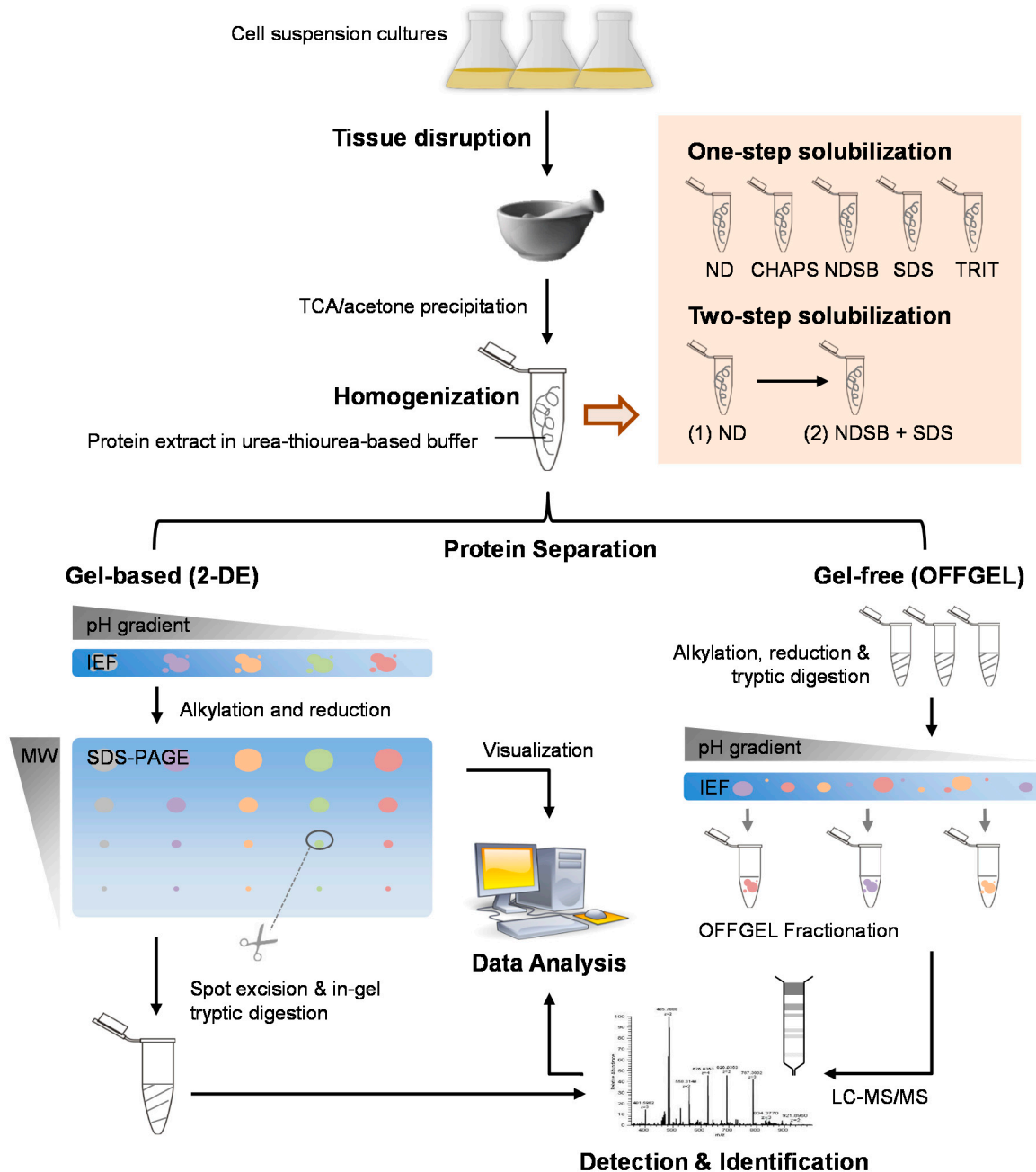
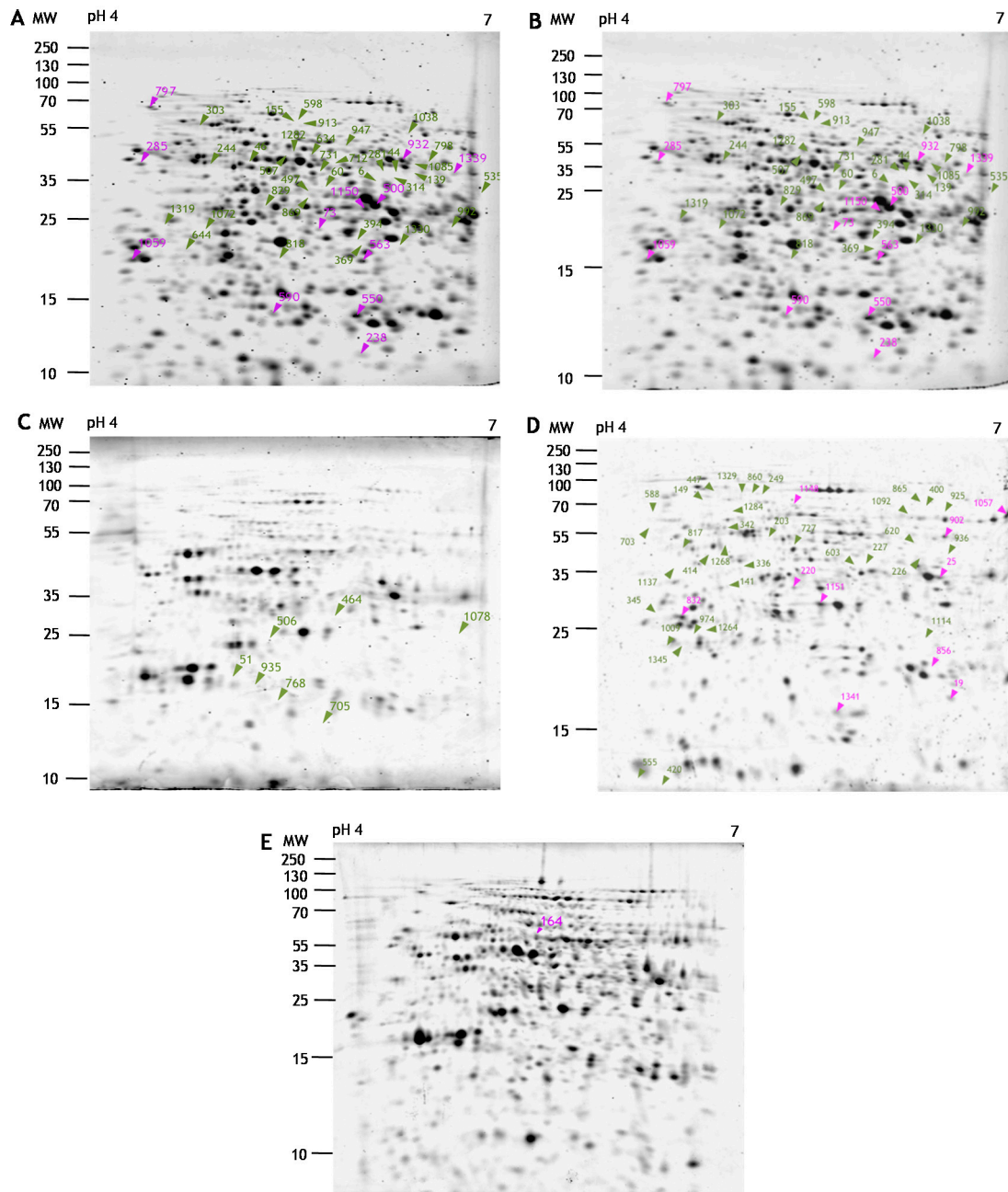


