Table S1. Primers and reaction conditions used for the determination of PHA isoforms expression by semi-quantitative RT-PCR.

	Primer sequence	**Annealing temperature (°C)**	**Number of cycles**
PHA1 forward	5’ GTGAGTGGGTGATAGAATGAAGAC 3’	46	20
PHA1 reverse	5’ GCCGATAATGAATGCTGTTATAG 3’	46	20
PHA2 forward	5’ AGAAAAGAAGAGACACACAAGC 3’	46	24
PHA2 reverse	5’ GACACAATCCCTTTCAATGG 3’	46	24
PHA3 forward	5' TGATCAAGTTCCTCATCCG 3'	47	26
PHA3 reverse	5' TTAAACGGTGTATGACTGCTG 3'	47	26
PHA4 forward	5' GACACAATGATCCAAAACAAGAC 3'	48	30
PHA4 reverse	5' ATTCAACAAAATGCCAGCAG 3'	48	30
PHA5 forward	5' GTG ATGCCTGGGATTCAATG 3'	48	30
PHA 5 reverse	5' CTCCCATAATTCATTGCATAATCTTAG 3'	48	30
PHA6 forward	5' CCTGGTTGTGATAGTCTCC 3'	47	35
PHA6 reverse	5' AATCACAATATGCTTTTCAAAAATCC 3'	47	35
PHA7 forward	5' GATCCCATCAAATTTGCTG 3'	46	30
PHA7 reverse	5' GGTGTAATGCGGATTGAC 3'	46	30
EF1-α forward	5´ GTATGGTTGTGACCTTTGG 3´	48	20
EF1-α reverse	5´ CAACATTCTTGACAACAC 3´	48	20

Table S2. Chromosome localization, coding region length, predicted protein length and molecular weight (MW) of the plasma membrane H^+-ATPases identified in *S. tuberosum* Phureja (Potato Genome Sequencing Consortium database).

name	transcript ID	peptide ID	chromosome localization	coding region length (bp)	protein length (aa)	protein MW (KDa)
PHA1	PGSC0003DM T400083041	PGSC0003DM P400055772	6	2871	956	105.0
PHA2	PGSC0003DM T400010497	PGSC0003DM P400007331	7	2859	952	105.0
PHA3	PGSC0003DM T400065168	PGSC0003DM P400043938	3	2973	990	109.4
PHA4	PGSC0003DM T400030913	PGSC0003DM P400021001	7	2856	951	104.5
PHA5	PGSC0003DM T400020414	PGSC0003DM P400013900	12	2775	924	101.6
PHA6	PGSC0003DM T400003602	PGSC0003DM P400002571	2	2739	912	101.7
PHA7	PGSC0003DM T400088585	PGSC0003DM P400060260	8	2901	966	106.2

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PHA6      -----------MGLDDLVDLENIPIEQVFENLKCNKEGLTYTDVEERLSIYGHNKLEEKT     49
PHA7      MGTEKTTTTLEAINNETVDLENIPIKEVFENLKCTEEGLNSAEVEKRLNVFGHNKLEEKK     60
PHA1      --MGEKPEVLDAVLKETVDLENIPIEEVFENLRCTKEGLTGTAAQERLAIFGYNKLEEKK     58
PHA3      --MAEKPEVLDAVLKETVDLENIPIEEVFENLRCTREGLTTTAAQERLSIFGYNKLEEKK     58
PHA2      ---MAKAISLEEIKNETVDLEKIPIEEVFEQLKCSREGLTSDEGANRLQIFGPNKLEEKK     57
PHA4      ---MASNLSLEDIKNEQIDLENIPVEEVFQQLKCSKEGLSSAEGQKRVEIFGPNKLEEKK     57
PHA5      ---MAANLSLEELKNEKVDLESIPVEEVFQILKCSKEGLTKEEGQKRIEIFGPNKLEEKK     57
                        .: :***.**:::**: *:*..***.     :*: ::* ******.

PHA6      ESKFLNFLRYSWNPLSRTMVAAAIMAIVLANGGGRPPDWQLFLGIVTFLIVTNSSYTFVA     109
PHA7      ESKILKFLGFMWNPLSWVMEAAAIMALFLPHGKHKGVDYQDFVGIVALLIINS-TISFME     119
PHA1      ESKFLKFLGFMWNPLSWVMEAAAIMAIALANGGGKPPDWQDFVGIITLLVINS-TISFIE     117
PHA3      ESKFLKFLGFMWNPLSWVMEAAAIMAIALANGGGKPPDWQDFVGIITLLIINS-TISFIE     117
PHA2      ESKILKFLGFMWNPLSWVMEAAAIMAIALANGNGKPPDWQDFVGIVCLLVINS-TISFIE     116
PHA4      DNKLLKFLGFMWNPLSWVMECAAIMAIVLANGGGKPPDWPDFVGITVLLIINS-TISFIE     116
PHA5      ENKVLKFLGFMWNPLSWVMEAAAIMSIVLANGGGKPPDWPDFVGIMVLLVINS-TISFIE     116
          :.*.*:** : ***** .* .****:: * .*  :  *:  *:**  :*::.. : :*:

