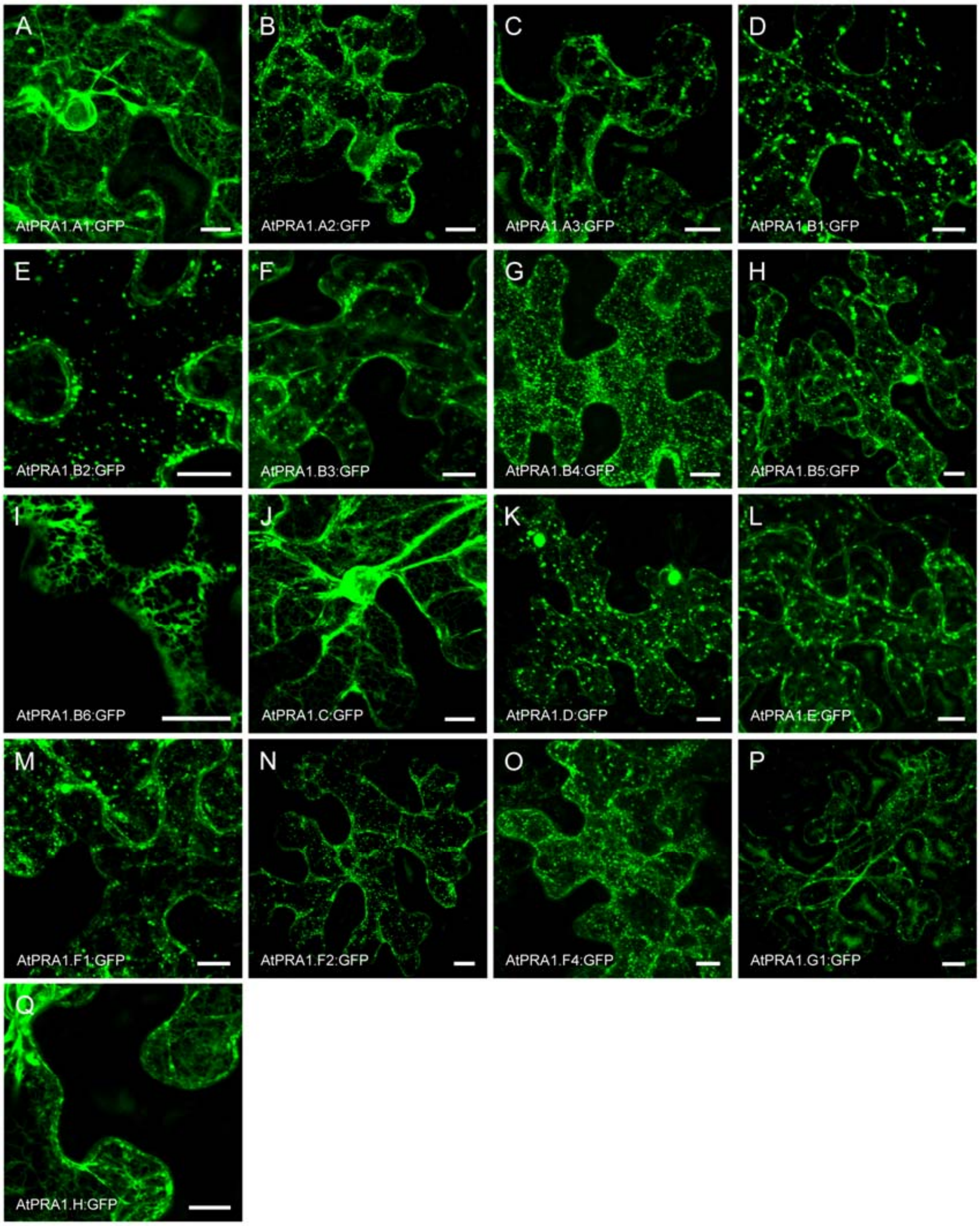

Figure S1. Subcellular distribution of AtPRA1 proteins in tobacco leaf epidermal cells. A, AtPRA1.A1; B, AtPRA1.A2; C, AtPRA1.A3; D, AtPRA1.B1; E, AtPRA1.B2; F, AtPRA1.B3; G, AtPRA1.B4; H, AtPRA1.B5; I, AtPRA1.B6; J, AtPRA1.C; K, AtPRA1.D; L, AtPRA1.E, M, AtPRA1.F1; N, AtPRA1.F2; O, AtPRA1.F4; P, AtPRA1.G1; Q, AtPRA1.H. Most AtPRA1 proteins were found as vesicular organelles, often associated with a light network of ER strands. Four AtPRA1 proteins (AtPRA1.A1, AtPRA1.B6, AtPRA1.C, AtPRA1.H) showed a unique localization specific to the ER compartment. The proteins AtPRA1.F3 and AtPRA1.G2, showed expression indicative of ER localization, but no strong detectable GFP cells were found to be imaged (data not shown). Scale bar = 10 µm.