## Supplementary Information



**Figure S1.** Proteins from Arabidopsis cell suspension cultures were extracted using trichloroacetic acid (TCA) in acetone precipitation followed by a one-step solubilization in urea-thiourea lysis buffer containing no detergent (ND), or either 3-[(3-Cholamidopropyl)dimethylammonio]-1-propanesulfonate (CHAPS), non-detergent sulfobetaine 201 (NDSB), sodium dodecyl sulfate (SDS), Triton X-100 (TRIT), or a two-step solubilization process that consists of an initial solubilization in ND-based buffer followed by a second solubilization in NDSB- and SDS-based buffer (orange). Solubilized proteins were separated by either gel-based (2DE) or gel-free (OFFGEL fractionation) methods prior to liquid chromatography-tandem mass spectrometry (LC-MS/MS analysis, identification, and the subsequent data analysis).



**Figure S2.** Two-dimensional gel electrophoresis (2DE) of protein extracts from *Arabidopsis thaliana* cell suspension cultures. Total soluble proteins (approximately 50  $\mu$ g) from cell suspension culture of *Arabidopsis thaliana* (cv. Columbia 0) were extracted by precipitation with 10% (w/v) trichloroacetic acid (TCA) in acetone and solubilized with 7 M urea and 2 M thiourea buffer containing either no detergent (**A**); 4% (w/v) 3-[(3-cholamido-propyl) dimethylammonio]-1-propanesulfonate (**B**); 4% (w/v) non detergent sulfobetaine 201 (**C**); 2% (v/v) Triton X-100 (**D**) or 1% (w/v) sodium dodecyl sulfate (**E**). Proteins were then resolved by 2DE using 7 cm-long IPG strip pH range 4–7 in the first dimension and 12% SDS-PAGE in the second dimension, visualized by SYPRO Ruby fluorescent stain and comparatively analyzed with the Delta 2D (Decodon) software. Purple and green numbers and arrows show spots present and absent, respectively, only in that particular buffer system.

**Table S1.** Unique protein spots from 2DE identified by LC-MS/MS. CHAPS: 3-[(3-cholamidopropyl) dimethylammonio]-1-propanesulfonate; ND: no detergent; SDS: sodium dodecyl sulfate; TM: transmembrane domain; TRIT: Triton X-100.

