62	0.74	0.07	0.25
gi30679979	Importin subunit alpha-1	2.63	1	5.08	918124.14	n.e.v.	401164.19	n.e.v.	0.44	n.e.v.	0.18
gi30680575	phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	6.96	2	29.39	1992158.45	1992198.52	n.e.v.	1.00	n.e.v.	1.00	n.e.v.
gi30681554	mitochondrial F1F0-ATP synthase subunit Fad	8.18	3	26.84	1610886.54	1433301.31	n.e.v.	0.89	n.e.v.	0.89	n.e.v.
gi30684617	40S ribosomal protein S12-1	9.72	3	16.78	2846509.27	3219454.91	n.e.v.	1.13	n.e.v.	0.68	n.e.v.
gi30685069	actin 2	9.16	4	42.33	3357618.94	3577611.88	3576788.97	1.07	1.07	0.91	0.90
gi30685117	protein TIC 62	2.03	3	22.25	69002.35	17514.64	152951.80	0.25	2.22	0.08	0.54
gi30686293	UTP--glucose-1-phosphate uridylyltransferase 1	4.87	5	48.59	1450948.83	1094512.27	n.e.v.	0.75	n.e.v.	0.75	n.e.v.
gi30688425	glyceraldehyde-3-phosphate dehydrogenase A subunit	52.78	77	450.77	81242522.66	76047925.39	73106267.74	0.94	0.90	0.46	0.31
gi30690089	myrosinase 1	27.41	21	124.3	13278437.04	14841298.57	17096281.87	1.12	1.29	0.38	0.17
gi30690772	glutathione S-transferase phi 8	26.62	11	65.44	6788362.06	6794127.05	5817236.85	1.00	0.86	0.99	0.36
gi30691626	heat shock protein 70-1	3.37	3	31.4	188265.72	272156.51	n.e.v.	1.45	n.e.v.	0.20	n.e.v.
gi30692256	glycine-rich RNA-binding protein 8	10.87	2	33.66	698293.28	1353769.66	1376822.72	1.94	1.97	0.10	0.54

gi30693659	thioredoxin Y2	7.78	2	13.59	519069.96	692890.35	n.e.v.	1.33	n.e.v.	0.55	n.e.v.
gi30693966	Luminal-binding protein 2	14.85	16	107.5	8289467.68	11707537.59	6164690.76	1.41	0.74	0.10	0.07
gi30694221	dihydrolipoyl dehydrogenase 1	20.12	13	123.15	6163307.86	7945663.52	9220652.47	1.29	1.50	0.46	0.28
gi30694420	40S ribosomal protein S7-1	13.61	2	18.22	1717103.77	897112.50	827261.13	0.52	0.48	0.39	0.54
gi30694694	BOI-related protein 1	5.62	2	16.69	1275732.92	899083.91	2205322.80	0.70	1.73	0.39	0.10
gi30695097	methylenetetrahydrofolate reductase 1	3.93	1	9.83	447853.00	710418.50	615742.26	1.59	1.37	0.56	0.27
gi30696124	haloacid dehalogenase-like hydrolase family protein	2.65	2	19.06	916173.19	463252.72	n.e.v.	0.51	n.e.v.	0.38	n.e.v.
gi30696347	thylakoid lumenal protein-17.4	5.53	1	29.04	625959.03	616986.80	314020.66	0.99	0.50	0.94	0.19
gi30696928	Monodehydroascorbate reductase	11.54	5	48.01	3949122.12	7913476.29	15285436.96	2.00	3.87	0.25	0.09
gi30696958	putative translation initiation factor	2.32	2	20.5	229399.29	1014820.51	287916.46	4.42	1.26	0.08	0.84
gi30697525	D-ribulose-5-phosphate-3-epimerase	6.76	2	14.74	2874421.77	2398466.43	4273742.89	0.83	1.49	0.76	0.52
gi334182539	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	48.29	65	401.4	73142777.61	70944483.40	63896360.22	0.97	0.87	0.82	0.20
gi334183715	60S ribosomal protein L17-2	7.63	1	16.01	641242.56	658019.40	666168.67	1.03	1.04	0.91	0.90
gi334183935	dehydrin ERD14	7.03	3	12.57	11088454.49	2563706.66	2715971.99	0.23	0.24	0.09	0.05
gi334184403	aminopeptidase family protein	6.4	4	29.31	27805757.78	7236942.83	n.e.v.	0.26	n.e.v.	0.39	n.e.v.
gi334184408	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	10.48	5	48.22	1734968.73	2607966.79	2170117.04	1.50	1.25	0.17	0.19
gi334184571	pentatricopeptide repeat-containing protein	3.38	1	26.26	24933209.76	13990005.89	16739281.23	0.56	0.67	0.16	0.11
gi334184593	photosystem II subunit P-2	33.6	14	77.55	14611974.02	6965997.82	5649735.72	0.48	0.39	0.18	0.13
gi334184607	uncharacterized protein	3.99	2	15.53	14474445.93	n.e.v.	17137938.78	n.e.v.	1.18	n.e.v.	0.84
gi334184908	O-acetylserine (thiol) lyase (OAS-TL) isoform oasB	21.43	9	78.06	6364019.49	7227752.92	8443883.31	1.14	1.33	0.67	0.23
gi334185190	heat shock protein 70-3	35.9	29	189.8	17067382.92	12777332.84	17925823.49	0.75	1.05	0.05	0.76
gi334185347	peroxisomal (S)-2-hydroxy-acid oxidase GLO2	29.97	23	179.83	13229672.94	9865556.29	13869670.66	0.75	1.05	0.04	0.61
gi334185547	O-acetylserine (thiol) lyase (OAS-TL) isoform A2	3.93	1	21.18	2208781.82	1246339.21	1776383.88	0.56	0.80	0.41	0.76
gi334185828	Clp ATPase	5.32	9	91.92	126955400.64	128213186.76	n.e.v.	1.01	n.e.v.	0.99	n.e.v.
gi334185964	fructose-1,6-bisphosphatase	6.47	4	32.97	2023228.46	2085174.65	2705395.96	1.03	1.34	0.83	0.17
gi334186158	transketolase	22.57	32	235.04	23897260.58	31624235.23	26323229.20	1.32	1.10	0.08	0.46
gi334186198	peptidyl-prolyl cis-trans isomerase CYP20-3	43.24	18	147.74	27863172.09	20291120.37	19599566.23	0.73	0.70	0.05	0.11
gi334187077	aspartate aminotransferase	6.7	4	32.4	720180.30	2025346.38	1733031.58	2.81	2.41	0.12	0.22
gi334187695	voltage dependent anion channel 3	21.9	5	47.03	2553408.50	2436988.95	1573957.74	0.95	0.62	0.89	0.22

