

Supplementary Materials: Aluminum Toxicity-Induced Alterations of Leaf Proteome in Two Citrus Species Differing in Aluminum Tolerance

Huan Li, Lin-Tong Yang, Yi-Ping Qi, Peng Guo, Yi-Bin Lu and Li-Song Chen

Table S1. List of differentially expressed proteins in Al-toxic *Citrus sinensis* leaves. Control and Al-toxic samples were labeled with 119 and 121 tags, respectively.

Accession	Homology in <i>Arabidopsis thaliana</i>	Proteins	Fold Change (121/119)
Energy and carbohydrate metabolism			
Ciclev10016525m PACid:20819165	AT4G05180.1	Photosystem II subunit Q-2	2.138
Ciclev10017247m PACid:20815638	AT3G21055.1	Photosystem II subunit T	2.328
Ciclev10005974m PACid:20791469	AT3G22840.1	Chlorophyll A-B binding family protein	2.243
Ciclev10002532m PACid:20787444	AT1G54500.1	Rubredoxin family protein	122.070
Ciclev10017081m PACid:20817328	AT2G27510.1	Ferredoxin 3	2.190
Ciclev10029499m PACid:20813098	AT2G27510.1	Ferredoxin 3	2.689
Ciclev10031620m PACid:20804829	AT2G39730.2	Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic	370.071
Ciclev10005029m PACid:20791411	AT1G79530.1	Glyceraldehyde-3-phosphate dehydrogenase	2.635
Ciclev10014974m PACid:20817138	AT3G07670.1	Rubisco methyltransferase family protein	0.451
Ciclev10014196m PACid:20818257	AT5G11720.1	α -glucosidase//Glycosyl hydrolases family 31 protein	2.086
Ciclev10017122m PACid:20815005	AT3G26720.1	Glycosyl hydrolase family 38 protein	2.203
Ciclev10028301m PACid:20813445	AT4G39010.1	Endo-1,4- β -glucanase//Endoglucanase 24	121.841
Ciclev10028656m PACid:20812272	AT4G34480.1	(1->3)- β -glucan endohydrolase 7// β -1,3-endoglucanase 7//Glucan endo-1,3- β -glucosidase 7//O-Glycosyl hydrolases family 17 protein	2.260
Ciclev10005195m PACid:20790202	AT3G57240.1	(1->3)- β -glucan endohydrolase// β -1,3-endoglucanase	2.439
Ciclev10005316m PACid:20792235	AT3G57270.1	(1->3)- β -glucan endohydrolase// β -1,3-endoglucanase	2.708
Ciclev10005491m PACid:20790391	AT5G24090.1	Acidic endochitinase	3.017
Ciclev10004369m PACid:20791173	AT5G49360.1	Arabinofuranosidase// β -D-xylosidase 1	0.388
Ciclev10004864m PACid:20791543	AT3G48950.1	Pectin lyase-like superfamily protein	0.439
Ciclev10031404m PACid:20803253	AT1G22360.1	UDP-glucosyl transferase 85A2	171.963
Ciclev10031408m PACid:20802707	AT1G22380.1	UDP-glucosyl transferase 85A3	40.098
Ciclev10000272m PACid:20786660	AT2G36390.1	1,4- α -glucan-branching enzyme//Q-enzyme	2.457
Ciclev10019346m PACid:20806605	AT1G32900.1	GBSSII-2//Granule-bound starch synthase 1, chloroplastic//amyloplastic//Granule-bound starch synthase I	2.211
Ciclev10015687m PACid:20818911	AT1G29050.1	Trichome birefringence-like 38	0.420
Ciclev10004731m PACid:20790470	AT5G19220.1	ADP glucose pyrophosphorylase large subunit 1	0.467
Ciclev10032014m PACid:20805824	AT3G04120.1	Glyceraldehyde-3-phosphate dehydrogenase C subunit 1	2.262
Ciclev10019997m PACid:20811450	AT5G56350.1	Pyruvate kinase family protein	2.481
Ciclev10011402m PACid:20797055	AT3G08590.1	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	2.354
Ciclev10011989m PACid:20798577	AT5G15140.1	Aldose 1-epimerase	16.397

Table S1. Cont.

Accession	Homology in <i>Arabidopsis thaliana</i>	Proteins	Fold Change (121/119)
Energy and carbohydrate metabolism			
Ciclev10022953m PACid:20808910	AT3G62810.1	Complex 1 family protein/LVR family protein	12.567
Ciclev10015546m PACid:20818719	AT4G22260.1	Alternative oxidase family protein	2.043
Ciclev10021931m PACid:20811193	AT4G19540.1	IND1(iron-sulfur protein required for NADH dehydrogenase)-like	2.474
Ciclev10021162m PACid:20807552	AT5G24400.1	NagB/RpiA/CoA transferase-like superfamily protein	2.126
Ciclev10009694m PACid:20793497	AT1G18270.3	Ketose-bisphosphate aldolase class-II family protein	0.459
Ciclev10010343m PACid:20793499	AT5G20830.2	Nodulin-100//Sucrose synthase	0.298
Ciclev10020692m PACid:20809157	AT3G14420.2	Aldolase-type TIM barrel family protein	0.495
Ciclev10018748m PACid:20811584	AT1G78580.1	Trehalose-6-phosphate synthase	0.494
Ciclev10016324m PACid:20816626	AT1G28960.1	Coenzyme A diphosphatase NUDT15//Nudix hydrolase 15, mitochondrial//Predicted protein/nudix hydrolase homolog 15	0.445
S metabolism			
Ciclev10004927m PACid:20791536	AT3G22890.1	ATP sulfurylase 1	3.166
Ciclev10032031m PACid:20803628	AT3G03630.1	Cysteine synthase 26	9.028
Ciclev10032680m PACid:20805511	AT1G10370.1	Glutathione S-transferase family protein	1682.737
Ciclev10012631m PACid:20798866	AT5G02790.1	Glutathione S-transferase family protein	3.157
Ciclev10022212m PACid:20809459	AT2G47730.1	Glutathione S-transferase F8, chloroplastic	3.548
Ciclev10030408m PACid:20812962	AT2G29420.1	Glutathione S-transferase tau 7	5.701
Ciclev10030418m PACid:20812954	AT2G29420.1	Glutathione S-transferase tau 7	5.328
Ciclev10022164m PACid:20810119	AT1G78380.1	Glutathione S-transferase TAU 19	2.056
Ciclev10009304m PACid:20794954	AT4G31870.1	Glutathione peroxidase 7	2.220
Ciclev10022130m PACid:20808338	AT4G11600.1	Glutathione peroxidase 6	2.542
Ciclev10000728m PACid:20785479	AT5G27380.1	Glutathione synthetase 2	384.080
Ciclev10008149m PACid:20793255	AT4G33030.1	UDP-sulfoquinovose synthase, chloroplastic	2.061
Ciclev10016894m PACid:20815716	AT3G54900.1	Monothiol glutaredoxin-S14, chloroplastic	22.681
Ciclev10002859m PACid:20787371	AT3G51030.1	Thioredoxin H-type 1	2.264
Ciclev10002332m PACid:20785936	AT1G76020.1	Thioredoxin superfamily protein	2.015
Ciclev10007750m PACid:20792997	AT4G29210.1	γ -glutamyl transpeptidase 4	0.479
Ciclev10017254m PACid:20817743	AT1G31170.4	Sulfiredoxin	0.405
Stress response			
Ciclev10001726m PACid:20787677	AT1G71695.1	ATP4a//PRXR6//Peroxidase 12	3.198
Ciclev10012554m PACid:20797449	AT3G09640.1	Ascorbate peroxidase	2.785
Ciclev10002765m PACid:20789304	AT1G08830.1	Superoxide dismutase [Cu-Zn]//copper/zinc superoxide dismutase 1	2.641
Ciclev10032661m PACid:20804250	AT3G10920.1	Mn/Fe superoxide dismutase//Superoxide dismutase [Mn], mitochondrial	2.518
Ciclev10000951m PACid:20786358	AT4G35090.1	Catalase	0.481
Ciclev10015870m PACid:20817415	AT4G21960.1	ATP1a//ATP1b//PRXR1	0.387
Ciclev10015090m PACid:20818685	AT3G27820.1	Probable monodehydroascorbate reductase, cytoplasmic isoform 2	0.301
Ciclev10020289m PACid:20810123	AT4G10720.1	Ankyrin repeat family protein//Ankyrin repeat-containing protein At2g01680	2.614
Ciclev10024221m PACid:20810180	AT5G54620.1	Ankyrin repeat family protein//Ankyrin repeat protein//Ankyrin repeat-containing protein At2g01680	2.159
Ciclev10016314m PACid:20818806	AT2G42590.3	14-3-3 protein homolog [<i>Maackia amurensis</i>]//14-3-3-like protein D//SGF14D//General regulatory factor 9	738.459

