

Organism	Gene/protein annotation discussed or used in this study		Annotation/prediction supported by transcriptome data of the organism or a closely related species (based on TSA available publicly)	
	Existing gene annotation/prediction: YES/NO (Details)	Existing gene annotation/prediction either modified /New annotation/prediction for this study: YES/NO (Details)	Partially supported: YES/NO (Details)	Completely supported: YES/NO (Details)
<i>Chlamydomonas eustigma</i>	NO (GAX74142, GAX74143) NCBI	NO	YES (GFWA01012995.1; GFWA01107356.1) ( <i>Chlamydomonas acidophila</i> , NCBI)	No
<i>Volvox carteri</i>	NO (Vocar.0009s0222) Phytozome	NO	NO	NO
<i>Bathycoccus prasinus</i>	YES (XP_007511896.1), NCBI	NO	YES (HBMR01008367; HBMR01008373; HBMR01008370), NCBI	NO
<i>Ostreococcus tauri</i>	YES (OUS42981.1), NCBI	NO	YES (HBDX01000727; HBLQ01004044), NCBI	NO
<i>Mesotaenium endlicherianum</i>	NO (ME000610S08690)	YES, (Described in methods)	NO	NO
<i>Chara braunii</i>	NO (GBG89877.1)	NO	YES (GGXX01117481.1), NCBI	NO

<i>Klebsormidium nitens</i>	NO (GAQ84758.1 , GAQ84757.1) Source: NCBI	YES (Described in methods)	YES (GBSO01008411.1) (GBSO01005714.1 ), NCBI	NO
<i>Marchantia polymorpha</i>	YES (Mapoly0069s0061.1) Source: Phytozome	NO	YES (GEFO01007190.1, GEFO01010847.1)	NO
<i>Physcomitrella patens</i>	YES (XP_024384633.1) Source: NCBI	NO	NO	YES (as per entry XM_024528865, 100% coverage of the annotated genomic feature by RNAseq alignments)
<i>Sphagnum fallax</i>	YES  (Sphfalx06G105000.1 )  Source: "Sphagnum fallax v1.1, DOE-JGI, <a href="http://phytozome.jgi.doe.gov/">http://phytozome.jgi.doe.gov/</a> ".	NO	NO	NO

<i>Anthoceros agrestis</i> [Oxford]	NO (AagrOXF_evm.mode l.utg000049l.749.1) Source: <a href="https://www.hornwort&lt;br/&gt;s.uzh.ch">https://www.hornwort s.uzh.ch</a>	YES (Described in methods) (scaffold_2012162, 1KP)	NO	YES (scaffold_2012162), 1KP
<i>Diphasiastrum complanatum</i>	YES (Dicom.17G090200.1)  Source: "Diphasiastrum complanatum v3.1, DOE-JGI, <a href="http://phytozome-&lt;br/&gt;next.jgi.doe.gov/">http://phytozome- next.jgi.doe.gov/</a>	NO	NO	NO
<i>Selaginella moellendorffii</i>	YES (XP_002965996.2)  XP_002989230.2	NO	NO	YES (NCBI entry:100% coverage of the annotated genomic feature by RNAseq alignments" And (GEMU01096076.1)
<i>Azolla filiculoides</i>	NO (Azfi_s0095.g043658)  Source: Fernbase.org	YES  (Described in methods)	YES (partial TSA, at NCBI) GBTV01032116.1 GBTV01032115.1 and at fernbase.org	
<i>salvinia cucullata</i>	NO (Sacu_v1.1_s0105.g0 20212) Source: Fernbase.org	NO	YES (at fernbase.org)	NO

<i>Ceratopteris richardii</i>	NO (Ceric.1Z120700) Source: Phytozome	YES (based on TSA)	No	YES (GIXU01015881)
<i>Pinus taeda</i>	NO	YES (Predicted from TSA, Described in methods)	Yes <i>Pinus taeda</i> TSA (GIYS01087684)	YES (GHWB01310569)( <i>Pinus flexilis</i> TSA)
<i>Sequoia sempervirens</i>	NO	YES  Predicted from TSA (GIBU01226047)	No	YES (GIBU01226047)
<i>Isoetes taiwanensis</i>	NO >Isoetes taiwanensis  Itaiw_v1_scaffold_24  14899984  14905902  Itaiw_v1_scaffold_24_t17467-RA  1  CDS  3473898239  3044  frame0 >Isoetes taiwanensis  Itaiw_v1_scaffold_24  14910580  14923530  Itaiw_v1_scaffold_24_t17468-RA  1  CDS  3473898242  4268  frame0	NO	NO	Annotated as two separate proteins.NO sufficient RNA support to determine the full length protein.

**Supplementary Table 1.** Details of putative DNA-PKcs gene/protein annotations used or discussed in the current study from different plant species.