

Lhcb1

D8QN27_SELML:

AT1G29930.1:

Os01g41710.1_ORYSA:

A9S6S7_PHYPA:

MAAMTATATMAAPSTFAGQTGLKPQNEFVARNASNGSRIAMRKtG-KAss 49
MAASTMALS---SPAFAGKAVKLsP---AAsEVLGSGRVTMRKtVAKPK- 43
MAAATMALS---SPALAGK-----AAAKVFGEGRITMRKSAAKPKP 38
MAACTATHS---TALAGQTALKSINELSRKVGNVQARVTMRK-ASSSDS 45
*** * : : .::**:

VGGGsPWYGPDRVKYLGPFGSGESPSYLTGEYPGDYGWDTAGLSADPETFA 99
GPSGsPWYGSDRVKYLGPFGSGESPSYLTGEFPGDYGWDTAGLSADPETFA 93
AASGSPWYGADRVLYLGPLSGEPPSYLTGEFPGDYGWDTAGLSADPETFA 88
I-----WYGADRPKYLGPLSGETPSYLTGEFAGDYGWDTAGLSADPETFA 90
. ** *:***.*****:*****:*****

KNRELEVIHSRWAMLGALGCVFPELLSKNGIKFGEAVWFKAGSQIFKEGG 149
RNRELEVIHSRWAMLGALGCVFPELLARNGVKFGEAVWFKAGSQIFSDGG 143
KNRELEVIHSRWAMLGALGCVFPELLARNGVKFGEAVWFKAGSQIFSEGG 138
RNRELEVIHARWAMLGALGCVTPELLAKNGVKFGEAVWFKAGSQIFSEGG 140
:*****:***** ****:***:*****:*****:***

LDYLGNP SLVHAQSILAIWASQVILMGAVEGYRIAG-GPLGEVTDPIYPG 198
LDYLGNP SLVHAQSILAIWATQVILMGAVEGYRVAGNGPLGEAEDLLYPG 193
LDYLGNP SLIHAQSILAIWAVQVILMGAVEGYRIAG-GPLGEVVDPLYPG 187
LDYLGNP SLVHAQSILAIWASQVILMGAVEGYRVAG-GPLGEVTDPIYPG 189
*****:***** **:*****:*** *****. * :***

GSFDPLGLAEDPEAFAELKVKEIKNGRLAMFSMFGFFVQAIVTGKGPLEN 248
GSFDPLGLATDPEAFAELKVKEIKNGRLAMFSMFGFFVQAIVTGKGPIEN 243
GSFDPLGLADDPEAFAELKVKEIKNGRLAMFSMFGFFVQAIVTGKGPLEN 237
GSFDPLGLADDPDTFAELKVKEIKNGRLAMFSMFGFFVQAIVTGKGPLEN 239
***** **::*****:*****:*****:***

LSDHLADPVANNAWAYATNFTPGS 272
LADHLADPVNNNAWAFATNFVPGK 267
LADHLADPVNNNAWAYATNFVPGK 261
LSDHLADPVANNAWAYATNFVPGN 263
*:***** *****:*****.***.

Lhcb2

D8SUF1_SELML:

AT2G05100.1:

Os03g39610.1_ORYSA:

A9S6S7_PHYPA:

```
MAASASAISSSSFSGQTALKSPNELSRKVGNLGEARTVMRRtRAStPDSI 50
-MATSAIQQS-SFAGQTALKPSNELLRKVGVS GGGRVTMRRtVKSTPQSI 48
-MAASALHQTTSTFLGTAPRR--DELVRRVGDSSG-RITMRRTVKSAPQSI 46
-MAACTATHSTALAGQTALKSINELSRKVGNV-QARVTMR--KASSSDSI 46
*:.: : : * .: : : ** *:** * .** *:.:**
```

```
WYGPDRPKFLGPFSEQTPSYLTGEFPGDYGWDTAGLSADPETFAKNRELE 100
WYGPDRPKYLGPFSENTPSYLTGEYPGDYGWDTAGLSADPETFAKNRELE 98
WYGPDRPKYLGPFSEQTPSYLTGEFPGDYGWDTAGLSADPETFARNRELE 96
WYGADRPKYLGPLSGETPSYLTGEFAGDYGWDTAGLSSDPETFARNRELE 96
***.****:***:* :*****:*****:*****:*****
```

```
VIHSRWAMLGALGCVTPELLAKNGIKFGEAVWFKAGSQIFKEGGLDYLGN 150
VIHSRWAMLGALGCTFPEILSKNGVKFGEAVWFKAGSQIFSEGGLDYLGN 148
VIHSRWAMLGALGCVFPEILSKNGVKFGEAVWFKAGAQIFSEGGLDYLGN 146
VIHARWAMLGALGCVTPELLAKNGVKFGEAVWFKAGSQIFSEGGLDYLGN 146
***:*****. **:*:***:*****:***.*****
```

```
PNLVHAQSILAIWASQVILMGAVEGYRVGGGPLGEGLDKIYPGGAFDPLG 200
PNLIHAQSILAIWAVQVVLMGFIEGYRIGGGPLGEGLDPLYPGGAFDPLN 198
PNLVHAQSILAIWAVQVVLMGFVEGYRVGGGPLGEGLDKVYPGGAFDPLG 196
PSLVHAQSILAIWASQVILMGAVEGYRVAGGPLGEVTDPIYPGGSFDPLG 196
*.:***** **:*** :****:***** * :****:*****.
```

```
LADDPDTFAELKVKEKNGRLAMFSMFGFFVQAIVTGKGPIENLLDHLDN 250
LAEDPEAFSELKVKEKNGRLAMFSMFGFFVQAIVTGKGPIENLFDHLAD 248
LADDPDTFAELKVKEKNGRLAMFSMFGFFVQAIVTGKGPIENLFDHVAD 246
LADDPDTFAELKVKEIKNGRLAMFSMFGFFVQAIVTGKGPLENLSHLAD 246
**:*:.*:*****:*****.*****:*** **: :
```

```
PTVNNAWAYATNFTPGS 267
PVANNAWSYATNFVPGN 265
PVANNAWAYATNFVPGK 263
PVANNAWAYATNFVPGN 263
*..****:*****.**.
```

EVLKLAIEIKHARLAMVAAGFAVQAAATGKGPLDNWVTHLSDFLHTTTIID 295
AQLQLAIEIKHARLAMVGFLGFAVQAAATGKGPLNNWATHLSDFLHTTTIID 282
ERLQLAIEIKHARLAMVAFLGFAVQAAATGKGPLNNWATHLSDFLHTTTIFD 284
ETLKLAIEIKHARLAMVAALGFAAQAAATGKGPLDNWATHLADFLHTTTIFD 292
* . * * * * * . * * * * . * * * * * * * . * * . * * * . * * * * * * . *

TFSK-- 299

TFSSS- 287

TFSSSS 290

TFSK-- 296

***.

PsbD

C7B2K2_SELML:

ATCG00270.1:

Os02g24634.1_ORYSA:

```
MtIIVVGRLSGGSTSFFDNTDDRPRRDRFAFVGRSGLSLLPRAYFSPGGWF 50
MtIALGKFTKDEKDLFDIMDDWLRRDRFVFBVGSGLLLFPCAYFALGGWF 50
MTIALGRVTKEENDLFDIMDDWLRRDRFVFBVGSGLLLFPCAYFALGGWF 50
***.:*::: ...:** ** *****.*** *** *: * ***: ****

TGTTSVTSRYTHGLASSYPEGRNSLTVAASTPANSPAHSPPLLWGPEAQG 100
TGTTFVTSWYTHGLASSYLEGCNFLTAAVSTPANSLAHSLLLLWGPEAQG 100
TGTTFVTSWYTHGLASSYLEGCNFLTAAVSTPANSLAHSLLLLWGPEAQG 100
**** ** ***** ** * *.*.***** *** *****

DFTRWCQLGGLWTFVALHGAFGLMGPMRLQSELARSVQSRPYNIAIAFSAP 150
DFTRWCQLGGLWAFVALHGAFALIGFMLRQFELARSVQLRPYNIAIAFSGP 150
DFTRWCQLGGLWTFVALHGAFALIGFMLRQFELARSIQFRPYNIAISFSGP 150
*****:*****.*:* **** *****:* *****:*. *

IAVSVPVSLIHPLGQSGRFSAPSSGVAAIFRSILLPQGLHNWTLNPFHMM 200
IAVFVSVFLIYPLGQSGWFFAPSFVAAIFRFILFFQGFHNWTLNPFHMM 200
IAVFVSVFLIYPLGQSGWFFAPSFVAAIFRFILFFQGFHNWTLNPFHMM 200
*** *. * *:***** * *** ***** **: *:*****

GVAGVPGAAPPRATHGATVENTLFEEDGDGANTFRASNPTQSEETYSMVTA 250
GVAGVLGAALLCAIHGATVENTLFEEDGDGANTFRAFNPQTAEETYSMVTA 250
GVAGVLGAALLCAILGATVENTLFEEDGDGANTFRAFNPQTAEETYSMVTA 250
***** ** * ***** *****:*****

NRFWSQTSQVAPPNKRSHFPMLFVPVTGSRMSAIGVVGLAPNLRAYDFV 300
NRFWSQIFGVAFSNKRWLHFFMLFVPVTGLWMSALGVVGLALNLRAYDFV 300
NRFWSQIFGVAFSNKRWLHFFMLFVPVTGLWMSAIGVVGLALNLRAYDFV 300
***** ** .*** ** ***** **:***** *****

SQEVRAAEDPEFETPYTKNILSNEGIRAWMAAQDQPHENLVFPPEEVLPRG 350
SQEIRAAEDPEFETFYTKNILLNEGIRAWMAAQDQPHENLIFPEEVLPRG 350
SQEIRAAEDPEFETFYTKNILLNEGIRAWMAAQDQPHENLIFPEEVLPRG 350
***:***** ***** *****:*****
```

NAL 353

NAL 353

NAL 353

PsbC

C7B2K3_SELML:

ATCG00280.1:

Os02g24632.1_ORYSA:

PSBC_PHYPA:

```
MKTSYSPRRFYPVETLFDGTLALGGRDQETTGF AWWAGNARLINLSGKSL 50
MKTLYSLRRFYHVETLFNGTLALAGRDQETTGF AWWAGNARLINLSGKLL 50
MKILYSLRRFYHVETLFNGTFVLAGRDQETTGF AWWAGNARLINLSGKLL 50
MKILYSQRRFYHVETLFNGTLALSGRDQETTGF AWWAGNARLINLSGKLL 50
```

*** ** **** *****:***:.*.***** * *

```
GAHVAHAGLIVFWAGAMTLFEVAHFVPEKPMYEQGLILLPHLATLGWGVG 100
GAHVAHAGLIVFWAGAMNLF EVAHFVPEKPMYEQGLILLPHLATLGWGVG 100
GAHVAHAGLIVFWAGAMNLF EVAHFVPEKPMYEQGLILLPHLATLGWGVG 100
GAHVAHAGLIVFWAGAMNLF EVAHFVPEKPMYEQGLILLPHLATLGWGVG 100
```

*****.*****

```
PGGEAVGVSPYLASGVLHLISSAVLGFGGIYHSLIGPDTLEESFPFFGYE 150
PGGEVIDTFPYFVSGVLHLISSAVLGFGGIYHALLGPETLEESFPFFGYV 150
PGGEVLDTFPYFVSGVLHLISSAVLGFGGIYHALLGPETLEESFPFFGYV 150
PGGEVIDTFPYFVSGVLHLISSAVLGFGGIYHALIGPETLEESFPFFGYV 150
```

****.:... **:.******:*.**:*****

```
WRNRNKMTTILGIHLILLGIGALLLVSKALYFGGVYDTWAPGGGDVREIT 200
WKDRNKMTTILGIHLILLGVGAFLLVFKALYFGGVYDTWAPGGGDVRKIT 200
WKDRNKMTTILGIHLILLGIGAFLLVLKALYFGGIYDTWAPGGGDVRKIT 200
WKDKNKMTTILGIHLILLGAGAFLLVFKALYFGGIYDTWAPGGGDVRKIT 200
```

*:::***** **:*** *****:*****:*

```
NLTASPSVISGYLLKSPFGGEGWIVSVDNLEDVIGGHLWLGSICILGGIF 250
NLTLSPSVIFGYLLKSPFGGEGWIVSVDDLEDIIGGHVWLGSICIFGGIW 250
NLTLSPGVIFGYLLKSPFGGEGWIVSVDDLEDIIGGHVWLGFICVFGGIW 250
NLTLSPGVIFGYLLKSPFGGEGWIVSVDNLEDIIGGHVWLGSICIFGGIW 250
```