Table S1. Cont.

Accession	Homology in <i>Arabidopsis thaliana</i>	Proteins	Fold Change (121/119)
Stress response			
Ciclev10007095m PACid:20790772	AT3G23400.1	Probable plastid-lipid-associated protein 6, chloroplastic	3.571
Ciclev10015934m PACid:20819295	AT4G22240.1	Probable plastid-lipid-associated protein 2, chloroplastic	2.171
Ciclev10008835m PACid:20793494	AT3G47860.1	Apolipoprotein D//Chloroplastic lipocalin	2.249
Ciclev10029251m PACid:20813153	AT1G09560.1	Germin-like protein 5	3.130
Ciclev10016799m PACid:20818836	AT4G03240.1	Frataxin, mitochondrial	20.281
Ciclev10022174m PACid:20810231	AT1G17100.1	SOUL heme-binding family protein	2.802
Ciclev10024466m PACid:20811465	AT1G17100.1	SOUL heme-binding family protein	2.676
Ciclev10022064m PACid:20808330	AT1G17100.1	SOUL heme-binding family protein	2.251
Ciclev10029029m PACid:20813663	AT1G60680.1	NAD(P)-linked oxidoreductase superfamily protein//Probable aldo-keto reductase 2	18.580
Ciclev10015901m PACid:20815543	AT5G19440.1	Alcohol dehydrogenase-like protein	20.223
Ciclev10023259m PACid:20809337	AT3G03080.1	Alcohol dehydrogenase, putative//NADP-dependent alkenal double bond reductase P2	3959.958
Ciclev10004594m PACid:20790507	AT3G66658.2	Aldehyde dehydrogenase 22A1	0.405
Ciclev10019095m PACid:20809601	AT5G52640.1	Heat shock protein 83//Heat shock protein 90.1	2.511
Ciclev10029467m PACid:20813389	AT3G46230.1	17.4 kDa class I heat shock protein	2.472
Ciclev10007067m PACid:20790805	AT4G15802.1	Heat shock factor binding protein	543.235
Ciclev10025114m PACid:20801969	AT1G16030.1	Heat shock 70 kDa protein 5//Heat shock protein 70-5//Heat shock protein, putative	2.146
Ciclev10026390m PACid:20801494	AT1G52560.1	26.5 kDa heat shock protein, mitochondrial//HSP20-like chaperones superfamily protein//Small heat-shock protein, putative	2.994
Ciclev10024164m PACid:20808067	AT1G53280.1	Chaperone protein YajL//Class I glutamine amidotransferase-like superfamily protein	508.524
Ciclev10021210m PACid:20811903	AT1G53280.1	Chaperone protein YajL//Class I glutamine amidotransferase-like superfamily protein	18.328
Ciclev10029386m PACid:20812277	AT2G16600.1	Peptidyl-prolyl <i>cis-trans</i> isomerase CYP19-1	2.267
Ciclev10010508m PACid:20794622	AT1G01470.1	Late embryogenesis abundant protein	222.637
Ciclev10009203m PACid:20796146	AT5G54110.1	Membrane-associated mannitol-induced	92.662
Ciclev10012028m PACid:20798669	AT1G17020.1	Protein SRG1//Senescence-related gene 1	9.830
Ciclev10029528m PACid:20813912	AT3G04720.1	Pathogenesis-related 4	3.179
Ciclev10029375m PACid:20814005	AT2G21620.1	Adenine nucleotide α hydrolases-like superfamily protein	2.092
Ciclev10029414m PACid:20814816	AT3G53990.1	Adenine nucleotide α hydrolases-like superfamily protein//Universal stress protein 1//Universal stress protein A-like protein	2.567
Ciclev10006096m PACid:20791940	AT1G24020.2	MLP-like protein 423//Major allergen Pru ar 1//Stress-related protein	2.279
Ciclev10032973m PACid:20802498	AT1G24020.1	MLP-like protein 423//Major latex-like protein	0.407
Low-P-responsive proteins			
Ciclev10026096m PACid:20800141	AT1G73010.1	Inorganic pyrophosphatase 1//Predicted protein	26.117
Ciclev10012723m PACid:20796310	AT3G53620.1	Soluble inorganic pyrophosphatase 4	2.770
Ciclev10016242m PACid:20815326	AT2G39780.2	Ribonuclease 2	3.253
Ciclev10016283m PACid:20815386	AT1G25230.1	Purple acid phosphatase 4	2.776
Ciclev10015905m PACid:20817929	AT2G01890.1	Purple acid phosphatase 8	2.149
Ciclev10013402m PACid:20797645	AT3G52780.1	Purple acid phosphatases superfamily protein	2.821
Ciclev10030896m PACid:20803277	AT1G13900.1	Purple acid phosphatases superfamily protein	2.346
Ciclev10015568m PACid:20815289	AT3G02040.1	Glycerophosphodiester phosphodiesterase GDE1	7.013
Ciclev10020540m PACid:20807368	AT5G08030.1	Glycerophosphoryl diester phosphodiesterase//PLC-like phosphodiesterases superfamily protein	2.366

Table S1. Cont.