Spot No.	Protein name	Accession No.	Molecular Weight (Da)	Protein Probability	No. Unique Peptides	Coverage	Peptide Sequences (Charge State)	GRAVY Index/TM	Detergent Specificity
25	Rubisco activase	AT2G39730.1, AT2G39730.2, AT2G39730.3	51,982.00	99.8%	1	3.16%	EGPPVFEQPEMTYEK (+2)	-0.308	TRIT
73	Aldolase superfamily protein	AT3G52930.1	38,540.40	100.0%	1	2.51%	NLNAMNQLK (+2)	-0.231	CHAPS
	Purin-rich $\alpha$ 1	AT2G32080.1,AT2G32080.2	32,201.10	99.8%	1	5.74%	TIDSPGQEETGMTGVSK (+2)	-0.442	
	Arginase	AT4G08900.1	37,345.20	98.6%	1	3.80%	DTVDGMTAMVAAK (+2)	-0.190	
	Selenium-binding protein 1	AT4G14030.1, AT4G14030.2	54,058.70	100.0%	3	9.59%	DTGFGVSALSSNMIR (+2)/GGPQMIQLSLDGK (+2)/YGGPGYATPLAAMSG PSEK (+2)	-0.273	
	Enolase	AT2G36530.1	47,719.70	100.0%	4	14.90%	AGWGVMTSHR (+2)/ LAMQEFMILPVGAASF (+2)/MTTECGTEVQIVGDD LLVTNPK (+2, +3)	-0.190	
	ATP synthase $\alpha/\beta$ family protein	AT5G08670.1, AT5G08680.1, AT5G08690.1	59,632.20	100.0%	7	18.70%	CALVYGQMNEPPGAR (+2)/EMIESGVK (+2)/ FEDQEGLPIMTSLEVQDH PTR (+3)/IMNVLGEPIDER (+2)/TIAMDGTEGLVR (+2)/TVLIMELINNVAK (+2)/YDDLSEQSFYMVGGI DEVVAK (+2)	-0.152	SDS
164	Nitrile specifier protein 1	AT3G16400.1, AT3G16400.2	51,669.50	100.0%	3	9.79%	GGEMGDVWDDGVYENVR (+2)/MVSVGSTLYVFGGR (+2)/VNDMTSEMITFLSIK (+2)	-0.305	

Table S1. *Cont.*

Spot No.	Protein name	Accession No.	Molecular Weight (Da)	Protein Probability	No. Unique Peptides	Coverage	Peptide Sequences (Charge State)	GRAVY Index/TM	Detergent Specificity
164	Cytosol aminopeptidase family protein	AT2G24200.1, AT2G24200.2	54,509.90	100.0%	4	9.42%	FDMGGSAAVLGAAK/ MPLEESYWEMMK/ SGVADMVNTGGR/ TGPGCSIELMK	0.042/TM predicted	SDS
	Alanine aminotransferase	AT1G17290.1	59,823.00	100.0%	4	8.10%	AEGAMYLFPCLHLPQK (+2, +3)/GGYMEVTGFTSDVR (+2)/LTAFHQSFMDDEF (+2, +3)/LTAFHQSFMDDEF (+2, +3)	-0.255	
	Glutamate-cysteine ligase	AT4G23100.1, AT4G23100.3	58,564.20	100.0%	2	5.56%	AVAEEMGIGFLGIGFQPK (+2)/VGTGLDMLLR (+2)	-0.262	
	Cytosolic enolase	AT2G29560.1	51,601.10	100.0%	3	8.84%	ANMVLPPVPAFTVLSGGK (+2)/ISEALIGMDPK (+2)/ LQGQIDQAMIDLK (+2)	-0.205	
	Tubulin $\alpha$ -3	AT5G19770.1, AT5G19780.1	49,654.00	100.0%	2	5.33%	AVISNNTAVAEVFSR (+2)/FDLMYAK (+2)	-0.154	
	Insulinase (Peptidase family M16) protein	AT1G51980.1	54,403.40	100.0%	8	24.70%	AALTSLDMPLQGVSLPPPLA DK (+2)/EAVTATVLQMLM GGGGSFSAGGPGK (+2)/ LNGELLEEFMTENFTAAR (+2)/MIAAEDIGR (+2)/ MKVEIAELAK (+2)/ MVLAASGVEHEELK (+2)/ SAVLMNLESR (+2)/ TYVPEMVEVLIDSVR (+2)	-0.126	

Table S1. *Cont.*

Spot No.	Protein name	Accession No.	Molecular Weight (Da)	Protein Probability	No. Unique Peptides	Coverage	Peptide Sequences (Charge State)	GRAVY Index/TM	Detergent Specificity
220	ATP synthase $\alpha/\beta$ family protein	AT5G08670.1, AT5G08680.1, AT5G08690.1	59,714.20	100.0%	3	8.27%	IMNVLGEPIDER (+2)/TVLIMELINNVAK (+2)/YDDLSEQSFYMVGGI DEVVAK (+2)	-0.152	TRIT
238	Rubisco activase	AT2G39730.1, AT2G39730.2, AT2G39730.3	51,982.00	99.8%	1	3.16%	EGPPVFEQPEMTYEK (+2)	-0.308	CHAPS
283	Lactate/malate dehydrogenase family protein	AT1G53240.1	35,805.20	100.0%	1	4.11%	SEVVGYMGDDNLAK (+2)	0.168/TM predicted	ND
	Rubisco activase	AT2G39730.1, AT2G39730.2, AT2G39730.3	51,982.00	100.0%	1	3.16%	EGPPVFEQPEMTYEK (+2)	-0.308	
285	P-loop containing nucleoside triphosphate hydrolases superfamily protein	AT4G21800.1, AT4G21800.2	42,551.90	100.0%	2	8.18%	AIEASAEEMYETKY (+2)/DMESSQGGTVVLNTG LK (+2)	-0.342	CHAPS
405	Binding to TOMV RNA 1L (long form)	AT5G04430.1, AT5G04430.2	36,019.30	100.0%	2	7.03%	AIQQAETMIK (+2)/ NIMEITQMTGAR (+2)	-0.473	ND
	Peroxidase superfamily protein	AT2G38380.1	38,109.20	100.0%	2	6.59%	AFIDAMIR (+2)/ MGNLRPLTGTQGEIR (+3)	0.036/TM predicted	CHAPS
500	Phosphoserine aminotransferase	AT4G35630.1	47,359.60	100.0%	3	9.77%	ASIYNAMPLAGVEK (+2)/ DLIGNAQDITPVMLDYK (+2)/SLMNVPTLEK (+2)	-0.229	
	Isovaleryl-CoA-dehydrogenase	AT3G45300.1	44,774.40	100.0%	2	6.11%	GVYVLMGSLDLER (+2)/VADMYTALQSSR (+2)	-0.201	