gi334187803	chaperonin 20	39.53	16	129.12	8900141.76	3512930.87	7728304.94	0.39	0.87	0.12	0.70
gi334188676	aldose 1-epimerase family protein	4.23	1	18.37	10115184.15	7457953.52	11751904.00	0.74	1.16	0.46	0.69
gi42565109	cell wall-plasma membrane linker protein	5.99	6	32.21	767266.12	1410541.96	443436.03	1.84	0.58	0.11	0.35
gi42570951	60S acidic ribosomal protein P2-2	46.09	3	28.87	4815558.97	4193326.20	2629681.31	0.87	0.55	0.82	0.41
gi42571269	protein disulfide-isomerase like 2-1	4.51	1	4.73	1039913.70	1123127.71	653382.41	1.08	0.63	0.88	0.38
gi42571485	FAD/NAD(P)-binding oxidoreductase	5.17	3	14.1	28955522.42	8866258.79	n.e.v.	0.31	n.e.v.	0.38	n.e.v.
gi42571761	photosystem II subunit S	8.78	1	4.97	9357610.35	12660103.66	10740853.83	1.35	1.15	0.76	0.76
gi42572347	adenosine kinase 1	19.54	16	73.05	6747926.29	7974740.92	4280554.05	1.18	0.63	0.27	0.35
gi42573658	putative sorbitol dehydrogenase	7.14	4	38.58	1556410.50	682673.19	978704.99	0.44	0.63	0.12	0.33
gi7525018	ATP synthase CF1 alpha subunit	36.88	77	526.65	42923992.28	34451920.91	40515113.37	0.80	0.94	0.04	0.46
gi7525019	ATP synthase CF0 B subunit	20.11	3	27.39	23301385.60	19283007.71	n.e.v.	0.83	n.e.v.	0.82	n.e.v.
gi7525028	photosystem II protein D2	6.23	2	12.59	2721427.96	2799609.70	2024427.17	1.03	0.74	0.86	0.11
gi7525029	photosystem II 44 kDa protein	6.98	4	24.11	6604190.43	n.e.v.	4210966.52	n.e.v.	0.64	n.e.v.	0.53
gi7525039	ATP synthase CF1 epsilon subunit	62.12	13	72.94	9871235.23	9544440.80	8738035.01	0.97	0.89	0.88	0.33
gi7525040	ATP synthase CF1 beta subunit	73.29	154	923.04	152946303.89	165866097.13	158572240.14	1.08	1.04	0.40	0.45
gi7525059	photosystem II 47 kDa protein	9.84	14	67.57	14694874.78	23514245.33	2193213.98	1.60	0.15	0.54	0.36
gi7525069	ribosomal protein L14	27.05	6	30.29	7234546.44	6422647.32	970013.24	0.89	0.13	0.91	0.14
gi7525086	photosystem I subunit VII	35.8	6	37.09	8060231.75	4040176.11	9649869.41	0.50	1.20	0.19	0.57
gi79313237	protein DJ-1-like A	10.84	5	44.69	5585106.28	5079143.43	2134560.51	0.91	0.38	0.77	0.07
gi79313261	PYK10-binding protein 1	40.6	22	116.98	14591927.22	20637703.83	8384935.03	1.41	0.57	0.26	0.12
gi79313265	JA-responsive protein 1	6.65	3	21.62	599592.69	670234.34	430925.72	1.12	0.72	0.81	0.48
gi79313434	gamma-hydroxybutyrate dehydrogenase	22.66	7	51.13	1128450.17	697459.97	928881.84	0.62	0.82	0.31	0.70
gi79314469	UDP-XYL synthase 5	4.11	2	23.01	2438322.22	3522720.91	n.e.v.	1.44	n.e.v.	0.44	n.e.v.
gi79314743	20S proteasome alpha subunit PAD1	5.76	1	8.96	666073.32	1022697.08	n.e.v.	1.54	n.e.v.	0.12	n.e.v.
gi79314806	ATP synthase subunit d	9.84	1	4.64	498240.74	1238428.06	n.e.v.	2.49	n.e.v.	0.18	n.e.v.
gi79316582	40S ribosomal protein S15-1	23.84	2	11.95	1619012.98	2400538.69	n.e.v.	1.48	n.e.v.	0.10	n.e.v.
gi79318406	glutamate:glyoxylate aminotransferase	30.16	22	139.49	32528026.49	29763682.00	6502816.33	0.92	0.20	0.83	0.10
gi79320443	PSI type III chlorophyll a/b-binding protein	30.28	12	63.1	7717406.00	9924177.78	10955181.72	1.29	1.42	0.03	0.35
gi79321061	glutamate--glyoxylate aminotransferase 2	21.62	17	98.13	11124045.31	10861661.13	14590417.20	0.98	1.31	0.72	0.20
gi79321468	V-type proton ATPase catalytic subunit A	6.74	6	28.17	2160932.37	3516398.50	3924180.77	1.63	1.82	0.14	0.12
gi79322198	20S proteasome subunit PAA2	12.27	3	22.07	207854.18	228354.99	n.e.v.	1.10	n.e.v.	0.27	n.e.v.
gi79322611	ubiquitin fusion degradation 1	6.58	2	9.52	42276.21	39782.03	n.e.v.	0.94	n.e.v.	0.92	n.e.v.
gi79322643	fructose-bisphosphate aldolase 1	17.36	10	104.58	37320828.38	11302287.13	24453894.04	0.30	0.66	0.20	0.62

