

Table 1 Suppl. HHP protein sequences from some different crops.

Name	GenBank accession No.	Protein sequence
AtHHP1	AT5G20270	MDQNGHNDEAETVSCGNGNCKSKIVPGDDHGGDESSGTKRRKKRKTQQKTMKRRELM SYCELPEYMKDNEYILNYYRADWSIRD AFFSVFSFHNESLNVWTHLIGFIFFVALTVANII HHDGFFPVDAKSPGNVTRWPFFVFLGGSMFCLLASSICHLFCCHSKELNVFLLRIDYAGIT AMIITSFFPPIFYIFQCTPRWYFIYLAGITSMGIFTIITLFTPSLSAPKYRAFRALLFASMGLFG IVPAAHALVVNWGNPQRNVTLVYELLMVVFYLVGTGFYVGRVPERLKPWFDRVGHSH QIFHV FVLLGALSHYAAALLFLDWRDHVGC
AtHHP2	AT4G30850	MQKRRTVKESTKIRNGKGMDSGEKKRSEKRLMKFEELPRYLKDNEFIHNHYRCEWSIKE TFLSAFSWHNETLNIWTHLCGFAIFTWMMVVSMMETTELGLAGFVSLLSGATIRWPWPS MAMSKDVYFSSDQTLHHDNLNVTHTRSLLNSQGDVNYEAIKPWPWLFLTGMGCLICSS MSHLFACHSRRFNLFFWRLDYAGISLMIVCSFFAPIYYAFSCHTYWRLFYLLSSISILGLLAIF TLLSPSLSAPRFRSFRAALFLTMGFSGVIPATHVLYLHKDHPNVLIALVYELAMAVLYAT GAAFYVTRIPERWKP GAFDIAGHSHQIFHV FVVLGALAHSVASLLIMDFRRASPSCAF
AtHHP3	AT2G24150	MKRRRSAKKSPAMVTVTDWKGLDCGEETRIVRRLMKFEDLPEYLKDNEFIHNHYRCQW SLKDTFLSAFSWHNETLNIWTHLIGFGIFLWMTVVSCLLETTEISLAGVFNGMAGVRICLSS NQTLHDSNVTHHISCLTSQGEAIPKPWPVLVYLVGAMGCLICSSVSHLLACHSKRFNVFF WRLDYAGISLMIVASFFAPIYYAFSCHPNFRLLYLSSISILGLLAITLSPALSTPRFRPFRA NLFLAMGSSAVIPATHVLCLYWDHPNVFIALGYEIATALS YFVGATFYVSRVPERWKPGA FDMAGHSHQIFHV FVVMGALAHCVTTLLIIDFSRASPSCGF
AtHHP4	AT4G37680	MGDEAEIKEHLKPQASSETMDKKHN VKGKRLWQKVYQLVEFHSLPAYLRDNEYIIGH YRSEWPIKQILLSIFTIHNETLNVWTHLIGFFLFLALTIYTATKVPSVVDLHSLQHRLPDLLR KTDLHKLHSELMARLPSSPSSWHVMDLLYNCLPERFSHGNYTDMCVLH SVREDLANLIA PLIFRPITRWPFYAFLGGAMFCLLASSTCHLLSCHSERVSYIMLRLDYAGIAALIATSFYPP VYYSFMCDPFFCNLYLGFITILGIATVLVSLLPVFQSPEFRVVRASLFFGMGFSGLAPILHK LIIFWDQPEALHTTG YEILMGLLYGLGALVYATRIPERWMPGKFDIAGHSHQLFHV LVVA GAFTHYRAGLVYLKWRDIEGC
AtHHP5	AT4G38320	MGDEAEIKEHLKPQASSETIDKKHN VKGKRLWQKVYQLVEFHSLPAYLRDNEYIIGHY RSEWPIKQILLSIFTIHNETLNVWTHLIGFFLFLALTIYTATKVPSVVDLHSLQHRLPDLLRK TDLHKLHSELMSRLPSSPSSWHVMDLLYNCLPERFSHGNYTDMCVLH SVREDLANLIAPL IFRPITRWPFYAFLGGAIFCLLASSTCHLLSCHSERVSYIMLRLDYAGIAALIATSFYPPVYY SFMCDPFFCNLYLGFITILGIATVLVSLLPVFQSLEFRVVRASLFFGMGFSGLAPILHKL IIF WDQPEALHMTG YEILMGLLYGLGAVVYATRIPERWMPGKFDIAGHSHQLFHV LVVAGA LTHYRAGL
BcHHP1	CabbageG_a_f_g01 2615	MDQDGPNYEPETVPCSNSSCKSKIVPGDGSSGPKKIKSQKTRKRRELM SYSELPEYMKDN EYILNYYRAEWSIRD AFFSVFSFHNESLNVWTHLLGFILFVGLTVANIMHHDKFFPVDAKS PGNVTRWPFFVFLGGSMFCLLSSSICHLFCCHSKDLNVFLLRIDYAGITAMIITSFFPPIYYIF QCTPRWYFIYLAGITSMGIFTIITLFTPSLS SPKYRGFRALLFASMGLFGIVPAVHAI VNVW ENPQRNVTLMYELGMAVFYLVGTGFYVGRVPERLKPWFDRVGHSHQIFHV FVVMLGAL SHYAAALLFLDWRDHVGC

BcHHP2	CabbageG_a_f_g00 0841	MQKRRPVRESSKTTPERNGKALDSGEKKKRSERRLMKFGELPRYLKDNEYIHNHYRCEW SLKETFLSAFSWHNETLNIWTHLGGFLIFGWMMVVSCEMETTEVGLAGFVNVFSGVTIRW PWPSMAKAVYFSSDHDSNVTHHTSFLNPQGEVNYETIPKWPWLVLFTGAMTCLICSSM SHLFACHSRRFNLFFWRLDYAGISLMIVCSFFAPIYYAFSCHTNWRLFYLSSISILGLLAIFA LLSPALSAPRFRSFRAALFLTMGFSGVIPASHVLYLHKDHPNVVIALVYELAMAVLYATG AGFYVSRIPERWKPGAFDIAGHSHQIFHVFFVLGALAHSVASLLIMDFRRASPCAF