Table S1. *Cont.*

Spot No.	Protein name	Accession No.	Molecular Weight (Da)	Protein Probability	No. Unique Peptides	Coverage	Peptide Sequences (Charge State)	GRAVY Index/TM	Detergent Specificity
550	20S proteasome $\beta$ subunit D1	AT3G22630.1	22,541.00	100.0%	1	6.86%	SDMSVEEAIELVDK (+2)	-0.034	CHAPS
	Glutathione S-transferase phi 8	AT2G47730.1	29,232.60	99.4%	1	6.84%	GMFGMTTDPAAVQELEGK (+2)	-0.220	
563	Vacuolar ATP synthase subunit E1	AT4G11150.1	26,060.40	100.0%	2	10.40%	IDYSMQLNASR (+2)/ VLQAQDDIVNAMK (+2)	-0.487	CHAPS
	Glyceraldehyde-3-phosphate dehydrogenase C subunit 1	AT3G04120.1	36,914.60	100.0%	2	7.40%	DAPMFVVGVEHEEYK (+2)/ VVDLIVHMSK (+2)	-0.129	
590	Adenine nucleotide $\alpha$ hydrolases-like superfamily protein	AT3G11930.1, AT3G11930.2, AT3G11930.3, AT3G11930.4	21,457.50	100.0%	1	5.53%	MHVDLLVVGSR (+2)	-0.011	CHAPS
	Rubisco activase	AT2G39730.1, AT2G39730.2, AT2G39730.3	51,982.00	100.0%	1	3.16%	EGPPVFEQPEMTYEK (+2)	-0.308	
661	Actin-related protein 7	AT3G60830.1	39,904.50	100.0%	2	9.09%	AGAAIPDQSPAMIIPSQMK (+2)/ TNPSMNLSMSDVEK (+2)	-0.171	ND
728	14-3-3 $\lambda$ G-box regulating factor 6	AT5G10450.1, AT5G10450.2, AT5G10450.3, AT5G10450.4	27,976.50	99.9%	2	11.30%	AAQDIAAADMAPTHPIR (+3)/ TAAEDTMLAYK (+2)	-0.358	ND
797	RNA-binding KH domain-containing protein	AT3G04610.1	63,401.40	100.0%	1	1.91%	HDSYYPPPEMR (+2)	-0.753	CHAPS
	PDI-like 1-4	AT5G60640.1	66,358.60	100.0%	1	1.51%	MFHLDPEK (+2)	-0.429	
827	Vacuolar ATP synthase subunit A	AT1G78900.1, AT1G78900.2	68,814.50	100.0%	2	4.82%	DMGYNVSMMDSTSR (+2)/ TTLVANTSMPVAAR (+2)	-0.172	ND

Table S1. *Cont.*

Spot No.	Protein name	Accession No.	Molecular Weight (Da)	Protein Probability	No. Unique Peptides	Coverage	Peptide Sequences (Charge State)	GRAVY Index/TM	Detergent Specificity
832	Nascent polypeptide-associated complex subunit $\alpha$ -like protein 5	AT1G33040.1	22,780.00	100.0%	1	6.22%	DIDLVMTQAGVSK (+2)	-0.628	TRIT
	Nascent polypeptide-associated complex subunit $\alpha$ -like protein 2	AT3G49470.1	23,711.90	100.0%	2	10.60%	DIDLVMTQAGVSR (+2)/ MPEIGATSQR (+2)	-0.699	
	Nascent polypeptide-associated complex (NAC), $\alpha$ subunit family protein	AT4G10480.1	23,171.60	100.0%	3	20.80%	IDDMSSQLQAQAAQR (+2, +3)/LGMKPVTDVSR (+3)/PGPVIEEVNEEALMDA IK (+2)	-0.642	
856	Glutamine synthetase 1.3	AT3G17820.1	38,595.30	100.0%	1	6.21%	GNNILVMCDAYTPAGDPIP TNK (+2)	-0.408	TRIT
	Binding to TOMV RNA 1L (long form)	AT5G04430.1, AT5G04430.2	36,019.30	97.7%	1	3.19%	AIQQAETMIK (+2)	-0.473	
902	ATPase, F1 complex, $\alpha$ subunit protein	AT2G07698.1	85,935.70	100.0%	2	2.45%	QMSLLLR (+2)/ VVDAMGVPIDGK (+2)	-0.066	TRIT
932	Glutathione reductase	AT3G54660.1	60,853.60	100.0%	2	4.60%	DFVGEQMSLR (+2)/ INLTPVALMEGGALAK (+2)	-0.137	CHAPS
	Lipoamide dehydrogenase 2	AT3G17240.1, AT3G17240.3	53,986.10	100.0%	3	7.50%	AIDTAEGMVK (+2)/ EAAMATYDKPIHM (+2)/ VSSVEVDLPAMLAQK (+2)	-0.023	