Accession	Homology in <i>Arabidopsis thaliana</i>	Proteins	Fold Change (121/119)
Low-P-responsive proteins			
Ciclev10018719m PACid:20805954	AT1G53310.3	Phosphoenolpyruvate carboxylase 3	2.706
Ciclev10012732m PACid:20798969	AT1G79790.1	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein//Phosphorylated carbohydrates phosphatase TM_1254	1142.463
Ciclev10032556m PACid:20804067	AT2G38740.1	Haloacid dehalogenase-like hydrolase domain-containing protein Sgpp	3.182
Ciclev10016366m PACid:20815584	AT5G44730.1	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	309.403
Ciclev10008400m PACid:20795268	AT2G25870.1	Haloacid dehalogenase-like hydrolase family protein	0.415
Nucleic acid metabolism			
Ciclev10009937m PACid:20796049	AT5G26170.1	Probable WRKY transcription factor 50	3.042
Ciclev10009720m PACid:20795220	AT5G11260.1	Basic-leucine zipper (bZIP) transcription factor family protein//Protein LONG HYPOCOTYL 5//Transcription factor HY5//bZIP transcription factor 56	17.626
Ciclev10002081m PACid:20786258	AT3G12480.1	Nuclear factor Y, subunit C11	23.136
Ciclev10025390m PACid:20800887	AT5G66730.1	C2H2-like zinc finger protein	70.035
Ciclev10033000m PACid:20804271		HAP3-like protein	2.050
Ciclev10016303m PACid:20816503	AT3G23250.1	Myb domain protein 15	0.310
Ciclev10004185m PACid:20791644	AT5G49930.1	Zinc knuckle (CCHC-type) family protein	0.438
Ciclev10015532m PACid:20815484	AT5G07900.1	Mitochondrial transcription termination factor family protein	0.459
Ciclev10010753m PACid:20792790	AT1G15340.1	Methyl-CPG-binding domain 11	2.060
Ciclev10033914m PACid:20802816	AT3G12640.1	RNA-binding (RRM/RBD/RNP motifs) family protein	368.818
Ciclev10025862m PACid:20801963	AT2G18510.1	RNA-binding (RRM/RBD/RNP motifs) family protein//Splicing factor 3B subunit 4	293.896
Ciclev10014272m PACid:20817277	AT3G02010.1	Pentatricopeptide repeat (PPR) superfamily protein	611.788
Ciclev10018370m PACid:20818993	AT4G03430.1	Putative pre-mRNA splicing factor	2.190
Ciclev10030532m PACid:20804921	AT3G55220.1	Spliceosome-associated protein 130	0.496
Ciclev10021761m PACid:20808316	AT1G18800.1	NAP1-related protein 2	0.493
Ciclev10004916m PACid:20791356	AT3G54470.1	Uridine 5'-monophosphate synthase	543.655
Ciclev10007580m PACid:20793771	AT5G11350.1	DNase I-like superfamily protein	0.466
Protein and amino acid metabolism			
Ciclev10004211m PACid:20790583	AT5G49030.3	tRNA synthetase class I (I, L, M and V) family protein	0.417
Ciclev10004807m PACid:20791740	AT3G06430.1	Tetratricopeptide repeat (TPR)-like superfamily protein	0.322
Ciclev10025061m PACid:20800270	AT5G08650.1	Elongation factor 4 homolog/Ribosomal back-translocase/Small GTP-binding protein/Translation factor GUF1 homolog, chloroplastic	0.489
Ciclev10006396m PACid:20789804	ATCG00800.1	Structural constituent of ribosome	0.453
Ciclev10022283m PACid:20810800	AT3G49010.1	60S ribosomal protein L13/Protein BBC1 homolog/Breast basic conserved 1	0.361
Ciclev10013047m PACid:20799080	AT3G56910.1	Plastid-specific 50S ribosomal protein 5	0.348
Ciclev10013049m PACid:20798310	AT2G38140.1	Plastid-specific ribosomal protein 4	0.319
Ciclev10009636m PACid:20793290	AT3G15190.1	Chloroplast 30S ribosomal protein S20, putative	0.494
Ciclev10022870m PACid:20811532	AT3G05560.1	Ribosomal L22e protein family	0.465
Ciclev10006136m PACid:20789692	AT2G33450.1	Ribosomal L28 family	0.298
Ciclev10009798m PACid:20796123	AT2G19730.1	Ribosomal L28e protein family	0.470
Ciclev10026623m PACid:20801707	AT5G65220.1	Ribosomal L29 family protein	0.384
Ciclev10033083m PACid:20804008	AT2G39390.1	Ribosomal L29 family protein	0.169
Ciclev10016875m PACid:20816724	AT5G45775.2	Ribosomal L5P family protein	0.473

Table S1. Cont.

Accession	Homology in <i>Arabidopsis thaliana</i>	Proteins	Fold Change (121/119)
Protein and amino acid metabolism			
Ciclev10021696m PACid:20808755	AT4G01310.1	Ribosomal L5P family protein	0.439
Ciclev10032705m PACid:20803904	AT5G13510.1	Ribosomal protein L10 family protein	0.446
Ciclev10021899m PACid:20808624	AT1G78630.1	Ribosomal protein L13 family protein	0.396
Ciclev10023476m PACid:20812085	ATCG00780.1	Ribosomal protein L14	0.448
Ciclev10016274m PACid:20815504	AT3G25920.1	Ribosomal protein L15	0.451
Ciclev10004001m PACid:20788151	ATCG00790.1	Ribosomal protein L16	0.429
Ciclev10032703m PACid:20802569	AT1G26910.1	Ribosomal protein L16p/L10e family protein	0.397
Ciclev10006182m PACid:20792369	AT1G02780.1	Ribosomal protein L19e family protein	0.355
Ciclev10030134m PACid:20813406	AT5G22440.1	Ribosomal protein L1p/L10e family	0.487
Ciclev10016308m PACid:20817308	AT4G36130.1	Ribosomal protein L2 family	0.273
Ciclev10002401m PACid:20788696	AT1G35680.1	Ribosomal protein L21	0.353
Ciclev10005921m PACid:20792152	ATCG00810.1	Ribosomal protein L22	0.393
Ciclev10023969m PACid:20810966	AT3G53020.1	Ribosomal protein L24	0.393
Ciclev10017015m PACid:20815733	AT1G29070.1	Ribosomal protein L34	0.343
Ciclev10022900m PACid:20806865	AT1G26880.1	Ribosomal protein L34e superfamily protein	0.302
Ciclev10033093m PACid:20804391	AT1G26880.1	Ribosomal protein L34e superfamily protein	0.295
Ciclev10013164m PACid:20798847	AT1G07070.1	Ribosomal protein L35Ae family protein	0.399
Ciclev10006273m PACid:20790606	AT3G53740.2	Ribosomal protein L36e family protein	0.382
Ciclev10011875m PACid:20799017	AT3G09630.1	Ribosomal protein L4/L1 family	0.456
Ciclev10020582m PACid:20810676	AT3G25520.1	Ribosomal protein L5	0.388
Ciclev10016107m PACid:20818376	AT5G39740.1	Ribosomal protein L5 B	0.412
Ciclev10009377m PACid:20794151	AT1G33140.1	Ribosomal protein L6 family	0.483
Ciclev10016578m PACid:20816737	AT1G05190.1	Ribosomal protein L6 family	0.459
Ciclev10032636m PACid:20805408	AT1G74050.1	Ribosomal protein L6 family protein	0.463
Ciclev10032494m PACid:20803323	AT2G47610.1	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	0.433
Ciclev10006259m PACid:20792027	AT1G77940.1	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	0.346
Ciclev10029219m PACid:20813782	AT3G44890.1	Ribosomal protein L9	0.440
Ciclev10016825m PACid:20818990	AT5G40950.1	Ribosomal protein large subunit 27	0.458
Ciclev10009763m PACid:20793057	AT5G23740.1	Ribosomal protein S11-beta	0.396
Ciclev10002692m PACid:20789374	AT5G14320.1	Ribosomal protein S13/S18 family	0.387
Ciclev10006145m PACid:20790323	AT4G00100.1	Ribosomal protein S13A	0.413
Ciclev10026679m PACid:20800350	AT1G79850.1	Ribosomal protein S17	0.475
Ciclev10003202m PACid:20788933	ATCG00650.1	Ribosomal protein S18	0.463
Ciclev10002819m PACid:20786600	AT3G04920.1	Ribosomal protein S24e family protein	0.402
Ciclev10029630m PACid:20813886	AT2G21580.2	Ribosomal protein S25 family protein	0.486
Ciclev10002825m PACid:20785887	AT3G56340.1	Ribosomal protein S26e family protein	0.464
Ciclev10009868m PACid:20794701	AT5G56670.1	Ribosomal protein S30 family protein	0.208
Ciclev10012508m PACid:20798906	AT4G34670.1	Ribosomal protein S3Ae	0.445

Table S1. Cont.