gi79324564	40S ribosomal protein S5-1	7.25	2	17.92	1352996.68	348663.03	825021.06	0.26	0.61	0.25	0.53
gi79324933	photosystem I P subunit	12.64	3	23.86	846968.07	788511.12	1139795.52	0.93	1.35	0.87	0.48
gi79325183	plasma-membrane associated cation-binding protein 1	10.22	7	41.88	5024048.44	247643.11	n.e.v.	0.05	n.e.v.	0.14	n.e.v.
gi79325203	pyruvate, phosphate dikinase regulatory protein 1	7.18	1	9.24	313770.49	183802.97	n.e.v.	0.59	n.e.v.	0.06	n.e.v.
gi79325233	glutamate-cysteine ligase	5.45	1	18.07	1746255.17	826218.90	n.e.v.	0.47	n.e.v.	0.30	n.e.v.
gi79325249	superoxide dismutase [Fe]	8.06	4	19.49	2486888.00	2937163.56	1578800.93	1.18	0.63	0.45	0.12
gi79326317	catalase 2	17.51	10	112.76	25330808.98	28163733.13	8517247.53	1.11	0.34	0.76	0.10
gi79327622	14-3-3-like protein GF14 lambda	11.79	5	38.95	813184.17	679163.40	770663.13	0.84	0.95	0.66	0.89
gi79327847	isopropylmalate dehydrogenase 1	3.87	4	22.15	2105395.21	1305985.46	1133527.76	0.62	0.54	0.31	0.34
gi79329027	biotin carboxylase subunit CAC2	10.02	3	36.15	673336.01	401108.57	n.e.v.	0.60	n.e.v.	0.35	n.e.v.
gi79329220	14-3-3-like protein GF14 psi	11.42	1	42.94	1856013.90	3176106.41	2921328.60	1.71	1.57	0.06	0.31
gi79329956	beta-ketoacyl-[acyl carrier protein] synthase I	9.09	6	39.81	4095417.81	2349312.57	3675944.65	0.57	0.90	0.15	0.75

Table S4. List of gene onthology annotations connected to development found in differential proteome of roots of *fra2* mutant.

Level GO	Term(Acc)	Term(Name)	#Seq	Score
6	GO:0009555	pollen development	4	3.36
6	GO:0048580	regulation of post-embryonic development	4	1.44
6	GO:0022622	root system development	4	0.73
6	GO:0048513	organ development	4	0.67
6	GO:0009664	plant-type cell wall organization	3	3.20
6	GO:0009720	detection of hormone stimulus	2	1.20
6	GO:0048468	cell development	2	0.26
6	GO:0009553	embryo sac development	1	0.60
6	GO:0048640	negative regulation of developmental growth	1	0.60
6	GO:0000902	cell morphogenesis	1	0.36
6	GO:0061458	reproductive system development	1	0.13

Table S5. List of gene onthology annotations connected to development found in differential proteome of roots of *ktn1-2* mutant.

LevelGO	Term(Acc)	Term(Name)	#Seq	Score
6	GO:0048513	organ development	5	1.37
6	GO:0061458	reproductive system development	4	1.40
6	GO:0048367	shoot system development	3	1.36
6	GO:0000902	cell morphogenesis	2	0.96
6	GO:0048468	cell development	2	0.96
6	GO:0022622	root system development	2	0.44
6	GO:0009553	embryo sac development	1	1.00
6	GO:0009555	pollen development	1	1.00
6	GO:0009846	pollen germination	1	1.00
6	GO:0048868	pollen tube development	1	0.60
6	GO:0090351	seedling development	1	0.60
6	GO:0048580	regulation of post-embryonic development	1	0.36

Table S6. List of gene onthology annotations connected to development found in differential proteome of above ground part of *fra2* mutant.

LevelGO	Term(Acc)	Term(Name)	#Seq	Score
6	GO:0048513	organ development	11	2.92
6	GO:0048367	shoot system development	9	3.37
6	GO:0009886	post-embryonic morphogenesis	5	3.00
6	GO:0022622	root system development	3	0.76
6	GO:0061458	reproductive system development	2	0.43
6	GO:0048468	cell development	2	0.26
6	GO:0090351	seedling development	1	0.60
6	GO:0000902	cell morphogenesis	1	0.36

Table S7. List of gene onthology annotations connected to development found in differential proteome of above ground part of *ktn1*- mutant.

LevelGO	Term(Acc)	Term(Name)	#Seq	Score
6	GO:0048513	organ development	9	2.35
6	GO:0048367	shoot system development	7	2.29
6	GO:0061458	reproductive system development	4	1.01
6	GO:0009886	post-embryonic morphogenesis	3	1.80
6	GO:0022622	root system development	2	0.68
6	GO:0000902	cell morphogenesis	1	0.36
6	GO:0048468	cell development	1	0.13

