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AtHHP1      1 ........MDQNG......................HNDEAETVSCGNGNCKSKIVPGDDHGGDESSGTKRRKKRKTQQKTMK
AtHHP2      1 ........MQKRR......................TVKES...........TKIR..NGKGMD..SGEKKRSEKR.......
AtHHP3      1 ........MKRRR......................SAKKSPAM........VTVT..DWKGLD..CGEETRIVRR.......
AtHHP4      1 ........MGDEA......................EIKEHLKP......QASSETMDKKHNVK...GKRLWQKVK.......
AtHHP5      1 ........MGDEA......................EIKEHLKP......QASSETIDKKHNVK...GKRLWQKVK.......
ScYOL002c   1 .......MLHVG........................EESFQMSTLLERTKSVQELKKRAAGKTSANPAEVAKAKKVL......
HsAdipoR1  17 ASNREADTVELA.ELGPLLEEKGKRVIANPPKAEEEQTCPVPQEEEEEVRVLTLPLQAHHAMEKMEEFVYKVWEGR......
HsAdipoR2  29 GTRRGDNDSHQG.DLEPILEASVLSSHHKKSSEEHEYSDEAPQEDEG.FMGMSPLLQAHHAMEKMEEFVCKVWEGR......
DmCG5315    1 ....MTEVLKAG..........VLS.........DEIDLG............ALAHNAAEQAEE...FVRKVWEAS......
CeC43G2.1  83 RATSFAGRIRAGSDDEAMPKHTILRYRRKKGGQWREINLQGTPDKRK.DDEDELEVDVKEDRSEQTGIVTKTYEAR......
HsMPRG      1 ..............................................................MLSLKLP.......
HsMPRA      1 ........MAMAQK......................LSHLLPSL........RQVIQEPQLSLQ......PEPVFT.......
HsMPRB      1 ......MTTAILER......................LSTLSVSG........QQLRRLPKILEDG....LPKMPCT.......

                                                                   TM1
AtHHP1     53 RREIMSYCELPEYMKDNEYILNYYRADWS.IRDAFFSVFSFHNESLNVWTHLIGFIFFVALTVAN.................
AtHHP2     30 ...LMKFEELFRYLKDNEFIHNHYRCEWS.IKETFLSAFSWHNETLNIWTHLCGFAIFTWMMVVSSMET.TELGLAGFVSLL
AtHHP3     33 ...LMKFEDLFEYLKDNEFIHNHYRCQWS.LKDTFLSAFSWHNETLNIWTHLIGFGIFLWMTVVSCLET.TEISLAGVFNGM
AtHHP4     36 .YQLVEFHSLPAYLRDNEYIIGHYRSEWP.IKQILLSIFTIHNETLNVWTHLIGFFLFLALTIYTATKVPSVVDLHSLQHRL
AtHHP5     36 .YQLVEFHSLPAYLRDNEYIIGHYRSEWP.IKQILLSIFTIHNETLNVWTHLIGFFLFLALTIYTATKVPSVVDLHSLQHRL
ScYOL002c  46 .RRLYSWDEIPEWQRDNDFLLHGYVKETSSFIETFKSLFYLHNESVNIYSHLIPALGFFTVLLLDKSTIKVFA.........
HsAdipoR1  91 .WRVIPYDVLPDWLKDNDYLLHGHRPPMPSFRACFKSIFRIHTETGNIWTHLLGFVLFLFLGILTMLRPNMYF.........
HsAdipoR2 102 .WRVIPHDVLPDWLKDNDFLLHGHRPPMPSFRACFKSIFRIHTETGNIWTHLLGCVFFLCLGIFYMFRPNISF.........
DmCG5315   38 .WKVCHYKNLPKWLQDNDFLHRGHRPPLPSFRACFKSIFRVHTETGNIWTHLLGCIAFIGVALYFISRPSV...........
CeC43G2.1 157 .WKVLKYEHLPEWLQDNEFLRHGHRPPLPSFSECFKSIWSLHTETGNIWTHLIGCVAFFFLACWFLTRPDN...........
HsMPRG      7 ..RLFSIDQIPQVFHEQGTLFG.YRHPQSSATACILSLFQMTNETLNIWTHLLPFWFFAWRFVTALYMTDIK..........
HsMPRA     32 ....VDRAEVPPLFWKP.YIYAGYRPLHQTWRFYFRTLFQQHNEAVNVWTHLLAALVLLLRLALFVETVDF...........
HsMPRB     36 ....VPETDVPQLFREP.YIRTGYRPTGHEWRYYFFSLFQKHNEVVNVWTHLLAALAVLLRFWAFAEAEALP..........