BcHHP3	CabbageG_a_f_g04 7327	MKRRRAARKSSAMVAVSDSKGLDSRMGRRLMRFEELPGYLQDNEFIHDHYRCQWSLKD TFLSAFSWHNETLNIWTHLIGFVIFMWMVVSLETTELSIAGLFNGISGAWIRLSSNQTL LRHDSNVTERIPLTSQEVNHHNYQEAVPKWPWLVYLAGAMGCLICSSVSHLLACHSKR YNLFFWRLDYAGISLMIVSSFFAPIYYAFSCHPNFRFLYLSSISILGLLAIITLLAPALSAPRF RPFRAYLFLAMGFCSVVPASHVLFYWGHPNVLFALACELATGLSYAVGAVFYVSRVPE RWKPGAFDIAGHSHQIFHVFFVLGALVHCVATLVIVDFRRASPCGV
BcHHP4	CabbageG_a_f_g00 0168	MGGEAEIKQQLQPKSLPAETIEKKQHNVKRRRLWQKVYQLVEYHALPAYLRDNEYIIG HYRSEWPIKQILLSIFTIHNETLNVWTHLIGFFLFLSLTIYTATKVPSSVDLHSLQDRPLDIL RKTDLHKLHSDLMShLPSSPKWHVMELLYNCLPERFSHGNYTDMCVLHVKEDLANM IAPLIFRPITRWPFYAFLLGGAMFCLLASSTCHLLSCHSERVSIMLRDLDYAGIAALIATSFYP PVYYSFMCDPFFCNLYLGFITTLGIATVLVSLIPVFQTPEFRVVRASLFFGMGFSGAAPILH KLIIFWDQPEALHTTCYEILMGLLYGLGALVYVTRIPERWMPGKFDIAGHSHQLFHVLVV AGAFTHYRAGLLYLKWRDIEGC
BcHHP5	CabbageG_a_f_g05 0850	MQKRRAVRDSSKITPRNGKTSDSGEKKRCERRLMKFEELPKYLKDNEFIHNHYRCEWSL KETFLSAFSWHNETLNIWTHLGGFLIFGWMMVVSCEMETTEVGLTSFVRLFSGKTIRWPWP SMAISKDVFFSSYQTLYHDSNVTHHTSFLNHQGEVNHETVPKWPWLLFLSGAMACLMC SSLSHLFACHSRKFNLFFWRLDYAGISLMIVSSFFAPLYYAFSCHPYWRLFYLSSISILGLL AIFTLLSPALSAPRFRPFRAALFLTMGFSGIVPVSHLVYLHKDHPNVVIALVYELAMAVLY ATGAGFYVSRIPERWKPGAFDVAGHSHQIFHVFFVLGALAHSVASLLIMDFRRASPCAF
BoHHP1	Bol034597	MDHDGSNDEPETVSCGNSSCKSKIVPGNGSSGPKKRKSQKTRKRRELMSSYSELPEYMKD NEYILNYYRAEWSIRDAFFSVFSFHNESLNVWTHLLGFILFVGLTVANIMHHDKFFPVDA KSPGNVTRWPFVFLGGSMFCLLSSSICHLFCCHSKELNVFLLRIDYAGITAMIITSFFPIY YIFQCTPRWYFIYLAGITSMGIFTIITLFTPSLSSPKYRGFRALLFASMGLFGIVPAVHAIVV NWENPQRNVTLMYELGMAVFYLVGTGFYVGRVPERLKPWFDRVGHSHQIFHVFMVL GALSHYAAALLFLDWRDHVGC
BoHHP2	Bol018049	MQKRRPVRESSKTTPERNGKALDSGEKKKRSERRLMKFEELPRYLKDNEYIHNHYRCEW SLKETFLSAFSWHNETLNIWTHLGGFLIFGWMMVVSCEMETTEVGLAGFVNVFSGVTIRW PWPSMAKAVYFSSDHDSNVTHHTSFLNSQGDVNYETIPKWPWLVLFTGAMTCLICSSM SHLFACHSRRFNLFFWRLDYAGISLMIVCSFFAPIYYAFSCHTYWRLFYLSSISILGLLAIFA LLSPALSAPRFRSFRAALFLTMGFSGVIPASHVLYLHKDHPNVVIALGYELAMAVLYATG AGFYVSRIPERWKPGAFDKAGHSHQIFHVFFVLGALAHSVASLLIMDFRRASPCAF

BoHHP3	Bol045785	MKRRRAARKSSAMVAVSDSKGLDSRMGRRLMKFDELPGYLQDNEFIHDHYRCQWSLR DTFLSAFSWHNETLNIWTHLIGFVIFMWMVMVSSLETTELSLAGLFNGISGAWIRLSSNQTL LLRHDSNVTEHIPLLTSEQEVNHQNYHEAVPKWPWL VYLAGAMGCLICSSVSHLLACHSK RYNLFFWRLDYAGISLMIVSSFFAPIYYAFSCHPNFRFLYLSSISILGLLAIITLLAPALSAPR FRPFRAYLFLAMGFCSVVPASHVLCLYWGHPNVLFALACELATGLSYAVGAVFYVSRVP ERWKPGAFDIAGHSHQIFHV FVVLGALVHC VATLVIVDFRRASPCGF