Accession	Homology in <i>Arabidopsis thaliana</i>	Proteins	Fold Change (121/119)
Protein and amino acid metabolism			
Ciclev10032800m PACid:20804334	AT5G39850.1	Ribosomal protein S4	0.444
Ciclev10029508m PACid:20812895	AT2G09990.1	Ribosomal protein S5 domain 2-like superfamily protein	0.497
Ciclev10006162m PACid:20790988	AT2G09990.1	Ribosomal protein S5 domain 2-like superfamily protein	0.382
Ciclev10005613m PACid:20790205	AT3G57490.1	Ribosomal protein S5 family protein	0.452
Ciclev10026340m PACid:20801998	AT5G10360.1	Ribosomal protein S6e	0.464
Ciclev10012856m PACid:20796870	AT5G16130.1	Ribosomal protein S7e family protein	0.478
Ciclev10009415m PACid:20792807	AT5G59240.1	Ribosomal protein S8e family protein	0.370
Ciclev10023063m PACid:20807474	AT3G10950.1	Zinc-binding ribosomal protein family protein	0.458
Ciclev10022990m PACid:20811127	AT4G14320.1	Zinc-binding ribosomal protein family protein	0.441
Ciclev10026841m PACid:20799774	AT3G16080.1	Ribosomal protein L37//Zinc-binding ribosomal protein family protein	0.235
Ciclev10009628m PACid:20794614	AT5G54600.1	Translation protein SH3-like family protein	0.492
Ciclev10026719m PACid:20802119	AT3G49910.1	Translation protein SH3-like family protein	0.428
Ciclev10012788m PACid:20797116	AT1G57860.1	Translation protein SH3-like family protein	0.347
Ciclev10001454m PACid:20789331	AT1G43170.8	60S ribosomal protein L3//ribosomal protein 1	0.424
Ciclev10001453m PACid:20788226	AT1G61580.1	60S ribosomal protein L3-2//R-protein L3 B	2.068
Ciclev10005170m PACid:20789963	AT4G13670.1	Plastid transcriptionally active 5	2.043
Ciclev10012870m PACid:20798639	AT3G12390.1	Nascent polypeptide-associated complex (NAC), alpha subunit family protein	374.508
Ciclev10022215m PACid:20807094	AT3G49470.1	Nascent polypeptide-associated complex subunit alpha-like protein 2	73.723
Ciclev10026634m PACid:20801099	AT4G37660.1	50S ribosomal protein L7/L12//Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein	196.542
Ciclev10018845m PACid:20809345	AT1G56070.1	Ribosomal protein S5/Elongation factor G/III/V family protein	576.342
Ciclev10029555m PACid:20813972	AT5G02960.1	Ribosomal protein S12/S23 family protein	25.756
Ciclev10009899m PACid:20793086	AT5G20160.1	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	22.210
Ciclev10022435m PACid:20810058	AT5G27850.1	Ribosomal protein L18e/L15 superfamily protein	71.594
Ciclev10003535m PACid:20787040	AT1G35340.1	ATP-dependent protease La (LON) domain protein	2.960
Ciclev10015814m PACid:20818497	AT2G27420.1	Cysteine proteinases	315.813
Ciclev10020859m PACid:20807278	AT1G02305.1	Cysteine proteinases superfamily protein	2.147
Ciclev10005038m PACid:20790402	AT1G03220.1	Eukaryotic aspartyl protease family protein	2.260
Ciclev10001060m PACid:20785798	AT1G73300.1	Serine carboxypeptidase, putative//Serine carboxypeptidase-like 18	2.432
Ciclev10029139m PACid:20813954	AT5G66140.1	Proteasome α subunit D2	1116.926
Ciclev10026339m PACid:20801160	AT5G66140.1	Proteasome α subunit D2	975.112
Ciclev10014351m PACid:20817403	AT2G04160.1	Subtilisin-like serine endopeptidase family protein	310.100
Ciclev10001054m PACid:20785799	AT1G47128.1	Granulin repeat cysteine protease family protein	2.617
Ciclev10002346m PACid:20788131	AT3G12490.2	Cystatin B	2.256
Ciclev10003705m PACid:20786256	AT5G47550.1	Cystatin/monellin superfamily protein	2.037
Ciclev10022001m PACid:20806490	AT1G17860.1	Kunitz family trypsin and protease inhibitor protein	3.039
Ciclev10022156m PACid:20808320	AT1G17860.1	Kunitz family trypsin and protease inhibitor protein	2.537
Ciclev10022211m PACid:20810798	AT1G17860.1	Kunitz family trypsin and protease inhibitor protein	2.293
Ciclev10011794m PACid:20796925	AT2G24280.1	α/β -Hydrolases superfamily protein	2.007

Table S1. Cont.

Accession	Homology in <i>Arabidopsis thaliana</i>	Proteins	Fold Change (121/119)
Protein and amino acid metabolism			
Ciclev10021018m PACid:20812099	AT4G10790.1	UBX domain-containing protein	346.152
Ciclev10023537m PACid:20809334	AT4G17510.1	Ubiquitin C-terminal hydrolase 3	597.747
Ciclev10009208m PACid:20795336	AT5G25770.3	α/β -Hydrolases superfamily protein	0.283
Ciclev10022124m PACid:20806488	AT1G17860.1	Kunitz family trypsin and protease inhibitor protein	0.454
Ciclev10008097m PACid:20793654	AT4G32940.1	Gamma vacuolar processing enzyme	0.454
Ciclev10014528m PACid:20815760	AT5G46210.1	Cullin4	0.498
Ciclev10032969m PACid:20804504	AT2G47110.1	Ubiquitin 6	0.268
Ciclev10008698m PACid:20793182	AT5G05920.1	Deoxyhypusine synthase	110.347
Ciclev10028599m PACid:20813645	AT5G64370.1	Beta-alanine synthase//N-carbamoyl-beta-alanine amidohydrolase//Predicted protein	294.686
Ciclev10021002m PACid:20809681	AT4G08900.1	Arginase	2.541
Ciclev10011621m PACid:20797657	AT3G08860.1	Alanine-glyoxylate aminotransferase 2 homolog 3, mitochondrial//Alanine-glyoxylate aminotransferase, putative	2.110
Ciclev10019032m PACid:20806055	AT4G12290.1	Copper amine oxidase family protein	2.846
Ciclev10015485m PACid:20818727	AT2G13360.1	Alanine:glyoxylate aminotransferase	0.382
Ciclev10007310m PACid:20794460	AT4G33010.1	Glycine decarboxylase P-protein 1	0.393
Ciclev10033729m PACid:20804854	AT1G69800.2	Cystathionine β -synthase (CBS) protein	0.423
Ciclev10032361m PACid:20805672	AT1G07780.1	Phosphoribosylanthranilate isomerase 1	0.227
Ciclev10027913m PACid:20814546	AT2G37040.1	Phenylalanine ammonia-lyase 1	0.325
Ciclev10001828m PACid:20788451	AT1G76730.1	Methenyltetrahydrofolate synthase domain-containing protein//NagB/RpiA/CoA transferase-like superfamily protein	0.486
Cell wall and cytoskeleton metabolism			
Ciclev10021884m PACid:20807416	AT4G17030.1	Expansin-like B1	3.008
Ciclev10033057m PACid:20802906	AT5G59890.2	Actin-depolymerizing factor 2//Actin depolymerizing factor 4	2188.468
Ciclev10011723m PACid:20796428	AT5G23860.2	Beta-8-tubulin	15.113
Ciclev10011719m PACid:20798687	AT5G12250.1	Tubulin beta-6 chain	0.383
Ciclev10028426m PACid:20814187	AT1G50010.1	Tubulin α -2 chain	0.433
Cellular transport			
Ciclev10013168m PACid:20798707	AT3G01390.1	V-type proton ATPase subunit G//Vacuolar proton pump subunit G//Vacuolar membrane ATPase 10	540.092
Ciclev10032471m PACid:20804478	AT2G40300.1	Ferritin 4	2.200
Ciclev10029240m PACid:20812600	AT2G16060.1	Non-symbiotic hemoglobin 1	2.113
Ciclev10006560m PACid:20791490	AT5G51720.1	CDGSH iron-sulfur domain-containing protein NEET	2.146
Ciclev10012107m PACid:20798800	AT2G40060.1	Clathrin light chain 2//Clathrin light chain protein	2.006
Ciclev10016438m PACid:20816862	AT1G61250.1	Secretory carrier-associated membrane protein 3//secretory carrier 3	9.400
Ciclev10032366m PACid:20805747	AT3G01280.1	Voltage dependent anion channel 1	3.454
Ciclev10006198m PACid:20791190	AT1G01490.2	Heavy-metal-associated domain-containing protein	2.917
Ciclev10020395m PACid:20809498	AT2G36070.1	Mitochondrial import inner membrane translocase subunit TIM44-2	2.032
Ciclev10008825m PACid:20793014	AT4G30840.1	Nucleoporin Nup43//Nup107-160 subcomplex subunit Nup43//Transducin/WD40 repeat-like superfamily protein	166.926
Ciclev10007941m PACid:20794860	AT2G18710.1	Preprotein translocase subunit SCY1, chloroplastic	0.241
Ciclev10014606m PACid:20818166	AT1G14830.1	Dynamin	0.484
Ciclev10000332m PACid:20789395	AT1G76850.1	Exocyst complex component 2//Exocyst complex component Sec5//Predicted protein	0.412