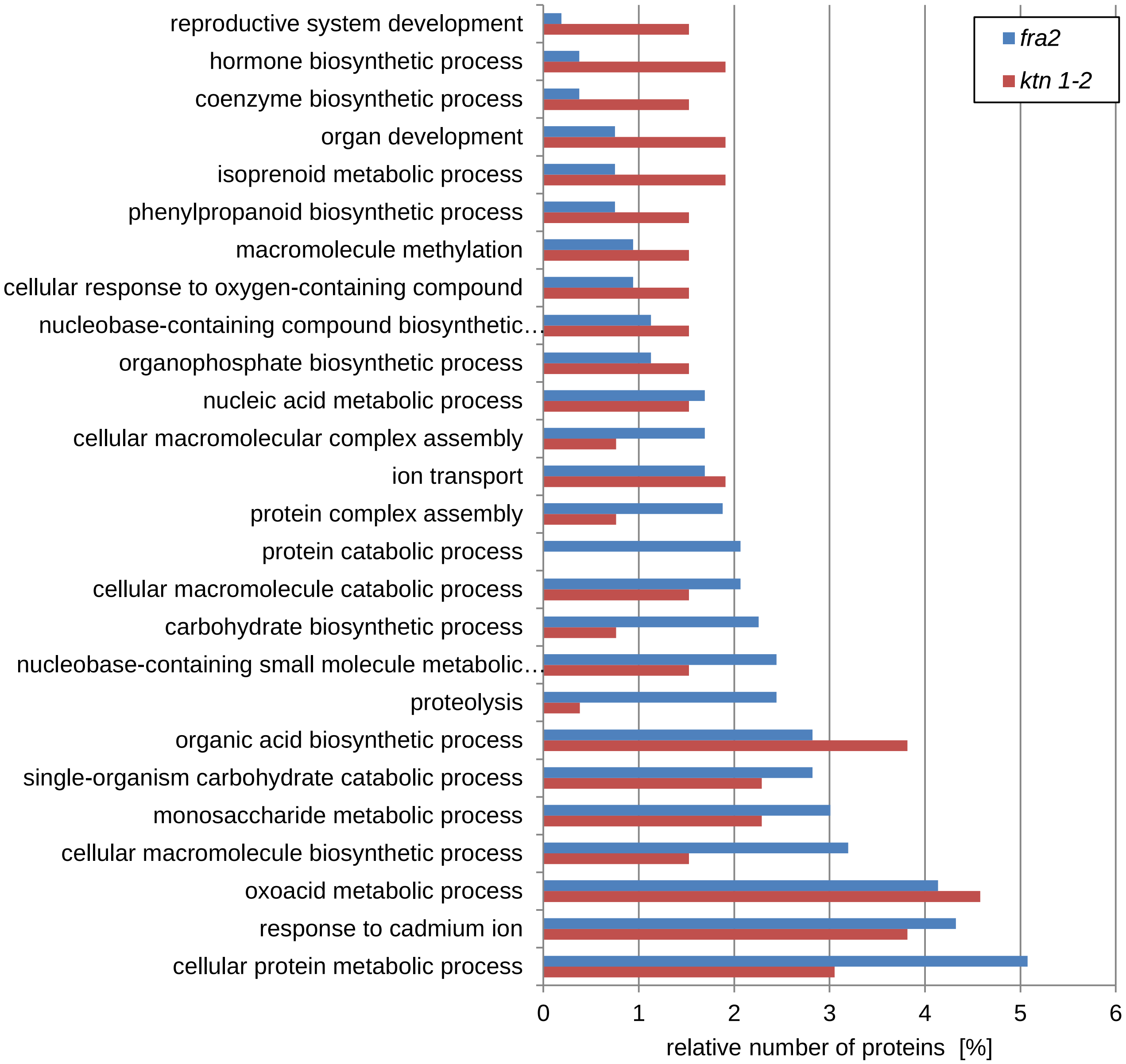

Figure S1 Comparison of gene onthology annotations (at 6th level of onthology) of differentially abundant proteins in *fra2* and *ktn1-2* mutant roots (as compared to Col-0) according to biological process. Relative numbers of proteins per annotation are presented in the graph.

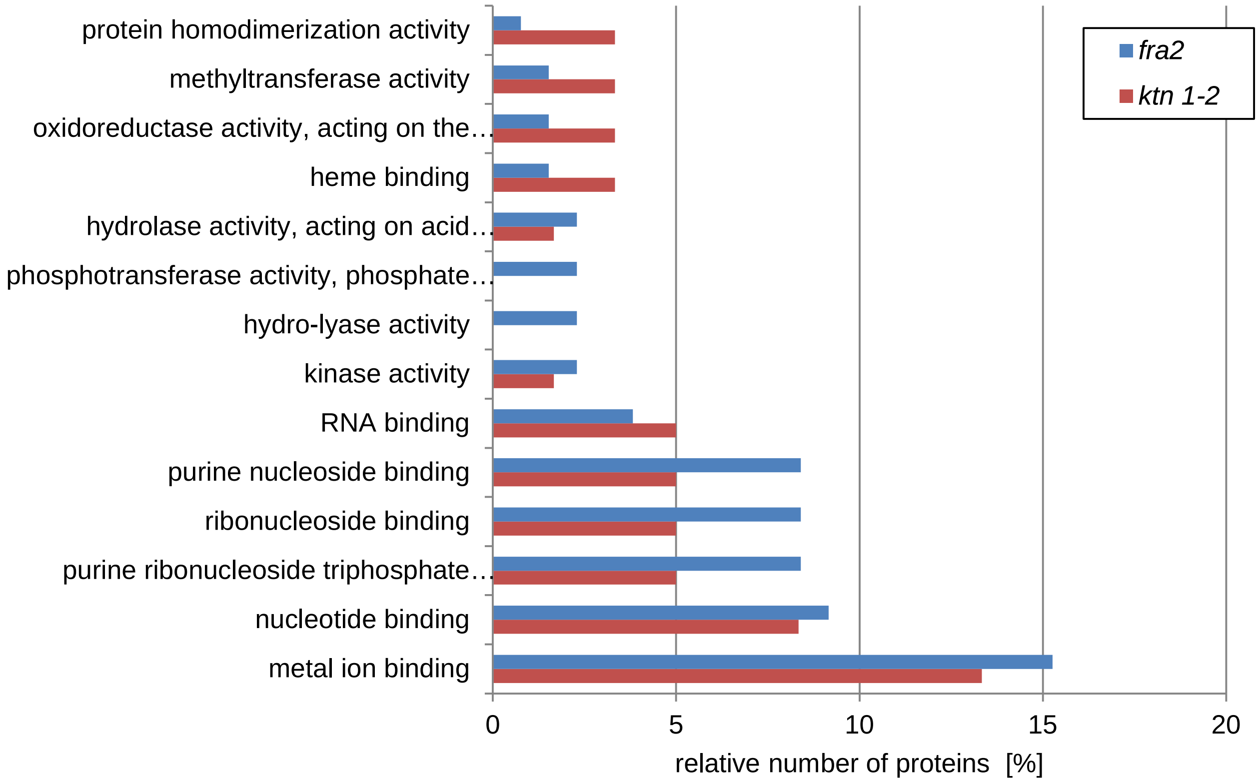

Figure S2 Comparison of gene onthology annotations (at 5th level of onthology) of differentially abundant proteins in *fra2* and *ktn1-2* mutant roots (as compared to Col-0) according to molecular function. Relative numbers of proteins per annotation are presented in the graph.