BoHHP4	Bol018601	MGGEAEIKQQLQPRSLPAEKKQHNVKRRRLWQKV KYQLVEYHALPAYLRDNEYIIGHY RSEWPIKQILLSIFTIHNETLNVWTHLIGFFLFLALTIYTATKVPSVVDLHSLQHRLPDILRK TDLHKLHSDLMSRLPSSPSKWHVMELLYNCLPERFYHGNYTDMCVLH SVKEDLANMIA PLIFRPITRWPFY AFLGGAMFCLLASSTCHLLSCHSERVSYIMLRD YAGIAALIATSFYPP VYYSFMCDPFFCNLYLG FITTLGIATVLVSLIPVFQTPEFRVV RASLFFGMGFSGAAPILHK LIIFWDQPEALHTTCYEVL MGLLYGLGALVYVTRIPERWMPGKFDIAGHSHQLFHV LVV AGAFTHYRAGLVYLKWRDIEGC
BoHHP5	Bol028895	MGGEAEVKERLQPKGKRLWQKV KYQLVEYHALPAYLRDNEYILGHYRSEWPIKQILLSI FTIHNETLNVWTHLIGFFLFLALTIYTATKVPSVVDLHSLQHRLPDLLRK TDLHKLHSDLM SRLPSSPSKWHVMELLYNCLPERFSHGNSTDMCVLH SVKEDLANMIAPLIFRPITRWPFY AFLGGAMFCLLASSTCHLLSCHSERVSYIMLRD YAGIAALISTSFYPPVYYSFMCDPFFC NLYLG FITILGISTVLVSLLPVQSPEFRVV RASLFFGMGFSGAAPILHKLIIFWDQPEALHT TGYEVL MGLLYGLGALVYATRIPERWMPGKFDIAGHSHQLFHV LVVAGAFTHYRAGLV YLKWRDIEGC
BrHHP1	Bra006551	MDQDGPNYEPETVPCSNSSCKSKIVPGDGSSGPKKIKSQKTRKRRELM SYSELPEYMKDN EYILNYYRAEWSIRDAFFSVFSFHNESLNVWTHLLG FILFVGLTVANIMHHDKFFPVD AKS PGNVTRWPFVFLGGSMFCLLSSSICPLFCCHSKDLNVFLLRIDYAGIPAMIITSFFPPIYYIF QCTPRWYFIYLAGITSMGIFTITLFTPSLSSPKYRGFRALLFASMGLFGIVPAVHAI VVNW ENPQRNVTLMYELGMAVFYLVGTGFYVGRVPERLKP GWFDRVGHSHQIFHV FVVMLGAL SHYAAALLFLDWRDHVGC
BrHHP2	Bra011228	MQKRRPVRESSKTTPERNGKALDSGEKKKRSERRLMKFEELPRYLKDNEYIHNHYRCEW SLTETFLSAFSWHNETLNIWTHLGGFLIFGWMMVVS CMETTEVGLAGFVN VFSRV TIRW PWPSMAKAVYFSSDHHDSNV THTSSFLNPQGDVNYETIPKWPWL VFLT GAMTCLICSSM SHLFACHSRRFNLF WRLDYAGISLMIVCSFFAPIYYAFSCHTNWRLFYLSSISILGLLAIFA LLSPALSAPRFRSFRAALFLTMGFSGVIPASHVLYLHKDHPNVVIALVYELAMAVLYATG AGFYVSRIPERWKPGAFDIAGHSHQIFHV FVVLGALAHSVASLLIMDFRRASPCAF
BrHHP3	Bra039234	MKRRRAARKSSAMVAVSDSKGLDSRMGRRLMRFEELPGYLQDNEFIHDHYRCQWSLRD TFLSAFSWHNETLNIWTHLIGFVIFMWMVMVSSVETTELSIAGLFNGISGAWIRLSSNQTL LRHDSNVTEHIPLLTSEQEVNHQNYHEAVPKWPWL VYLAGAMGCLICSSVSHLLACHSKR YNLFFWRLDYAGISLMIVSSFFAPIYYAFSCHPNFRFLYLSSISILGLLAIITLLAPALSAPRF RPFRAYLFLAMGFCSVVPASHVLFLYWGHPNVLFALACELATGLSYAVGAVFYVSRVPE RWKPGAFDIAGHSHQIFHV FVVLGALVHC VATLVIVDFRRASPCGV

BrHHP4	Bra000570	MGGEAEIKQRLQPNAGKRLWQKVYQLVEYHALPAYLRDNEYILGHYRSEWPIKQILL SIFTIHNETLNVWTHLIGFFLFLALTIYTATKVPSVVDLHSLQHRLPDVLRKTDLHKLHSDL MSRLPSSPSKWHVMELLYNCLPERFSHGNNDMCVLHSHVEDLANMIAPLIFRPITRWPF YAFLGGAMFCLLASSTCHLLSCHSERVSYIMLRDLYAGIAALISTSFYPPVYYSFMCDPFF CNLYLGFITILGISTVLVSLLPVFQSPEFRVVRASLFFGMGFSGAAPILHKLIIFWDQPEALH TTGYEVLMLLYGLGALVYATRIPERWMPGKFDIAGHSHQLFHVLLVAGAFTHYRAGL VYLKWRDIEGC
BrHHP5	Bra024038	MGGEAEIKQQLQPKSLPAETIEKKQHNVKRRRLWQKVYQLVEYHALPAYLRDNEYIIG HYRSEWPIKQILLSIFTIHNETLNVWTHLIGFFLFLALTIYTATKVPSVVDLHSLQDRLPDIL RKTDLHKLHSDLMHLPSSPSKWHVMELLYNCLPERFSHGNYTDMCVLHSHVEDLANM IAPLIFRPITRWPFYAFLGGAMFCLLASSTCHLLSCHSERVSYIMLRDLYAGIAALIATSFYF PVYYSFMCDPFFCNLYLGFITTLGTATVLVSLIPVFQTPEFRVVRASLFFGMGFSGAAPILH KLIIFWDQPEALHTTCYEVLMLLYGLGALVYVTRIPERWMPGKFDIAGHSHQLFHVLLV VAGAFTHYRAGLVYLKWRDIKGC
