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PP2CA  MAGICCGVGETEPAAP-----VDST--S----RASLR-----RRLD-----LLPSIKIVADSAVAP 46
ABI1    MEEVSPAIGPFRPFS-----ETQ--M---DFTGIRLG---KGYCNN-----QYSNQDSENGD--LMVSLPETSSCSVSG 60
ABI2    MDEVSPAIVPFRPFT-----DP-----HAGLR-----GYCN-----GE--SRVTLPE--SSCSGDG 43
HAB1    MEEMTPAVAMTSLAANTMCES---SPVETIQKKNVTDAAADLLSDSENQSFCCNGGTECTMEDVSELEEVEQDLLKTLSDTRSGSSNV 85
HAB2    MEEISPAVALTLGLAN-TMCDSGISSTFDISELENVTDAADMLCNQKRQRYNSGVVDCIMGSVSEKTLSE---VRLSSDSFVTVQE 84

PP2CA  PLEN-----CRKQKRETVVLS---TLPGNLDDSNVRSENKAR-----SAVTNSNSVT 93
ABI1    SHGSESR-----KVLII-----SRINSPNLNMKES---AAADIVVVDISAGDEINGSD-----I---TSEKKMISRT 115
ABI2    AMKDSS-----FEINTRQDSLTS---SSA-MAGVDISAGDEINGSDEFDP---RSMN---QSEKKVLSRT 99
HAB1    FDEDDVLSVVEDNSAVISEGLLVVDAGSELSLNTAMEIDNGRVLATAIIVGESSIEQVPTAEVLIAGVNDTN---TSEVVIRLPD 169
HAB2    SEEDEPL---VSDATIISEGLIVVDARSEISLPDT-VETDNGRVLATAIILNETTIEQVPTAEVLIASLNHDVNMVEVATSEVVIRLPE 168

PP2CA  E-----AESFFS--DVPKIGTTSVCGRRRDMEDAVSIHPSFLQRNS---E-----NHHFYGVFCHGGCSHVAEKCRER 156
ABI1    E-----SRSLFEFKSVPLYGFTSICGRPEMEDAVSTI PRFLQSSSGSMLDGR----FDPSAAHFFGVYCHGGGSQVANYCRER 191
ABI2    E-----SRSLFEFKCVPLYGFTSICGRPEMEDSVSTI PRFLQVSSSSLLDGRV-TNGFNPHLSAHFFGVYCHGGGSQVANYCRER 179
HAB1    ENSNHLVKGRSVYELDCIPLWGTVSIQGNRSEMEDAFAVSPHFLKLPKMLMGDHEGMSPSLTHLTGHFFGVYCHGGGHKVADYCRDR 257
HAB2    ENPNVARGSRSVYELECIPLWGTISICGGRSEMEDAVRALPHFLKLPKMLMGDHEGMSPSLPYLTHFFGVYCHGGGAQVADYCHDR 256

PP2CA  LHDIVKKEVEVMASDEWTETMVKSFOKMDKEVSQRECNLVNGATRSMKN-----SCRCELQSPCCDAVGSTAVVSVVTPEKIIIVSN 238
ABI1    MHLALAEELAKEK-PMLCD---GDTWLEKWKKALFNSFLRVDSIESVA-----PETVGSTSVVAVVFPSHIFVAN 258
ABI2    MHLALTEEIVKEK-PEFCD---GDTWQEKWKKALFNSFMRVDSIEITVAH-----APETVGSTSVVAVVFPTHIFVAN 248
HAB1    LHFALAEELIERIK-DELCKRNTGEGRQVQWQDKVFTSCLTVDGEIEGKIGRAVVGSSD-KVLEAVASETVGSTAVVALVCSSHIVVSN 343
HAB2    IHSALAEELIERIK-EELCRRNTGEGRQVQWEKVFVDCYLKVDDEVKGINRPVVGSSDRMVLEAVSPETVGSTAVVALVCSSHIIVSN 343

PP2CA  CGDSRAVLCRNGVAIPLSVDHKPDRPDELIRIQAGGRVTYWDGARVLGVLAMSRAGDNYLKPYVTPDPEVTVTDRTDEDECLILAS 326
ABI1    CGDSRAVLCRGKTALPLSVDHKPDREDEAARIEAAGGKVIQWNGARVFGVLAMSRSIGDRYLKPSIIPDPEVTVAVKRVKEDDCLILAS 346
ABI2    CGDSRAVLCRGKTPALASVDHKPDRDDEAARIEAAGGKVIQWNGARVFGVLAMSRSIGDRYLKPSVIIPDPEVTVSVRRVKEDDCLILAS 336
HAB1    CGDSRAVLFRGKEAMPLSVDHKPDREDEYARIENAGGKVIQWQGARVFGVLAMSRSIGDRYLKPYVPEPEVTFMPRAREDECLILAS 431
HAB2    CGDSRAVLLRGKDSMPLSVDHKPDREDEYARIEKAGGKVIQWQGARVSGVLAMSRSIGDQYLEPFVTPDPEVTFMPRAREDECLILAS 431

PP2CA  RGLWVVPNETACGVAR----MCLRGAGAG-----DDSDAAHNACSDAALLTKLALARQSSINVSVVVDLKRNRNQASS 399
ABI1    RGVWVMTDEEACEMARKRILLWHKKNVAGDASLLADERRKEGKDPAAMSAAEYLSKLAIQRGSKNISVVVVDLKRKFKSKPLN 434
ABI2    RGLWVMTNEEVCDLARKRILLWHKKNAMAGEA-LLPAEKRGEGKDPAAMSAAEYLSKMLAQGSKNISVVVVDLKGIRKFKSKSLN 423
HAB1    RGLWVVMNQEVCEIARRRILMWHKKNAGP-----PLAERGGIDPNCQAAADYLSMLALQGSKNISIIVIDLKAQRKFKTRT 511
HAB2    RGLWVMSNQEACDFARRRILAWHKKNGAL-----PLAERGVGEDQACQAAAEYLSKLAIQGSKNISIIVIDLKAQRKFKTRT 511

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Supplementary information Figure S1 Sequence comparison of five Clade A PP2Cs from *Arabidopsis thaliana*. Invariant residues are shaded yellow. The active residues that coordinate the catalytic cations are shaded red. The PP2CA-unique motif that constitutes a new interface with PYL13 is shaded orange with the key residues highlighted by red circles above. The sequences were aligned with ClustalW.