Table S1. Cont.

Accession	Homology in <i>Arabidopsis thaliana</i>	Proteins	Fold Change (121/119)
Cellular transport			
Ciclev10014840m PACid:20817945	AT4G25650.1	ACD1-like	0.464
Ciclev10007246m PACid:20793324	AT3G43300.1	HOPM interactor 7	0.449
Ciclev10030708m PACid:20805624	AT2G35800.1	Mitochondrial substrate carrier family protein	0.470
Ciclev10006055m PACid:20792243	AT4G14870.1	Preprotein translocase subunit SECE1//SecE/SEC61-gamma protein transport protein	0.363
Ciclev10018709m PACid:20805894	AT2G46520.1	Cellular apoptosis susceptibility protein homolog//Exportin-2//Importin-alpha re-exporter	0.498
Ciclev10007348m PACid:20795660	AT5G11560.1	Catalytic, putative//ER membrane protein complex subunit 1//Catalytics	0.498
Lipid metabolism			
Ciclev10032510m PACid:20802930	AT3G25780.1	Allene oxide cyclase 3	111.562
Ciclev10014204m PACid:20816226	AT3G45140.1	Lipoxygenase 2	3.025
Ciclev10004649m PACid:20791288	AT3G16910.1	Acetate/butyrate-CoA ligase AAE7, peroxisomal//Acyl-activating enzyme 7	195.305
Ciclev10022587m PACid:20810567	AT3G61200.1	Acyl-CoA thioesterase, putative//Thioesterase superfamily protein	150.409
Ciclev10020242m PACid:20811380	AT1G01710.1	Acyl-CoA thioesterase family protein	4.523
Ciclev10019200m PACid:20807021	AT4G23850.1	Long chain acyl-CoA synthetase 4	0.449
Ciclev10010427m PACid:20796029	AT1G53920.1	GDSL esterase/lipase 5	2.526
Ciclev10020550m PACid:20810248	AT3G60510.1	3-hydroxyisobutyryl-CoA hydrolase-like protein 1, mitochondrial	61.285
Ciclev10031489m PACid:20804761	AT5G17540.1	HXXXD-type acyl-transferase family protein	2.148
Ciclev10025939m PACid:20800257	AT4G39330.1	Cinnamyl alcohol dehydrogenase 9	0.475
Ciclev10020721m PACid:20807101	AT4G00400.1	Glycerol-3-phosphate acyltransferase 8	0.371
Ciclev10026558m PACid:20800793	AT5G48930.1	Hydroxycinnamoyl transferase	0.365
Ciclev10013542m PACid:20799197	AT5G54160.1	O-methyltransferase 1	0.383
Ciclev10008761m PACid:20795154	AT4G33110.1	Coclaurine N-methyltransferase	0.417
Ciclev10010749m PACid:20792814	AT3G18000.1	Phosphoethanolamine N-methyltransferase 1//Phosphoethanolamine N-methyltransferase, putative	0.232
Ciclev10033579m PACid:20803972	AT5G19290.1	HU-K5//Lysophospholipase-like//Monoacylglycerol lipase//Monoglyceride lipase	0.488
Signal transduction			
Ciclev10031755m PACid:20803828	AT1G14000.1	VH1-interacting kinase	2.151
Ciclev10012334m PACid:20797162	AT5G39790.1	5'-AMP-activated protein kinase-related	2.088
Ciclev10006977m PACid:20789643	AT5G52200.1	Phosphoprotein phosphatase inhibitors	1700.715
Ciclev10002098m PACid:20789158	AT1G34750.1	Protein phosphatase 2C family protein	22.049
Ciclev10021603m PACid:20811358	AT4G11240.1	Serine/threonine-protein phosphatase PPI isozyme 6	2.246
Ciclev10009194m PACid:20796151	AT5G06740.1	Concanavalin A-like lectin protein kinase family protein	0.250
Ciclev10018681m PACid:20806123	AT5G23060.1	Calcium sensing receptor	360.223
Ciclev10017002m PACid:20819306	AT5G47710.1	Calcium-dependent lipid-binding (CaLB domain) family protein	52.792
Ciclev10005548m PACid:20792350	AT3G16510.1	Calcium-dependent lipid-binding (CaLB domain) family protein	18.237
Ciclev10005575m PACid:20789955	AT3G10300.3	Calcium-binding EF-hand family protein//Calmodulin-like protein 49//Probable calcium-binding protein CML49	7.611
Ciclev10003554m PACid:20787567	AT2G21830.1	Cysteine/Histidine-rich C1 domain family protein	2.480
Ciclev10032615m PACid:20804275	AT3G07390.1	Auxin-induced in root cultures protein 12//Auxin-responsive family protein	456.371
Ciclev10022378m PACid:20809005	AT4G01900.1	GLNB1 homolog//Nitrogen regulatory protein P-II homolog//Protein PII-like	3.131
Ciclev10000962m PACid:20788421	AT5G63910.1	Farnesylcysteine lyase	143.231
Ciclev10021008m PACid:20809776	AT3G59380.1	Farnesyltransferase A	0.374

Table S1. Cont.