DcHHP1	DCAR_017777	MSCGEGFVWKRRGMSSDQMDDETSSITSKIMMSNKSTKKKKKNQKKMKMKNMRETNA KSGGCSSCDLVSFDELPEYMKDNEFIRDYYRADWSLKQALFSIFRWHNETLNVWTHLIGF VLFVGLTCSNLMHVLPVDQLLNIFTTWSFPLGPEVNVSHNSKNFFSDTTEFIDLKHSSSLG MQMTPTKLEATRWPFVFLGGSMFCLLSSICHLSCHSHPLNVLLLRIDYVGITVMIITSF FPPIYYIFQCTPHWQFLYLGGITVMGIFTIITLLSPVFSTSKFRAFASLFFVGMGLFGLIPAV HAMLNVNHEPSRNILGYELAMALSYLIGTVFYVSRIPERWRPGWFDLAGHSHQIFHVFV IMGALSHYGAALVFLDFRSKIGCEVNM
DcHHP2	DCAR_014800	MERRGGKSLNMGISVKIENVRNKIPVPKDKRLIKYEDLPEYLDNEFILDYYRCEWPLK DLITSTFAWHNETLNIWSHLIGFLVFLTLTLLSVTEKVDVERLIGRIFRWFDDEALTMIMSK PNKLSDASSTMSDGKQELSGWWAGKSCVYTGLYARQLVESLILKLSASADNPAAIPRWP WYVFLGGAMGCLLSSSLHLFACHSHRLNIFFWRDLYAGISLMIVCSFFAPIYYAFPCNPY SRIFYLTSITVLGILAITLLSPSLAPRYRSFRASLFFCMGFSGVIPAAHAIVLNWGHQPITT TLVYEIAMGLLYATGVVFYVRRIPERWKPAGFDIAGHSHQIFHAFVVAGALTHAAATLA VMDWRQGGPSCSVGHDTLVWT
DcHHP3	DCAR_014904	MEFKKAPIRSPVGERRRVGADGSRLKGGDVLAQAMSELALCWWCATVLTSSIVGDGRST AAIKRARSMAARGAGSICACIMCWILDILILIYGFMVGRMSSEHQMDQSQLLLTSAATN KMIINKKKKNQKNKKNKWRKYTSAKNGAANHTYDLVSFEELPAYMKDNEYIRNYR ANWPLKQALFSIFRWHNETLNVWTHLVGFILFVGLTCSNMIQVPPVVEFFNILTTSWSSPLG SAGNVSHDSKSFFSDTTKLIDLKHSFMDITLPELEVTRWPFVFLGGSMFCLLSSICH FCCHSHPMNILMLRIDYVGIAVMIITSFFPIYYIFQCSPHWQILYLSGITIMGIFTIVTLLSPV FSTNKFRSFRASLFFVAMGLFGLVPAVHAMVNVNWDPSRNILGYELAMALSYLIGTLFYV TRIPERWRPGWFDLAGHSHQIFHVFVIMGALSHYGAALVFLDFRSKIGCETNM

DcHHP4	DCAR_021463	MQRMTKSVGADSRRASTDSSSELQSERDSSGKGKRLWKKVKYQLVEYHSLPAYLKDNEFI LAHYRSEWPIKHIFMSIFTIHNETLNVWTHLIGFFLFLVLTITYTAMEVPKVVDSNTLQHLH DVLRKADMHKLREDLLTCLPSFPTLPDLHNFRDALKNSLPLTDLLTSLSNWHIVELLTNC LPESFSHINHTDNCVLRNVKDDMVSMIAPQTTRQITRWPFYFSFMGGAMFCLLASSVCHLF SCHSKRLSYVMLRIDYAGIAALISTSFYPIVYYFSMCPFFCMFYMGFITILGVATVLVSL PVFDRPEYRSVRAALFFGMGFSGVAPVLHKLILFSHQPEALHTTGYEILMGVFYIGVVLV YAMRIPERWMPGKFDIAGHSHQLFHVLVVAGAYTHYCAGLVYLKWRDMEGC
DcHHP5	DCAR_021464	MDNCEQEYRRKVGHRAESPKEKGKMLWKKVKYQLVEYHSLPAFLKDNEFILGHYRSE WPLKQIFFSVFSIHNETLNVWTHLIGFLLFLTLTIHTVMKIPYVVDLHKFENVREDLKTSLP LAHVLPSSLSSWRSKFLPNYIPEQFSQRNHSVDCALHSIKENVANTIAPVMVRPITRWPF AFLGGAMFCLLASSMCHLLSCHSKRLSYIMLRDLYAGIATIISTSFYPPVYYFSMCNPF NLYLGFITLLGMGTIIGSLLPVFDRSEFRSIRASLFFAMGFSGVVPIHLKLIMFWHQPEALH TTGYEVLMGSLYGLGALVYAMRVERWIPGKVDIAGHSHQLFHILVLGALHATHYRAGLV YLKWRDLEG
GmHHP1	Glyma.17G109800	MNYIQTKCVVKRKGKETAETETLCFTKSKDNNNMCDRHSKGKRYPLLSFWELPEYMKD NEYILRYYRANWPFKQALFSLFRWHNETLNVWTHLIGFLLFLGLTLANLMKPTVVDLLE LFTRSFSSSAEKNVSHNVKDLFQGTLLFDLNHQTPLTIELQSTALVIARWPFVFLGGSM FCLLSSSMCHLFCCHSRDLNLFWRMDYVGIVVMIITSFFPQIYYVFLCEPHWQIIYLAGIT AMGLFTIATMLSPTLSTSKYRAFRAMLFCSMGLFGIVPAIHACFVNWSNPRRNITLAYEIG MALSYLTGTLFYVTRIPERWKPGWFDLAGHSHQIFHALVVVGALAHYAATLQMLEWRD SFGCDTVL