PHA6      VKLT-SDIAARVQFLHKFCRVLRHGRWCEVDSSNLVPGDIIHIKMGDIVPADVRILNFFT     168
PHA7      ENNAGNAAAALMARLAPKAKVLRDGKWNEEDAAVLVPGDIISIKLGDIIPADARLLN---     176
PHA1      ENNAGNAAAALMARLAPKAKVLRDGKWNEEDAAVLVPGDIISIKLGDIVPADARLLE---     174
PHA3      ENNAGNAAAALMARLAPKAKVLRDGKWDEEDAAVLVPGDIISIKLGDIIPADARLLE---     174
PHA2      ENNAGNAAAALMAGLAPKTKVLRDGRWSEQEAAILVPGDIISVKLGDIVPADARLLE---     173
PHA4      ENSAGNAASALMANLAPKTKILRDGKWSEEEASILVPGDIISIKLGDIVPADARLLE---     173
PHA5      ENNAGNAAAALMANLAPKTKVLRDGKWSEEDASLLVPGDLISVKLGDIIPADARLLE---     173
           : : .  :* :  *    ::**.*:* * ::: *****:* :*:***:***.*:*:

PHA6      TDPVVKIDLSDLTGESLPVTKSRIGDCAYSGSTCQKGEIIAVVIAIGVRTRYRNAAAPHV     228
PHA7      -GDPLKIDQSALTGESLPVTKN-PGDGVYSGSTCKQGEIEAVVIATGVHTFFGKA--AHL     232
PHA1      -GDPLKIDQSALTGESLPVTKG-PGDGVYSGSTCKQGEIEAVVIATGVHTFFGKA--AHL     230
PHA3      -GDPLKIDQSALTGESLPVTKG-PGDGVYSGSTCKQGEIEAVVIATGVHTFFGKA--AHL     230
PHA2      -GDPLKIDQSALTGESLPVTKN-PGDEVFSGSTCKQGELEAVVIATGVHTFFGKA--AHL     229
PHA4      -GDPLKVDQAALTGESLPATKF-PGAEVFSGSTVKQGEIEAIVIATGVHTFFGKA--AHL     229
PHA5      -GDPLKIDQAALTGESLPVTKQ-PGDEVFSGSTVKQGELDAVVIATGVHTFFGKA--AHL     229
              :*:* : *******.**   *  .:**** ::**: *:*** **:* : :*   *:

PHA6      VKSSNQVECFRR----------------------------------VSKGIGNFCIHFVA     254
PHA7      VENTTHVGHFQK----------------------------------VLTSIGNFCICSIA     258
PHA1      VDSTNQVGHFQK----------------------------------VLTAIGNFCICSIA     256
PHA3      VDSTNQVGHFQKASRLFTLLFDAMIWINVSDFYEILHYKFMYGYRQVLTAIGNFCICSIA     290
PHA2      VDSTNNVGHFQK----------------------------------VLTAIGNFCICSIA     255
PHA4      VDSTNNVGHFQK----------------------------------VLTAIGNFCICSIA     255
PHA5      VDSTNQVGHFQK----------------------------------VLTAIGNFCICSIL     255
          *..:..*  *::                                  * ..******  :

PHA6      VVMMVEIIVMYCIQHRAYRSGIDNLLVLLIGGIPIGMPLTLLLIMRHGTV--TSSHYVIK     312
PHA7      TGMIIELIVIFGGQHRHPREAVDSLLVLLIGGIPIAMPTVLSVTMAIGSHRLSQQGAITK     318
PHA1      VGMIIEIIVMYPIQHRKYRPGIDNLLVLLIGGIPIAMPTVLSVTMAIGSHRLAQQGAITK     316
PHA3      VGMIIEIIVMYPIQHRKYRPGIDNLLVLLIGGIPIAMPTVLSVTMAIGSHRLAQQGAITK     350
PHA2      VGMLIEIIVMYPIQHRKYRDGIDNLLVLLIGGIPIAMPTVLSVTMAIGSHRLSQQGAITK     315
PHA4      VGMVIEIVVMYPIQKRNYRDGIDNLLVLLIGGIPIAMPTVLSVTMAIGSHRLAQQGAITK     315
PHA5      VGIVIEIVVMWPIQKRKYRDGIDNLLVLLIGGIPIAMPTVLSVTMAIGSHRLSQQGAITK     315
          . :::*::*::  *:*  * .:*.***********.** .* : *  *:   :..  : *

PHA6      RMTTIIDMACMDVLCSDMTGTLTLGMLDVQRDLIEVFANDINKDTVALMAARACNSEECA     372
PHA7      RMTAIEEMAGMDVLCSDKTGTLTLNKLSVDKNLIEVFAKDVEKDMVVLMAARASRLENQD     378
PHA1      RMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLVEVFAKGVDADTVVLMAARASRTENQD     376
PHA3      RMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKALIEVFAKGIDADTVVLMAARASRIENQD     410
PHA2      RMTAIEEMAGMDVLCSDKTGTLTLNKLSVDKTLVEVFVKGVDKEYVLLLAARASRVENQD     375
PHA4      RMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLIEVFPKDADKDTVMLLGARASRIENQD     375
PHA5      RMTAIEEMAGMDVLCSDKTGTLTLNKLTVDQTLIEVFPKNADADTVMLLAARASRVENQD     375
          ***:* :** ******* ******  * *:: *:*** :  : : * *:.***.. *:

PHA6      ---------------RRAGIS--LRLRCCPTEKQISHTYSDGKGKKHRVSIGKPEHILNH     415
PHA7      AIDTAIVSMLADPKEARAGITEVHFLPFNPTDKRTALTYLDSAGKMHRVSKGAPEQILNL     438
PHA1      AIDTAIVGMLSDPKEARAGIREIHFLPFNPTDKRTALTYLDGEGKMHRVSKGAPEQILNL     436
PHA3      AIDTAIVGMLADPQEARAGIREIHFLPFNPTDKRTALTYLDGEGKMHRVSKGAPEQILNL     470
PHA2      AIDACMVGMLADPKEARAGIREVHFLPFNPVDKRTALTYIDNNGNWHRASKGAPEQILDL     435
PHA4      AIDTCIVNMLGDPKEARAGIQEVHFLPFNPVEKRTAITYIDDKGNWHRASKGAPEQIIEL     435
PHA5      AIDACIVNMLGDAKLAREGIQEVHFFPFNPVDKRTAITYIDGNGDWHRASKGAPEQIIEL     435
                          * **     :   *.:*: : ** *  *. **.* * **:*::
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PHA6        YAHNKSDIEHRVHSVINMFAEKGLKSMAVAYQEFPSDIEHRVHSAMDIFAEKVLHSIAEQ    475
PHA7        -AWNKSDIKNRVHSVIDKFAERGLRSLA--------------------------------    465
PHA1        -AHNKSDIERRVHAVIDKFAERGLRSLG--------------------------------    463
PHA3        -AHNKSDIERRVHTVIDKFAERGLRSLG--------------------------------    497
PHA2        -CNCKEDVRRKVHSMIDKYAERGLRSLA--------------------------------    462
PHA4        -CELKGDIKKKALEIIDDYANRGLRSLG--------------------------------    462
PHA5        -CGLSGSVLKKSHEIIDNFANRGLRSLG--------------------------------    462
             .  . .: .:   :*: :*::**:*:.

PHA6        ANPSDIEQSVHSVIDMFAEKVLHSITLAFQEIPSDIKHTVRSMIDVFSEKVLHSIAEAYQ    535
PHA7        --------------------------------------------------------VARQ    469
PHA1        --------------------------------------------------------VAYQ    467
PHA3        --------------------------------------------------------VAYQ    501
PHA2        --------------------------------------------------------VARQ    466
PHA4        --------------------------------------------------------LARQ    466
PHA5        --------------------------------------------------------VARQ    466
                                                                     * *

PHA6        EVPHGSKEKSGSPWQLIGLLPFVDPPREDCASSIRELLNHGVNVKMITRDHMVIGKEIGR    595
PHA7        EVPEGTKDSPGGLWEFVGLLPLFDPPRHDSAETIRRALELGVSVKMITGDQLAIGKETGR    529
PHA1        EVPEGRKESSGGPWQFIGLLPLFDPPRHDSAETIRRALNLGVNVKMITGDQLAIGKETGR    527
PHA3        EVPEGRKESAGGPWQFIALLPLFDPPRHDSAETIRRALNLGVNVKMITGDQLAIGKETGR    561
PHA2        EVPEKSKESAGGPWQFVGLLPLFDPPRHDSAETIRRALNLGVNVKMITGDQLAIAKETGR    526
PHA4        TVPEKNKESEGSPWEFVGLLPLFDPPRHDSAETIRKALELGVAVKMITGDQLAIGKETAR    526
PHA5        TVPEKDKESAGSPWEFVGLLPLFDPPRHDSAETIRKALELGVNVKMITGDQLAIGKETGR    526
             **.  *:. *. *:::.***:.****.*.*.:**. *: ** ***** *::.*.** .*

PHA6        RLGMGTNMYPSSALLGHNDKSIAADNDLSIDEIIENADGFVSCALPEQKYEIIKHLQSRK    655
PHA7        RLGMGTNMYPSSFLLGEQKDSSA--AVLPIEELIESADGFAG-VFPEHKYEIVRILQSRK    586
PHA1        RLGMGTNMYPSSALLGQTKDESI--ASLPIDELIEKADGFAG-VFPEHKYEIVKRLQARK    584
PHA3        RLGMGTNMYPSSALLGQTKDESI--AALPIDELIEKADGFAG-VFPEHKYEIVKRLQARK    618
PHA2        RLGMGTNMYPSASLLGQDKDSSI--ASLPVEELIEKADGFAG-VFPEHKYEIVKKLQERK    583
PHA4        RLGMGTNMYPSSALLGEHKDAAI--ASIPVDELIEKADGFAG-VFPEHKYEIVKKLQDMK    583
PHA5        RLGMGTNMYPSSALLGDHKDESI--AQIPVEELIEQADGFAG-VFPEHKYEIVKKLQERK    583
            ***********: ***. ..       : ::*:**.****.. .:**:****:: **  *

PHA6        HVCGMIGGGVDDIPALKKADIRIAPYGVTEAAQNAADIVLMESGLKYLCEAVLTSRSITV    715
PHA7        HICGMTGDGVNDAPALKKADIGIAVADATDAARGASDIVLTEPGLSVIIHAVLTSRAIFQ    646
PHA1        HICGMTGDGVNDAPALKKADIGIAVDDATDAARSASDIVLTEPGLSVIISAVLTSRAIFQ    644
PHA3        HICGMTGDGVNDAPALKKADIGIAVDDATDAARSASDIVLTEPGLSVIISAVLTSRAIFQ    678
PHA2        HIVGMTGDGVNDAPALKKADIGIAVADATDAARGASDIVLTEPGLSVIISAVLTSRAIFQ    643
PHA4        HICGMTGDGVNDAPALKKADIGIAVDDATDAARSASDIVLTEPGLSVIVSAVLTSRAIFQ    643
PHA5        HICGMTGDGVNDAPALKKADIGIAVADATDAARGASDIVLTEPGLGVIISAVLTSRAIFQ    643
            *: ** * **:* ******** **   .*:**: *:**** * **  :  ******:*

