Ancestry & molecular evolutionary analyses of heat shock protein 47 kDa (HSP47/SERPINH1)

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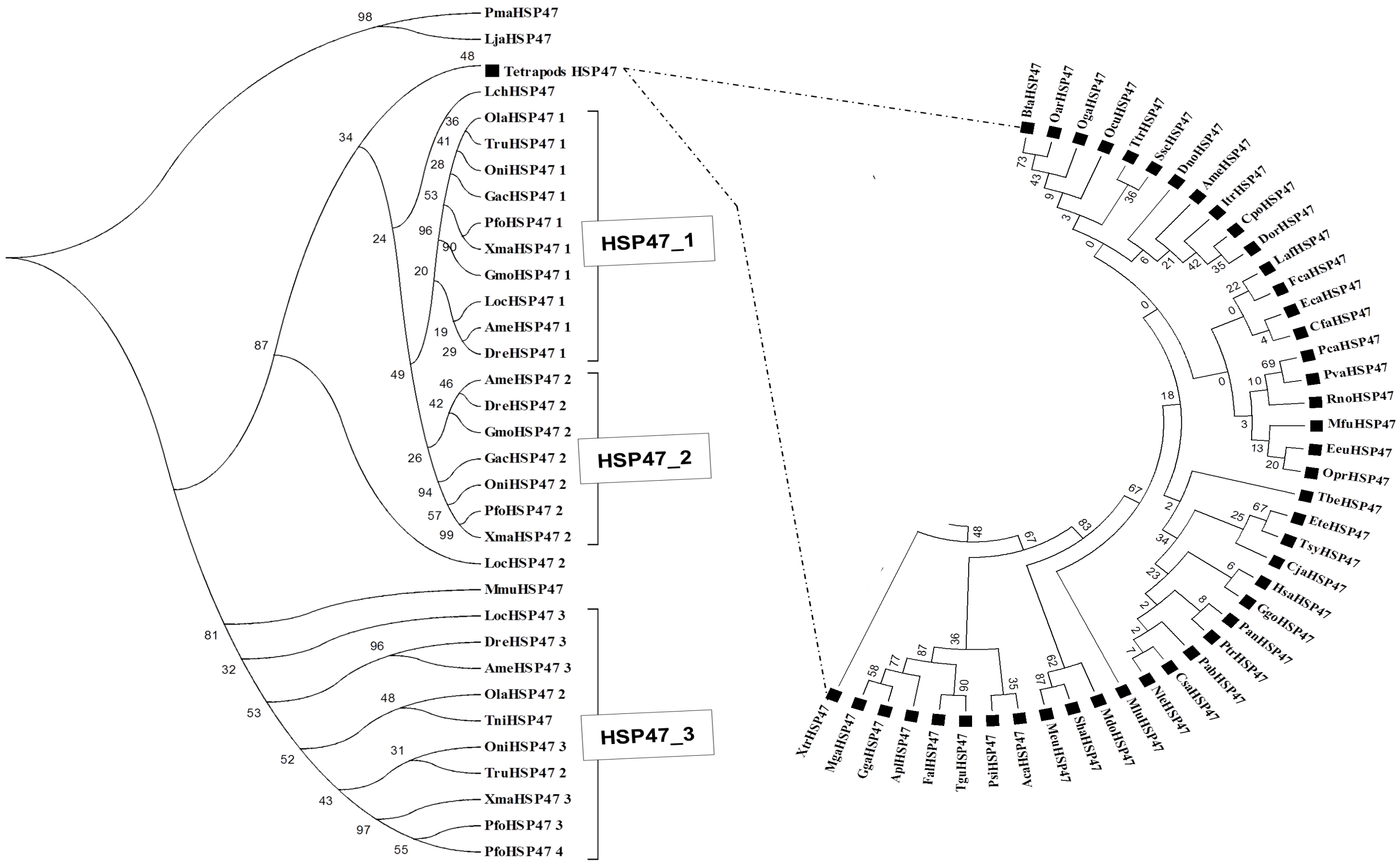
Fig S1. Detailed phylogenetic tree of HSP47 proteins reveals three sets of HSP47 in ray-finned fishes. This tree was obtained using MEGA7 with maximum likelihood method using bootstrap of 1000. Ame - Ailuropoda melanoleuca;Apl - Anas platyrhynchos;Aca - Anolis carolinensis;Ame - Astyanax mexicanus;Bta - Bos taurus;Cja - Callithrix jacchus;Cfa - Canis lupus familiaris;Cpo - Cavia porcellus;Csa - Chlorocebus sabaeus;Dre - Danio rerio;Dno - Dasypus novemcinctus;Dor - Dipodomys ordii;Ete - Echinops telfairi;Eca - Equus caballus;Eeu - Erinaceus europaeus;Fca - Felis catus;Fal - Ficedula albicollis;Gmo - Gadus morhua;Gga - Gallus gallus;Gac - Gasterosteus aculeatus;Ggo - Gorilla gorilla;Hsa - Homo sapiens;Itr - Ictidomys tridecemlineatus;Lch - Latimeria chalumnae;Loc - Lepisosteus oculatus;Lja - Lethenteron japonicum;Laf - Loxodonta africana;Mmu - Macaca mulatta;Meu - Macropus eugenii;Mga - Meleagris gallopavo;Mmur - Microcebus murinus;Mdo - Monodelphis domestica;Mmu - Mus musculus;Mfu - Mustela putorius furo;Mlu - Myotis lucifugus;Nle - Nomascus leucogenys;Opr - Ochotona princeps;Oni - Oreochromis niloticus;Ocu - Oryctolagus cuniculus;Ola - Oryzias latipes;Oga - Otolemur garnettii;Oar - Ovis aries;Ptr - Pan troglodytes;Pan - Papio anubis;Psi - Pelodiscus sinensis;Pma - Petromyzon Marinus;Pfo - Poecilia formosa;Pab - Pongo abelii;Pca - Procavia capensis;Pva - Pteropus vampyrus;Rno - Rattus norvegicus;Sha - Sarcophilus harrisii;Ssc - Sus scrofa;Tgu - Taeniopygia guttata;Tru - Takifugu rubripes;Tsy - Tarsius syrichta;Tni - Tetraodon nigroviridis;Tbe - Tupaia belangeri;Ttr - Tursiops truncatus;Xtr - Xenopus tropicalis;Xma - Xiphophorus maculatus;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TruHSP47 1
OniHSP47 1
GacHSP47 1
PfoHSP47 1
XmaHSP47 1
GmoHSP47 1
LocHSP47 1
AmeHSP47 1
DreHSP47 1
HSP47_1
AmeHSP47 2
DreHSP47 2
GmoHSP47 2
GacHSP47 2
OniHSP47 2
PfoHSP47 2
XmaHSP47 2
HSP47_2
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DreHSP47 3
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TniHSP47
OniHSP47 3
TruHSP47 2
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PfoHSP47 3
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AcaHSP47
PsiHSP47
TguHSP47
FalHSP47
AplHSP47
GgaHSP47
MgaHSP47
XtrHSP47

Fig S2. Sequence alignment of different HSP47 proteins. Percentage identity scores of 90-100, 70-89, 50-69 are marked by black, grey and yellow shades, respectively. Known conserved (≥70%) amino acids (proposed by Irving et al 2000) are marked by different colors of hashes (above the alignment), #, # and # for presence, absence and partial presence (<50% of HSP47 proteins) of residues, respectively. Structural elements are marked above the alignment: **α**-helices and **β**-sheets as ~~ and ==>, respectively. Three serpin motifs are shown with black boxes. Intron position and phasing are shown above alignment with green and cyan shades for standard introns and additional intron insertions (confined to only HSP47_1 of selected ray-finned fishes at the positions 36b and 102b), respectively. @@@ indicates N-glycosylation site (NxT, where x - any residue).