GmHHP2	Glyma.17G070900	MINLRRSGENIPAKSKRFKRQLVKFEELPEYLDSEFILDYRSEWPVKEALWSIFAWHN ETLNIWTHVGGFLIFAVLAAMSATSELWNLLRSSTALGLSTTAAEMNGSNSDAFPDLHFR HVLDDSSILGEMKGSVETIPRWPFVFLAGGMGCLACSSSHLLACHSKGYNLFFWRDL YAGISLMIVCSFFAPIYYVFCNPYARLFYLASISVLGVLAITLLAPSLSTPRFRPLRASLFL SMGFSGIIPAAHAVVLFWGHPHILVALGYELAMAILYATGAGFYVARIPERWKPGAFDIT GHSHQIFHVFFVLGALAHSVAILVILDFRHGSPTCVH
GmHHP3	Glyma.02G207000	MISLRRSVNKPASKRFKCRVLKFEELPEYLDSEFILDYRSEWPVKEALWSIFAWHNE TLNIWTHIGGFLIFAVLAAMSTSELWNLLRSSTALGLSTTTAAEMNGSNSDAFPDLHFRH VLDPSILGEMKGSVETVPRWPWFVFLAGGMGCLACSSSHLLACHSKGFNLFFWRLDY AGISLMIVSSFFAPIYYAFCNPARNARLFYLASISVLGVLAITLLAPSLSTPRFRPLRASLFLS MGFSGIIPAAHAVALYWGQPHIFVALGYELVMAILYATGAGFYVARVPERWKPGAFDIA GHSHQIFHVFFVLGALAHSVATLVILDFRLGSPTCAN
GmHHP4	Glyma.01G194900	MGGEELSLMENERKGRRLWKKVKYQLVEYHSLPGYLDRDNEYILAHYRSEWPIKQVLLS AFTIHNETLNVWTHLIGFFIFLALTIYTAMKIPKVVDLNSLQHFPDMLKKADLHKLQSEIL TCLPSMPDLHRLRDEISSWHIKEYLYNCLPVRFSNHTDACVLLSVKDDLANIAPLMIRP ITRWPFFAFLGGAMFCLLASSICHLLSCHSARMAYIMLRDLYAGIAALISTSFYPPVYYSF MCDPFFCNLYLGFITVLGIATILFSLPVFQNPFEFRTIRASLFFGMGLSGAAPILHKLFLFW GQPEVFHTTAYEILMGVLYGIGALVYATRIPERWMPGKFDIAGHSHQLFHILVVAGAYAH YRAGLVYLRWRDLQGC

GmHHP5	Glyma.11G046900	MGGEELCLMENSGKGKRLWKKVKYQLVEYHSLPGYLRDNEYILGHYRSEWPIRQVLLS AFTIHNETLNVWTHLIGFFIFLALTIYTAMNLNSLQQFPDMLKKADLHKLQSEILTCLPSM PDLHILREGISSWHIKEYLYNCLPVRFSSSNHTDACVLHSVKDDLANIAPLMIRPITRWPF FAFLGGAMFCLLASSICHLLSCHSARMAYIMLRDLDYAGIAALISTSFYPPVYYSFMCYPFF CNLYLGFITVLGISTILFSLLPVFQNPFEFRTIRASLFFGMGLSGAAPILHKLYLFWGQPEVFH TTGYEILMGVLYGIGALVYATRIPERWMPGKFDIAGHSHQLFHILVVAGAYAHYRAGLV YLRWRDLQGC
OsHHP1	LOC_Os06g43620	MGEEAAMATMESAYHDELAPAAAPAPAKGGGSKKKRKQKREEKRKECRLVSYHELP DYMKENEFILDYRSEWPILNALLSLFSWHNETINIWTHLLGFVLFFGLTVLHLGQYFPQV ADLIGHLSWPISKVAENVSSNIGDVLSGAASF MQASPASSAGAMAAWPVTA AAAAATTR WPFVFLAGAMFCLLSSAACHLLSCHSHRLNLFRLDYTGIAVMIVVSFFPPIYYIFQCEP RWQVVYLSAITAAGVATVYALMSPRLSAARYRAHRALLFVAMGLSGVVPAAHAVAVN WHEPRRNVTLAYEGAMAASYLAGTAFYLTRVPERWRP GFMFDLCGHSHQIFHALVIAGA LAHYAAAIVFIQARDEMGC PAP
OsHHP2	LOC_Os06g44250	MTT VT TETAAAAAANTVARRRHRGGWCCAGGGAEEEEEEVVALSSSSSSSAPGKKVG AAAGGLPRLVRFEELPDY LK DNEFIRGHYRCEWSVRDALRSAFAWHNETLNVWTHLGG FFLFLWLAVAGGTERPAAAAAGVNAAPGIMTFLVASSANNASWETNSTSLEGKDSPALL GGGEHALARWPRTVFLVGAMTCLAVSATAHLLACHSRRFSRLFWQLDYAGIAVMIVAS FFPPVYYAFLGRAVAQVAYLSAITALGALVVAALLAPARSSPRLRHIRAGLFVSMGLSGV VPALHALWLNWGHPECYLALSLELVMLVYAAGAGFYVARVPERWRPGAFDCVGHSH QIFHVLVLAGALTHYAATAILIDWREAAIAAGGGAA AFL
OsHHP3	LOC_Os03g10300	MASSTVTLEKTTTIRSEAVVAADAAVDRAATLKSPLLEGKKCGDGGVAKRCCERKYELV SYDALPAFLKHNEFIIDYRSEWPIKQALLSAFAVHNETVNVWTHLIGFFMFLALTVCAA TMVPMESSATSMTMANNTGNPMVLMMSYGSNGAAMAVQALRNVSESELA AAAALS AAGDQVARWP FYAYLCGAMFCLLMSSACHLLACHSEHASVLLRLDYAGITGLIVTSFY PLVYYTFLCDPFFRTL YLGFITLFGAAAVAVSLMPVF EKPEL RWARAGLFACMGMSGLV PIVHKMLVFGARPEAVLT TGYEMVMGAFYLAGVVVYATRVPERWMPGKFDLAGHSHQ LFHVLVIAGAYAHYLAGVVYLSWRDGEAC