*** *.** *****:***:***:*** **:::***:

```
HILTKPFAWARRAFVWSGEAYLSYSLGALSIFGFIACCFVWFNNTVYPSE 300
HILTKPFAWARRALVWSGEAYLSYSLAALSVCGFIACCFVWFNNTAYPSE 300
HILTKPFAWARRAFVWSGEAYLSYSLGALSVEFGFIACCFVWFNNTAYPSE 300
HILTKPFAWARRALVWSGEAYLSYSLGAIAVFGFIACCFVWFNNTAYPSE 300
```

*****:*****.*::: *****.****

FYGPTGPEASQAQAF TFLVRDQRLGANAGSAQGPTGLGKYLMRSPtGEII 350
FYGPTGPEASQAQAF TFLVRDQRLGANVGS AQGPTGLGKYLMRsptGEVI 350
FYGPTGPEASQAQAF TFLVRDQRLGANVGS AQGPTGLGKYLMRSPTGEVI 350
FYGPTGPEASQAQAF TFLVRDQRLGANVGS AQGPTGLGKYLMRSPTGEII 350
*****.*****:*

FGGETMRFWDLRAPWLEPLRGPNGLDLSKLRDIQPWQERRSAEYMTHAP 400
FGGEtMRFWDLRAPWLEPLRGPNGLDLSRLKKDIQPWQERRSAEYMTHAP 400
FGGETMHFWDLRAPWLEPLRGPNGLDLSRLKKDIQPWQERRSAEYMTHAP 400
FGGETMRFWDLRAPWLEPLRGPNGLDLSKLRKKDIQPWQERRSAEYMTHAP 400
*****:*****:*.*****

LGSLNSVGGVATEINAVNYVSPRSLATSHFVLGFFFFVGHLWHAGRARA 450
LGSLNSVGGVATEINAVNYVSPRSLSTSHFVLGFFLFVGHLWHAGRARA 450
LGSLNSVGGVATEINAVNYVSPRSLATSHFVLGFFFFVGHLWHAGRARA 450
LGSLNSVGGVATEINAVNYVSPRSLATSHFVLGFFFFVGHLWHAGRARA 450
*****:*****:*****

AAAGFERGIDRDSEPVL SMTPLN 473
AAAGFEKGIDRDFEPVLsMTPLN 473
AAAGFEKGIDRDLEPVLYMTPLN 473
AAAGFEKGIDRDFEPVLSMTPLN 473
*****:***** *****

PsbO

D8TBN9_SELML:

AT3G50820.1:

Os01g31690.1_ORYSA:

A9RS28_PHYPA:

```
MAASVVAAGKAGPSLLQPKLDASAGSSASLRPVSVSKAFGLRSNGGGARLT 50
MATSLQAAATFLQPAKIAASPS-RNVHLRSNQTVGKSFGGLDS--SQARLT 47
MAASLQAAATLMQPAKLGGASSAALPSRPSSHVARAFGVDTG-AAGRIT 49
MAASVASVGCKVTAALAS-SAKVEKIQAVRSVMSNAFGLKP--AVARVS 47
**:*: ..          :...:**: . . .*::
```

```
CSMEDIVKRAT----DVGKVAVATAAATLLVAGTAAAN--PKRLTYDEVQ 94
CSLHSDLKDFAGKCSDAKIAGFALATSALVVSGAGAEGAPKRLTYDEIQ 97
CSLQSDIREVANKCADAAGLAGFALATSALLVSGASAEGVPRRLTFDEIQ 99
CNLEENVKSIV----DNAKAAAIVLASSALVAGAAFAEGVPQRLTFDEVN 93
*.... :: . * . * * . *:: *... * *: *::***:**::
```

```
AQTYLEVKGSGTANQCPILSGGDEGFKFKPGSVSVKKFCLEPTSFTVKKE 144
SKTYMEVKGTGTANQCPTIDGGSETFSFKAGKYTGKKFCFEPTSFTVKAD 147
SKTYMEVKGTGTANQCPTVEGGVDSFAFKAGKYNMKKFCLEPTSFTVKAE 149
AQTYMDVKSGTANQCPIVAEGSDKFAFKDGNYTMRKFCLEPTSFTVKAE 143
::**::***:***** : * : * ** *.*. :***:***** :
```

```
SPFKGGGDQYVDTKLMTRLTYTLDEIEADLSVDEKGNLKLVEKDGDIDYAA 194
SVSKNAPPDFQNTKLMTRLTYTLDEIEGPFVEVGSDGSVKFKEEDGDIDYAA 197
GVAKNAPPEFQTKLMTRLTYTLDEIEGPLEVSSDGTIKFEEKDGIDYAA 199
SQFKGGNEGFPQTKLMTRLTYTLDEIEGPLTVQ-NGNLRFEEDGDIDYAA 192
. *.. : *****. : * *.*::: * *****
```

```
VTVQLPGGERVPFLFTIKELVATGSPDGFSGSFLVPSYRGSSFLDPKGRG 244
VTVQLPGGERVPFLFTVKQLEASGKPESFSGKFLVPSYRGSSFLDPKGRG 247
VTVQLPGGERVPFLFTIKNLVATGKPESFGGPFLVPSYRGSSFLDPKGRG 249
VTVQLPGGERVPFLFTVKELVAEGKPEAFGGSFLVPSYRGSSFLDPKGRG 242
*****:*:* * *.*.*. *****
```

```
GSTGYDNAVALPAGGAGDEEELGKENLKDTSGSTGNITLKVAESNTATGE 294
GSTGYDNAVALPAGGRGDEEELSKENVKNTAASVGEITLKITSKPKETGE 297
GSTGYDNAVALPAGGRGDEEELAKENVKNASSSTGNITLSVTKSKPKETGE 299
GSTGYDNAVALPAGGAGDEEELAKENEKNTAALNGNITFSIAKSNVQTGE 292
***** *****.* ** *::: *::*:::*: **
```

IAGVFESIQPSDSDLGSKAPKEVKIQGIWYAQLD 328
VIGVFESLQPSDSDLGAKVPKDVKIQGVWYGQIE 331
VIGVFESVQPSDSDLGAKVPKDVKIQGVWYAQLE 333
IAGTFESFQPSDSDLGSKAPKEVKIEGIFYAQLD 326
: *.***.*****:*.**:*:*:*::*.*::

PsbQ

D8S1M9_SELML:

AT4G05180.1:

Os07g36080.3_ORYSA:

A9S1E8_PHYPA:

MVGLVAVAAGVLAVEES----- 17
MAQAVTSMAGLRGASQAVLEGLQING---SNRLNISRVSVGSQRTGLVI 47
MAQAALAEA----- 9
MAN-TVAMAGLCGTSQALTQGGLVSCNNVINGSSRVNSVCVSKPAVVVAR 49
* . . *

-----RALTGIKINGPPPPSG 33
RAQQNVSVPESSRRSVIGLVAAGLAGGSFVKAVFAEAPIKVGGPPLPSG 97
-----AKPIKLGPPPPPSG 23
AEQSDAAASVQSRRSVLSLLAATIVGTAVVNEARADARSVKLEPPPPLSG 99
*: ** **

GLPGTENADQPRDLPLKERFFIQPLsPAEAVGRIKDASKDIVGVKELI 83
GLPGTDNSDQARDFSLALKDRfyIQPLspEAAARAKDSAKEIINVKSFI 147
GLPGTLNSDQARDTDLPLRERFYLQPLPPAEAAARAKESAQDIINLKPLI 73
GLPGTENADQARDTDLPLRERFFIQPLSPADAAQRAKFSQDIINVKSLI 149
***** *:**.** .*.*:**:**.*:*. * * ::*:*:*: *

DKKSWPYVRNDLRNKATYLRDYLKTIMDAKPKAERKALKKLTDLNLFVID 133
DKKAWPYVQNDLRLRASYLRYDLNTVISAKPKEEKQSLKDLTAKLFQTID 197
EKKQWPFVRDDLRLRASYLRYDLKTVINSKPKDEKKGLKDLTGKLFATID 123
DKKAWPYVQNGLRSSAGYLRDYLNTVITSKSKEDRKSLKALSCLKLFESLN 199
:** **:*:**.** * ******: : :*. * ::*.** *: **: :

KLDFAARAKNPTDAGKCYAEAVAALDTVIAKISA 167
NLDYAARSKSSPDAEKYYSETVSSLNNVLAKLG- 230
GLDHAARIKSPEEAEKYYTLTKSALGDVLAKLG- 156
ALDYAARSKSTKDAEKYYSTVTLLNDVLSKIA- 232
.: *. . :* * *: : : *. **:*:.