PHA6        RMKSCMVHAVSIAIHNVLGFMLLALVWKFDFPPFKMLIIALANCFINVIASQNRVKSSPL    775
PHA7        RMKNYTIYAVSITIRIVLGFMLLTAFWKFNFPPFMVLVIAILNDGTIMTISKDRVKPSPL    706
PHA1        RMKNYTIYAVSITIRIVLGFMLLALIWKFDFPPFMVLIIAILNDGTIMTISKDRVKPSPL    704
PHA3        RMKNYTIYAVSITIRIVLGFMLLALIWKFDFPPFMVLIIAILNDGTIMTISKDRVKPSPL    738
PHA2        RMKNYTIYAVSITIRIVFGFMLIALIWKYDFSAFMVLIIAILNDGTIMTISKDRVKPSPM    703
PHA4        RMKNYTIYAVSITIRVVMGFMLIALIWKFDFSPFMVLIIAILNDGTIMTISKDRVVPSPL    703
PHA5        RMKNYTIYAVSITIRVVMGFMLIALIWEFDFPPFMVLIIAILNDGTIMTISKDRVKPSPL    703
            ***.  ::****:*: *:****:: .*:::*  * :*:**: *    :  *::**  **:

PHA6        PVNWSLSEILTTGIVLGSYLAMSTVIFFWAVYETNFFSLDKT------------------    817
PHA7        PDSWKLSEIFAIGIVLGSYLALMTALFFYLTFETSFFANAFHVTDFNKHIPENKVITDSL    766
PHA1        PDSWKLAEIFTTGVVLGGYLAMMTVIFFWAAYETDFFPRVFGVSTLQRTATD-------D    757
PHA3        PDSWKLAEIFTTGVILGGYLAMMTVIFFWAAYKTNFFPRVFGVSTLEKTATD-------D    791
PHA2        PDSWKLNEIFATGVVLGGYQALMTVLFFWAMHDTKFFSDKFGVKDIRES-----------    752
PHA4        PDSWKLNEIFATGVVLGTYQAIMTVVFFYLAADTDFFTENFHVRSIRNS-----------    752
PHA5        PDSWKLNEIFATGIILGTYQALMTVLFFYLAASTDFFTEKFGVRSIREN-----------    752
            * .*.* **:: *::** * *: *.:**:   .*.**
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PHA6      YMKFVLAVLLQVSSSNYALIFVTRTGKLL----PGCDSLLFIWVSYQLL-------FTML     866
PHA7      NAKLASAVYLQVSTISQALIFVTRSRGWSFMERPGLL-LVVAFIVAQLVATFMSAMVTSV     825
PHA1      FRKLASAIYLQVSTISQALIFVTRSRSWSFVERPGLL-LVVAFLIAQLVATLIA-VYASW     815
PHA3      FRKLASAIYLQVSTISQALIFVTRSRSWSFVERPGLL-LVFAFFVAQLVATLIA-VYANW     849
PHA2      DEEMMSALYLQVSIISQALIFVTRSRSWSFVERPGAL-LMIAFLIAQLVATLIA-VYADW     810
PHA4      PNELTAALYLQVSIISQALIFVTRSRSWSFVERPGLM-LVGAFFAAQLVATVLA-VYADW     810
PHA5      EHGLTAAVYLQVSIISQALIFVTRSRSWSFVERPGFL-LVVAFFLAQFVATLIT-VYANW     810
             :  *: ****  . *******:        **   *:  :.  *::        :

PHA6      AVSGDQSICWSCAGKIWLYNIVFYVPLYCIKFFNQRSRKGFLKSIL*-------------     912
PHA7      KFAGIEKIGWRWTGVIWLFNIITYFLLDPIKFAVRYALSGRAWGLLLNQKTAFTNRKDFG     885
PHA1      SFAAIEGIGWGWAGVIWLYNLVFYFPLDIIKFLIRYALSGRAWDLVLEQRIAFTRKKDFG     875
PHA3      SFAAIEGIGWGWAGVIWLYNIVTYIPLDLIKFLIRYALSGKAWDLVLEQRIAFTRKKDFG     909
PHA2      TFARVKGCGWGWAGVIWIFSIVTYFPLDIMKFAIRYILSGKAWNNLLDNKTAFTTKKDYG     870
PHA4      EFARIKGVGWGWAAVIWVYTIITYLPQDVLKFIIRFGLSGRAWDTMIQNKTAFTTKKDYG     870
PHA5      NFARIHGIGWGWAAIIWVYTIITYLPLDVLKFISRYALSGDAWDSMIQNKTAFTTKKDYG     870
           .:  .   *  :. **::.:: *.    :**  :   .*     :

PHA6      ------------------------------------------------------------     912
PHA7      KEAREAAWAAEQRTIHGLQSVET-KTFPENYTFREISVMAEEAKRRADIARLRELHTLKG     944
PHA1      KEQRELQWAHAQRTLHGLQVPDT-KLFSESTNFNELNQLAEEAKRRAEIARQRELHTLKG     934
PHA3      KELRELQWAHAQRTLHGLQVPDP-KIFSETTNFNELNQLAEEAKRRAEIARLRELHTLKG     968
PHA2      KEEREAQWALAQRTLHGLQPPEASNLFNEKNSYRELSEIAEQAKRRAEMARLRELHTLKG     930
PHA4      RGEREAQWALAQRTLHGLQTPEAAGLFNDK-NYRELSEIAEQAKRRAEVARLRELHTLKG     929
PHA5      KGEREAQWAVDQRTRHGLQTAESNGLFHDK-NYRELNEIAEQAKRRAEVAKYTHE*----     924