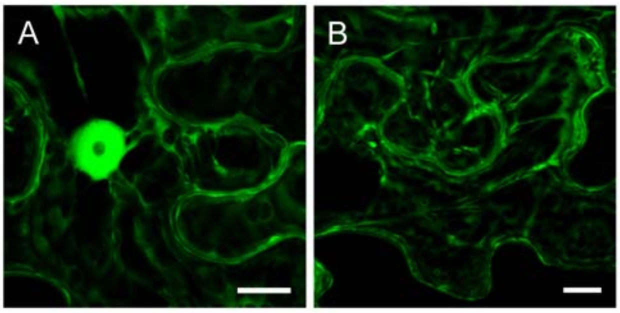

Figure S2. Subcellular distribution of free GFP protein in tobacco epidermal cells. A, Median section with nucleus; B, Cortical section. The expression of the GFP gene driven by the CaMV 35S promoter led to the fluorescent protein accumulation in the nucleus and the cytoplasm, denoted by thick transvacuolar strands. Scale bar = 10 µm.

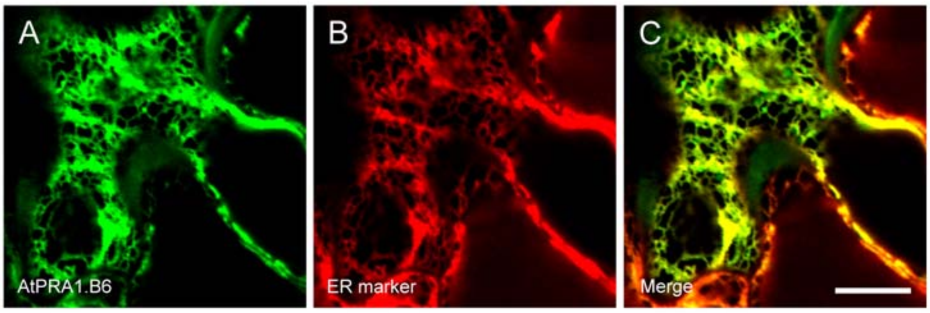

Figure S3. Subcellular distribution of AtPRA1.B6 over the ER in tobacco leaf epidermal cells. Out of the four ER-specific AtPRA1, AtPRA1.B6 was chosen as representative. The adopted ER marker corresponds to a chimeric fusion of the signal peptide AtWAK2 and the HDEL retention signal to the fluorescent marker gene. A, AtPRA1.B6; B, ER-marker; C, Merge. Scale bars = 10 µm.

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dme2861       100 AGALLG-GYLLLHLLSAVLLTIFTVLLPISLTFIHASLRLRNNKLTNSAPSTPMGSLLDAL 159
hsa32764      92  LAAVLAVGLLVLWVAGGACTFLFSIAGPVLLILVHASLRLRNNKIENKKRTPM-GLLLEAL 151
mmu28592      92  LAAVLAISLFILWAVGGAFTFLLSITAPVFLILLHASLRLRNNKIENKKRTPM-GLLLEAL 151
dre22987      95  LAAILGSSYLFLSVLGGVAVFLVGIAFPILMILVHASVRLRSNKLENKKRTPM-GLVLEAL 154
tni2594       98  LSIL--FTGYLFMSVLGGVVFLFGVAFPILMVLVHASLRLRSNKMENKKRTPM-GLLLEAL 155
cin1427       94  VAGIVGVSTVAMYMLGSIAAFVFSIALPMLLILLHASFRMRNNKVQNKKRTPM-GVIMRAL 153
tni26839      98  VLLVLVASYILLSLLGSVMVFMSAITFPLVCVFAHASFRLRNNKLENKKRSPM-GILLEAL 157
tni25068      96  VIGVMVTSYFLLSLCGGVMVFIFGITFPLLLILIHASLRLRNNRLENKKRTPM-GVIMDLL 155
dre14921      92  VVAVMGISYFLLSLCGGVMVFLFGITFPMLLILIHASLRLRSNKLENKKKTPM-GVILDLL 151
hsa22741      94  VMVVMLASYFLISMFGGVMVFVFGITFPLLLMFIHASLRLRNNKLENKKRTPM-GIVLDAL 153
mmu22402      94  VMVVMLASYFLISMFGGVMVFVFGITLPLLLMFIHASLRLRNNKLENKKKTPM-GIILDAL 153
rno21900      94  VMVVMLASYFLISMFGGVMVFVFGITFPLLLMFIHASLRLRNNKLENKKKTPM-GIILDAL 153
cme1623       100 GGLLTL----MLFLTDVVALALTSASLAAAVTLAHAALHDPVAVLSARNAEYTVAP----- 151
cme3337       99  VVLV--FSLVILWLTGAGATFSTLLFVVATIAIAHAAIRKPPADFESG--------IPGA- 148
Pt_594536     97  LGLIAVATMIELIATEAGLHLVITSAATVPIVLIHAVLWVRDDFCVEEGGGGD-GELVPLV 156
