

Supplemental Figure 4

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SNRK2.1      -----MAAASTINPDPPLASEGTFHKIKDLGSGSFGHVALYSR-LGHDEP---VAVKCLPVR--VVDYNNVVKREVRSHCSLNHPHVLVLFKRLGLTPDKRVLFMVMEYADCG
SAC3/SNRK2.2 MAAAANQKPGPARPPEPLHGHPRYEKIKDLNSCTFGFVQLARD-KLTGET---WAVKFLBRGDKITKY--VEREINHRCLVHPHVLVQFREVFLTP--THLCLVMEYAPGG
SNRK2.3      ----MASAPAPPNPLSGQSGYQVFKALGTCAFQSVLHYRQLTFGGPIEBVAVKVIISRE-ECSDENLVSREVHSHRLLVHPHVLVRFKRLGLTPDKRVLFMVMEYADRG
SNRK2.4      -----MDNLSLQVVDPLLGNACQYCKVKDLGITGSGFSGVALYTRNEGRGEP-SLCAVKFMNRSRGGVDINLIQREIQSHRVLRRHPHVLVRFKQLGLTP--THIFMCMEEADQG
SNRK2.5      -----MERFQVITQSLGSGSFGTIVRVKD-VAAEKI---LAKMVLNRRD-ASKY--VEAEIVNHSLLRHPHVLVHFREVFLTD--PHLCLVMEYANGG
SNRK2.6      -----MAAEPDPMRETRGRYERVQSLGKCAFQFVQLGRN-LQNGEI---AAIKFLRGRD-VNKY--VESEILNHSVLRHPHVLVQFKEVFLTS--EYIALAMEYATGG
SNRK2.7      -----MNAAPDPLKCHGRYAKVQPLSSGSGFQVHLCKN-LQNGEI---VAIKFLRGRERVNKY--VEEVLNHRMLRHPHVLVQFKEVFLTP--EYICTOMEYASGG
SNRK2.8      -----MDKFEFVADLGSNFGVAKLMRD-RASGQI---VANKFLRGRERVDRN--VEREINHRMLNHPNIVAFMEVFLTP--SHLCLVMEYAAAG

SNRK2.1      DLFKYVQOHGRPEADARWFFQQLILGLDYCHRRGVVNRDLKLENLLRSAAEVPPPPGQ--LEQPRNLHTRKVAADFGLCK-ASVNSLPKSRVGTLYYLPAPEVLRASADRP
SAC3/SNRK2.2  DMFEYVVRKNGHREDEARWFFQQLIVGLDYCHRRMGVVNRDIKLENTLLD-----SSRPLVVICDFGYSKHEKFOASAPCSRVTGPAYLPAPEVLLTTKGT
SNRK2.3      DLLDYLRRRGCFRREHARWFFQQLVFGLDYCHORGVVNRDLKLENLLKRTTPDARQELTQGDLEHPFNLHLKIADFGLSK-EGMHSQPKSRVGTLYYMAPEVLRAGPSRR
SNRK2.4      DLGFLRRKCPLEADSRWLFQQLIFGLDYCHLKGVVNRDLKLENLLK-----LTPEASKRRHSNTFNLHLKIADFGLSK-RAAHSLPKTRVGTLYYMAPEVLRAGPAQR
SNRK2.5      SLFSMVRQORRLKESMARWFFQQLILAVDYCHKRGVANRDIKLENLLH-----LEEGLHPPLKMCDFGYSK-ADFRSAAKSOVGTLSYMAPEVMKSCG-AY
SNRK2.6      SLFHHVQKQTRLKEAVARWFFQQLILGVDYCHKRGVANRDIKLENTLLO-----KVNGLPLPLKICDFGYSK-ADFRSAAKSKVG-----
SNRK2.7      NLFQYVQRAVRLKEPARWFFQQLICGLDYCHRRGVVNRDIKLENTLLT-----MVPGLPLPLKICDFGYSK-AHFMSAPKSKVGTLYYMAPEVLRAT--DQ
SNRK2.8      ELFERIVRACRFSEDEARWFFQQLISGVDYCHASGVCHRDLENTLLD-----GNPAPRLKICDFGYSK-SAFDSQPKSTVGTLPAYLPAPEVLRQ--KE

