

**Supplementary Table S2.** *In vitro* plant kinase assay using *Arabidopsis* kinase extract and synthetic peptides.

Accession No.	Putative function	Sequence of synthetic peptides <sup>a</sup>	Kinase assay <sup>b</sup>
AT1G19870	IQ-domain 32 (IQD32)	HHHHHHKHSLKRKVS*NPSFIAAQSK	<i>N/P</i>
AT1G20696	High mobility group 3 (HMGB3)	HHHHHHKWKSLS*DSEKAPYVAK	<i>N/P</i>
AT1G24180	IAA-conjugate-resistant 4 (IAR4)	HHHHHHEMDTYRYHGHS*MSDPGSTYRTR	<i>N/P</i>
AT1G62630	Disease resistance protein (CC-NBS-LRR class) family	HHHHHHRLQLIFGSNIFS*PDRQL	<i>N/P</i>
AT1G74910	ADP-glucose pyrophosphorylase family protein	HHHHHHRATLKRVS*FEALQPATR	<i>N/P</i>
AT2G19810	CCCH-type zinc finger family protein	HHHHHHLLSRS*LGSNLGNDVVASLR	<i>N/P</i>
AT2G26570	Weak chloroplast movement under blue light 1 (WEB1)	HHHHHHRTVSSPRFSGS*PVSTGTPKNVD	<i>N/P</i>
AT2G28000	Chaperonin-60alpha (CPN60A)	HHHHHHGRNVVLDEFGS*PKVVNDG	<i>N/P</i>
AT2G46180	Golgin candidate 4 (GC4)	HHHHHHRKLFPS*KTEDLSR	<i>N/P</i>
AT3G13224	RNA-binding (RRM/RBD/RNP motifs) family protein	HHHHHHKSLNRS*PPSYGSHPR	<i>N/P</i>
AT3G27580	Protein kinase superfamily protein (ATPK7)	HHHHHHTSARSMS*FVGTHEYLAPEIHK	<i>N/P</i>
AT4G30160	Villin 4 (VLN4)	HHHHHHKSQQRSRSMSFS*PDRVRVRGR	<i>N/P</i>
AT4G31700	Ribosomal protein s6 (RPS6)	HHHHHHRSESLAKKRSRLS*SAAAKPSVTA	<i>N/P</i>
AT4G35785	RNA-binding (RRM/RBD/RNP motifs) family protein	HHHHHHRRKRPTPT*PGHYLGLK	<i>N/P</i>
AT5G10360	Embryo defective 3010 (EMB3010)	HHHHHHRSESLAKKRSRLS*SAPAKPVAA	<i>N/P</i>
AT5G52040	RNA-binding (RRM/RBD/RNP motifs) family protein (ATRSP41)	HHHHHHRKGRGESRS*PPPYEKR	<i>N/P</i>
AT1G05150	Calcium-binding EF hand family protein	HHHHHHMRDNDVPVSYSGSGGPTKSIRK	<i>N</i>
AT1G20760	Calcium-binding EF hand family protein	HHHHHHHPSTPLSRFGNS*PPRFSDASAR	<i>N</i>
AT2G17410	ARID/BRIGHT DNA-binding domain-containing protein	HHHHHHPESKLSEDTGS*PHHHADILMVR	<i>N</i>
AT2G39730	Rubisco activase (RCA)	HHHHHHDRWRGLAYDTS*DDQQDITRGK	<i>N</i>
AT3G08940	Light harvesting complex photosystem II (LHCB4.2)	HHHHHHKNLYGEVIGTRT*EAVDPKSTPF	<i>N</i>
AT3G45780	Phototropin 1 (PHOT1)	HHHHHHVEAVKRPRALS*ESTNLHPFMTK	<i>N</i>
AT3G50370	unknown protein	HHHHHHKSSLTQVRPVSGGGREANAWR	<i>N</i>
AT3G57610	Adenylosuccinate synthase (ADSS)	HHHHHHLLRLAGQEFGT*TTGRPRRCGW	<i>N</i>
AT4G17720	RNA recognition motif (RRM)-containing protein	HHHHHHDEFARVHLSSES*PKAASSTQEAER	<i>N</i>
AT5G52040	RNA-binding (RRM/RBD/RNP motifs) family protein (ATRSP41)	HHHHHHRRDRRRERVAS*PENGAVRNRSR	<i>N</i>
AT5G62810	Peroxin 14 (PEX14)	HHHHHHNGSNVDYDTRS*ASPPAAPADSSAPPHPK	<i>N</i>

<sup>a</sup> Sterisk stands for the MS-detected phosphosites either from *in vitro* or *in vivo* experiments.<sup>b</sup> MS-identification of substrate peptides from *in vitro* plant kinase assay: *N* stands for non-phosphorylated peptide identified; *P* stands for phosphorylated peptide identified.