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TguHSP47      1  -------------------------------MWI---------IMGLALL   10
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PsiHSP47      1  -------------------------------MWV---------TSLLALC   10
LchHSP47      1  -------------------------------MWM---------TRLLSLS   10
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LocHSP47_1    1  ---------------------IAQLPSITESMWV---------TKLVALS   20
DreHSP47_1    1  -------------------------------MWV---------SSLIALC   10
GacHSP47_1    1  -------------------------------MWM---------TNLVAFC   10
GmoHSP47_1    1  -------------------------------MWM---------TSVLALC   10
OlaHSP47_1    1  -------------------------------MWT---------TTIVALC   10
OniHSP47_1    1  -------------------------------MWM---------TNIVGLC   10
PfoHSP47_1    1  -------------------------------MWM---------TRAVALC   10
TruHSP47_1    1  ----------------------------LRLLWLLWKTETMRAANIVVLS   22
XmaHSP47_1    1  -------------------------------MWM---------TTAVALC   10
DreHSP47_2    1  -------------------------------MLA---------SNVLLLC   10
OniHSP47_2    1  -------------------------------MWV---------TNLVSLV   10
GmoHSP47_2    1  -------------------------------MLV---------TSLVALA   10
XmaHSP47_2    1  -------------------------------MWL---------TLLVSLA   10
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LocHSP47_2    1  -------------------------------AMA---------FKAAVVS   10
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TruHSP47_2    1  ----------------------------SRAAML---------PRLPVYI   13
TniHSP47      -  --------------------------------------------------    -
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LocHSP47_3    1  -------------------------------AML----------LLPATV    9
PfoHSP47_3    1  ----------------------------------------------LAVC    4
PfoHSP47_4    1  ------------------------------RPAM---------LLRLAVC   11
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               ------------------------------------------N-terminal
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RnoHSP47     11   LLA---VALAAEVK-------KPVEATAPGT---AEKLSSKATTLAERST    47
GgaHSP47     11   GLA---AAV-------------------PSE---DRKLSDKATTLADRST    35
TguHSP47     11   GLA---AAV-------------------PSE---DRKLSDKATTLAERST    35
MgaHSP47     19   MLPEPSLAAAV-----------------PSE---DRKLSDKATTLADRST    48
PsiHSP47     11   ALV---AAV-------------------PSE---DKKLSDKAATLADRSA    35
LchHSP47     11   ILA---AVA-------------------ICE---EKKLSEHATTLADRSS    35
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GacHSP47_1   11   LLA---VVA-------------------SAE---EKKLSSYATALADHSA    35
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XmaHSP47_1   11   LLA---FVA-------------------SAE---DKKLSSHANTLADNSA    35
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GmoHSP47_2   11   LLA---HTASS--------------ATSASP---DKVLSTHASLLADNSA    40
XmaHSP47_2   11   LLA---PAISA--------------ATATTA---DKVLSNHATILADNSA    40
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DreHSP47_3   12   LLLAQQSVWSS-----------------TPQEPKVQGSPPEISSLHHPTW    44
OniHSP47_3    9   LLISLPVLLVQGSATN-----SSKKSADTPAGPVSRPPPLPPPPQGDPSW    53
OlaHSP47_2    1   --------------------------------------------LSDPSW     6
TruHSP47_2   14   LLF---LPLAP----------VQRSTADSSEKSSASSPHLPPPPLGDPSW    50
