Supplemental Figure 1. Alignment of *A. thaliana* AHA2 with its *S. cerevisiae* counterpart Pma1p with phosphosites indicated. A CLUSTAL 2.1 multiple sequence alignment is shown. AHA2 sequence: *Green residues*, phosphorylated *in planta* (this study and other studies); *Boxed residues*, phosphorylated *in fungus* when AHA2 is expressed heterologously in yeast. Pma1p sequence: *Cyan residues,* phosphorylated *in fungus*.

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AHA2     --------------------------MSSLEDIKNETVDLEKIP--IEEVFQQLKCSRE- 31
Pma1p    MTDTSSSSSSSSASSVSAHQPTQEKPAKTYDDAASESSDDDDIDALIEELQSNHGVDDED 60
                                   .: :*  .*: * :.*   ***: .:   . *

AHA2     --------------------------GLTTQEGEDRIQIFGPNKLEEKKESKLLKFLGFM 65
Pma1p    SDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLKRRKKYGLNQMADEKESLVVKFVMFF 120
                                  ***::*  .* : :* *:: ::*** ::**: *:

AHA2     WNPLSWVMEMAAIMAIALANGDGRPPDWQDFVGIICLLVINSTISFIEENNAGNAAAALM 125
Pma1p    VGPIQFVMEAAAILAAGLS-------DWVDFGVICGLLMLNAGVGFVQEFQAGSIVDELK 173
          .*:.:*** ***:* .*:       ** **  *  **::*: :.*::* :**. .  *

AHA2     AGLAPKTKVLRDGKWSEQEAAILVPGDIVSIKLGDIIPADARLLEGD-PLKVDQSALTGE 184
Pma1p    KTLANTAVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGRIVTEDCFLQIDQSAITGE 233
           ** .: *:***:  *  *  :*****:.:: * :**:*.*::  *  *::****:***

AHA2     SLPVTKHPGQEVFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTN-QVGHFQKVLTAI 243
Pma1p    SLAVDKHYGDQTFSSSTVKRGEGFMVVTATGDNTFVGRAAALVNKAAGGQGHFTEVLNGI 293
         **.* ** *::.**.** *:**   ** *** :**.*:** **:.:    *** :**..*

AHA2     GNFCICSIAIGMVIEIIVMYPIQRRKYRDGIDNLLVLLIGGIPIAMPTVLSVTMAIGSHR 303
Pma1p    G-IILLVLVIATLLLVWTACFYRTNGIVRILRYTLGITIIGVPVGLPAVVTTTMAVGAAY 352
         * : :  :.*. :: : .    : .     :   * : * *:*:.:*:*::.***:*:

AHA2     LSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLSVDKNLVEVFCKGVEKDQVLLFAA 363
Pma1p    LAKKQAIVQKLSAIESLAGVEILCSDKTGTLTKNKLSLHE---PYTVEGVSPDDLMLTAC 409
         *::: **.::::***.:**:::********** ****:.:       :**. *:::* *.

AHA2     MASRVENQ--DAIDAAMVG---MLADPKEARAGIREVHFLPFNPVDKRTALTYIDGSGNW 418
Pma1p    LAASRKKKGLDAIDKAFLKSLKQYPKAKDALTKYKVLEFHPFDPVSKKVTAVVESPEGER 469
         :*:  :::  **** *::      ...*:* :  : :.* **:**.*:.: .  . .*:

AHA2     HRVSKGAPEQILELAKASN----DLSKKVLSIIDKYAERGLRSLAVARQVVPEKTKESPG 474
Pma1p    IVCVKGAPLFVLKTVEEDHPIPEDVHENYENKVAELASRGFRALGVARKRG--------E 521
             ****  :*: .: .:    *: ::  . : : *.**:*:*.***:

AHA2     APWEFVGLLPLFDPPRHDSAETIRRALNLGVNVKMITGDQLAIGKETGRRLGMGTNMYPS 534
Pma1p    GHWEILGVMPCMDPPRDDTAQTVSEARHLGLRVKMLTGDAVGIAKETCRQLGLGTNIYN- 580
         . **::*::* :****.*:*:*: .* :**:.***:*** :.*.*** *:**:***:*

AHA2     SALLGTHKDANLASIPVEELIEKADGFAGVFPEHKYEIVKKLQERKHIVGMTGDGVNDAP 594
Pma1p    AERLGLGGGGDMPGSELADFVENADGFAEVFPQHKYRVVEILQNRGYLVAMTGDGVNDAP 640
         :  **   ..::..  : :::*:***** ***:***.:*: **:* ::*.**********

AHA2     ALKKADIGIAVADATDAARGASDIVLTEPGLSVIISAVLTSRAIFQRMKNYTIYAVSITI 654
Pma1p    SLKKADTGIAVEGATDAARSAADIVFLAPGLSAIIDALKTSRQIFHRMYSYVVYRIALSL 700
         :***** **** .******.*:***:  ****.**.*: *** **:** .*.:* :::::

AHA2     RIVFGFMLIALIWEFDFSAFMVLIIAILNDGTIMTISKDRVKPSPTPDSWKLKEIFATGV 714
Pma1p    HLEIFLGLWIAILDNSLDIDLIVFIAIFADVATLAIAYDNAPYSPKPVKWNLPRLWGMSI 760
         :: : : *   * : .:.  ::::***: * : ::*: *..  **.* .*:* .::. .:

AHA2     VLGGYQAIMTVIFFWAAHKTDFFSDTFGVRSIRDNNHELMGAVYLQVSIISQALIFVTRS 774
Pma1p    ILG----IVLAIGSWITLTTMFLPK----GGIIQNFGAMNGIMFLQISLTENWLIFITRA 812
         :**    *: .*  * : .* *:..     .* :*   : * ::**:*: .: ***:**:

AHA2     RSWSFVERPGALLMIAFLIAQLIATLIAVYANWEFAKIRGIGWGWAGVIWLYSIVTYFPL 834
Pma1p    AGPFWSSIPSWQLAGAVFAVDIIATMFTLFGWWSEN--------------WTDIVTVVRV 858
          .  : . *.  *  *.: .::***:::::. *.                 .*** . :

AHA2     DVFKFAIRYILSGKAWLNLFENKTAFTMKKDYGKEEREAQWALAQRTLHGLQPKEAVNIF 894
Pma1p    WIWSIGIFCVLGGFYYEMSTSEAFDRLMNGKPMKEKKSTRSVEDFMAAMQRVSTQHEKET
          ::.:.*  :*.*  :           *     ** :

AHA2     PEKGSYRELSEIAEQAKRRAEIARLRELHTLKGHVESVVKLKGLDIETPSHYTV 948
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