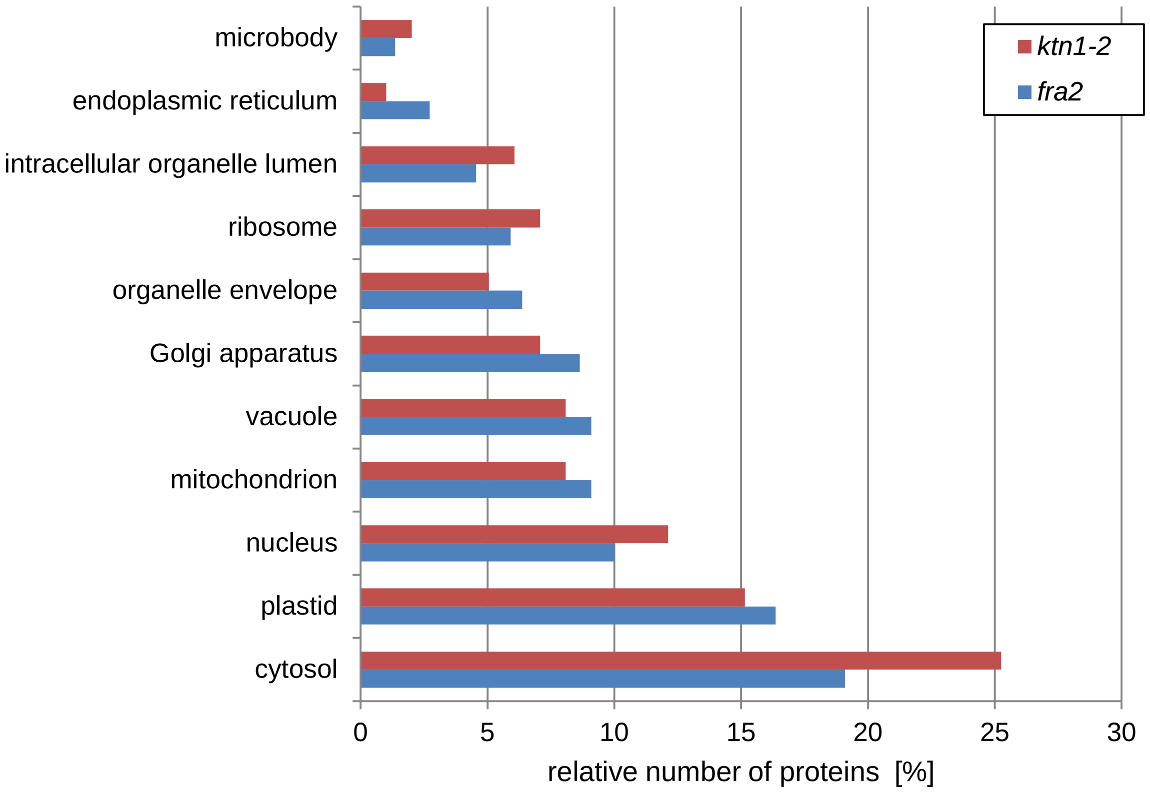

Figure S3 Comparison of gene onthology annotations (at 8th level of onthology) of differentially abundant proteins in *fra2* and *ktn1-2* mutant roots (as compared to Col-0) according to localization. Relative numbers of proteins per annotation are presented in the graph.

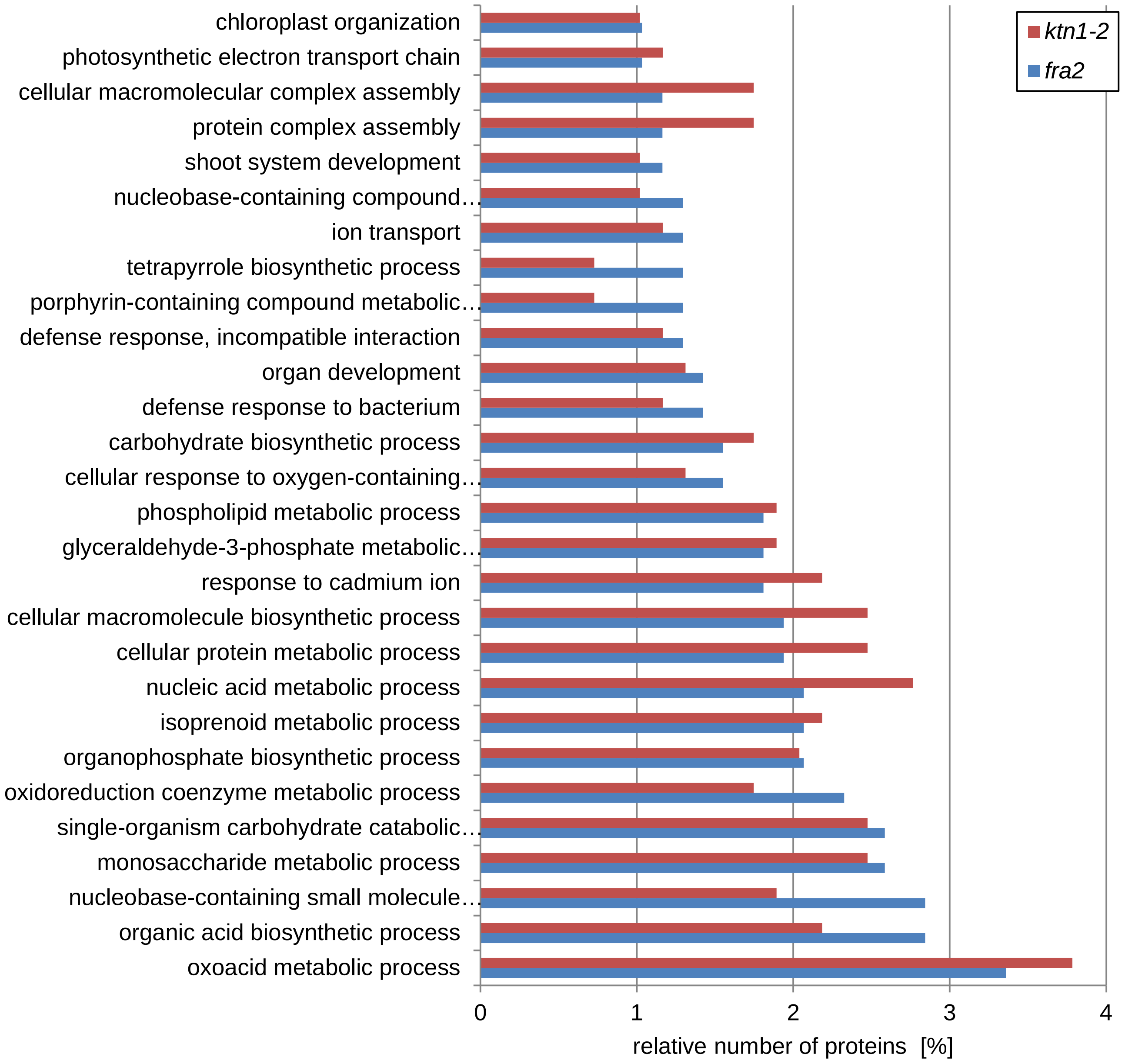

Figure S4 Comparison of gene onthology annotations (at 6th level of onthology) of differentially abundant proteins in *fra2* and *ktn1-2* mutant above ground parts (as compared to Col-0) according to biological process. Relative numbers of proteins per annotation are presented in the graph.