Accession	Homology in <i>Arabidopsis thaliana</i>	Proteins	Fold Change (121/119)
Others			
Ciclev10002486m PACid:20787718	AT4G31950.1	Cytochrome P450	0.226
Ciclev10007096m PACid:20791221	AT1G64940.1	Cytochrome P450, family 87, subfamily A, polypeptide 6	0.467
Ciclev10004785m PACid:20790316	AT3G26300.1	Cytochrome P450, family 71, subfamily B, polypeptide 34	0.239
Ciclev10000866m PACid:20786710	AT3G26300.1	Cytochrome P450, family 71, subfamily B, polypeptide 34	0.403
Ciclev10031280m PACid:20805703	AT3G26300.1	Cytochrome P450, family 71, subfamily B, polypeptide 34	0.299
Ciclev10017346m PACid:20815057	AT5G04750.1	F1F0-ATPase inhibitor protein, putative	2.385
Ciclev10005457m PACid:20791540	AT5G24020.1	Septum site-determining protein (MIND)	9.392
Ciclev10021578m PACid:20810267	AT1G53520.1	Chalcone-flavonone isomerase 2	17.473
Ciclev10001946m PACid:20787842	AT1G75280.1	Isoflavone reductase homolog P3	0.401
Ciclev10008386m PACid:20794913	AT5G53860.2	Embryo defective 2737	12.485
Ciclev10012793m PACid:20797650	AT2G04690.1	Pyridoxamine 5'-phosphate oxidase family protein	2.225
Ciclev10031003m PACid:20805689	AT4G19170.1	Probable carotenoid cleavage dioxygenase 4, chloroplastic	0.315
Ciclev10000425m PACid:20787673	AT1G21680.1	DPP6 N-terminal domain-like protein	4.505
Ciclev10005724m PACid:20790262	AT3G23600.1	α/β -Hydrolases superfamily protein	2.136
Ciclev10015803m PACid:20818801	AT2G36290.1	α/β -Hydrolases superfamily protein	0.405
Ciclev10014035m PACid:20817344	AT5G47690.3	Uncharacterized binding protein	0.427
Ciclev10016821m PACid:20815954	AT5G14030.1	Translocon-associated protein beta (TRAPB) family protein	15.251
Ciclev10026171m PACid:20801938	AT4G36850.1	PQ-loop repeat family protein/transmembrane family protein	2.084
Ciclev10016230m PACid:20818084	AT4G21470.1	Bifunctional riboflavin kinase/FMN phosphatase	2.259
Ciclev10008512m PACid:20793764	AT1G04970.1	Lipid-binding serum glycoprotein family protein	2.080
Ciclev10001991m PACid:20787158	AT3G04830.1	Protein prenyltransferase superfamily protein	0.473
Ciclev10020109m PACid:20808858	AT5G50150.1	Protein of Unknown Function (DUF239)	2.983
Ciclev10026423m PACid:20799876	AT1G15860.1	DCN1-like protein 4//DCUN1 domain-containing protein 4//Defective in cullin neddylation protein 1-like protein 4	0.499
Ciclev10016630m PACid:20817048	AT3G20790.1	NAD(P)-binding Rossmann-fold superfamily protein	0.393

Table S2. List of differentially expressed proteins in Al-toxic *Citrus grandis* leaves. Control and Al-toxic samples were labeled with 114 and 117 tags, respectively.

Accession	Homology in <i>Arabidopsis thaliana</i>	Proteins	Fold Change (117/114)
Energy and carbohydrate metabolism			
Ciclev10016116m PACid:20816432	AT3G26710.1	Cofactor assembly of complex C	2.072
S metabolism			
Ciclev10002119m PACid:20786689	AT2G47730.1	Glutathione S-transferase ϕ 8	0.431
Stress response			
Ciclev10009502m PACid:20793097	AT2G24440.1	Selenium binding	0.457
Low-P-responsive proteins			
Ciclev10026096m PACid:20800141	AT1G73010.1	Inorganic pyrophosphatase 1//Predicted protein	2.808
Ciclev10015568m PACid:20815289	AT3G02040.1	Glycerophosphodiester phosphodiesterase GDE1	2.407
Nucleic acid metabolism			
Ciclev10014026m PACid:20818243	AT3G01460.1	Methyl-CPG-binding domain 9	4.615
Ciclev10031009m PACid:20805801	AT3G48710.1	DEK domain-containing chromatin associated protein	0.422
Protein and amino acid metabolism			
Ciclev10004119m PACid:20790317	AT1G65810.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	0.441
Ciclev10029619m PACid:20813697	AT3G44590.1	60S acidic ribosomal protein family	0.412
Ciclev10007222m PACid:20793486	AT1G55860.2	Ubiquitin-protein ligase 1	2.416
Cellular transport			
Ciclev10025542m PACid:20801125	AT1G80310.1	Molybdate transporter 2//Sulfate transporter like protein 5.1//Sulfate transporter, putative//Sulfate transmembrane transporters	2.623
Ciclev10005024m PACid:20791376	AT1G05370.1	Sec14p-like phosphatidylinositol transfer family protein	0.282
Signal transduction			
Ciclev10027740m PACid:20813291	AT3G45780.1	Non-phototropic hypocotyl protein 1//Root phototropism protein 1	0.456
Ciclev10009194m PACid:20796151	AT5G06740.1	Concanavalin A-like lectin protein kinase family protein	0.439
Others			
Ciclev10008649m PACid:20793993	AT4G27520.1	Early nodulin-like protein 2	0.460
Ciclev10009420m PACid:20795288	AT3G20570.1	Early nodulin-like protein 9	0.325
Ciclev10032528m PACid:20805031	AT3G55605.1	Mitochondrial glycoprotein family protein	0.468

Table S3. Specific primer pairs used for qRT-PCR expression analysis.

Accession	Proteins	Forward Primers (5'→3')	Reverse Primers (5'→3')
Ciclev10015568m PACid:20815289	Glycerophosphodiester phosphodiesterase GDE1	AATCGGCGTCGTTTAG	GGGATATTTAGCGGAAGA
Ciclev10025542m PACid:20801125	Molybdate transporter 2	CTCCTCGCCCTCACAG	GGGTATTGCCGACAGA
Ciclev10002119m PACid:20786689	Glutathione S-transferase phi 8	TGGCAACTCCAGTAAAA	ACAAACATAGCGGCATA
Ciclev10009420m PACid:20795288	Early nodulin-like protein 9	GCCAGCAAATGGAGTA	CACGAGGATGAGGATAAT
Ciclev10008649m PACid:20793993	Early nodulin-like protein 2	AACTGGATTCCGGTGA	GGAGACTTAGGAGACGG
Ciclev10004927m PACid:20791536	ATP sulfurylase 1	TGCTCCTCCCTCACA	ACTTCCAAAGCCAATGAGACT
Ciclev10000272m PACid:20786660	1,4- α -glucan-branching enzyme//Q-enzyme	GGATGGAGGACGAGACAG	GACAACAATAAGGAATACGAGGA
Ciclev10019346m PACid:20806605	Granule-bound starch synthase 1, chloroplastic	GGAACCCCTTGACTGA	CGGACGAATGAATGTGGGT
Ciclev10018845m PACid:20809345	Ribosomal protein S5/Elongation factor G/III/V family protein	GCTGCCCTTCGTACTACT	TCTCCTCACTCAATCCCAACT
Ciclev10008097m PACid:20793654	Gamma vacuolar processing enzyme	GCTCCAGCAACCAATC	GGTTTATGTTGGAGGAGTAGGAT
Ciclev10001726m PACid:20787677	ATP4a//PRXR6//Peroxidase 12	CCCAGTAGCGAAAGGT	GAGGGACTAAAGGACCGACA
Ciclev10022164m PACid:20810119	Glutathione S-transferase τ 19	TTACTTTCGGCGTGTT	ACCAGAAGCCAGCAACAAT
Ciclev10028656m PACid:20812272	(1- \rightarrow 3)- β -glucan endohydrolase 7	CATCCGCCAAGACACTAT	CCGCACAAATGATTCCAGT
Ciclev10000951m PACid:20786358	Catalase	TTTTCTGCTTCCTCC	CAAGAAGCCCAAGGAAGC
Ciclev10007941m PACid:20794860	Preprotein translocase subunit SCY1	TCTCCAGACTCAGAAAC	TGCAAGTGGCTGAACAGAA
Ciclev10010749m PACid:20792814	Phosphoethanolamine N-methyltransferase 1	TGGCAGAAAGGATGGT	AGGGCTATAATGGGCAGTG
Ciclev10006055m PACid:20792243	Preprotein translocase subunit SECE1	AAAGCCGCCACCTGTA	CAGATAGCCAAGAAGAGGAGC
Ciclev10015870m PACid:20817415	ATP1a/ATP1b//PRXR1	CCTTTAGTGAGTGAAGAGTAG	GGACTACCGTAATAGTAAAGTCGC
Ciclev10027913m PACid:20814546	Phenylalanine ammonia-lyase 1	ACGGAACAGGAGTGGG	CCGTAACCATTCCCTCCATC
Ciclev10022212m PACid:20809459	Glutathione S-transferase F8, chloroplastic	CACGGTTCTGTTTTCTCA	TTGGGGAGCAGGTTGGA
GU911361.1	Actin	AGAACTATGAACTGCCTGATGGC	GCTTGGAGCAAGTCTGTGATT