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XmaHSP47_3    9   LPVSLLVLL------------VQSSTTKSSKSPAASVSPSLRPLVNDPSW    46
LocHSP47_3   10   LWG---VLL-------------------SAH---CKPPGDHAATLAEGSW    34
PfoHSP47_3    5   LLVSLRVLL------------VQSGAATSSQSPAASVSPSLPPLVNDPSW    42
PfoHSP47_4   12   LLVSLRVLL------------VQSGAATSSQSPAASVSPSLPPLVNDPSW    49
PmaHSP47     12   LAA---AAAADGKKATVSKADAAAANNATAP---PKNLSEHAKKVGEGNW    55
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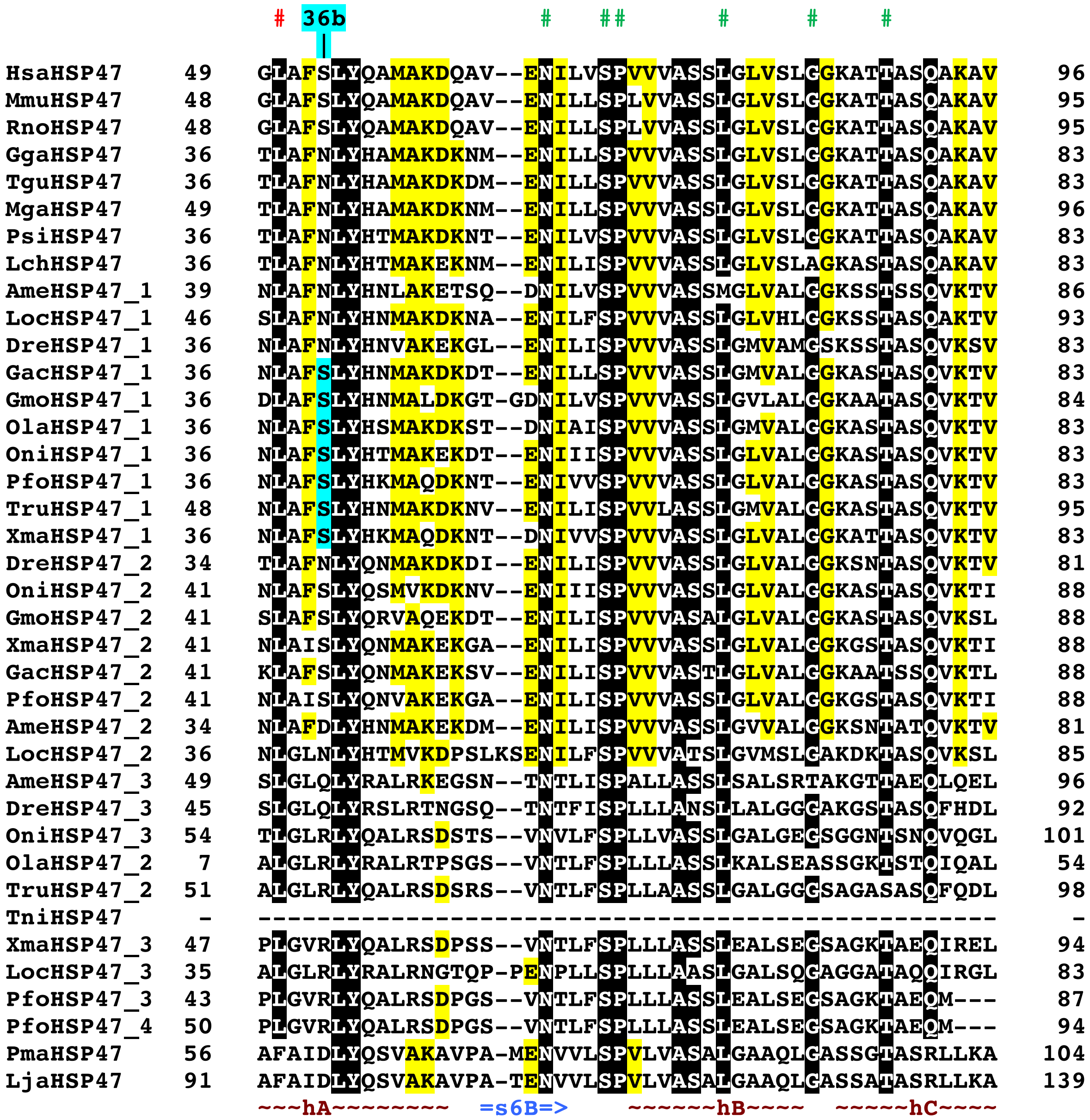

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GgaHSP47        36   TLAFNLYHAMAKDKNM--ENILLSPVVVASSLGLVSLGGKATTASQAKAV    83
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MgaHSP47        49   TLAFNLYHAMAKDKNM--ENILLSPVVVASSLGLVSLGGKATTASQAKAV    96
PsiHSP47        36   TLAFNLYHTMAKDKNT--ENILVSPVVVASSLGLVSLGGKATTASQAKAV    83
LchHSP47        36   TLAFNLYHTMAKEKNM--ENILISPVVVASSLGLVSLAGKASTASQAKAV    83
AmeHSP47_1      39   NLAFNLYHNLAKETSQ--DNILVSPVVVASSMGLVALGGKSSTSSQVKTV    86
LocHSP47_1      46   SLAFNLYHNMAKDKNA--ENILFSPVVVASSLGLVHLGGKSSTASQAKTV    93
DreHSP47_1      36   NLAFNLYHNVAKEKGL--ENILISPVVVASSLGMVAMGSKSSTASQVKSV    83
GacHSP47_1      36   NLAFSLYHNMAKDKDT--ENILLSPVVVASSLGMVALGGKASTASQVKTV    83
GmoHSP47_1      36   DLAFSLYHNMALDKGT-GDNILVSPVVVASSLGVLALGGKAATASQVKTV    84
OlaHSP47_1      36   NLAFSLYHSMAKDKST--DNIAISPVVVASSLGMVALGGKASTASQVKTV    83
OniHSP47_1      36   NLAFSLYHTMAKEKDT--ENIIISPVVVASSLGLVALGGKASTASQVKTV    83
PfoHSP47_1      36   NLAFSLYHKMAQDKNT--ENIVVSPVVVASSLGLVALGGKASTASQVKTV    83
TruHSP47_1      48   NLAFSLYHNMAKDKNV--ENILISPVVLASSLGMVALGGKASTASQVKTV    95
XmaHSP47_1      36   NLAFSLYHKMAQDKNT--DNIVVSPVVVASSLGLVALGGKATTASQVKTV    83
DreHSP47_2      34   TLAFNLYQNMAKDKDI--ENILISPVVVASSLGLVALGGKSNTASQVKTV    81
OniHSP47_2      41   NLAFSLYQSMVKDKNV--ENIIISPVVVASSLGLVALGGKASTASQVKTI    88
GmoHSP47_2      41   SLAFSLYQRVAQEKDT--ENILISPVVVASALGLVALGGKASTASQVKSL    88
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GacHSP47_2      41   KLAFSLYQNMAKEKSV--ENILISPVVVASTLGLVALGGKAATSSQVKTL    88
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DreHSP47_3      45   SLGLQLYRSLRTNGSQ--TNTFISPLLLANSLLALGGGAKGSTASQFHDL    92
OniHSP47_3      54   TLGLRLYQALRSDSTS--VNVLFSPLLVASSLGALGEGSGGNTSNQVQGL   101
OlaHSP47_2       7   ALGLRLYRALRTPSGS--VNTLFSPLLLASSLKALSEASSGKTSTQIQAL    54
TruHSP47_2      51   ALGLRLYQALRSDSRS--VNTLFSPLLAASSLGALGGGSAGASASQFQDL    98
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LocHSP47_3      35   ALGLRLYRALRNGTQP-PENPLLSPLLLAASLGALSQGAGGATAQQIRGL    83
PfoHSP47_3      43   PLGVRLYQALRSDPGS--VNTLFSPLLLASSLEALSEGSAGKTAEQM---    87
PfoHSP47_4      50   PLGVRLYQALRSDPGS--VNTLFSPLLLASSLEALSEGSAGKTAEQM---    94
PmaHSP47        56   AFAIDLYQSVAKAVPA-MENVVLSPVLVASALGAAQLGASSGTASRLLKA   104
LjaHSP47        91   AFAIDLYQSVAKAVPA-TENVVLSPVLVASALGAAQLGASSATASRLLKA   139
                     ~~~hA~~~~~~~~  =s6B=>    ~~~~~~hB~~~~  ~~~~~hC~~~~
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                 #                    102c
                                       |  @@@           @@@
HsaHSP47     97   LSAEQL--RDEEVHAGLGELLRSLSNSTA---------RNVTWKLGSRLY   135
MmuHSP47     96   LSAEKL--RDEEVHTGLGELLRSLSNSTA---------RNVTWKLGSRLY   134
RnoHSP47     96   LSAEKL--RDEEVHTGLGELLRSLSNSTA---------RNVTWKLGSRLY   134