OsHHP4	LOC_Os03g13040	MAAAAGEEVEAARWAEADERKEGLRRRRRYGLVEYRALPGYMRDNEYILRH YRCEW PLPQVLLSAFSIHNETLNVWTHLIGFFIFLVLT IYTATQVPNVVDLQSLQHLPDVL RNADL HKIQTELVA CLPSLPHLSDLQKLKDELKSSWNSIEVLP SLRWHLLLELLSSCLPHRFTHSNE TSLSVLQSMKEDIANMIAPQLIRPIRWPFY AFLGGAMFCLLASSTCHLLSCHSRRLAYIM LRLDYAGIAALIATSFYPPVYYSFMCYPFFCNLYLSCITILGVATIAFSLLPVFQNPFEFRTIR ACLFFGMGASGVIPVIHKLILFWHQPEALHTTAYEVLMLGLFYGIGALVYATRVPERWMP GKFDIAGHSHQLFHVLVVAGAYTHYHSGLVYLKWRDVQGC

OsHHP5	LOC_Os12g32640	MEMMSLEEEETMASPTTSSCGTCKCGANDDKAKKMKTKTKKCELVGYEELPEWLKDN EFIHGYRCEWPMKETILSIFSIHNETLNVWTHLIGFLLFLCLAIFTAMVIPSGDNLHSNSSR SRSNATAMDYYYIHGDLMVMSNMTRVLRHEALAAAACLLHDPADLSQHEQISTSCPTN TSSCYTSSSSFSHLHNVRQHAIQDAGKVTAATAAAIAEPITRWPVFAYLGGAMACLLAST ACHLLLCHSERANYVTLRLDYAGIAALIVASFLPIVHYSFLCDPWLRRAYTAAIACAGAA TVTASLVPAFQSPRLRPLRAALFSGLAASGVVPVAHKMVLYGGTVREAATSARCEAAMG ALYALGVAVYAARVPERWFPGRFDLVGHSHQLFHLLVVAGAYAHYLGALLEYLKWRDA VKC
SIHHP1	Solyc07g007800	MIKSSKGSVWKRKNMNQEKENEKNIANKNCKKNIEKITKKGENYNNYNNNINNYPLVC YEELPGYMKDNEFILNYYRANWPIKQALLSIFRWHNETLNVWTHLLGFILFVALTLSNVV QVPQLSDFMTMFIWNFPMGGDANVSNNSEFFQGSPRLIDLKQDQHLQLENMMSTKSIQ SETTWPFYVFLVGSMFCLLSSSICHLFCCHSHKLNILLRMDYVGITVMIITSFFPIYYIFQ CSPHWQIVYLGICITIMGICTIITLLSPVFSTGKYRSFRAVLFMSMGFFGLIPAVHAVVLNWD EPERNVTLAYELAMALSYLIGTIFYMARIPERWRPGFFDLAGHSHQIFHVVFILGALSHYG AAQVFLEYRSRLSCDT
SIHHP2	Solyc12g010480	MKSMMNNGTKSSKIGKTEISESGILKEKKMNSYKEEEKKFKRRMLKFEELPVYLQDNE FIRDYYRCEWPLKEVALSVFSWHNETLNIWTHLVGFVVFVTLTVTSLMEKTAMETLLAG FSRPAGMGWPPTMKSNGSADSFPSYTSNISNPSFLGAYGDGYEVAIWPWFVFLGGAMI CLVFSSVSHLFACHSHKFTLFFWRLDYSGISIMIICSFFAPVYYTFCCQPYWCLLYLSSITIV GILVIFTLFAPALTSGKFRSFRAVLFLAMGFSGVIPAAHAVSLYFHHQPVLVALVYEITMG LLYAAGAVFYVTRFPERWKPGTFDLVGQSHQIFHVLVVAALSHSIATLVIMDWRRGLP PCNAGILG
SIHHP3	Solyc07g006020	MKRRGKKISKLRDGERVDSADRIDKTIRKNDQKLDRRKKLVKYEALPEYLQDNEFIRDY YRCEWPLKDIALSLFSWHNETLNIWTHLGGFVVFVTLTVMSLTEKTTTVENLFAGIFRG GDEWMNMKNNGSGDSFPDSYARQITNPSFLDINRDGYEVAIWPWFVFLGGAMGCLIAST LSHLFACHSLRYNLFFWRLDYAGISLMIVCSFFCPIYYIFCDQPHWCIFYLTTITIFGILAIT LLSPALFSGRFRSFRATLFLAMGFSGLIPATHALFLHYGHPQVLLALS YEIIMGILYATGAV FYMTRFPERCKPGAFDLVGHSHQIFHVVFVAAALAHCVASLVIMDWRRGMGLPTLQ
SIHHP4	Solyc02g092230	MGKGKEKLTGNGSREDNELLSPSKEGKGKRLWKKVKYQLVEYHSLPGYLKDNEYILGH YRAEWPLKQALLSIFTIHNETLNVWTHLIGFFLFLALTIYTATKVPKVVDLHSLQNLDPVL RKADLHKLQAELLTCLPSLPYMPDLHKL RDGLLRSPSNWHIIDLLHNCLPERFHSNHTD VCVLRSVKEDVANILAPLLVRPITRWPFYAFLGGAMFCLLASSTCHLLSCHSERLSYIMLR LDYAGIAALISTSFYPPVYYSFMCYPFFCNLYLGFITLLGIGTILGSLLPVFQTPEYRVIRAS LFFGMGLSGAVPILHKLVLFWHQPEALHTTG YELLMGIFYGIGALVYAMRVPERWMPGK FDIAGHSHQLFHVLVVAGAYTHYRAGLVYLRWRDLQGC