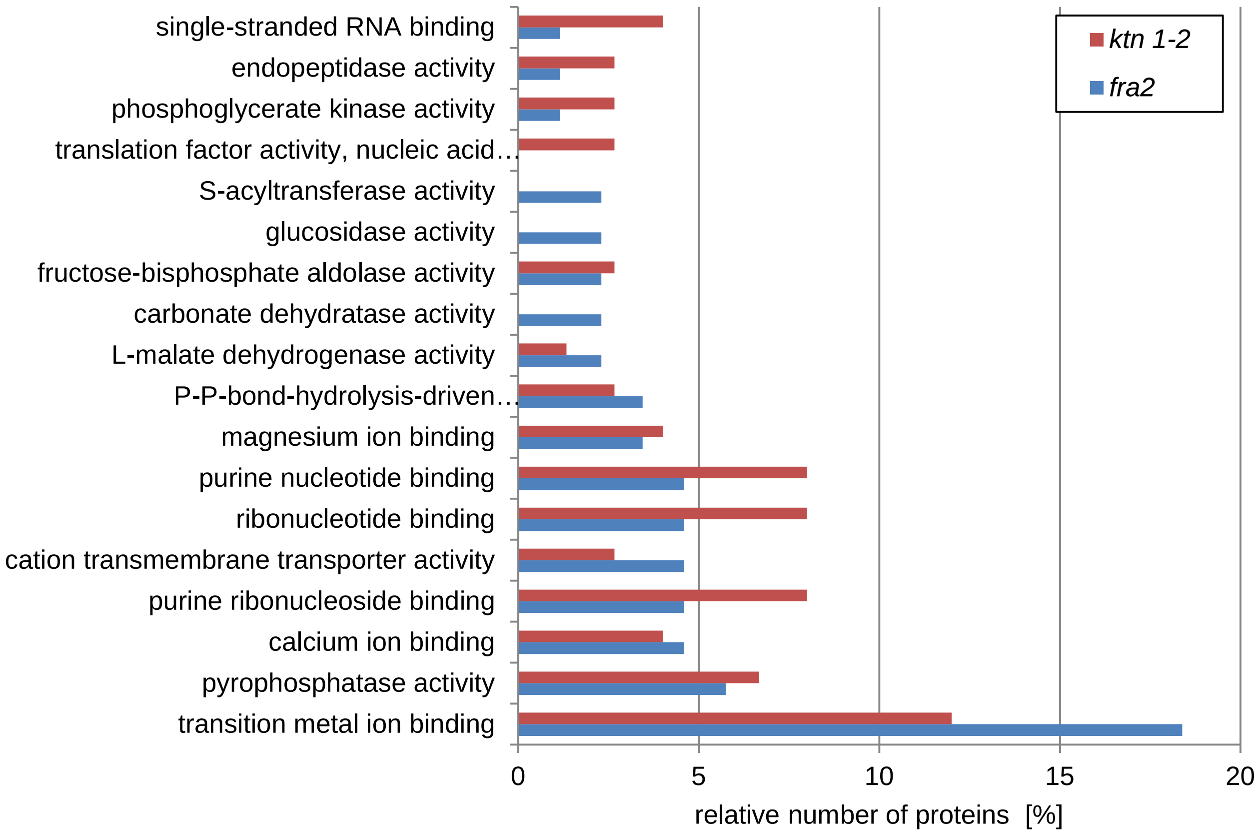

Figure S5 Comparison of gene onthology annotations (at 5th level of onthology) of differentially abundant proteins in *fra2* and *ktn1-2* mutant above ground parts (as compared to Col-0) according to molecular function. Relative numbers of proteins per annotation are presented in the graph.