GgaHSP47     84   LSADKL--NDDYVHSGLSELLNEVSNSTA---------RNVTWKIGNRLY   122
TguHSP47     84   LSADKL--NDDYVHSGLSELLSEVSNSTA---------RNVTWKIGNRLY   122
MgaHSP47     97   LSADKL--NDDYVHSGLSELLNEVSNSTA---------RNVTWKIGNRLY   135
PsiHSP47     84   LSADKL--NDEYVHSGLSELLSEVSNSTA---------RNVTWKLGNRLY   122
LchHSP47     84   LSVDKL--KDEHLHAGLSELLNEVSNSTA---------RNVTWKMGSRLY   122
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LocHSP47_1   94   LSADKV--KDDQLHTGLSELLTEVSNSTA---------RNVTWKIGSRLY   132
DreHSP47_1   84   LKADAL--KDEHLHTGLSELLTEVSDPQT---------RNVTWKISNRLY   122
GacHSP47_1   84   LSADKL--KDEHLHAGLSELLSEVSDAKS---------RNTTWKINNRLY   122
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OlaHSP47_1   84   LSADKL--KDEHLHSGLSELLSEVSDTKA---------RNTTWKINNRLY   122
OniHSP47_1   84   LSADKL--KDEHLHAGLSELLTEVSNAKT---------RNTTWKINNRLY   122
PfoHSP47_1   84   LSADKL--KDEHLHAGLSELLSEVSDQKT---------RNSTWKINNRLY   122
TruHSP47_1   96   LSADKL--KDEHLHAGLSELLTELSDADK---------RNTTWKINNRLY   134
XmaHSP47_1   84   LSADKL--KDEHLHAGLSELLSVVSNQKT---------RNSTWKINNRLY   122
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GmoHSP47_2   89   LKADKL--KDEQLHAGLGELLSEVSDPAV---------RNVTWKIRSRLY   127
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PfoHSP47_2   89   LNAAKV--QDEQLHSGLAELLTEVSDPKE---------RNVTWKISNRLY   127
AmeHSP47_2   82   LSGNKV--KDENLHSSLAEILTEVSNSTE---------RNVTWKISNRLY   120
LocHSP47_2   86   LRVN-L--HEDKLHPAFSELFNDVSNETA---------RNTTWKVGSRLY   123
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DreHSP47_3   93   LRITK---NENVVGETLTTAQKAVHESNG---------TSYILHSSSALF   130
OniHSP47_3  102   LNPPSPVKADTQVPERLAEALKSFSEANG---------TSFHLHASSAVF   142
OlaHSP47_2   55   LRPET---PSETSDGVLSGALKRFTEADG---------SSFHLRWSSAVF    92
TruHSP47_2   99   LKASSS--AKAGAEL-LSESLKSLGKSNG---------TSFHAHASTALF   136
TniHSP47      -   --------------------------------------------------     -
XmaHSP47_3   95   LQPPSG--TKEAVGELLSMALESFVKANG---------TSFQIHASSGVF   133
LocHSP47_3   84   LGAGAM--TPDALAGALAGLLDELHARHN---------ASYALHAAGALF   122
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PfoHSP47_4   95   --PPSG--TKEAVGGLLSVALESFVKANG---------TSFQIHASSCVF   131
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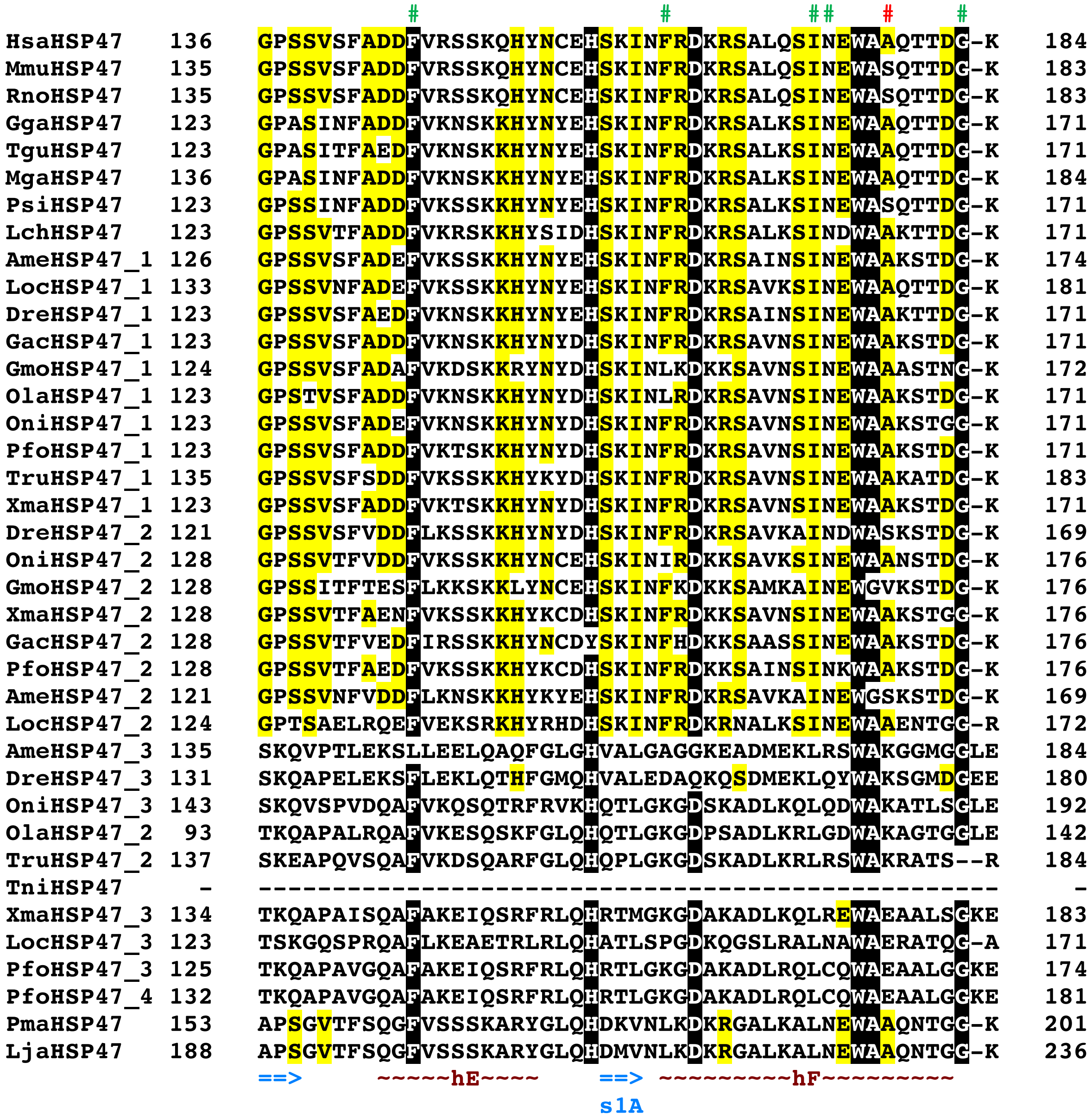

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TguHSP47    123    GPASITFAEDFVKNSKKHYNYEHSKINFRDKRSALKSINEWAAQTTDG-K    171
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LchHSP47    123    GPSSVTFADDFVKRSKKHYSIDHSKINFRDKRSALKSINDWAAKTTDG-K    171
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GmoHSP47_1  124    GPSSVSFADAFVKDSKKRYNYDHSKINLKDKKSAVNSINEWAAASTNG-K    172
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OniHSP47_1  123    GPSSVSFADEFVKNSKKHYNYDHSKINFRDKRSAVNSINEWAAKSTGG-K    171
PfoHSP47_1  123    GPSSVSFADDFVKTSKKHYNYDHSKINFRDKRSAVNSINEWAAKSTDG-K    171
TruHSP47_1  135    GPSSVSFSDDFVKSSKKHYKYDHSKINFRDKRSAVNSINEWAAKATDG-K    183
XmaHSP47_1  123    GPSSVSFADDFVKTSKKHYNYDHSKINFRDKRSAVNSINEWAAKSTDG-K    171
DreHSP47_2  121    GPSSVSFVDDFLKSSKKHYNYDHSKINFRDKRSAVKAINDWASKSTDG-K    169
OniHSP47_2  128    GPSSVTFVDDFVKSSKKHYNCEHSKINIRDKKSAVKSINEWAANSTDG-K    176
GmoHSP47_2  128    GPSSITFTESFLKKSKKLYNCEHSKINFKDKKSAMKAINEWGVKSTDG-K    176
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GacHSP47_2  128    GPSSVTFVEDFIRSSKKHYNCDYSKINFHDKKSAASSINEWAAKSTDG-K    176