**Supplementary Table S3. *rcn1-1* specific phosphopeptides.**

Accession No.	Phosphopeptide <sup>a</sup>	Motif category	Protein	Subcellular location	Homologs in Human (identity) <sup>b</sup>
<b>Hydrolase activity</b>					
AT1G22620	<sup>443</sup> ASQLSHANTAREP <i>p</i> SLR	Rxx[pS]	Suppressor of actin 1 (ATSAC1)	Golgi apparatus, nucleus	O94964 (27.0%)
AT1G23240	<sup>1</sup> MSHQ <i>p</i> TVALASK		Caleosin-related family protein	extracellular region	
<b>Kinase activity</b>					
AT3G13530, AT3G07980	<sup>874,877</sup> ISLSANRT <i>p</i> STDKLQK		MAP3K epsilon protein kinase 1/2 (MAP3KE1/E2)	cytosol, plasma membrane, vacuole	O95819 (35.0%)
AT4G33240	<sup>1141</sup> NV <i>p</i> SLEKLSDEKVK	Rxx[pS]	Forms aploid and binucleate cells 1A (FAB1A)	cytoplasm	
<b>Nucleic acid binding</b>					
AT1G51140	<sup>276</sup> RPPLAHHM <i>p</i> SLPK		Flowering bHLH 3 (FBH3)	nucleus	Q13136 (24.0%)
AT1G58380, AT1G58983, AT1G59359, AT1G58684	<sup>270,270,270,270</sup> AV <i>p</i> SATKVITEGEDQA		XW6 / Ribosomal protein S5 family protein	cell wall, chloroplast, intracellular, membrane, nucleus, plasma membrane, ribosome	
AT1G79950	<sup>106</sup> KSLGSFS <i>p</i> TR	[pT]xxD/E	RAD3-like DNA-binding helicase protein	mitochondrion, nucleus	
AT2G20280	<sup>358</sup> TSIQIREPNDEGS <i>p</i> S		Zinc finger C-x8-C-x5-C-x3-H type family protein	cytoplasm	
AT2G41840	<sup>255</sup> FSR <i>p</i> SPYQEHTDFLASK	[pS]P	Ribosomal protein S5 family protein	cytosol, intracellular, membrane, nucleolus, ribosome	
<b>Protein binding</b>					
AT1G30280	<sup>48</sup> KF <i>p</i> SGDFSR	Rxx[pS]	Chaperone DnaJ-domain superfamily protein	cytoplasm	
<b>Other binding</b>					
AT3G01500, AT5G14740	<sup>142,137</sup> EKYETNPALYGELAKGQ <i>p</i> SPK	[pS]P	Carbonic anhydrase 1/2 (CA1/CA2)	chloroplast, cytoplasm, cytosol, membrane	
AT3G15290	<sup>285</sup> EATQKL <i>p</i> SPRL	[pS]P	3-hydroxyacyl-CoA dehydrogenase family protein	cytoplasm, peroxisome	
AT5G66190	<sup>164</sup> LVY <i>p</i> TNDGGEIVK		Ferredoxin-NADP(+)-oxidoreductase 1 (FNR1)	chloroplast	
<b>Structural molecule activity</b>					
AT3G60770, AT4G00100	<sup>20</sup> RS <i>p</i> SPSWLK	[pS]P	Ribosomal protein S13/S13A (RPS13/RPS13A)	cell wall, chloroplast, cytosol, intracellular, membrane, nucleolus, ribosome	Q6P9B9 (32.0%)
<b>Transferase activity</b>					
AT1G26850	<sup>111</sup> D <i>p</i> SoxMIYR		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	Golgi apparatus, membrane	Q5TF21 (41.0%), Q9UL03 (27.0%)
AT2G13360	<sup>31</sup> NNEDYR <i>p</i> SPAIPALTK	[pS]P	Alanine:glyoxylate aminotransferase (AGT)	chloroplast, membrane, peroxisome, plasma membrane	
<b>Transporter activity</b>					
AT1G75220	<sup>16</sup> RPFHTG <i>p</i> SWYR		ERD6-like 6 (ERDL6)	Golgi apparatus, membrane, plant-type vacuole membrane, plasma membrane, vacuolar membrane	
AT1G62020, AT2G21390	<sup>358,358</sup> RP <i>p</i> GTPSLNQSPR	Rxx[pT]P	Coatomer, alpha subunit	cytosol, intracellular, membrane, plasma membrane	
AT4G33530	<sup>203</sup> I <i>p</i> SGFGLKVPSELER		K <sup>+</sup> uptake permease 5 (KUP5)	membrane, plasma membrane, vacuolar membrane	

<sup>a</sup> The phosphorylated amino acids (Ser, Thr, or Tyr) are marked by *p* and the oxidized Met are marked by *ox*.