PsaC

C7B2J3_SELML:

ATCG01060.1:

Os10g21406.1_ORYSA:

PSAC_PHYPA:

MAHPAKIHGTCIGRTQCVRACPTDVSETIPWDGCKANQIASAPRTEDRVG 50

MSHSVKIYDTCIGCTQCVRACPTDVLEMIPWDGCKAKQIASAPRTEDCVG 50

MSHSVKIYDTCIGCTQCVRACPTDVLEMIPWDGCKAKQIASAPRTEDCVG 50

MAHSVKIYDTCIGCTQCVRACPTDVLEMVPWDGCKASQIASAPRTEDCVG 50

:.*.**:.***** ***** * :*****.****** **

CKRRESACPTDPSSARVYLGS^EETTRSTGLAHQ 82

CKRCESACPTDFLSVRVYLWHETTRSMGLAY- 81

CKRCESACPTDFLSVRVYLGPE^TTRSMALSY- 81

CKRCESACPTDFLSVRVYLGAETTRSMGLAY- 81

*** ***** *.***** ***** .*::

PsaF

D8QPQ3_SELML:

AT1G31330.1:

Os03g56670.1_ORYSA:

A9TWD4_PHYPA:

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-----
MSLTIPANLVLNPRSNKSLTQSVPKSSARFVCSDD-----KSSSSTPQ 43
MAALAAASTAFAAKPRLARAPSSPAARFSVSCSASGNNGGAGEMAQSLAA 50
-----MFVKNTKARTVCSAS-----ADETATVAQ 24

---MAAALAAAAIIGSAPIVAAPPEAAADVAGLTKCKDSAAFAKREKKE 46
SMKAFSAAVALSSILLS-----APMPAVADISGLTPCKDSKQFAKREKQQ 88
SAKTFSAALALSSVLLSS-AATSPPPAAADIAGLTPCKESKAFKREKQS 99
TAGKFATALALAAIVGGSDMVVP--EARADVAGLTPCKESKGFARQKQE 72
:::*:* :::: . . * **::*** **:* *****:*.

IKKLQSRLKLYADDSAPALAINATIEKTKRRFKFYGDAGLLCGADGLPHL 96
IKKLEssSLKLYyAPESsAPALALNAQIEKTKRRFDNYGKYGLLCGSDGLPHL 138
IKKLQSSLKKYAPDSAPALAINATIEKTKRRFENYGKFGLLCGADGLPHL 149
IKKLESRLKLYAPDSAPALAINATIEKTKRRFEFYGKQGLLCGTDGLPHL 122
*****:* ** ** :*****:* *****. **. *****:*****

IVDGDQQHLGEFVYPGLIFLYIAGWIGWVGRSYLIAVSTEAKPTQKEIII 146
IVNGDQRHWGEFITPGILFLYIAGWIGWVGRSYLIAISGEKKPAMKEIII 188
IVSGDQRHWGEFITPGLLFLYIAGWIGWVGRSYLIAISGEKKPAMREIII 199
IVDGDQAHLGEFVYPGLVFLYIAGWIGWVGRAYLIDVRTSKKPTKEKEIII 172
**.* ** * ***: **:*****:*** : . **: :****

DVPLATSLIWKGFVWPLAAVSEFRNGKLVVDAGNITVsPR 186
DVPLASRIIFRGFIWPVAAYREFLNGDLIAKDV----- 221
DVELAVKLLPRGFIWPVAAYRELITGNLVVDDADIGY--- 236
DVPLALRVMSKGFTWPLAAIGELRSGKLVEKSGNITVSPR 212
** ** :: :** **:** *: .*.*: .
```

Supplementary Figure S2. Complete ClustalW sequence alignment of Selaginella photosynthesis proteins with Arabidopsis, rice and moss orthologs. Phosphosites identified by our group and other groups are highlighted in red and yellow, respectively. The moss sequences are included as a reference although no phosphorylation information is available.