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AmeHSP47_2  121    GPSSVNFVDDFLKNSKKHYKYEHSKINFRDKRSAVKAINEWGSKSTDG-K    169
LocHSP47_2  124    GPTSAELRQEFVEKSRKHYRHDHSKINFRDKRNALKSINEWAAENTGG-R    172
AmeHSP47_3  135    SKQVPTLEKSLLEELQAQFGLGHVALGAGGKEADMEKLRSWAKGGMGGLE    184
DreHSP47_3  131    SKQAPELEKSFLEKLQTHFGMQHVALEDAQKQSDMEKLQYWAKSGMDGEE    180
OniHSP47_3  143    SKQVSPVDQAFVKQSQTRFRVKHQTLGKGDSKADLKQLQDWAKATLSGLE    192
OlaHSP47_2   93    TKQAPALRQAFVKESQSKFGLQHQTLGKGDPSADLKRLGDWAKAGTGGLE    142
TruHSP47_2  137    SKEAPQVSQAFVKDSQARFGLQHQPLGKGDSKADLKRLRSWAKRATS--R    184
TniHSP47      -    --------------------------------------------------      -
XmaHSP47_3  134    TKQAPAISQAFAKEIQSRFRLQHRTMGKGDAKADLKQLREWAEAALSGKE    183
LocHSP47_3  123    TSKGQSPRQAFLKEAETRLRLQHATLSPGDKQGSLRALNAWAERATQG-A    171
PfoHSP47_3  125    TKQAPAVGQAFAKEIQSRFRLQHRTLGKGDAKADLRQLCQWAEAALGGKE    174
PfoHSP47_4  132    TKQAPAVGQAFAKEIQSRFRLQHRTLGKGDAKADLRQLCQWAEAALGGKE    181
PmaHSP47    153    APSGVTFSQGFVSSSKARYGLQHDKVNLKDKRGALKALNEWAAQNTGG-K    201
LjaHSP47    188    APSGVTFSQGFVSSSKARYGLQHDMVNLKDKRGALKALNEWAAQNTGG-K    236
                   ==>     ~~~~~hE~~~~    ==> ~~~~~~~~~hF~~~~~~~~~
                                          s1A
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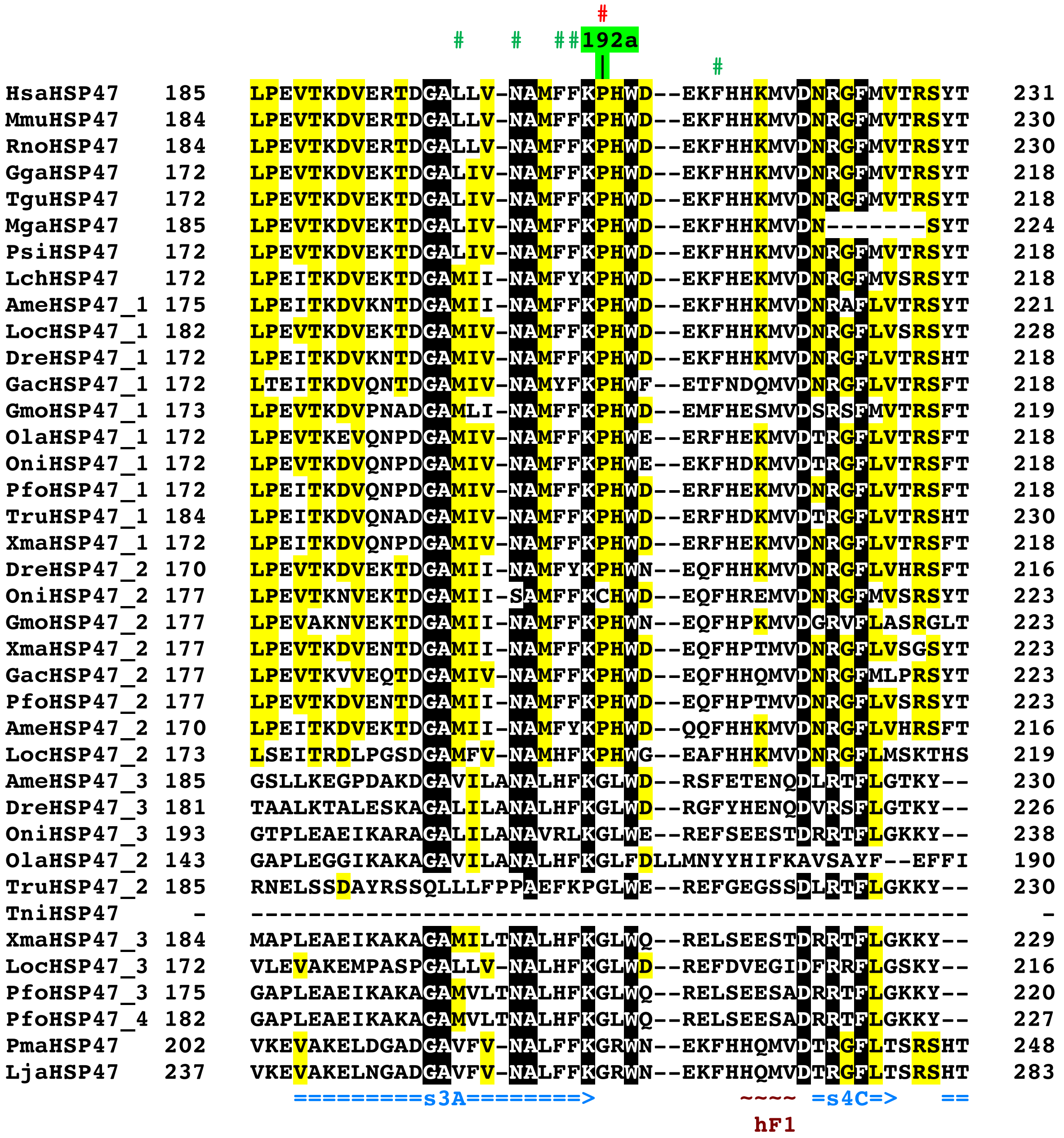

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MmuHSP47    184    LPEVTKDVERTDGALLV-NAMFFKPHWD--EKFHHKMVDNRGFMVTRSYT   230
RnoHSP47    184    LPEVTKDVERTDGALLV-NAMFFKPHWD--EKFHHKMVDNRGFMVTRSYT   230
GgaHSP47    172    LPEVTKDVEKTDGALIV-NAMFFKPHWD--EKFHHKMVDNRGFMVTRSYT   218
TguHSP47    172    LPEVTKDVEKTDGALIV-NAMFFKPHWD--EKFHHKMVDNRGFMVTRSYT   218
MgaHSP47    185    LPEVTKDVEKTDGALIV-NAMFFKPHWD--EKFHHKMVDN-------SYT   224
PsiHSP47    172    LPEVTKDVEKTDGALIV-NAMFFKPHWD--EKFHHKMVDNRGFMVTRSYT   218
LchHSP47    172    LPEITKDVEKTDGAMII-NAMFYKPHWD--EKFHEKMVDNRGFMVSRSYT   218
AmeHSP47_1  175    LPEITKDVKNTDGAMII-NAMFFKPHWD--EKFHHKMVDNRAFLVTRSYT   221
LocHSP47_1  182    LPEVTKDVEKTDGAMIV-NAMFFKPHWD--EKFHHKMVDNRGFLVSRSYT   228
DreHSP47_1  172    LPEITKDVKNTDGAMIV-NAMFFKPHWD--EKFHHKMVDNRGFLVTRSHT   218
GacHSP47_1  172    LTEITKDVQNTDGAMIV-NAMYFKPHWF--ETFNDQMVDNRGFLVTRSFT   218
GmoHSP47_1  173    LPEVTKDVPNADGAMLI-NAMFFKPHWD--EMFHESMVDSRSFMVTRSFT   219
OlaHSP47_1  172    LPEVTKEVQNPDGAMIV-NAMFFKPHWE--ERFHEKMVDTRGFLVTRSFT   218
OniHSP47_1  172    LPEVTKDVQNPDGAMIV-NAMFFKPHWE--EKFHDKMVDTRGFLVTRSFT   218
PfoHSP47_1  172    LPEITKDVQNPDGAMIV-NAMFFKPHWD--ERFHEKMVDNRGFLVTRSFT   218
TruHSP47_1  184    LPEITKDVQNADGAMIV-NAMFFKPHWD--ERFHDKMVDTRGFLVTRSHT   230
XmaHSP47_1  172    LPEITKDVQNPDGAMIV-NAMFFKPHWD--ERFHEKMVDNRGFLVTRSFT   218
DreHSP47_2  170    LPEVTKDVEKTDGAMII-NAMFYKPHWN--EQFHHKMVDNRGFLVHRSFT   216
OniHSP47_2  177    LPEVTKNVEKTDGAMII-SAMFFKCHWD--EQFHREMVDNRGFMVSRSYT   223
GmoHSP47_2  177    LPEVAKNVEKTDGAMII-NAMFFKPHWN--EQFHPKMVDGRVFLASRGLT   223
XmaHSP47_2  177    LPEVTKDVENTDGAMII-NAMFFKPHWD--EQFHPTMVDNRGFLVSGSYT   223
GacHSP47_2  177    LPEVTKVVEQTDGAMIV-NAMFFKPHWD--EQFHHQMVDNRGFMLPRSYT   223
PfoHSP47_2  177    LPEVTKDVENTDGAMII-NAMFFKPHWD--EQFHPTMVDNRGFLVSRSYT   223
AmeHSP47_2  170    LPEITKDVEKTDGAMII-NAMFYKPHWD--QQFHHKMVDNRGFLVHRSFT   216
LocHSP47_2  173    LSEITRDLPGSDGAMFV-NAMHFKPHWG--EAFHHKMVDNRGFLMSKTHS   219