Pt_827148     97  LGLIAVATMIELIATKAGLHLVITSAATVPIVLIHAVLWVREDFCVEEGGGGG-GELVPLV 156
AT5G56230.    100 LLFLVLASVWAIWFTNSAVNLAVGVSVGLLLCIIHAVFRNSDELFLEEDAING-GLIGSNL 159
AT1G55640.    100 FGLI-LGSLWALWFINSLQCLILGVVTSVLLCLVHAIIRNSDDLFVQEKDVVV-PSNFLHW 158
Pt_550673     100 LIGLVLVSVLGVWLSGAAWNLVWGVLIGFLVCAIHAVLRNSDGLLVPGEEAAFVGSVSGSY 160
AT4G29658.    100 LVLL-VLTIGIFLLTDVSRGIVIGVLAGLPVVLVHGMCRRTEMLFVLEDDEEK-VAMNTSS 158
Op11g00150    100 MGMSALSAFVIFMLTSAGTVLFSGLGVALLGVGAHAAARVPDDLFVEDANDNK-GF-FSFL 158
Ot11g00120    100 MGMTALSAFVIFMLTSAGTVLFSGMGVALLGIGAHAAARVPDDLFVEDAESNK-GF-FSFL 158
AT1G04260.    100 AVLLIGLSIGSLVTTGVWLRALTTVGFGVLVLILHAALRGTDDLVSDDLESPY-GPMLSTS 159
Pt_230928     100 LVVLFVVDFLVVIWGGVFQNVVVGGIAVVLMLLHAALRSTDDLVADDETSPYANLLSDDD 160
AT1G08770.    100 LVLLSLVTVLALVYTDVGENVLVSLIIGLLIVGAHGAFRNTDDLFLDESARRG-GLVSAGS 159
AT1G17700.    100 LIIMSVITLSILFLTDAKLNIAVAIVAGALAVLSHAAVRKTEDLFQTDEETSLLNP----- 155
Pt_595411     100 LCVLGLVTILALVFTHVGLNVLIALIIGVVIVGVHAAFRGTEDLFLDEESAVE-GGLLSVV 159
Pt_651854     100 LGLLSIVTIIALIFTHVWLNVLVSVLIGAAVVVLHAAFRGTENLYLDEHDLAD-EGLFSVV 159
Pt_551089     100 LGLLGVATIVALIFTHVWLNVLVSLLIGAAIVVLHAAFRRTDDMYSDDQDVAD-GSLLSFV 159
Pt_754227     93  LGLLGVATIVALIFTHVWLNVLVSLLIGAAIVLLHAAFRRTDDLYLDEMASPSRDPVPPEF 153
Os67_00962    100 LAALAAVTLVLLLLTGATANIVSSLLIGVLLVVLHAALHKENDEFNVD------TISFTLL 154
Os82_01045    100 LAVLSVLTLVLLLLTGATVNILTSLLVGVVIVLLHAVFHRPADSIDEEGRYYT-PVPPQPS 159
Pt_288981     100 MIVLGVLTIFFLLLTHVTWNVLVSLLVGVVLVLIHGVTRK--DLSLDE------------- 145
AT1G55190.    100 LIGLSVLTVVMLLLTHATSNILGSLLTAAVLVLIHAAVRRSDNLFLDEEAAAVTEALMSYP 160
AT3G13710.    100 LIGLSVITIVLLLLTNATFNIVAALMAGAVLVLIHAVIRKTDDLFLDEEAATT-ETLTSHP 159
AT3G13720.    100 LIVLSVLTVVLLLLTNATFNIVGALVTGAVLVLIHSVVRKTEDLFLDEEAATT-ETLTSYP 159
Cr_171434     100 IGMSAISFITIFFLTSVGTVFFSALSISIALIALHGAFREPDNLFIDEGETQQ-GFMNIFA 159
Os69_05922    100 LAALSVATVLAVALSRAGLNLLVSLVLAAAAIGAHAAFRM--NVYLDERDAYD-GSMGSSY 157
Os69_05367    100 LAALTGVTVIALLFTNVGWNVIGSVMIGAALVAAHATLRSTDDLFLTEQEAAGDGLVAAGM 160
Pp_216234     100 LLGMSLFTVALVFMTNVGSTLISALAIGAAICFLHGAFRVPDDLFLDEQETTG-GFFLSSG 159