SNRK2.1      YDAKLSDIWSGVILYVLLFKAYPFQVI---SDRDNKAORDAILRRIANAENQLPAHPVIGEAQRDLLSRILVSDPAKRITMEGIMSHSWSFREDLPEGALEFNEGLVEEQ
SAC3/SNRK2.2  YDGKIADIWSCGVMLYVMLVGAYPFEPF---EDKHDNQLQKMIQRIILHVDYHIPPVHRASEDCDILLAKILVADHHRITVDGYNHRKWLKGLPPGVREMNDRVQ---
SNRK2.3      YDGNKADIWSACHVLYVMLFARAPFDDP---LATTDKARRDATMOQILRGEWNVPAFVVAPECDLLRGIILSPDPNTRFTLAQIMSHPWFSVGLPPAALTMNTVLRQQ
SNRK2.4      YDGAKADIWSAGVLYVMLFSRVPFPE-----IQRIIDGAVAVPPEGMIVSPOVLHLLTQMLQPPDARRIPMSAIMEHPWFRAGLPPAALTMNTALVRQQ
SNRK2.5      YDAKIADVWSCGVLYVMLYGHYYPFDNQGEDAGLSAQKVRKMLEREMENAYALNPQVPTPECDLMLRGLLKPAPESRFTLTKIMEHPWENKLLPQAREMNVYLN--
SNRK2.6      ----VADIWSCGVMLYVVMFYGRYPFETP-AGSAMPKATEILAMLD---NMRYELSEHVEISDOGDLRKMILLPDPKORITLEAVMTHPWFTTNLPPAATMNSYLR--
SNRK2.7      YAGQAADIWSCGVMLYVMLVGAYPFESP-QSRHQQKARMDSMQRIILRMEWSPADVBSPECRDLLCKLLVGDPRHRLTMAQIQHPWFLTNLPPDALAMNDNLAHT
SNRK2.8      YNGQPADVWSCGVLYVMLVGAYPFEPF---ADPRN---FRKTIQRIIMNVKYSFPFQLAISAECADLIGRIIVANPAQRIALADLRHPWFLKLNLAELADPNN-FRSRP

SNRK2.1      AADPPRCBQSM~EETDAILLSAEDPLHGCGGLGAGLAGGGAAGGTAAGVMAMIGSSGIDDEIDELHAEHPSQFGMND-----
SAC3/SNRK2.2  ---PPP-EGLOSVEEIKRLIEEARHVG-VGAPGYVNPV-----ETDEY-IDDAMDNMYDEGSLDYND-----
SNRK2.3      TAQPPPYE--QSVEDVNTVLEEATQ--RHGHQGGGLGGSEITDSGFMTMIADEMEENRRRHNPYMVDPYPGQGPAGRP-GQP-AAPOQR
SNRK2.4      AQQAA-----AGTATSGEQGG-----
SNRK2.5      --LPVPPYQR-PEQIKSLEEARA--VGGR-----
SNRK2.6      AGFPAGHQVQSPPEIKRLIEEAKGHRHT-----
SNRK2.7      DYTGV----QSEDIKKVLSAAILPAPMSKYAFAT-GGDDENY-----EDLDAALDPEMGHAGAGCKPAAA---GRPAGNGGAAPG-R
SNRK2.8      E-----PHOSLDEIRALIRARARTLGDTCPKPGGGGCGGGHLPLEFN-----EDDYMDA--DELA-----

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Supplemental Figure 3. Alignment of SNRK2 protein family in *Chlamydomonas*. The predicted SNRK2 proteins were aligned with BioEdit 7.0.5.3 software. The black and grey boxes indicate identical and similar amino acids, respectively. The extra loop segment present in SNRK2.1, SNRK2.3 and SNRK2.4 (dotted line), the conserved NLH motif (***) , the putative phosphorylation sites present in this extra segment (red letters) and the conserved phosphorylated Ser (#) are noted. The sequences of SNRK2.4, 5, 6 and 8 may be incomplete or partially incorrect since the transcript sequences have not been confirmed and the genomic sequence information is not complete.