AmeHSP47_3  185    GSLLKEGPDAKDGAVILANALHFKGLWD--RSFETENQDLRTFLGTKY--   230
DreHSP47_3  181    TAALKTALESKAGALILANALHFKGLWD--RGFYHENQDVRSFLGTKY--   226
OniHSP47_3  193    GTPLEAEIKARAGALILANAVRLKGLWE--REFSEESTDRRTFLGKKY--   238
OlaHSP47_2  143    GAPLEGGIKAKAGAVILANALHFKGLFDLLMNYYHIFKAVSAYF--EFFI   190
TruHSP47_2  185    RNELSSDAYRSSQLLLFPPAEFKPGLWE--REFGEGSSDLRTFLGKKY--   230
TniHSP47      -    --------------------------------------------------     -
XmaHSP47_3  184    MAPLEAEIKAKAGAMILTNALHFKGLWQ--RELSEESTDRRTFLGKKY--   229
LocHSP47_3  172    VLEVAKEMPASPGALLV-NALHFKGLWD--REFDVEGIDFRRFLGSKY--   216
PfoHSP47_3  175    GAPLEAEIKAKAGAMVLTNALHFKGLWQ--RELSEESADRRTFLGKKY--   220
PfoHSP47_4  182    GAPLEAEIKAKAGAMVLTNALHFKGLWQ--RELSEESADRRTFLGKKY--   227
PmaHSP47    202    VKEVAKELDGADGAVFV-NALFFKGRWN--EKFHHQMVDTRGFLTSRSHT   248
LjaHSP47    237    VKEVAKELNGADGAVFV-NALFFKGRWN--EKFHHQMVDTRGFLTSRSHT   283
                      =========s3A========>          ~~~~ =s4C=>   ==
                                                      hF1
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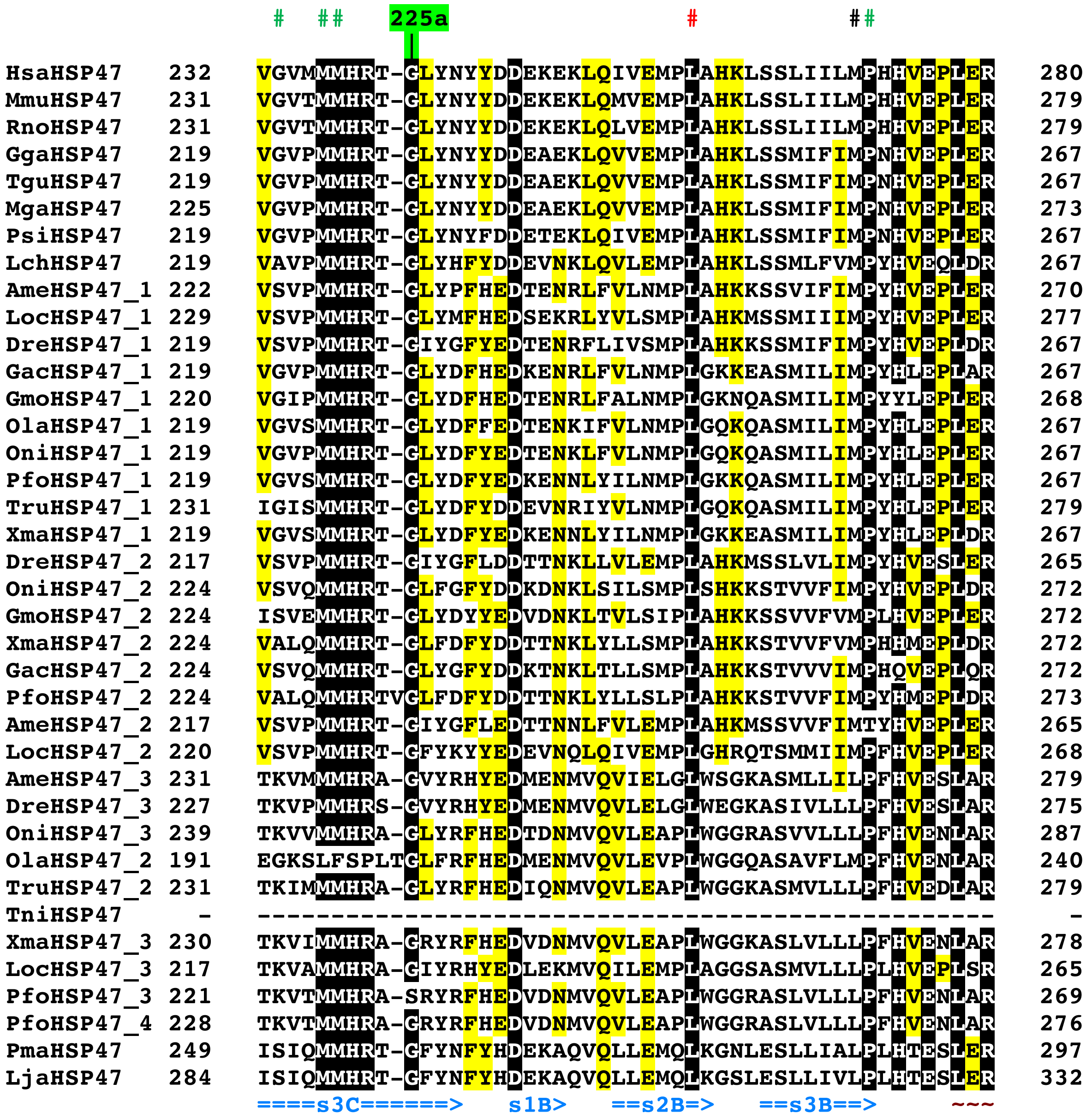
Motif 1



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RnoHSP47    231   VGVTMMHRT-GLYNYYDDEKEKLQLVEMPLAHKLSSLIILMPHHVEPLER    279
GgaHSP47    219   VGVPMMHRT-GLYNYYDDEAEKLQVVEMPLAHKLSSMIFIMPNHVEPLER    267
TguHSP47    219   VGVPMMHRT-GLYNYYDDEAEKLQVVEMPLAHKLSSMIFIMPNHVEPLER    267
MgaHSP47    225   VGVPMMHRT-GLYNYYDDEAEKLQVVEMPLAHKLSSMIFIMPNHVEPLER    273
PsiHSP47    219   VGVPMMHRT-GLYNYFDDETEKLQIVEMPLAHKLSSMIFIMPNHVEPLER    267
LchHSP47    219   VAVPMMHRT-GLYHFYDDEVNKLQVLEMPLAHKLSSMLFVMPYHVEQLDR    267
AmeHSP47_1 222   VSVPMMHRT-GLYPFHEDTENRLFVLNMPLAHKKSSVIFIMPYHVEPLER    270
LocHSP47_1 229   VSVPMMHRT-GLYMFHEDSEKRLYVLSMPLAHKMSSMIIIMPYHVEPLER    277
DreHSP47_1 219   VSVPMMHRT-GIYGFYEDTENRFLIVSMPLAHKKSSMIFIMPYHVEPLDR    267
GacHSP47_1 219   VGVPMMHRT-GLYDFHEDKENRLFVLNMPLGKKEASMILIMPYHLEPLAR    267
GmoHSP47_1 220   VGIPMMHRT-GLYDFHEDTENRLFALNMPLGKNQASMILIMPYYLEPLER    268
OlaHSP47_1 219   VGVSMMHRT-GLYDFFEDTENKIFVLNMPLGQKQASMILIMPYHLEPLER    267
OniHSP47_1 219   VGVPMMHRT-GLYDFYEDTENKLFVLNMPLGQKQASMILIMPYHLEPLER    267
PfoHSP47_1 219   VGVSMMHRT-GLYDFYEDKENNLYILNMPLGKKQASMILIMPYHLEPLER    267
TruHSP47_1 231   IGISMMHRT-GLYDFYDDEVNRIYVLNMPLGQKQASMILIMPYHLEPLER    279
XmaHSP47_1 219   VGVSMMHRT-GLYDFYEDKENNLYILNMPLGKKEASMILIMPYHLEPLDR    267
DreHSP47_2 217   VSVPMMHRT-GIYGFLDDTTNKLLVLEMPLAHKMSSLVLIMPYHVESLER    265
OniHSP47_2 224   VSVQMMHRT-GLFGFYDDKDNKLSILSMPLSHKKSTVVFIMPYHVEPLDR    272
GmoHSP47_2 224   ISVEMMHRT-GLYDYYEDVDNKLTVLSIPLAHKKSSVVFVMPLHVEPLER    272
XmaHSP47_2 224   VALQMMHRT-GLFDFYDDTTNKLYLLSMPLAHKKSTVVFVMPHHMEPLDR    272
GacHSP47_2 224   VSVQMMHRT-GLYGFYDDKTNKLTLLSMPLAHKKSTVVVIMPHQVEPLQR    272
PfoHSP47_2 224   VALQMMHRTVGLFDFYDDTTNKLYLLSLPLAHKKSTVVFIMPYHMEPLDR    273
AmeHSP47_2 217   VSVPMMHRT-GIYGFLEDTTNNLFVLEMPLAHKMSSVVFIMTYHVEPLER    265
LocHSP47_2 220   VSVPMMHRT-GFYKYYEDEVNQLQIVEMPLGHRQTSMMIIMPFHVEPLER    268
AmeHSP47_3 231   TKVMMMHRA-GVYRHYEDMENMVQVIELGLWSGKASMLLILPFHVESLAR    279
DreHSP47_3 227   TKVPMMHRS-GVYRHYEDMENMVQVLELGLWEGKASIVLLLPFHVESLAR    275
OniHSP47_3 239   TKVVMMHRA-GLYRFHEDTDNMVQVLEAPLWGGRASVVLLLPFHVENLAR    287
OlaHSP47_2 191   EGKSLFSPLTGLFRFHEDMENMVQVLEVPLWGGQASAVFLMPFHVENLAR    240
TruHSP47_2 231   TKIMMMHRA-GLYRFHEDIQNMVQVLEAPLWGGKASMVLLLPFHVEDLAR    279