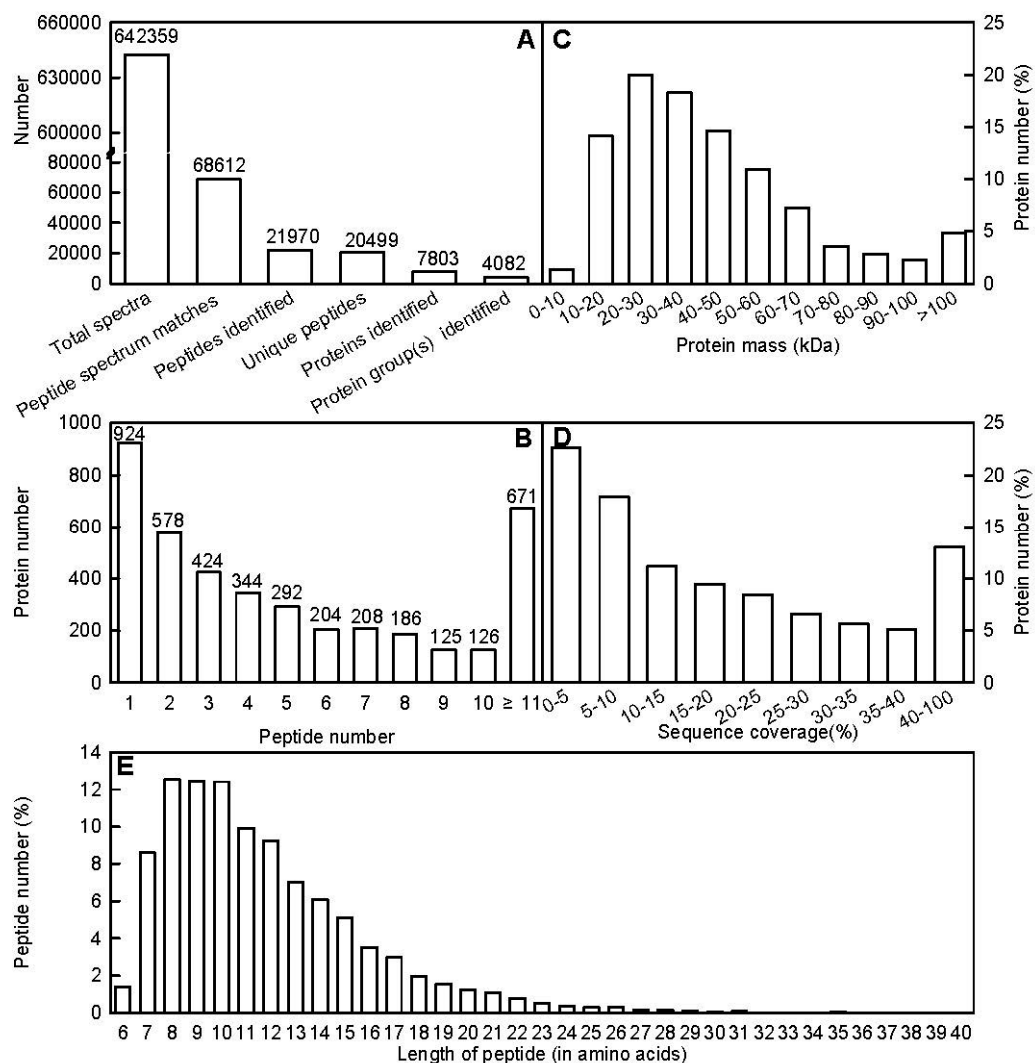


Figure S1. Spectra, peptides and proteins identified from iTRAQ proteomics (A); number of peptides that match to proteins (B); protein mass distribution (C); distribution of protein sequence coverage (D); and distribution of peptide length (E) in *C. sinensis* leaves.