AtHHP1    116 ......................................IIHHDG...FFPVDAKSPG...........NVTRWPFFVFLGG
AtHHP2    108 SGATIRWPWPSMAMSKDVYFSSD...............QTLHHDLNVTHTRSLLNSQGDV......NYEAIPKWPWLVFLTG
AtHHP3    111 AGVRI.............CLSSN...............QTLLHDSNVTHHISCLTSQG.......EAIPKWPWLVYLVG
AtHHP4    117 PDLLRKTDLHKLHSELMARLPSSPSSWHVMDLLYNCLPERFSHGNYTDMCVLHSVREDLANLIAPLIFRPITRWPFYAFLGG
AtHHP5    117 PDLLRKTDLHKLHSELMSRLPSSPSSWHVMDLLYNCLPERFSHGNYTDMCVLHSVREDLANLIAPLIFRPITRWPFYAFLGG
ScYOL002c 118 ..............................................................TTTWLDHMVIDLFYSG
HsAdipoR1 163 ..............................................................MAPLQEKVVFGMFFLG
HsAdipoR2 174 ..............................................................VAPLQEKVVFGLFFLG
DmCG5315  108 ..............................................................EIQTQEKIVFGAFFIG
CeC43G2.1 227 ..............................................................HIQFQEKVVFSFFFAG
HsMPRG    76 ..............................................................NDSYSWPMLVYMCT
HsMPRA    98 ..............................................................WGDPHALPLFIIVLA
HsMPRB   103 ..............................................................WASTHSLPLLLFILS

                TM2                      TM3                                TM4
AtHHP1    146 SMFCLLASSICHLFCCHSKELNVFLLRIDYAGITAMIITSFFPPIFYI...FQCTPRWYFIYLAGITSMGIFTIITLFTPSL
AtHHP2    169 AMGCLICSSMSHLFACHSRRFNLFFWRLDYAGISLMIVCSFFAPIYYA...FSCHTYWRLFYLSSISILGLLAIFTLLSPSL
AtHHP3    155 AMGCLICSSVSHLLACHSKRFNVFFWRLDYAGISLMIVASFFAPIYYA...FSCHPNFRLLYLSSISILGLLAIITLLSPAL
AtHHP4    199 AMFCLLASSTCHLLSCHSERVSYIMLRLDYAGIAALIATSFYPPVYYS...FMCDPFFCNLYLGFITILGIATVLVSLLPVF
AtHHP5    199 AIFCLLASSTCHLLSCHSERVSYIMLRLDYAGIAALIATSFYPPVYYS...FMCDPFFCNLYLGFITILGIATVLVSLLPVF
ScYOL002c 135 AFACLILSSSFHCLKSHSLRIATLGNKLDYLGICILIVTSMVSILYYG...YFEKFSLFCLFALITVSFGIACSIVSLKDKF
HsAdipoR1 180 AVLCLSFSWLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVPWLYYS...FYCSPQPRLIYLSIVCVLGISAIIVAQWDRF
HsAdipoR2 191 AILCLSFSWLFHTVYCHSEGVSRLFSKLDYSGIALLIMGSFVPWLYYS...FYCNPQPCFIYLIVICVLGIAAIIVSQWDMF
DmCG5315  125 AIVCLGFSFAFHTLSCHSVEMGRLFSKLDYCGIALLIMGSFVPWLYYG...FYCHYQPKVIYLSVVSILGILSIVVSLWDKF
CeC43G2.1 244 AVLCLGLSFAFHTLSCHSVNVVKIFCKLDYMGISLLIIGSFIPWIYYG...FYCRREPKITYIAMVSVLGIGAIVVSLWDKF
HsMPRG     91 SCVYPLVSSCAHTFSSMSKNARHICYFLDYGAVNLFSLGSAIAYSAYTFPDALMCTTFHDYYVALAVLNTILSTGLSCYSRF
HsMPRA    114 SFTYLSFSALAHLLQAKSEFWHYSFFFLDYVGVAVYQFGSALAHFYYAI.EPAWHAQVQAVFLPMAAFLAWLSCIGSCYNKY
HsMPRB    119 SITYLTCSLLAHLLQSKSELSHYTFYFVDYVGVSVYQYGSALAHFFYSS.DQAWYDRFWLFFLPAAAFCGWLSCAGCCYAKY