PHA6      -----------------------   912
PHA7      KVESFAKLRGLDVDHVNPHYTV*   966
PHA1      HVESVVKLKGLDIETIQQSYTV*   956
PHA3      HVESVVKLKGLDIETIQQSYTV*   990
PHA2      HVESVVKLKGLDIETIQQHYTV*   952
PHA4      HVESVVKLKGLDIETIQQHYTV*   951
PHA5      -----------------------   924
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Fig. S1. Alignment of the protein sequences of the plasma membrane H^+-ATPases identified in *S. tuberosum* Phureja (PHA1: PGSC0003DMP400055772 PHA2: PGSC0003DMP400007331, PHA3: PGSC0003DMP400043938 PHA4: PGSC0003DMP400021001, PHA5: PGSC0003DMP400013900, PHA6: PGSC0003DMP400002571, PHA7: PGSC0003DMP400060260). Sequences were aligned with the Clustal Omega program (http://www.ebi.ac.uk/Tools/msa/clustalo/*).* Identities are indicated by asterisks below the sequence. Conserved substitutions are marked with two vertical dots and semi-conserved substitutions are marked with a single dot. Unaligned residues are shown as dashes within the sequence line. The putative transmembrane domains (identified using the Phobius program, EMBL, version 1.1, http://www.ebi.ac.uk/Tools/pfa/phobius/) are shaded in gray. The 14-3-3 binding site is marked in blue. The conserved sequences common to P-ATPases (TGES, DKTGTLT, GDGVNDA and KGAP) are indicate in red.

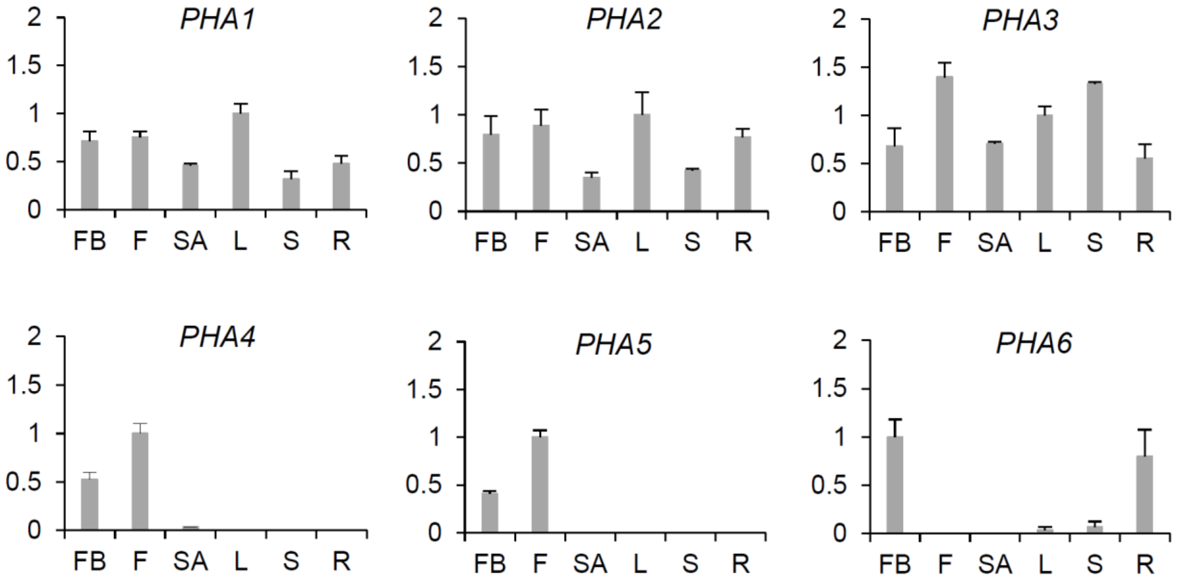

Fig. S2. Quantification of RT-PCR bands of Fig. 2A. Quantitative data of RT-PCR bands (mean ± SEM) of three independent experiments are displayed in the bar graph (arbitrary units). FB: flower bud, F: flower, SA: shoot apex, L: leaf, S: stem, R: root.

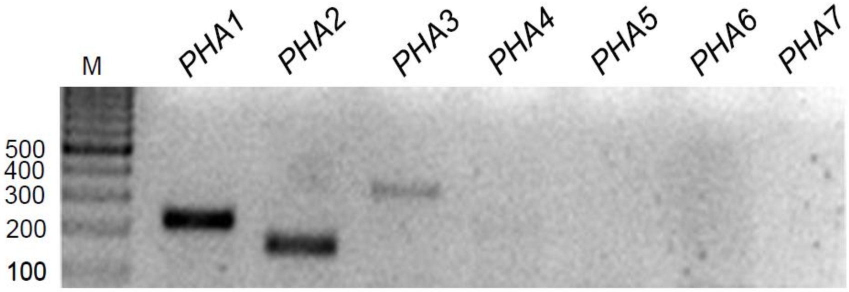

Fig. S3. RT-PCR analysis of PHA genes in stolons cultured *in vitro* under tuber-inducing conditions (MS medium plus 8% sucrose) for 15 days. The expected molecular weight of the amplicons are: 206 base pairs (bp) for PHA1, 141 bp for PHA2, 341 bp for PHA3, 372 bp for PHA4, 357 bp for PHA5, 203 bp for PHA6 and 339 bp for PHA7. M: molecular weight marker (numbers indicate the size of the DNA fragments in bp). A representative analysis of three independent experiments is shown.