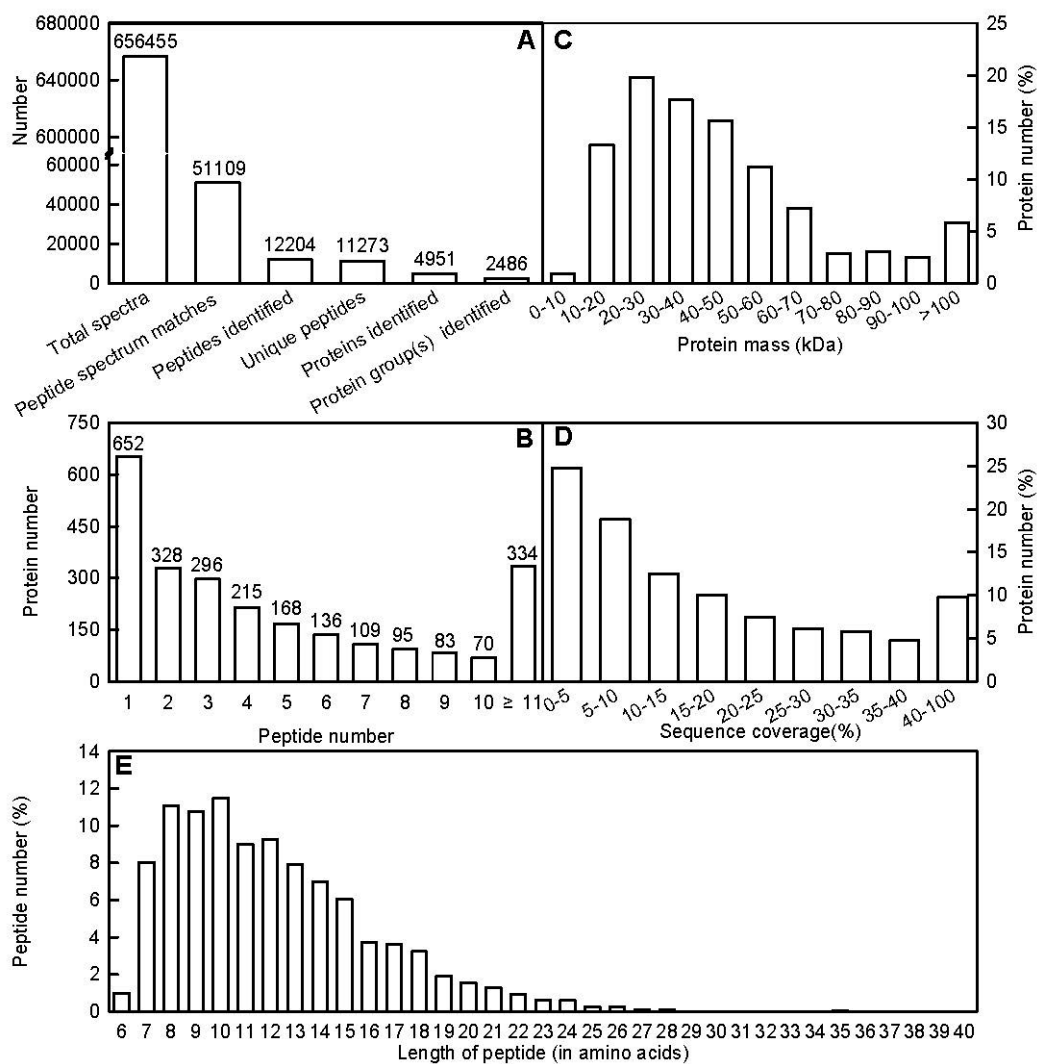


Figure S2. Spectra, peptides and proteins identified from iTRAQ proteomics (A); number of peptides that match to proteins (B); protein mass distribution (C); distribution of protein sequence coverage (D); and distribution of peptide length (E) in *C. grandis* leaves.

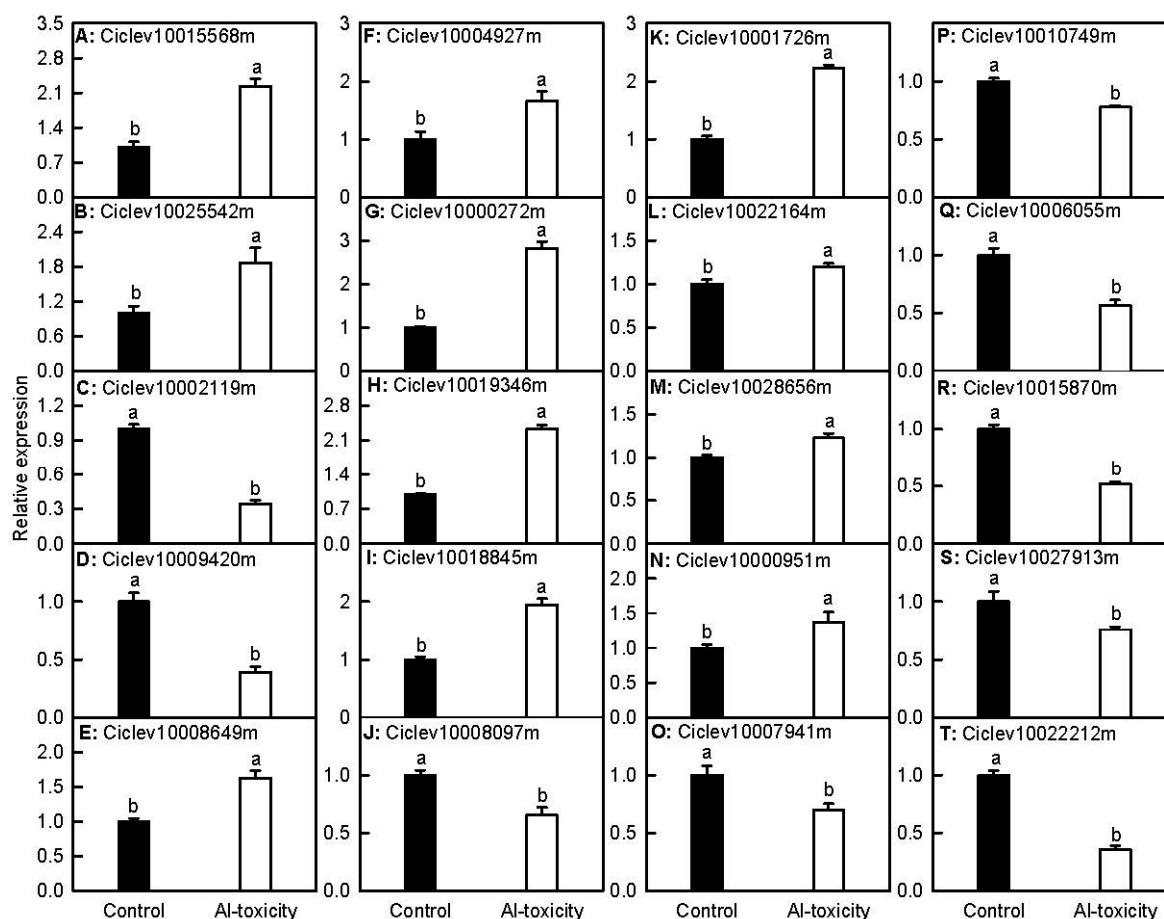


Figure S3. Relative expression levels of genes for differentially abundant proteins from *C. grandis* (A–E) and *C. sinensis* (F–T) leaves. qRT-PCR was run in three biological replicates with two technical replicates. For the normalization of gene, citrus *actin* (GU911361.1) was used as an internal standard and the sample from control plants was used as reference sample, which was set to 1. Bars represent means \pm standard error. Significant tests between means were carried out by unpaired *t*-test. Different letters above the bars indicate a significant difference at $p < 0.05$.

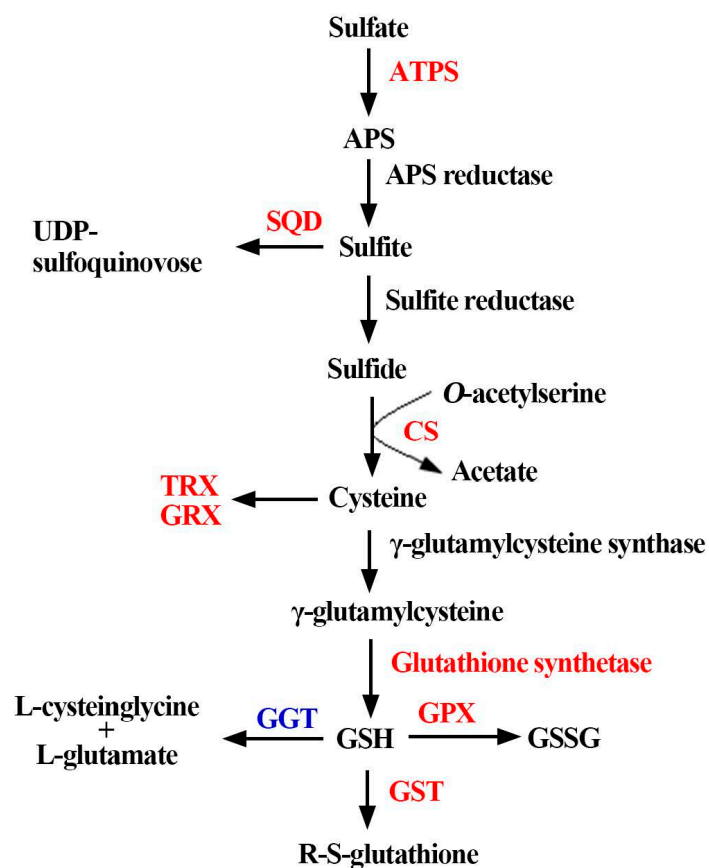


Figure S4. Al-induced alterations of S metabolism in *C. sinensis* leaves. Proteins with increased (decreased) abundances were highlighted in red (blue). APS: adenosine phosphosulphate; GGT: gamma-glutamyl transpeptidase; GST: glutathione S-transferase; SQD: UDP-sulfoquinovose synthase.