Table S1. *Cont.*

Spot No.	Protein name	Accession No.	Molecular Weight (Da)	Protein Probability	No. Unique Peptides	Coverage	Peptide Sequences (Charge State)	GRAVY Index/TM	Detergent Specificity
1057	Glycosyl hydrolase superfamily protein	AT3G09260.1	59,722.40	100.0%	2	5.53%	HLLSMQEAVCIDK (+2)/ MSIAWPR (+2)/ YKEDIQLMK (+2, +3)	−0.442	TRIT
1059	Calcium-dependent lipid-binding (CaLB domain) family protein	AT1G23140.1	18,568.90	99.7%	2	16.40%	DSNTSDPFVVVTMGSSQK (+2)/ILQDMILQLR (+2)	−0.441	CHAPS
1087	Glyceraldehyde-3-phosphate dehydrogenase C subunit 1	AT3G04120.1	36,914.60	100.0%	2	7.40%	DAPMFVVGVNEHEYK (+2)/VVDLIVHMSK (+2)	−0.129	ND
	Vacuolar ATP synthase subunit E1	AT4G11150.1	26,060.40	99.8%	2	10.40%	IDYSMQLNASR (+2)/VLQAQDDIVNAMK (+2)	−0.487	
	Mitochondrial HSO70 2	AT5G09590.1	72,992.20	100.0%	3	7.33%	EVDEVLLVGGMTR (+2)/GVNPDEAVAMGAALQGGI LR (+2)/IINEPTAAAL SYGMTNK (+2)	−0.306	
1148	Glycine-rich protein	AT1G27090.1	46,017.90	100.0%	3	9.05%	IMASDYFTTTPPEMK (+2)/ITQMEESISQGK (+2)/SQNEFTSIMLTR (+2)	−0.825	TRIT
	Vacuolar ATP synthase subunit A	AT1G78900.1, AT1G78900.2	68,814.50	100.0%	3	7.54%	DMGYNVSMMDSTSR (+2)/LAEMPADSGYPAYLAAR (+2)/TTLVANTSNNMPVAAR (+2)	−0.172	



Table S1. *Cont.*

Spot No.	Protein name	Accession No.	Molecular Weight (Da)	Protein Probability	No. Unique Peptides	Coverage	Peptide Sequences (Charge State)	GRAVY Index/TM	Detergent Specificity
1150	GTP binding elongation factor Tu family protein	AT4G02930.1	49,410.20	100.0%	2	5.29%	LMDAVDEYIPDPVR (+2)/ STVTGVEMFK (+2)	-0.117	CHAPS
	Peroxidase superfamily protein	AT2G38380.1	38,109.20	100.0%	2	6.59%	AFIDAMIR (+2)/ MGNLRPLTGTQGEIR (+3)	0.036/TM predicted	
1151	PYK10-binding protein 1	AT3G16420.1, AT3G16420.2, AT3G16420.3	32,158.20	100.0%	1	4.36%	IFGSDGSVITMLR (+2)	-0.303	TRIT
	Rubisco activase	AT2G39730.1, AT2G39730.2, AT2G39730.3	51,982.00	100.0%	1	3.16%	EGPPVFEPQEMTYEK (+2)	-0.308	
1165	Triosephosphate isomerase	AT3G55440.1	27,168.20	100.0%	1	5.51%	EAGSTMDVVAAQTK (+2)	0.076	ND
	Glutathione S-transferase PHI 10	AT2G30870.1	24,230.60	99.2%	1	6.05%	GVSFETVNVDLMK (+2)	-0.075	
1190	Ferretin 1	AT5G01600.1	28,178.10	100.0%	1	5.88%	GDALYAMELALSLEK (+2)	-0.253	ND
	Aluminium induced protein with YGL and LRDR motifs	AT4G27450.1	27,623.00	99.8%	1	5.20%	TTNEAMFVIEAYR (+2)	-0.099	
	Glutathione S-transferase PHI 10	AT2G30870.1	24,230.60	98.8%	1	6.05%	GVSFETVNVDLMK (+2)	-0.075	
1339	Lipoamide dehydrogenase 2	AT3G17240.1, AT3G17240.3	53,986.10	100.0%	2	4.93%	AIDTAEGMVK (+2)/ VSSVEVDLPAMLAQK (+2)	-0.023	CHAPS
1341	Rotamase CYP 4	AT3G62030.1, AT3G62030.2, AT3G62030.3	28,208.10	100.0%	2	9.23%	HVVFGQVIEGMK (+2)/ IVMGLFGEVVPK (+2)	-0.170	TRIT
	Double Clp-N motif protein	AT4G25370.1	26,051.10	100.0%	3	16.80%	SDMYFFSPEHPPLTEPAQK (+3)/SLAMGELEAR (+2)/SMNEDVDLSFK (+2)	-0.274	

**Table S2.** Detection of palmitoylation and glycosylphosphatidylinositol modifications to signaling proteins and their buffer system specificity.