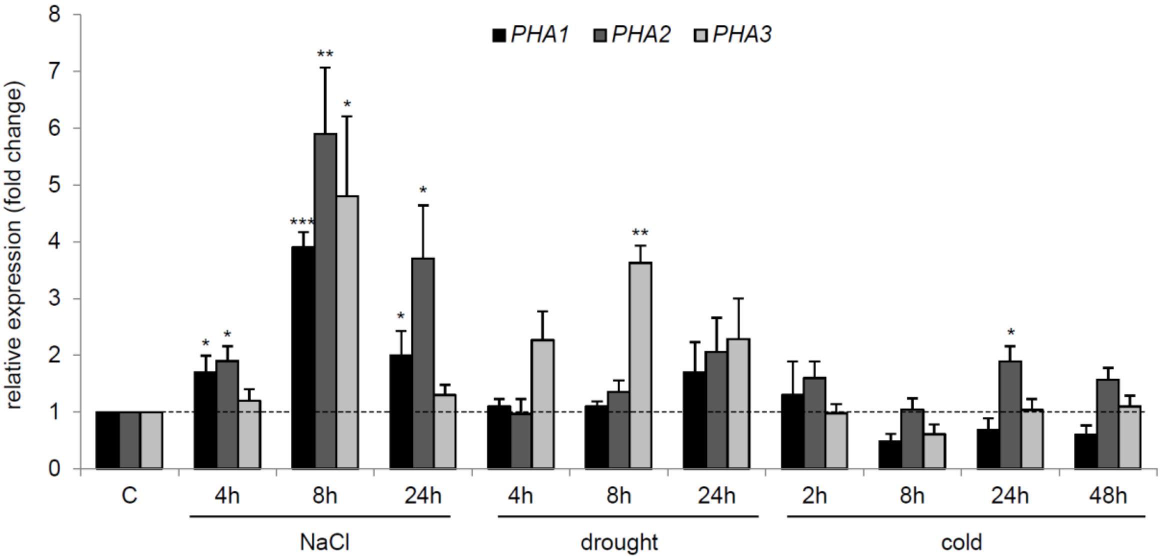

Fig. S4. Expression of PHA genes in response to abiotic stress. Detached leaves from soil-grown potato plants were treated with 250 mM NaCl or deprived of water (drought) for the indicated times. *In vitro*-grown potato plants were exposed to 4°C (cold) for the indicated times, while control plants remained at 22ºC. Total RNA was isolated from leaves and quantitative PCR was performed to determine the expression of PHA genes. Data are presented as expression level relative to the respective controls (C). Quantitative data (mean ± SEM) of three independent experiments, each consisting of four technical replicates, are displayed in the bar graph. The asterisks indicate statistical significance (*p<0.05, **p<0.01, ***p<0.005, with respect to controls).