Pp_109789     100 FLGMSVFTVIMVFMTNVGSILISALIIGAAICFAHGAYRVPDDLFLDEQEASG-GFFLSSG 159
Pp_119721     100 LLGMSLFTIIMIFMTSVGSILITALLIGGAICSAHGAYRVPDDLFLDEQETTG-GFFLTSG 159
Pp_196148     100 LLGMSVFTIIMIFMTSVGSILISALLIGGAICFAHGAYRVPDDLFLDEQESAG-GFFLSSG 159
AT5G07110.    100 LGILCLSTVVVMFMTSVGSLLMSTLAVGIMGVAIHGAFRAPEDLFLEEQEAIGSGLFAFFN 160
Pt_809747     100 LGILVLVTVIVVFLTSVGSLIITAVLVGVGIVCVHGAFRDPEDLFMDDQDTAGSTGLFSFI 160
Os86_00075    100 LGGLIVASAFVIFLTSVGSLIFSALALGAAIVCAHGAFRIPEDLFLDEDQANGAASLLSFI 160
Os11687_00    100 LGGLIVASAFVVFLTSVGSLIFSALALGAAIVCAHGAFRIPEDLFLDEDQANGAASLLSFI 160
Os67_06093    98  LLGLVVASVLAFFMTSVASLIISGLLVGGAIVAVHGAFRVPEDLFLDDNTTSR---LLSFL 155
Os82_03767    100 LGLV-VASFVAFFFTSVASLIISGLLVGGAIVAVHGACRMPEDLFLDDNSAAQ-GLL-SFL 157
AT5G01640.    100 LGGLILSTIAVIFFTSVGSVLISALMIGIATICVHGAFRAPDDLFLDEQDHAASGFFIGVP 160
Pt_724377     100 LGILVVSTIVVIFLTSVGSLLISASMVGFALVCAHGAFRVPEDLFLDDQEPASAG-LLSFL 159
Pt_832605     100 LGILVVLTIVVIFLTSVGSLLISALMVGFALVCAHGAFRVPDDLFLDDQEPASAGF-LSFL 159
AT5G05380.    100 LGVLVILTIVVVFLTSVGSLLTSALMIGFGIVCLHGAFRVPEDLFLDDQEPANTGLFLSGA 160
AT2G40380.    100 LLGLVLTTIVVVFMTSVGSLLTSALTIGIAIVCLHGAFRVPDDLFLDEQEPANAGLFIGNS 160
AT3G56110.    100 LLALVLSTIVVVFMTSVGSLLTSALMIGVAIVCVHGAFVVPDDLFLDEQEPANAG-LLSFL 159
AT2G38360.    100 LGCLILFSIFVIFLTDVGSVLVSAMMIGVALICAHGAFRAPEDLFLDEQEPAATGFFLGGA 160
Pt_560953     100 LGILIALSVFVVFLTSVGSVIISALLVGVGIVCAHGAFRVPEDLFLDDPENANTGFLSSFL 160
Pt_577062     100 LGILIVLSVFVVFLTNVGSVIISALLVGVGIVCAHGAFRVPEDLFLDDQENASTGFLSSFL 160
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Figure S4. Sequence alignments of PRA1 proteins. The program hmmsearch from the HMMER package together with the PRA1 PFAM domain (PF03208) was used to identify putative *PRA1* genes, as well as BLASTP searches with known *PRA1* genes. The PRA1 domain is marked by asterisks above the alignment. Predicted protein annotations were kept as retrieved from different used databases. Protein sequences were aligned with T-Coffee and manually edited with BioEdit. Conserved and identical amino acids are marked in grey and black, respectively.