Protein Name	Accession Number	Localization	TM	Number Palmitoylation Sites (Amino Acid Position/ Prediction Score)	Glycosylphosphatidyl-inositol (Amino Acid Position/ Prediction Score)	Buffer
Small GTPase mediated signal transduction (19 proteins)						
<i>Arabidopsis</i> RAS 5	AT1G02130	GA	–	2 (200/3.843; 201/3.479)	175/–80.34	NDSB
<i>Arabidopsis</i> RAC-like 9	AT2G44690	PM	–	1 (206/1.521)	192/–76.2	NDSB
RAB GTPase homolog A1G	AT3G15060	Cytosol	–	2 (214/4.033; 215/2.264)	195/–69.5	NDSB
RAB GTPase homolog 1C	AT4G17530	PM, GA	–	2 (199/1.62; 200/3.355)	178/–787	NDSB
ARF GTPase-activating protein	AT5G13300	GA, cytosol, vesicles	–	1 (827/1.24)	801/56.02	NDSB
Ypt/Rab-GAP domain of gyp1p	AT5G41940	GA	3	2 (174/0.433; 225/0.348)	524/–43.91	NDSB
ARF-GAP domain 8	AT4G17890	Nucleus	1	1 (28/0.509)	389/–47.95	CHAPS
SEC7-like guanine nucleotide exchange protein	AT1G01960	Nucleus, cytosol	1	5 (418/1.579; 1489/0.4; 1722/0.34; 1749/5.6; 1750/4.2)	1725/–26.69	ND
Ypt/Rab-GAP domain of gyp1p	AT4G29950	Cytoplasm	2	2 (390/0.395; 726/0.34)	808/–49.45	ND
RAB GTPase homolog A1E	AT4G18430	PM, GA	–	2 (214/1.744; 215/2.37)	195/–81.34	ND
RAB GTPase homolog C2A	AT5G03530	GA	1	3 (156/0.93; 208/2.6; 209/3.98)	187/–107.72	ND
RAB GTPase homolog G3E	AT1G49300	PM, GA	–	–	189/–102.34	SDS
RAB GTPase homolog B1C	AT4G17170	PM, GA	–	3 (121/0.34; 209/1.46; 210/2.27)	194/–80.77	SDS
RAB GTPase homolog A1C	AT5G45750	PM, nucleus, vacuole	–	1 (214/2.612)	189/–66.66	SDS
Calcium-dependent ARF-type GTPase activating protein	AT4G21160	Nucleus, vacuole	–	1 (53/0.752)	306/–71.50	SDS
GTP-binding 2	AT4G35860	GA, chloroplast	–	3 (121/0.38; 209/3.4; 210/2.3)	182/–65.59	SDS

Table S2. *Cont.*

Protein Name	Accession Number	Localization	TM	Number Palmitoylation Sites (Amino Acid Position/ Prediction Score)	Glycosylphosphatidyl-inositol (Amino Acid Position/ Prediction Score)	Buffer
<sup>a</sup> ADP-ribosylation factor-like A1D	AT5G67560	VM	–	3 (157/1.73; 158/1.51; 163/0.36)	166/–107	SDS
RAB GTPase homolog A5E	AT1G05810	Chloroplast	1	3 (4/3.405; 257/2.42; 258/3.314)	246/–87	TRIT
Endoplasmic reticulum morphology 1/ GNOM-Like 1	AT5G39500	Chloroplast	–	4 (191/1.037; 1177/0.843; 1208/0.495; 1248/111)	1423/–108.85	TRIT
<sup>a</sup> Cell surface receptor linked signal transduction (32 proteins)						
LRR protein kinase family protein	AT1G06840 *	Er. PM	1	2 (21/1.095; 876/0.638)	921/–30.43	NDSB
LRR-like protein kinase family	AT5G10020	PM	1	1 (8/3.413)	1029/–69.01	NDSB
KH domain-containing protein	AT1G33680	Nucleus	1	–	737/–52.61	NDSB
STRUBBELIG-receptor family 7	AT3G14350 *	Er. PM	1	3 (14/0.767; 184/0.32; 672/0.95)	690/–83.02	NDSB
Sodium bile acid symporter	AT3G25410	Chloroplast	10	3 (207/0.71; 208/1.74; 391/1.58)	403/–61.89	NDSB
Sphingosine kinase 1	AT4G21540	Nucleus, vacuole	1	1 (232/0.319)	464/–608	NDSB
Sec23/Sec24 transport protein	AT3G07100	COPII vesicle coat	1	1 (754/0.495)	1021/–64.04	CHAPS
STRUBBELIG-receptor family 4	AT3G13065 *	Er. PM	2	1 (15/0.576)	654/–36.08	CHAPS
Transmembrane kinase-like 1	AT3G24660 *	PM	1	4 (21/0.333; 23/0.533; 631/19; 632/0.4)	657/–81.78	CHAPS
LRR protein kinase family protein	AT2G31880 *	PM	2	3 (134/0.36; 616/0.51; 618/1.33)	622/–82.67	CHAPS
LRR protein kinase family protein	AT2G45340 *	PM	4	3 (301/0.51; 446/0.48; 666/0.4)	670/–47.83	CHAPS