TniHSP47      -   --------------------------------------------------      -
XmaHSP47_3 230   TKVIMMHRA-GRYRFHEDVDNMVQVLEAPLWGGKASLVLLLPFHVENLAR    278
LocHSP47_3 217   TKVAMMHRA-GIYRHYEDLEKMVQILEMPLAGGSASMVLLLPLHVEPLSR    265
PfoHSP47_3 221   TKVTMMHRA-SRYRFHEDVDNMVQVLEAPLWGGRASLVLLLPFHVENLAR    269
PfoHSP47_4 228   TKVTMMHRA-GRYRFHEDVDNMVQVLEAPLWGGRASLVLLLPFHVENLAR    276
PmaHSP47   249   ISIQMMHRT-GFYNFYHDEKAQVQLLEMQLKGNLESLLIALPLHTESLER    297
LjaHSP47   284   ISIQMMHRT-GFYNFYHDEKAQVQLLEMQLKGSLESLLIVLPLHTESLER    332
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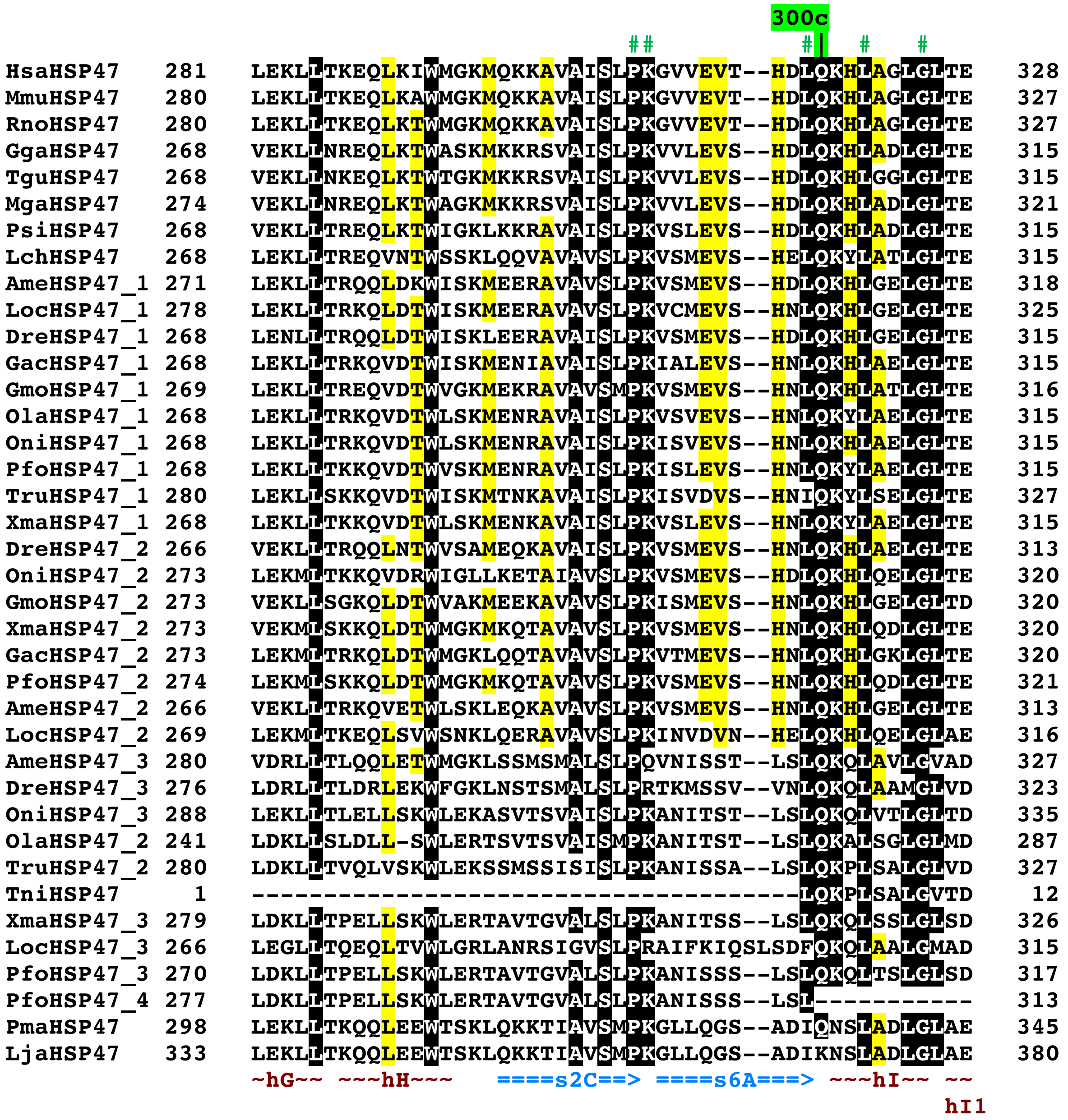

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MmuHSP47    280   LEKLLTKEQLKAWMGKMQKKAVAISLPKGVVEVT--HDLQKHLAGLGLTE    327
RnoHSP47    280   LEKLLTKEQLKTWMGKMQKKAVAISLPKGVVEVT--HDLQKHLAGLGLTE    327
GgaHSP47    268   VEKLLNREQLKTWASKMKKRSVAISLPKVVLEVS--HDLQKHLADLGLTE    315
TguHSP47    268   VEKLLNKEQLKTWTGKMKKRSVAISLPKVVLEVS--HDLQKHLGGLGLTE    315
MgaHSP47    274   VEKLLNREQLKTWAGKMKKRSVAISLPKVVLEVS--HDLQKHLADLGLTE    321
PsiHSP47    268   VEKLLTREQLKTWIGKLKKRAVAISLPKVSLEVS--HDLQKHLADLGLTE    315
LchHSP47    268   LEKLLTREQVNTWSSKLQQVAVAVSLPKVSMEVS--HELQKYLATLGLTE    315
AmeHSP47_1  271   LEKLLTRQQLDKWISKMEERAVAVSLPKVSMEVS--HDLQKHLGELGLTE    318
LocHSP47_1  278   LEKLLTRKQLDTWISKMEERAVAVSLPKVCMEVS--HNLQKHLGELGLTE    325
DreHSP47_1  268   LENLLTRQQLDTWISKLEERAVAISLPKVSMEVS--HDLQKHLGELGLTE    315
GacHSP47_1  268   LEKLLTRKQVDTWISKMENIAVAISLPKIALEVS--HNLQKHLAELGLTE    315
GmoHSP47_1  269   LEKLLTREQVDTWVGKMEKRAVAVSMPKVSMEVS--HNLQKHLATLGLTE    316
OlaHSP47_1  268   LEKLLTRKQVDTWLSKMENRAVAISLPKVSVEVS--HNLQKYLAELGLTE    315
OniHSP47_1  268   LEKLLTRKQVDTWLSKMENRAVAISLPKISVEVS--HNLQKHLAELGLTE    315
PfoHSP47_1  268   LEKLLTKKQVDTWVSKMENRAVAISLPKISLEVS--HNLQKYLAELGLTE    315
TruHSP47_1  280   LEKLLSKKQVDTWISKMTNKAVAISLPKISVDVS--HNIQKYLSELGLTE    327
XmaHSP47_1  268   LEKLLTKKQVDTWLSKMENKAVAISLPKVSLEVS--HNLQKYLAELGLTE    315
DreHSP47_2  266   VEKLLTRQQLNTWVSAMEQKAVAISLPKVSMEVS--HNLQKHLAELGLTE    313
OniHSP47_2  273   LEKMLTKKQVDRWIGLLKETAIAVSLPKVSMEVS--HDLQKHLQELGLTE    320
GmoHSP47_2  273   VEKLLSGKQLDTWVAKMEEKAVAVSLPKISMEVS--HNLQKHLGELGLTD    320
XmaHSP47_2  273   VEKMLSKKQLDTWMGKMKQTAVAVSLPKVSMEVS--HNLQKHLQDLGLTE    320
GacHSP47_2  273   LEKMLTRKQLDTWMGKLQQTAVAVSLPKVTMEVS--HNLQKHLGKLGLTE    320
PfoHSP47_2  274   LEKMLSKKQLDTWMGKMKQTAVAVSLPKVSMEVS--HNLQKHLQDLGLTE    321
AmeHSP47_2  266   VEKLLTRKQVETWLSKLEQKAVAVSLPKVSMEVS--HNLQKHLGELGLTE    313
LocHSP47_2  269   LEKMLTKEQLSVWSNKLQERAVAVSLPKINVDVN--HELQKHLQELGLAE    316
AmeHSP47_3  280   VDRLLTLQQLETWMGKLSSMSMALSLPQVNISST--LSLQKQLAVLGVAD    327
DreHSP47_3  276   LDRLLTLDRLEKWFGKLNSTSMALSLPRTKMSSV--VNLQKQLAAMGLVD    323
OniHSP47_3  288   LEKLLTLELLSKWLEKASVTSVAISLPKANITST--LSLQKQLVTLGLTD    335
OlaHSP47_2  241   LDKLLSLDLL-SWLERTSVTSVAISMPKANITST--LSLQKALSGLGLMD    287
TruHSP47_2  280   LDKLLTVQLVSKWLEKSSMSSISISLPKANISSA--LSLQKPLSALGLVD    327
TniHSP47      1   --------------------------------------LQKPLSALGVTD     12
XmaHSP47_3  279   LDKLLTPELLSKWLERTAVTGVALSLPKANITSS--LSLQKQLSSLGLSD    326
LocHSP47_3  266   LEGLLTQEQLTVWLGRLANRSIGVSLPRAIFKIQSLSDFQKQLAALGMAD    315
PfoHSP47_3  270   LDKLLTPELLSKWLERTAVTGVALSLPKANISSS--LSLQKQLTSLGLSD    317
PfoHSP47_4  277   LDKLLTPELLSKWLERTAVTGVALSLPKANISSS--LSL-----------    313