SIHHP5	Solyc03g043930	MSHQHDFIPVFPFLSPHFNSEILSGRIIFIQLSESPFFKSVFPFFQLMVQWKMGSDVEKLEEA LNGSGSSETQPFDRDSISKKEKQKRLWKKVNNQLVEYHSLPGYLKDFILGHYRCEWPV KQALLSVFTIHNETLNIWTHLIGFFLFLVLTITYTAKKVPDIVDLQTLQNLPEKLSKIDLHLK PADLLPCIPSLPNMPDLHLKRENLLQLLSNCLPDRFSHGHNHTDVGVLHHSVVDVANVIAPL MVKPITRWPFYAFLGGAMFCLLASSTCHLLCCHSERLSYVMLRFDYAGIAALISTSFYPPV YYSFMCYPFFLNLYLGFITVLGVGAMLASLLPVFQKPKFRSLRAGLFFGMGMSGVAPILH KLILYWNQPEALHTTGYEVLGMVLYGIGALIYALRVPERWMPGKFDIAGHSHNLFHVLV VAGAYTHYRAGLIYLQWRDQQGC
ZmHHP1	GRMZM2G169321	MASEEVATTVCADADQEAASAAAAAAMKEEGGRGKRRRRRQPRKGEEEGGRKKYALVS YHELPEYMKENEFILNYYRSEWPVLNAVLSLFSWHNETINVWTHLLGFMLFFGLTLVHL GQYFPQVADLIGHLSWPISKVAENVSSNIGDVLGAAMFIQTNPASLASHGTAVASQTTRW PFFVFLAGAMFCLSSSACHLLSCHSHRLNLLIRLDYTGIAVMIVVSFFPPIYYIFQCEPR WRAAYLSAITAAGAGTVYALMSPRLSAPRYRARRALLFVGMGLSGVVPAAHAAAAANW HEPRRNVTLAYEGAMAASYLVGTAFYLARVPERWRPGAFDLAGHSHQIFHALVIAGALA HYGAAIVFLRARDEMGCAS
ZmHHP2	GRMZM2G030099	MATTTVTTTAEASAPGKRRGGGCCALAAAAAASVVPVKAAGEQQQPLPLPRLVRF EELPDYLRDNEFIHAHYRCEWSVRDALRSAFAWHNETLNVWSHLGGFFLFLYLAVAEPT GTVAGAGAGVGAGAAPSIVTFVLASANTSWSSWEASSNSLTKASKGLMAVFGSSDGDH AVPRWPRTVFLAGAMACLAVSAAAHLACHSRRFTRLFWQLDYAGIAVMIVASFFPPVY YAFGRARTQLVYLSAVTLLGLLVVALLPARSSPRLRHLRAGLFVSMASFGVLPALHA LWLNWAHRECHLALALELLMGLVYAAGAGFYVTRVPERWSPGRFDCVGHSHQIFHLLV LVGALTHYAATAILIDWREAMAVAAGGASVLS
ZmHHP3	GRMZM2G363982	MGAATAPTARRRGPSTQEEAMARASPEARRRPRRLVGYEELPEYLKDNEYIRGHYRA EWPVRDALLSAFAWHNETLNVWTHLGGFLFLALAVAGGRKEAADGAAPGIMRFVRL DSWGSDDPGQPRHDDAGASLPSVPRWPRTVFLVGAMSLAISAAHLLACHSRRASAVF WQLDYAGISVMIVASFVPPVYYAFLCHPPARAAYLCAIAALGALVVAALLSPSCSSPRYR RLRAALFLAMGLSGVVPALHALWLNWGHAAACYLALGIEVVMGLTYATGAWFYVSRVP EKWRPGVFDVVGHSHQIFHVLVLGAVTHYVAVAVLIHWREKVAVACGAASA
ZmHHP4	GRMZM2G161780	MAATAAEEMERMVEAEWEEGKQGMKRKRYGLVEYRALPAYLRDNEYIHRHYRCEW PLPQVLLSAFSIHNETLNVWTHLIGFFIFLALTIYTATQVPNAVDIRSLQHLDPVLRKADIH KIQAEVLSCLPSLPHLSDLQKLKDELKTSWNSMEVLPPLSRWHLELLANCLPHRFTHPN ETSLSVLQSMKEDLASLIAPQLIRPIARWPFYAFLGGAMFCLLASSTCHLLSCHSRRLAYI MLRLDYAGIAALIATSFYPPVYYSFMCYPFFCNLYLSFITILGVATIAFSLPVFQNPFEFTI RACLFFGMGASGVIPVLHKLVLFWHQPEALHTTGYEILMGLFYGLGALVYAARVPERW MPGKFDIAGHSHQLFHVLVAGAYTHYHAGLVYLKWRDLQGC
ZmHHP5	GRMZM2G380789	MSSTVTLEKTTAIQSDGGRAGVAGSPKQAANRSPLLVAKKGAEGGAKEKARCCGRRCCL VSYDKLPEFLKHNEFIVDHYRSEWPVKEALLSAFSIHNETINVWTHLIGFFVFLALTVCAA TMVPTTEYESPHLALATSSSTGLTMTNITGNAMVLRYSADDGAVMAMKALRNVSAAE TAAAVLPAGAGRGRVARWPFYAFLCGAMFCLLMSSACHLLACHSEHASVFLRLDYAG ITGLIVTSFYPLVYYTFLCDPFYQALYLGFITVSGAAAVASLLPVFERPELRWARAGLFA CMGMSGLVPIVHKMLVFGARPEALLTTGYEVAMGAFYLAGVVVYATRVPERWMPGRF DLAGHSHQLFHVLVIAGAYAHYLAGLVYLGWDRMEGC

Table 2 Suppl. The qBcHHP1 and qBcACTIN primers used to amplify the core fragment by real-time qPCR analysis. The open reading frame of *BcHHP1* cDNA was amplified with the primers gBcHHP1. *Underlined* sequences represent gateway adapter sequences.