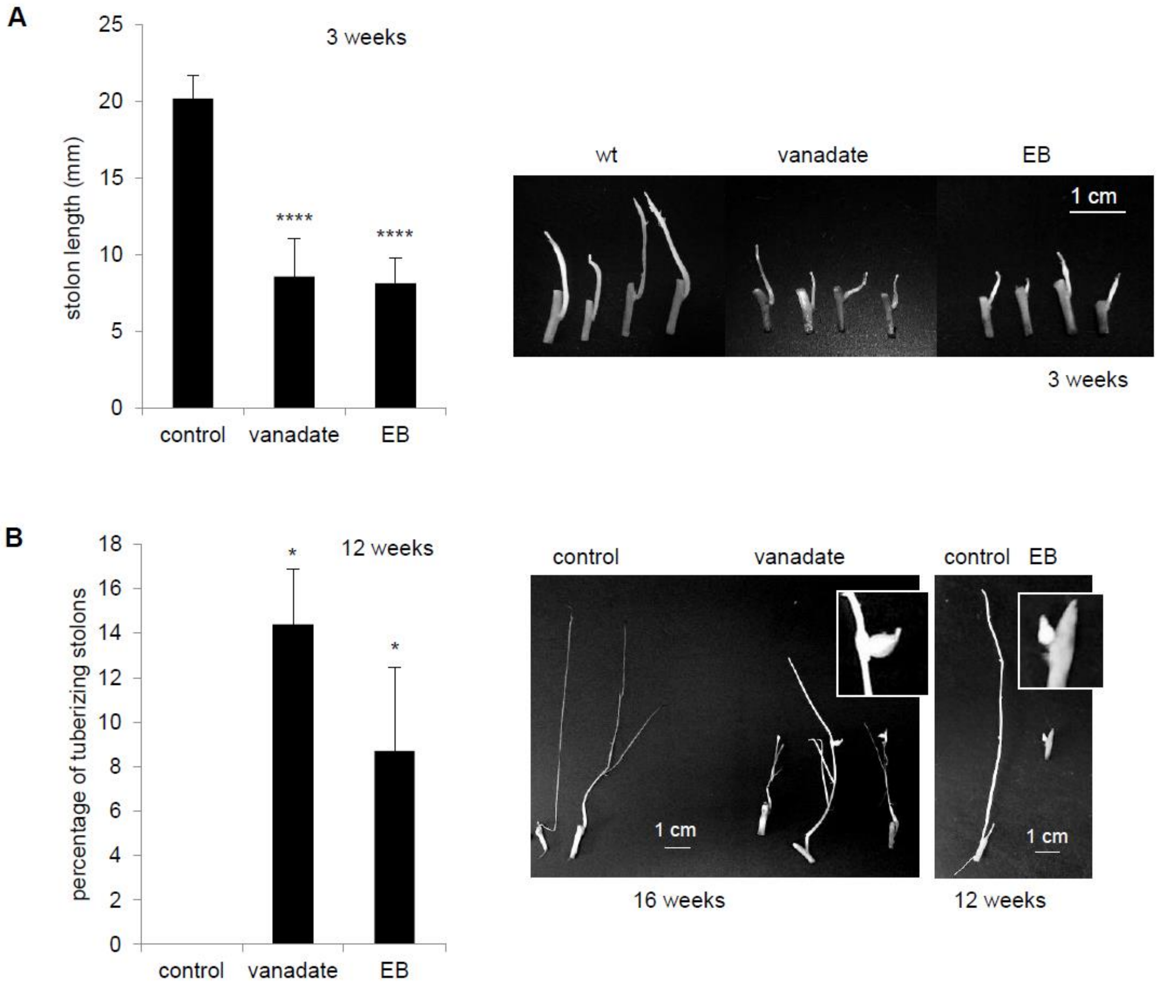

Fig. S5. Effect of vanadate and erythrosine B on stolons cultured under non-inducing conditions. Stolons were cultured under non-inducing conditions (MS medium plus 2% sucrose) in the absence (control) or presence of 1 mM vanadate or 50 μM erythrosine B (EB). (A) Stolon length, determined after 3 weeks of culture in the absence or presence of inhibitors; a representative image is shown. (B) The percentage of tuberizing stolons was determined after 12 weeks of culture in the absence or presence of inhibitors; a representative image is shown. Quantitative data of three independent experiments (mean ± SEM) are displayed in the bar graphs. The asterisks indicate statistical significance (*p<0.05, ****p<0.001, with respect to control). In these experiments performed under non-inducing conditions, the process was studied for 12-16 weeks, since tuber formation is significantly delayed with respect to tuber-inducing conditions.

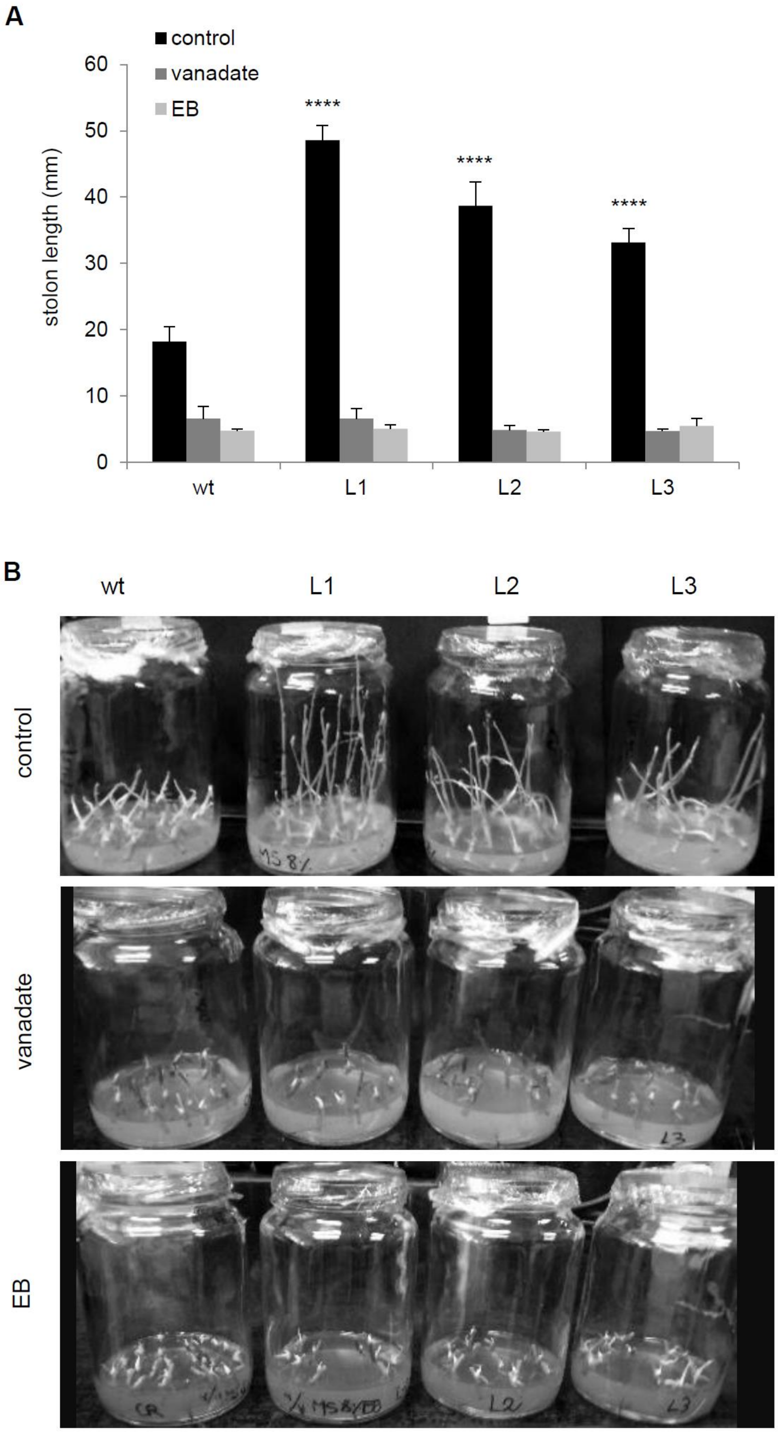

Fig. S6. Stolon length of PHA1-OE cultured in the presence of PM H^+-ATPase inhibitors. Stolons were cultured under tuber-inducing conditions (MS medium plus 8 % sucrose) for two weeks, in the absence or presence of 1 mM vanadate or 50 μM erythrosine B (EB). (A) Stolon length; data of three independent experiments (mean ± SEM; ****$p<0.001$, with respect to wt). (B) Representative image of stolons.