<sup>b</sup> Amino acid residues ( ±50 ) at vicinity of the phosphorylation sites were employed to BLAST against the human genome. Only the UniProt entries of the proteins that have been found in PP2A protein interaction network (Herzog *et al.*, 2012) are listed.

**Supplementary Table S3. *Rcn1-I* specific phosphopeptides (cont'd)**

Accession No.	Phosphopeptide <sup>a</sup>	Motif category	Protein	Subcellular location	Homologs in Human (identity) <sup>b</sup>
<b>Unknown functions</b>					
AT1G11110	<sub>162</sub> EpTFNFAEK		LisH and RanBPM domains containing protein	nucleus	
AT1G20890	<sub>45</sub> ETLPLKSGpSR		unknown protein		
AT1G35220	<sub>308</sub> LIDPSSVLHDKIGpSPR	[pS]P	unknown protein	nucleus	
AT1G70100	<sub>97</sub> Na <sub>p</sub> SFRPNIQNR	Rxx[pS]	unknown protein	nucleus	
AT1G70180	<sub>182</sub> NAGSFIGIPREPpSPPR	Rxx[pS]P	Sterile alpha motif (SAM) domain-containing protein	nucleus	
AT2G46180	<sub>319</sub> KLFPKpSTEDLSR	[pS]xxD/E	Golgin candidate 4 (GC4)	Golgi apparatus	Q13136 (27.0%), Q5TF21 (29.0%), O75334 (31.0%)
AT3G08780	<sub>197</sub> GHYGSFpSPK	[pS]P	unknown protein	nucleus	
AT3G58440	<sub>536</sub> LLFVDLEpSQLQK		TRAF-like superfamily protein	cytoplasm	
AT3G60380	<sub>412</sub> KAEFFpSKK	[pS]xxD/E	unknown protein	nucleus	Q562F6 (27.0%)
AT4G21930	<sub>90</sub> HVATpSAPVKVPDWSK		Protein of unknown function, DUF584	cellular_component	O94964 (35.0%)
AT4G37210	<sub>478</sub> KPALEFSDKADGNpSS		Tetratricopeptide repeat (TPR)-like superfamily protein	nucleus	Q6P9B9 (52.0%), Q5VSL9 (50.0%)
AT5G04550	<sub>347</sub> oxMGQpTPERPSISSVKK	[pT]P	Protein of unknown function (DUF668)	nucleus	
AT5G18590	<sub>16</sub> KVQLSDSVQGYKpSPLR	[pS]P	Galactose oxidase/kelch repeat superfamily protein	cytosol, nucleus	
AT5G63190	<sub>32</sub> SHTLFADLNIKpSPTGGK	[pS]P	MA3 domain-containing protein	nucleus	

<sup>a</sup> The phosphorylated amino acids (Ser, Thr, or Tyr) are marked by *p* and the oxidized Met are marked by *ox*.

<sup>b</sup> Amino acid residues ( ±50 ) at vicinity of the phosphorylation sites were employed to BLAST against the human genome. Only the UniProt entries of the proteins that have been found in PP2A protein interaction network (Herzog *et al.*, 2012) are listed.