                                TM5                          TM6
AtHHP1    225 SAPK....YRAFRALLFASMGLFGIVPAAHALVVN.WGNPQRNVTLVYELLMAVFYLVGTGFYVGRVPERLKPGWFDRVGHS
AtHHP2    248 SAPR....FRSFRAALFLTMGFSGVIPATHVLYLH.KDHPNVLIALVYELAMAVLYATGAAFYVTRIPERWKPGAFDIAGHS
AtHHP3    234 STPR....FRPFRANLFLAMGSSAVIPATHVLCLY.WDHPNVFIALGYEIATALSYFVGATFYVSRVPERWKPGAFDMAGHS
AtHHP4    278 QSPE....FRVVRASLFFGMGFSGLAPILHKLIIF.WDQPEALHTTGYEILMGLLYGLGALVYATRIPERWMPGKFDIAGHS
AtHHP5    278 QSLE....FRVVRASLFFGMGFSGLAPILHKLIIF.WDQPEALHMTGYEILMGLLYGLGAVVYATRIPERWMPGKFDIAGHS
ScYOL002c 214 RKRE....WRPYRAGLFVCFGLSSIIPIFSGLYCYSFSEIWTQIQLFWVLLGGVLYIIGAVLYGMRFPEKICPGKFDIWGHS
HsAdipoR1 259 ATPK....HRQTRAGVFLGLGLSGVVPTMHFTIAEGFVKATTVGQMGWFFLMAVMYITGAGLYAARIPERFFPGKFDIWFQS
HsAdipoR2 270 ATPQ....YRGVRAGVFLGLGLSGIIPTLHYVISEGFLKAATIGQIGWLMLMASLYITGAALYAARIPERFFPGKCDIWFHS
DmCG5315  204 SEPA....LRPLRAGVFMSFGLSGVIPAIHYSIMEGWFSQMSRASLGWLILMGLLYILGALLYALRVPERWFPGKFDIWGQS
CeC43G2.1 323 SESR....FRPIRAAVFVGMGCSGVIPTIHYIITDGVHSLFADNSFHWLLLMAFLYLLGAGLYATRTPERFFPGKCDIWFQS
HsMPRG    173 LEIQK.PRLCKVIRVLAFAYPYTWDSLPIFYRLFLFPGESAQNEATSYHQKHMIMTLLASFLYSAHLPERLAPGRFDYIGHS
HsMPRA    195 IQKP..GLLGRTCQEVPSVLAYALDISPVVHRIFVSSDPTTDDPALLYHKCQVVFFLLAAAFFSTFMPERWFPGSCHVFGQG
HsMPRB    200 RYRRPYPVMRKICQVVPAGLAFILDISPVAHRVALCHLAGCQEQAAWYHTLQILFFLVSAYFFSCPVPEKYFPGSCDIVGHG

                TM7
AtHHP1    302 HQIFHVFVLLGALSHYAAALLFLDWR.........................DHVGC.....................
AtHHP2    325 HQIFHVFVVLGALAHSVASLLIMDFR.........................ASPSCAF....................
AtHHP3    311 HQIFHVFVVMGALAHCVTTLLIIDFSR.........................ASPSCGF....................
AtHHP4    355 HQLFHVLVVAGAFTHYRAGLVYLKWR..........................DIEGC.....................
AtHHP5    355 HQLFHVLVVAGALTHYRAGL................................................................
ScYOL002c 292 HQLFHFLVVIAALCHLRGLLNSYELVH........................IKMENGIVS...................
HsAdipoR1 337 HQIFHVLVVAAAFVHFYGVS.NLQEFR.........................YGLEGGCTDDTLL...............
HsAdipoR2 348 HQLFHIFVVAGAFVHFHGVS.NLQEFR.........................FMIGGGCSEEDAL...............
DmCG5315  282 HQIFHILVIAAAFVHYHGIS.EMAMYR.........................VMYSECTVPIEPITF............
CeC43G2.1 401 HQLFHTCVVIAAFVHYYGIS.EMAFAR.........................LN.EQCPVR..................
HsMPRG    254 HQLFHVCVILATHMQMEAILLDKTLRKEWLLATSKPFSFSQIAGAILLCIIFSLSNIIYFSAALYRIPKPELHKKET
HsMPRA    275 HQLFHIFLVLCTLAQLEAVALDYEARRPIYEPLHTHWPHNFSG....L.FLLTVGSSILTAFLLSQLVQRKLDQKTK
HsMPRB    282 HQIFHAFLSICTLSQLEAILLDYQGRQEIFLQRHGPLSVHMAC....LSFFFLAACSAATAALLRHKVKARLTKKDS
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Fig. S1. Sequence alignment of *Arabidopsis* HHPs, yeast YOL002c, human AdipoRs, human mPRs and their representative homologs from *Drosophila* and *C. elegans*. Identical and similar amino acid residues are shaded in black and gray, respectively. The locations of the seven transmembrane domains TM1 to TM7 are indicated with solid lines above the sequences. At, *Arabidopsis thaliana*; Sc, *Saccharomyces cerevisiae*; Hs, *Homo sapiens*; Dm, *Drosophila melanogaster*; Ce, *Caenorhabditis elegans*.