Table S2. *Cont.*

Protein Name	Accession Number	Localization	TM	Number Palmitoylation Sites (Amino Acid Position/ Prediction Score)	Glycosylphosphatidyl-inositol (Amino Acid Position/ Prediction Score)	Buffer
LRR protein kinase family protein	AT3G08680 *	Er. PM	1	4 (20/1.87; 283/1.7; 283/1.61; 593/0.7)	618/−45.83	CHAPS
LRR protein kinase family protein	AT5G51560 *	PM	–	3 (472/0.63; 676/1.43; 679/2.74)	657/−55.23	CHAPS
LRR protein kinase family protein	AT2G41820 *	PM	1	3 (5/4.05; 21/0.338; 865/0.39)	869/−94.75	ND
LRR protein kinase family protein	AT3G56370 *	PM	2	4 (334/1.653; 471/0.329; 852/0.39; 953/1.23)	932/−69.84	ND
Proline-rich extensin-like receptor kinase 10	AT1G26150	PM	1	3 (350/2.719; 351/1.505; 685/0.405)	740/−88	ND
Unknown protein	AT1G62240	EM	1	–	203/−53.70	ND
Cyclin/Brfl-like TBP-binding protein	AT2G01280	Nucleus	1	3 (4/148; 7/0.629; 428/0.314)	534/−107.55	ND
Unknown protein	AT4G01985	EM	1	1 (13/324)	544/−39.57	ND
Extra-large GTP-binding protein 2	AT4G34390	PM	1	2 (217/1.298; 257/1)	843/−102.47	ND
LRR receptor-like protein kinase	AT3G24240 *	PM	1	3 (27/0.36; 857/1.38; 1045/0.58)	1108/−66.65	SDS
LRR transmembrane protein kinase	AT5G48940 *	PM	1	3 (857/1.214; 1079/0.414; 1083/1.444)	1115/−45.34	SDS
PLAC8 family protein	AT4G23470	Nucleus	2	6 (43/0.769; 89/0.529; 136/0.33; 153/232; 162/2.79; 164/2.426)	236/−79.77	SDS
Diacylglycerol kinase 7	AT4G30340	PM, nucleus	1	2 (34/0.314; 142/0.324)	472/−61.23	SDS
Unknown protein (DUF803)	AT5G11960	Chloroplast	8	2 (6/3.719; 213/0.381)	315/−53.08	SDS
Unknown protein (DUF247)	AT3G50180	PM	2	–	554/−57.86	TRIT

Table S2. *Cont.*

Protein Name	Accession Number	Localization	TM	Number Palmitoylation Sites (Amino Acid Position/ Prediction Score)	Glycosylphosphatidyl-inositol (Amino Acid Position/ Prediction Score)	Buffer
Receptor-like kinase 1	AT1G48480 *	PM, VM	1	2 (291/2.543; 621/0.4)	621/−116.41	TRIT
Transferase	AT5G06550	Nucleus	1	1 (4/3.248)	477/−93.9	TRIT
STRUBBELIG-receptor family 2	AT5G06820 *	Er	1	2 (673/0.843; 718/1.388)	703/−503	TRIT
Golgi vesicle transport associated proteins (11 proteins)						
<i>Arabidopsis</i> RAS 5	AT1G02130 EG, EMA, NT, PTL, ST	PM, GA, Vacuole	–	2 (200/3.843; 201/3.479)	175/−80.34	NDSB
Sec23/Sec24 transport family protein	AT3G23660 EG, EMA, IT, PTL	COPII vesicle coat	–	3 (81/0.676; 411/0.395; 412/1.372)	759/−21.93	NDSB
SNARE-like superfamily protein	AT5G02280 EG, EMA	Cis-Golgi network, GA	–	1 (22/0.429)	122/−75.64	NDSB
Transport protein particle component	AT5G54750 EG, EMA	GA	–	2 (86/1.372; 121/1.438)	176/−80.36	NDSB
Target of Myb protein 1	AT5G16880 EMA, PTL	Nucleus, PM	–	–	387/−94.97	NDSB
Sec24a/ER morphology 2	AT3G07100 cST, EG, EMA, PTL	COPII vesicle coat	1	1 (754/0.495)	1021/−64.04	CHAPS
Sec23/Sec24 transport family protein	AT4G14160 EG, PTL, IT	Cytoplasm	–	2 (90/0.546; 432/0.62)	747/−19.69	CHAPS
AT-RAB GTPase homology B1C	AT4G17170 EG, EMA, IT, NT, PTL, ST	GA, PM, Vacuole	–	3 (121/0.34; 209/1.46; 210/2.27)	194/−80.77	SDS
Dynamin-like protein 6	AT1G10290 EMA	PM, VM, cytoplasm	–	2 (623/0.348; 759/0.519)	891/−48.35	SDS

**Table S2. Cont.**

Protein Name	Accession Number	Localization	TM	Number Palmitoylation Sites (Amino Acid Position/ Prediction Score)	Glycosylphosphatidyl-inositol (Amino Acid Position/ Prediction Score)	Buffer
Sec23/Sec24 transport family protein	AT5G43670 EG, EMA	COPII vesicle coat	–	1 (224/1.264)	768/–24.71	TRIT
Sorting nexin 1	AT5G06140 EMA, PTL, RT	Chloroplast, cytosol	–	–	383/–36.55	TRIT

\* Protein also enriched in transmembrane receptor, tyrosine kinase signaling pathway; <sup>a</sup> proteins also involved in cell surface receptor linked signal transduction; EM, endomembrane; Er, extracellular region; GA, Golgi apparatus; GV, Golgi vesicle; LRR, leucine-rich repeat; PM, plasma membrane; TM, transmembrane domains; VM, vacuolar membrane; <sup>cST</sup>, Cell surface receptor linked signal transduction (GO:0007166); <sup>EG</sup>, ER to Golgi vesicle-mediated transport (GO:0006888); <sup>EMA</sup>, Establishment and maintenance of cellular localization; <sup>IT</sup>, Ion transport; <sup>NT</sup>, Nucleocytoplasmic transport (GO:0006913); <sup>PTL</sup>, Protein transport and localization; <sup>RT</sup>, Root development (GO:0048364); <sup>ST</sup>, Small GTPase mediated signal transduction (GO:0007264).