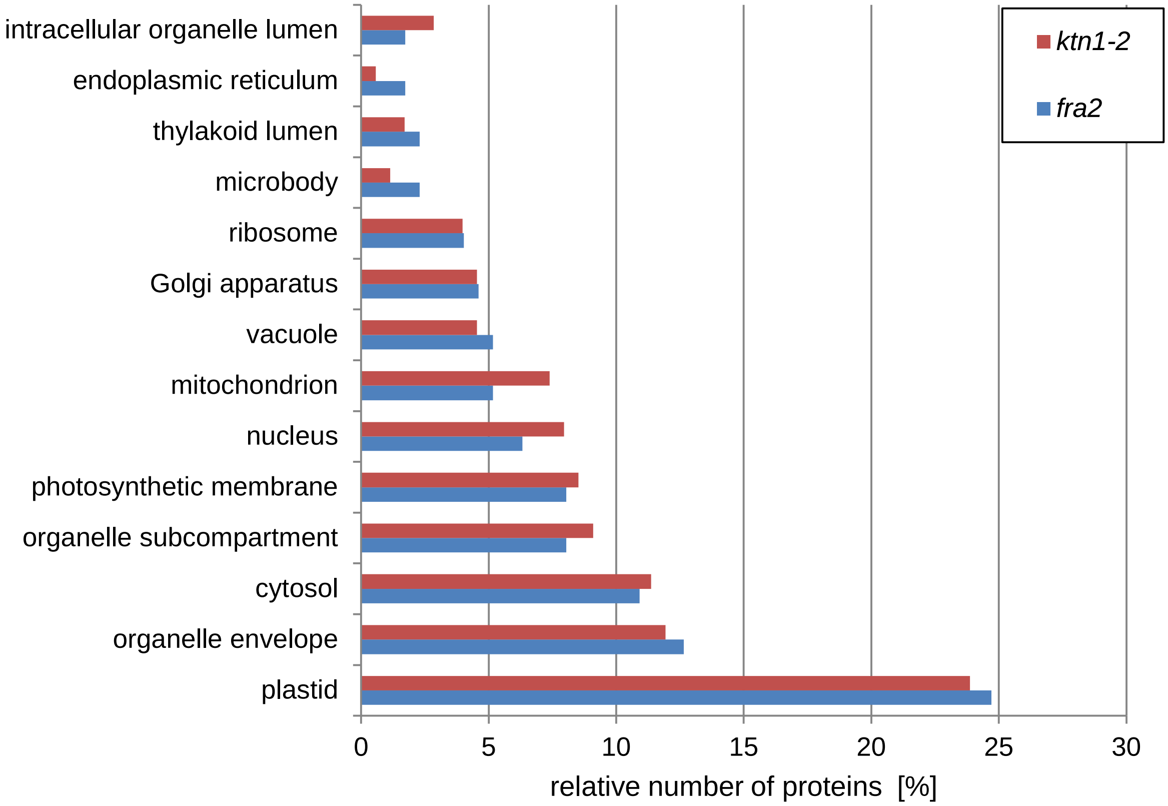

Figure S6 Comparison of gene onthology annotations (at 5th level of onthology) of differentially abundant proteins in *fra2* and *ktn1-2* mutant above ground parts (as compared to Col-0) according to localisation. Relative numbers of proteins per annotation are presented in the graph.

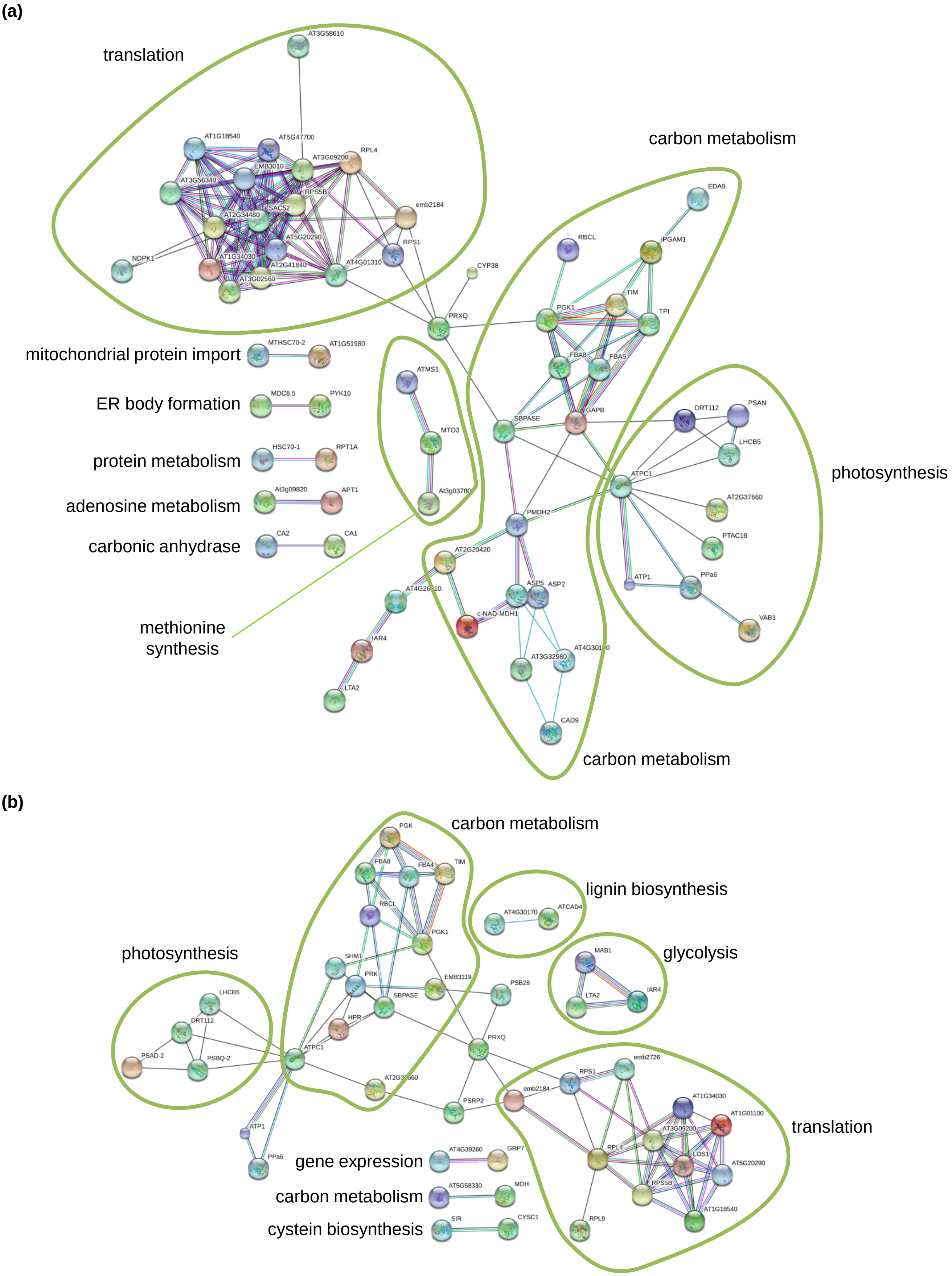

Figure S7 Prediction of protein inteaction networks in differential proteome of *fra2* (a) and *ktn1-2* (b) roots and aerial parts as predicted by STRING web-based application.