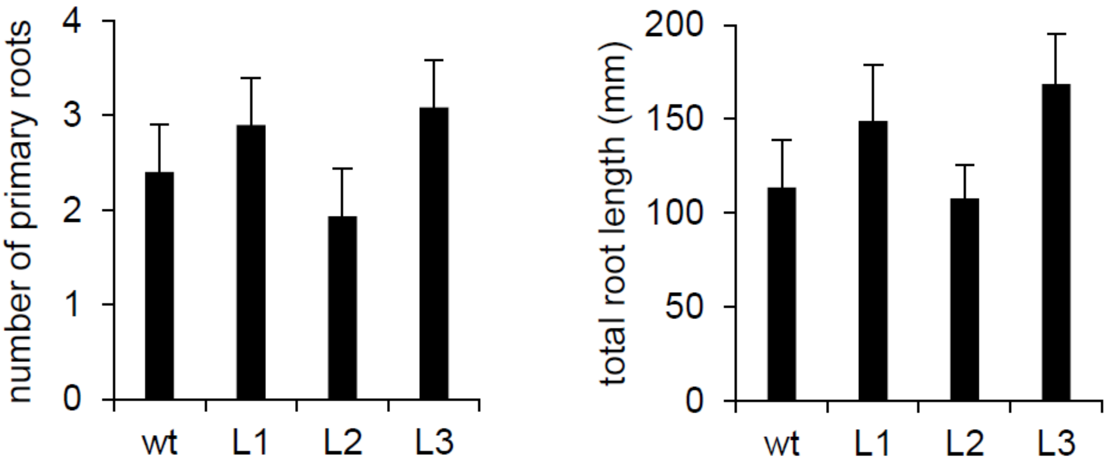

Fig. S7. Phenotypic analysis of PHA1-OE plants grown *in vitro*. Wild type (wt) and transgenic (L) plants generated from single-node cuttings were grown on MS medium plus 2% sucrose. After 2 weeks, the number of primary roots and total root length (calculated as the sum of the primary root lengths) were determined. Quantitative data of four independent experiments (mean ± SEM) are displayed in the bar graphs. No significant differences were detected between wt and transgenic lines (evaluated by Student's t test).

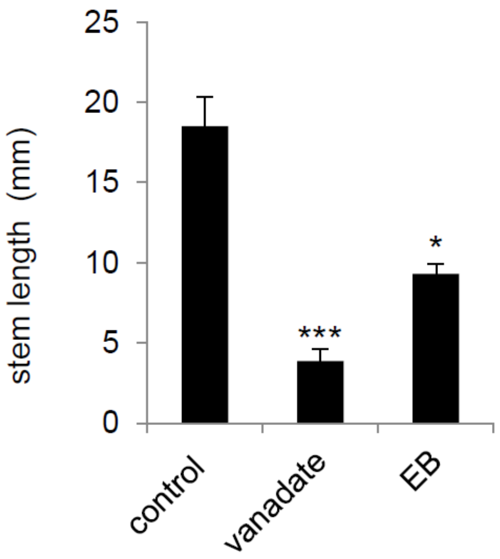

Fig. S8. Stem length of wild type plants generated from single-node cuttings, grown on MS medium plus 2 % sucrose in the absence (control) or presence of of 1 mM vanadate or 50 µM erythrosine B (EB). Quantitative data of three independent experiments (mean ± SEM) are displayed in the bar graph. The asterisks indicate statistical significance (*p<0.05, ***p<0.005, with respect to control).

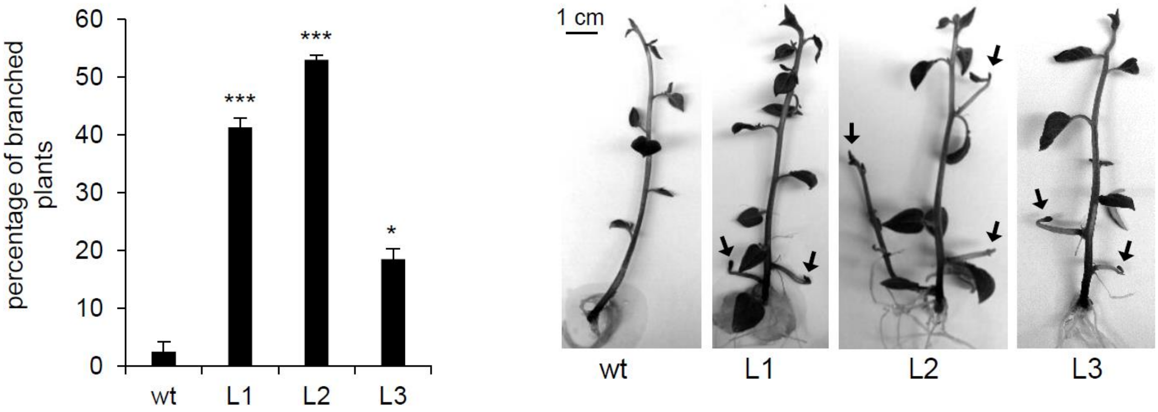

Fig. S9. Branching of PHA1-OE plants. Wild type (wt) and transgenic lines (L) generated from shoot apexes were grown on MS medium plus 2% sucrose for 3 weeks. The percentage of branched plants was determined as the number of plants presenting at least one branch equal or longer than 5 mm, with respect to the total number of plants (10-15 plants). A representative image of the plants is shown; arrows indicate branches. Quantitative data of three independent experiments (mean ± SEM) are displayed in the bar graph. The asterisks indicate statistical significance (*p<0.05, ***p<0.005, with respect to wt).