**Table S4.** Detection of palmitoylation and glycosylphosphatidylinositol modifications to myristoylated proteins.

Protein Name	Accession Number	Peptide	Location	TM	Palmitoylated Peptide (P/S)	MYR Signal Peptide (P/S)	GPI (P/S)	Detergent
Protein phosphatase 2C	AT2G46920	1	PM		GTSRVVGC FVPSNDK (11/0.376)	GNGTSRVVGC FVPSNDK (2/0.286)	181/–101.28	CHAPS
Adenine nucleotide $\alpha$ hydrolases-like protein	AT3G01520	1	PM		VGTVSAFCVKHA ECP (150/0.648)	GSEPTKVMVAVNASTIK (2/–1.193 twilight zone)	154/–105.67	CHAPS
Unknown protein	AT3G27210	1	PM			GSSSSSSLNNSPIRADS (2/3.105)	214/–52.51	CHAPS
$\alpha$ -/ $\beta$ -hydrolases protein	AT3G30380	1	Extracellular	2	MIRSVGFCNIDCFKP (387/1) VGFCNIDCFKPTATA (391/1.3)	GAVTSSMAAKFAFFPPN (2/–1.246 twilight zone)	383/–89.00	CHAPS
TRAF-like family protein	AT1G69650	1	Chloroplast, Vacuole		MGASCSAPVSST (5/3.661)	GASCSAPVSSTIKKNWR (2/3.959)	274/–69.40	ND
Regulatory particle AAA-ATPase 2B	AT2G20140	1	Cytosol, PM			GQGPGGGLNRQGDRKPD (2/1.239)	426/–88.73	ND

Table S4. *Cont.*

Protein Name	Accession Number	Peptide	Location	TM	Palmitoylated Peptide (P/S)	MYR Signal Peptide (P/S)	GPI (P/S)	Detergent
Calmodulin-binding family protein	AT2G26190	1			SPRVQVNC(532/1.355)	GLSLSLLLSAWKEVVT (2/-0.743 twilight zone)	500/-68.75	ND
LOG2-kike ubiquitin ligase 1	AT5G03200	1			NLISLIFCCGRRQRS (10/3.162) LISLIFCCGRRQRSN (11/1.429) VDQYPGNCLPPPVE (58/0.602) VLPCRHMCMCSGCAK (304/0.75) QTNLCPVCRQPVEML (323/1.289)	GNLISLIFCCGRRQRSN (2/-0.773 twilight zone)	308/-53.61	NDSB
Serine/threonine protein kinase 3	AT5G08160	1	PM		* MGCSFSGSLNA (3/1.281)	GCSFSGSLNALYDAVNGGG (2/1.566)	324/-42.85	NDSB
Tetratricopeptide repeat-like protein	AT2G17210	1	Mitochondria	1	MGSHLCSKLQALS (6/4.289) VVQSLHRCMKLDDTA (704/1.162)	GSHLCSKLQALSSKIKQ (2/1.398)	690/-62.76	SDS
Calmodulin-domain protein kinase 9	AT3G20410	1	PM		MGNCFAKNHGL (4/1.09) QFGVTYLCTENSTGK (108/0.405)	GNCFAKNHGLMKPQQNG (2/1.798)	530/-100.47	SDS
Impaired in BABA-induced sterility 1	AT1G18670	1	PM		MGCVNSKQTV (3/1.886) LHKIFKLCGSPPEY (349/0.75)	GCVNSKQTVSVTPAIDH (2/3.685)	681/-115.75	TRIT
Clumped chloroplasts 1	AT1G62390	1			ATVVKNHCSNEAAAT (734/0.338)	GKSGGRKKKSGGSNSNS (2/-0.7 twilight zone)	736/-83.87	TRIT
Brassinosteroid-signaling kinase 7	AT1G63500	1	PM		MGCEVSKLCA (3/0.867) GCEVSKLCAFCVSD (9/2.028) VSKLCAFCVSDPEG (12/3.62) SKLCAFCVSDPEGS (13/2.167) RMANLLGCCYEGEER (121/0.762) MANLLGCCYEGEERL (122/1.241) LIRLASRCLQYEPRE (292/0.917)	GCEVSKLCAFCVSDPE (2/2.069)	468/-90.93	TRIT

Table S4. *Cont.*

Protein Name	Accession Number	Peptide	Location	TM	Palmitoylated Peptide (P/S)	MYR Signal Peptide (P/S)	GPI (P/S)	Detergent
Brassinosteroid-signaling kinase 6	AT3G54030	1	PM		MGARCSKFSFCL (5/3.364)	GARCSKFSFCLFPSHFK (2/−1.018 twilight zone)	470–3.39	TRIT
					RCSKFSFCLFPSHFK (11/2.194)			
					RLANLIGCCFEGEER (118/0.629)			
					LANLIGCCFEGEERL (119/1.176)			
					LVRLATRCLQYEARE (289/1.028)			
Neurofilament triplet H protein	AT5G64690	1	PM		MGNCAIKPKVL (4/1.781)	GNCAIKPKVLKDSDEDL (2/0.365)	325/−70.82	TRIT

GPI, glycosylphosphatidylinositol; MYR, myristoylation; P/S, position/score; \* Prediction of potential myristoylation sites by NMT-MYR predictor; PM, plasma membrane.