Analysis	Primer name	Forward primers (5'-3')	Reverse primers (5'-3')
cDNA amplification	BcHHP1-F/R	ATGGACCAAGATGGTCCGAACT	ACAACCAACATGGTCGCGCCAG
	BcHHP2-F/R	ATGCAGAAACGGAGACCG	TCAAAAGGCACAAGAAGGTG
	BcHHP3-F/R	ATGAAGAGACGAAGAGCGGC	CTAAACCCACAGGGAGAC
	BcHHP4-F/R	ATGGGTGGTGAGGCAGAGAT	TCAACAGCCTTTAATGTCTCTCC
	BcHHP5-F/R	ATGAAACCCAGCGTTGTTGATC	TCAACATCCTTCAATGTCTCTCC
Gateway cloning	gBcHHP1-F/R	<u>GGGGACAAGTTTGTACAAAAAAGCAGG</u> <u>CTTCATGGACCAAGATGGTCCGAA</u>	<u>GGGGACCACTTTGTACAAGAAAGCTGG</u> <u>GTGACAACCAACATGGTCGCGC</u>
Real-time qPCR	qBcHHP1-F/R	CAAGATTGTTCTGGAGATG	ACTGAAGACGCTGAAGAA
	qBcACTIN-F/R	CTCAGTCCAAAAGAGGTATTCT	GTAGAATGTGTGATGCCAGATC

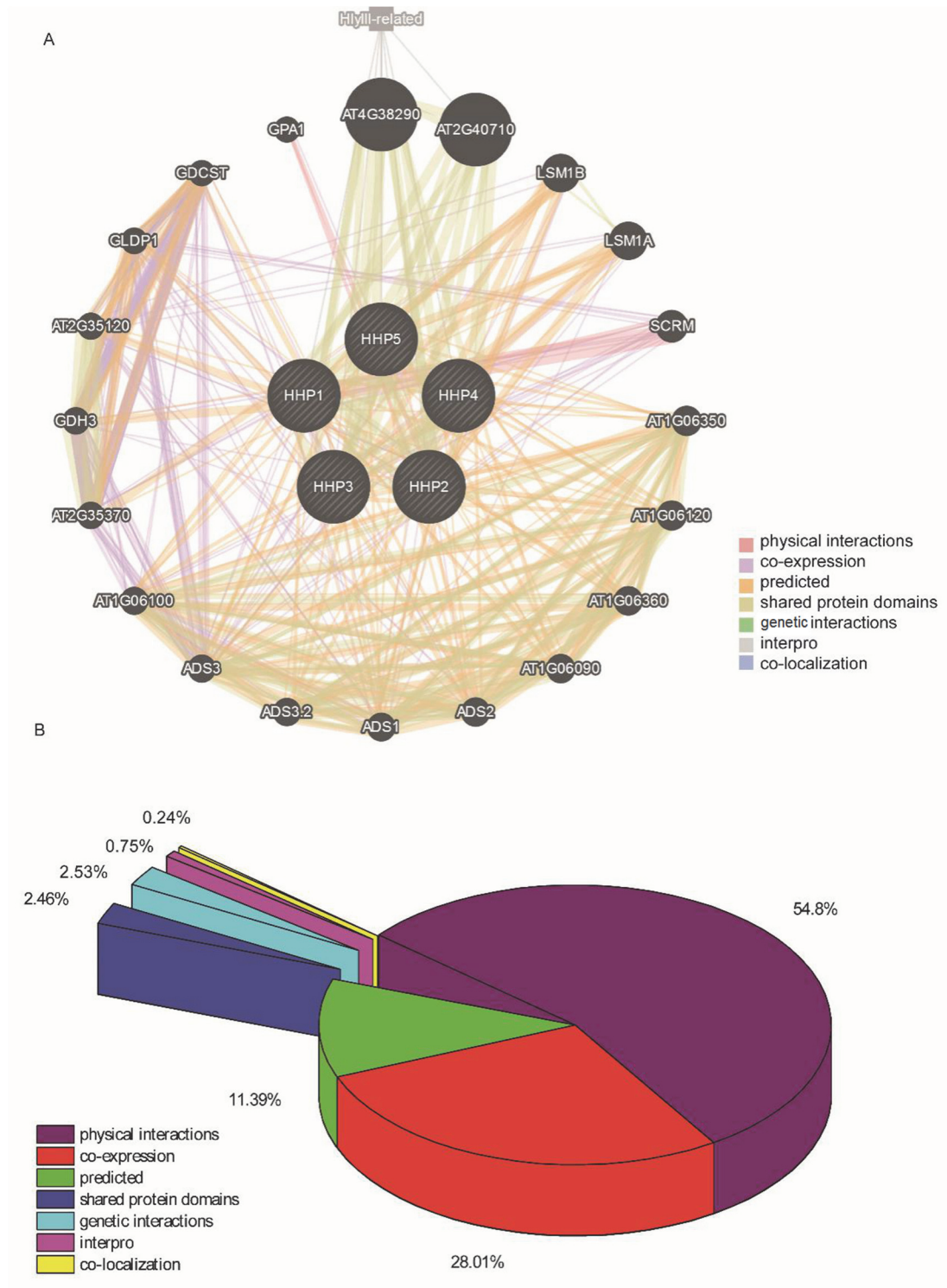


Fig. 1 Suppl. The interaction networks of HHPs in Pak-choi according to the orthologs in *Arabidopsis*. *A* - The interaction network of *BcHHP* genes. *B* - The purple, red, green, blue, cyan, It magenta and yellow lines, respectively, standing for physical interactions, co-expression, predicted, shared protein domains, genetic interactions, interpro and co-localization in the pie chart.