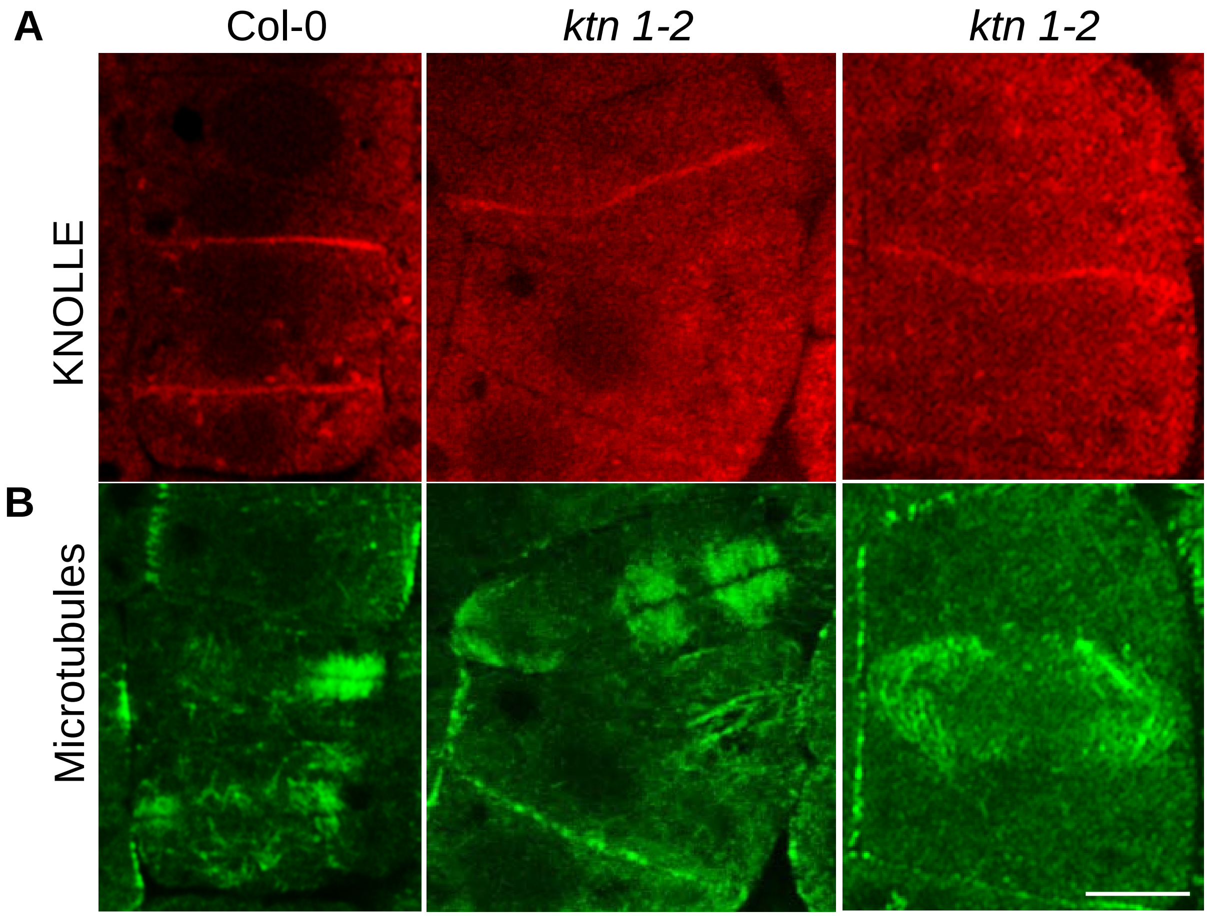

Figure S8 Co-immunolocalization of cell plate marker KNOLLE (A) with phragmoplast microtubules (B) during late cytokinesis in root epidermal cells of Col-0 and *ktn1-2* mutant. Note asymetric and aberrant cell plate deposition and bending in *ktn1-2* mutant. Bar represents 5 μm.

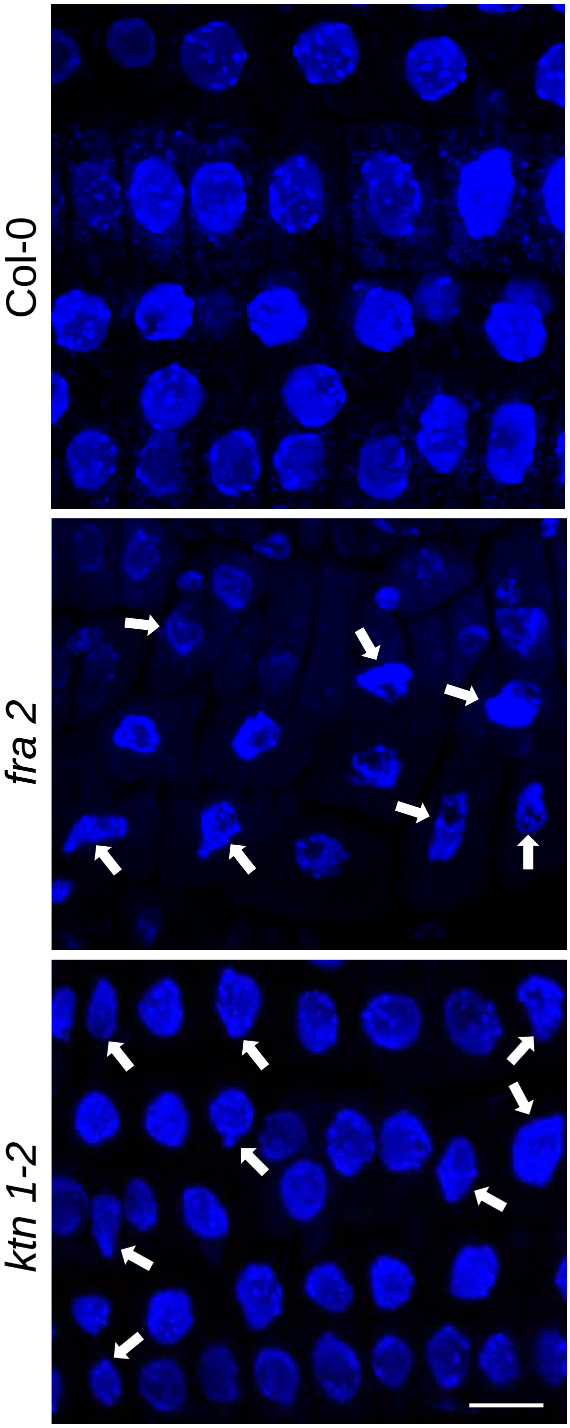

Figure S9 Changes in nuclear shape (arrows) as revealed by DAPI staining of Col-0 and *KATANIN 1* mutants *fra 2* and *ktn1-2*. Bar represents 10 µm.