**Supplementary Table S4.** Phosphopeptides affected by 1-minute ethylene treatment in *rcn1-1*.

Accession No.	Fold-change	<i>p</i> -value <sup>a</sup>	Phosphopeptide <sup>b</sup>	Motif category	Protein	Subcellular location
<b>Ethylene enhanced</b>						
AT2G02070	1.15	3.16E-02	<sup>60</sup> TPNSDAEVIAL <p><i>p</i>SPK</p>	[pS]P	Indeterminate-domain 5 (IDD5)	intracellular, nucleus
AT2G18960	1.14	3.12E-02	<sup>937</sup> GLDIDTAGHHY <p><i>p</i>TV</p>		H(+)-ATPase 1 (HA1)	Golgi apparatus, membrane, nucleus, plasma membrane, vacuole
AT1G20693, AT1G20696	1.10	7.41E-03	<sup>79,76</sup> SL <p><i>p</i>SDSEKAPYVAK</p>	[pS]D/E	High mobility group B2/B3 (HMGB2/B3)	nucleus
AT1G29920, AT1G29910, AT1G29930, AT2G34420	1.09	1.95E-03	<sup>38,38,38,36</sup> <i>p</i> TVAKPKGPSGSPWYGSDR		Light harvesting chlorophyll A/B binding protein 1.1/1.2/1.3/1.5 (LHCB1.1/1.2/1.3/1.5)	chloroplast, membrane, mitochondrion
AT1G37130	1.07	1.68E-02	<sup>532</sup> SV <p><i>p</i>STPFoxMNTTAK</p>		Nitrate reductase 2 (NR2)	cytosol, mitochondrion, plasma membrane, vacuole
AT3G57610	1.07	2.78E-03	<sup>357</sup> LAGQEFG <p><i>p</i>TTTGRPR</p>		Adenylosuccinate synthase (ADSS)	chloroplast, cytoplasm, plastid
AT2G05100, AT2G05070, AT3G27690	1.06	2.98E-02	<sup>40,40,41</sup> <i>p</i> TVKSTPQSIWYGPDRPK		Photosystem II light harvesting complex gene 2.1/2.2.2/3 (LHCB2.1/2.2/2.3)	chloroplast, membrane, vacuolar membrane
AT5G01530	1.05	3.99E-03	<sup>104</sup> NLAGDVIGTR <p><i>p</i>TEAADAK</p>	[pT]D/E	Light harvesting complex photosystem II (LHCB4.1)	chloroplast, membrane
AT5G01530	1.05	1.86E-02	<sup>104</sup> NLAGDVIG <p><i>p</i>TRTEAADAK</p>	[pT]xxD/E	Light harvesting complex photosystem II (LHCB4.1)	chloroplast, membrane
AT2G30710	1.05	4.32E-03	<sup>41</sup> RSDPPPYIP <p><i>p</i>SPTYQR</p>	[pS]P	Ypt/Rab-GAP domain of gyp1p superfamily protein	Golgi apparatus, intracellular
<b>Ethylene suppressed</b>						
AT1G07650	-1.27	1.17E-02	<sup>987</sup> SL <p><i>p</i>SFSTSGPR</p>	Rxx[pS]	Leucine-rich repeat transmembrane protein kinase	plasma membrane
AT1G70730, AT1G23190	-1.12	9.09E-03	<sup>115,114</sup> ATGAFILTA <p><i>p</i>SHNPGGPTEDFGIK</p>		Phosphoglucosyltransferase 2/3 (PGM2/3)	chloroplast, cytoplasm, cytosol, nucleus, plasma membrane
AT5G52040	-1.12	7.63E-04	<sup>270</sup> GE <p><i>p</i>SRpSPPPYEKR</p>	Rxx[pS], [pS]P	Arginine/serine-rich splicing factor (ATRSP41)	nucleus
AT1G16610	-1.10	1.28E-03	<sup>181</sup> VS <p><i>p</i>SPPKPVSAAPK</p>	[pS]P	Arginine/serine-rich 45 (SR45)	nuclear speck, nucleolus, nucleoplasm
AT1G29920, AT1G29910, AT1G29930, AT2G34430, AT2G34420	-1.09	4.65E-02	<sup>44,44,44,43,42</sup> GPSG <p><i>p</i>SPWYGSDRVK</p>	[pS]P	Light harvesting chlorophyll A/B binding protein 1.1/1.2/1.3/1.4/1.5 (LHCB1.1/1.2/1.3/1.4/1.5)	chloroplast, membrane, mitochondrion
AT2G39730	-1.08	4.72E-02	<sup>73</sup> GLAYD <p><i>p</i>TSDDQDITR</p>	[pT]xxD/E	Rubisco activase (RCA)	cell wall, chloroplast, membrane, nucleus
AT3G46780	-1.06	4.64E-02	<sup>447</sup> VQVA <p><i>p</i>TVRGQAK</p>		Plastid transcriptionally active 16 (PTAC16)	chloroplast, membrane

<sup>a</sup> Given by two-tailed Student's *t*-test. All phosphopeptides listed were selected using two-tailed Student's *t*-test (*p*<0.05).<sup>b</sup> The phosphorylated amino acids (Ser, Thr, or Tyr) are marked by *p* and the oxidized Met are marked by ox.

The results listed in Table 3 are highlighted in bold.

**Supplementary Table S5. *CTR1* gene-regulated phosphopeptides<sup>a</sup>.**

Accession No.	Fold-change	<i>p</i> -value <sup>b</sup>	Phosphopeptide <sup>c</sup>	Motif category	Protein	Subcellular location
<b><i>CTR1-enhanced</i></b>						
AT3G46780	1.77	4.06E-03	<sup>447</sup> VQVA <b>p</b> TVR		Plastid transcriptionally active 16 (PTAC16)	chloroplast, membrane
AT5G23060	1.73	3.08E-10	<sup>378</sup> pSGTKFLPSSD		Calcium sensing receptor (CaS)	chloroplast, mitochondrion
AT1G29920, AT1G29910, AT1G29930, AT2G34430, AT2G34420	1.71	2.05E-04	<sup>44,44,44,43,42</sup> GPSG <b>p</b> SPWYGSDRVK	[pS]P	Light harvesting chlorophyll A/B binding protein 1.1/1.2/1.3/1.4/1.5 (LHCB1.1/1.2/1.3/1.4/1.5)	chloroplast, membrane, mitochondrion
AT1G64500	1.61	2.04E-02	<sup>112</sup> KSA <b>p</b> SFHTLDELEVR		Glutaredoxin family protein	nucleus
AT1G29920, AT1G29910, AT1G29930, AT2G34430, AT2G34420	1.60	3.62E-03	<sup>44,44,44,43,42</sup> GPSGSPWYG <b>p</b> SDRVK	[pS]D/E	Light harvesting chlorophyll A/B binding protein 1.1/1.2/1.3/1.4/1.5 (LHCB1.1/1.2/1.3/1.4/1.5)	chloroplast, membrane, mitochondrion
AT2G42600, AT3G14940, AT3G42628	1.54	1.79E-02	<sup>9,9,9</sup> oxMA <b>p</b> SIDSQLR		PEP carboxylase 2/3 (PPC2/3)/PEP carboxylase-related	chloroplast, cytoplasm, cytosol, plasma membrane
AT1G07110	1.32	3.70E-02	<sup>301</sup> SL <b>p</b> SASSFLIDTK		Fructose-2,6-bisphosphatase (F2K)	cytosol, nucleus, plasma membrane
AT2G34310	1.31	2.87E-03	<sup>179</sup> SDEKEEIL <b>p</b> SPR	[pS]P	unknown protein	nucleus
AT3G08940	1.30	2.91E-02	<sup>33</sup> FGFG <b>p</b> TKK		Light harvesting complex photosystem II (LHCB4.2)	chloroplast, membrane
AT5G14720	1.25	3.70E-02	<sup>541</sup> FKVTSADL <b>p</b> SPK	[pS]P	Protein kinase superfamily protein	nucleus, plasma membrane
AT1G37130	1.17	4.07E-02	<sup>532</sup> SV <b>p</b> S*TPF <b>ox</b> MNTTAK		Nitrate reductase 2 (NIA2, B29, NIA2-1, CHL3, NR, NR2, ATNR2)	cytosol, mitochondrion, plasma membrane, vacuole
AT1G10290	1.10	2.09E-02	<sup>531</sup> AT <b>p</b> SPQPDGPTAGGSLK	Rxx[pS]P	Dynammin-like protein 6 (ADL6)	Golgi apparatus, cytoplasm, membrane, plasma membrane, vacuolar membrane
<b><i>CTR1-suppressed</i></b>						
AT3G53420, AT2G37170, AT2G37180	-1.82	2.64E-03	<sup>277,275,275</sup> SLG <b>p</b> SFR <b>p</b> SAANV		Plasma membrane intrinsic protein 2A/B/C (PIP2A/B/C)	chloroplast, membrane, plasma membrane, vacuole
AT3G22850	-1.42	8.53E-03	<sup>238</sup> VG <b>p</b> SVQNWSK	Rxx[pS]	Aluminium induced protein with YGL and LRDR motifs	cytoplasm, cytosol, nucleus, plasma membrane
AT4G32180	-1.21	2.39E-02	<sup>44</sup> <b>p</b> SGSRPQLDLK		Pantothenate kinase 2 (PANK2)	cytoplasm, cytosol
AT4G15545	-1.20	3.57E-02	<sup>229</sup> TTSR <b>p</b> I <b>p</b> SPR	Rxx[pS]P	unknown protein	
AT3G61860	-1.16	1.72E-02	<sup>180</sup> R <b>p</b> SL <b>p</b> SPVYR	Rxx[pS]P	RNA-binding (RRM/RBD/RNP motifs) family protein (RSP31)	cytoplasm, nuclear speck

<sup>a</sup> Both the wild type and *ctr1-1* mutant Arabidopsis were grown in the presence of ACC.<sup>b</sup> Given by two-tailed Student's *t*-test. All phosphopeptides listed were selected using two-tailed Student's *t*-test (*p*<0.05).<sup>c</sup> The phosphorylated amino acids (Ser, Thr, or Tyr) are marked by *p* and the oxidized Met are marked by *ox*.

The results listed in Table 2 are highlighted in bold.