PmaHSP47    298   LEKLLTKQQLEEWTSKLQKKTIAVSMPKGLLQGS--ADIQNSLADLGLAE    345
LjaHSP47    333   LEKLLTKQQLEEWTSKLQKKTIAVSMPKGLLQGS--ADIKNSLADLGLAE    380
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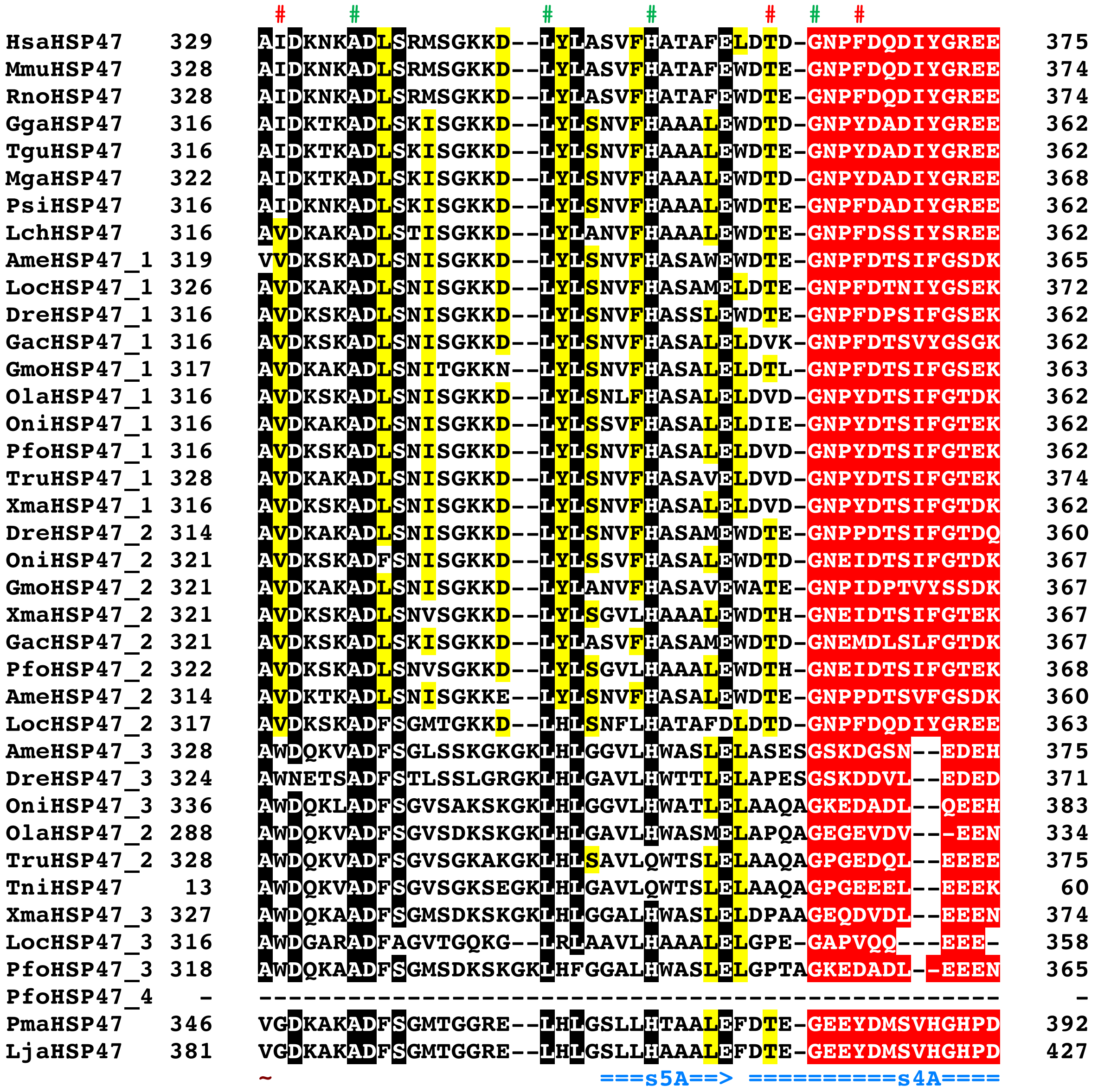

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RnoHSP47   328   AIDKNKADLSRMSGKKD--LYLASVFHATAFEWDTE-GNPFDQDIYGREE   374
GgaHSP47   316   AIDKTKADLSKISGKKD--LYLSNVFHAAALEWDTD-GNPYDADIYGREE   362
TguHSP47   316   AIDKTKADLSKISGKKD--LYLSNVFHAAALEWDTE-GNPYDADIYGREE   362
MgaHSP47   322   AIDKTKADLSKISGKKD--LYLSNVFHAAALEWDTD-GNPYDADIYGREE   368
PsiHSP47   316   AIDKNKADLSKISGKKD--LYLSNVFHAAALEWDTE-GNPFDADIYGREE   362
LchHSP47   316   AVDKAKADLSTISGKKD--LYLANVFHAAALEWDTE-GNPFDSSIYSREE   362
AmeHSP47_1 319   VVDKSKADLSNISGKKD--LYLSNVFHASAWEWDTE-GNPFDTSIFGSDK   365
LocHSP47_1 326   AVDKAKADLSNISGKKD--LYLSNVFHASAMELDTE-GNPFDTNIYGSEK   372
DreHSP47_1 316   AVDKSKADLSNISGKKD--LYLSNVFHASSLEWDTE-GNPFDPSIFGSEK   362
GacHSP47_1 316   AVDKSKADLSNISGKKD--LYLSNVFHASALELDVK-GNPFDTSVYGSGK   362
GmoHSP47_1 317   AVDKAKADLSNITGKKN--LYLSNVFHASALELDTL-GNPFDTSIFGSEK   363
OlaHSP47_1 316   AVDKSKADLSNISGKKD--LYLSNLFHASALELDVD-GNPYDTSIFGTDK   362
OniHSP47_1 316   AVDKAKADLSNISGKKD--LYLSSVFHASALELDIE-GNPYDTSIFGTEK   362
PfoHSP47_1 316   AVDKSKADLSNISGKKD--LYLSNVFHASALELDVD-GNPYDTSIFGTEK   362
TruHSP47_1 328   AVDKAKADLSNISGKKD--LYLSNVFHASAVELDVD-GNPYDTSIFGTEK   374
XmaHSP47_1 316   AVDKSKADLSNISGKKD--LYLSNVFHASALELDVD-GNPYDTSIFGTDK   362
DreHSP47_2 314   AVDKAKADLSNISGKKD--LYLSNVFHASAMEWDTE-GNPPDTSIFGTDQ   360
OniHSP47_2 321   AVDKSKADFSNISGKKD--LYLSSVFHASALEWDTD-GNEIDTSIFGTDK   367
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XmaHSP47_2 321   AVDKSKADLSNVSGKKD--LYLSGVLHAAALEWDTH-GNEIDTSIFGTEK   367
GacHSP47_2 321   AVDKSKADLSKISGKKD--LYLASVFHASAMEWDTD-GNEMDLSLFGTDK   367
PfoHSP47_2 322   AVDKSKADLSNVSGKKD--LYLSGVLHAAALEWDTH-GNEIDTSIFGTEK   368
AmeHSP47_2 314   AVDKTKADLSNISGKKE--LYLSNVFHASALEWDTE-GNPPDTSVFGSDK   360
LocHSP47_2 317   AVDKSKADFSGMTGKKD--LHLSNFLHATAFDLDTD-GNPFDQDIYGREE   363
AmeHSP47_3 328   AWDQKVADFSGLSSKGKGKLHLGGVLHWASLELASESGSKDGSN--EDEH   375
DreHSP47_3 324   AWNETSADFSTLSSLGRGKLHLGAVLHWTTLELAPESGSKDDVL--EDED   371
OniHSP47_3 336   AWDQKLADFSGVSAKSKGKLHLGGVLHWATLELAAQAGKEDADL--QEEH   383
OlaHSP47_2 288   AWDQKVADFSGVSDKSKGKLHLGAVLHWASMELAPQAGEGEVDV---EEN   334
TruHSP47_2 328   AWDQKVADFSGVSGKAKGKLHLSAVLQWTSLELAAQAGPGEDQL--EEEE   375
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XmaHSP47_3 327   AWDQKAADFSGMSDKSKGKLHLGGALHWASLELDPAAGEQDVDL--EEEN   374
LocHSP47_3 316   AWDGARADFAGVTGQKG--LRLAAVLHAAALELGPE-GAPVQQ---EEE-   358
PfoHSP47_3 318   AWDQKAADFSGMSDKSKGKLHFGGALHWASLELGPTAGKEDADL--EEEN   365
PfoHSP47_4   -   --------------------------------------------------     -
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LjaHSP47   381   VGDKAKADFSGMTGGRE--LHLGSLLHAAALEFDTE-GEEYDMSVHGHPD   427
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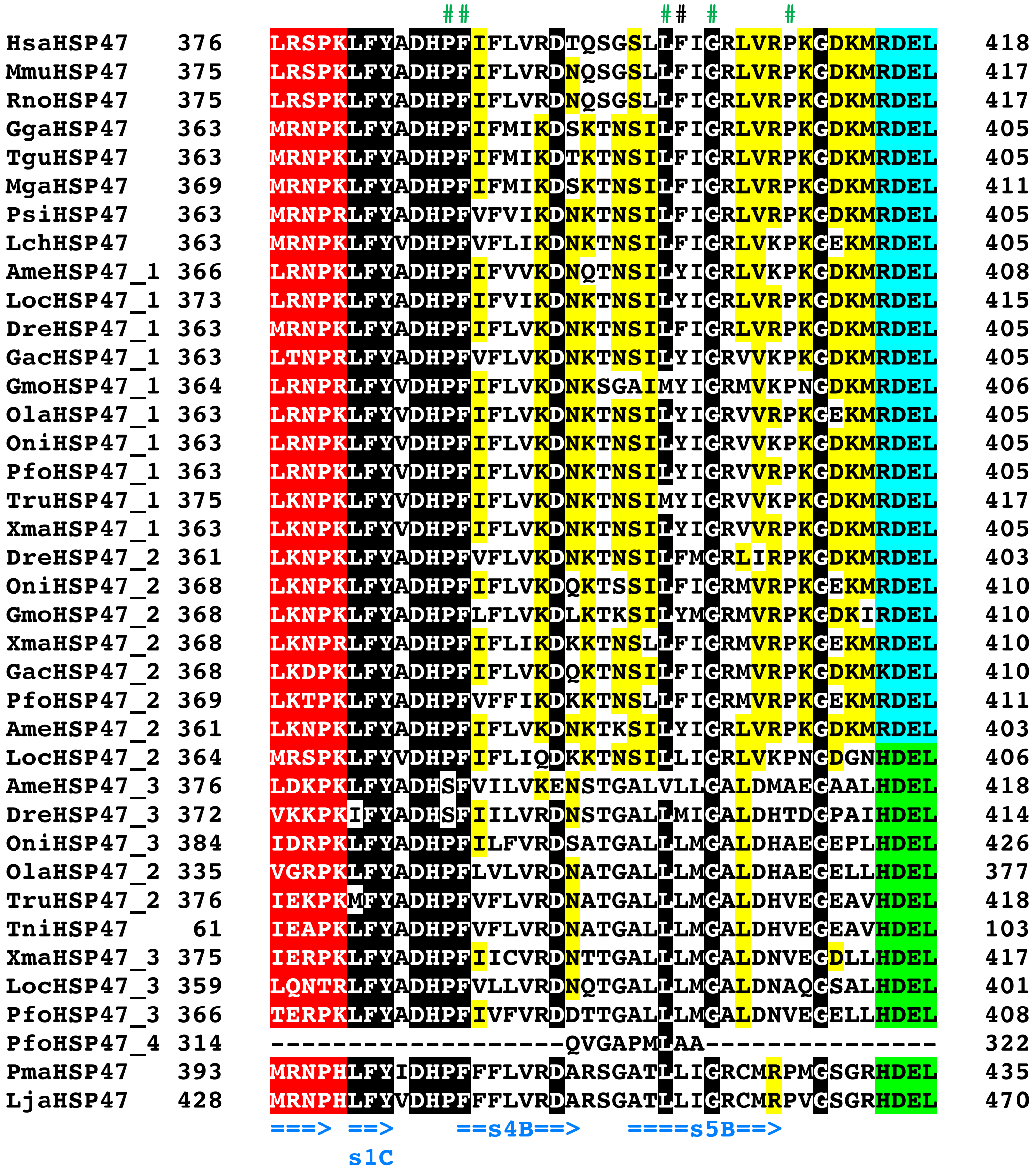
Motif 2



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RnoHSP47     375  LRSPKLFYADHPFIFLVRDNQSGSLLFIGRLVRPKGDKMRDEL  417
GgaHSP47     363  MRNPKLFYADHPFIFMIKDSKTNSILFIGRLVRPKGDKMRDEL  405
TguHSP47     363  MRNPKLFYADHPFIFMIKDTKTNSILFIGRLVRPKGDKMRDEL  405
MgaHSP47     369  MRNPKLFYADHPFIFMIKDSKTNSILFIGRLVRPKGDKMRDEL  411
PsiHSP47     363  MRNPRLFYADHPFVFVIKDNKTNSILFIGRLVRPKGDKMRDEL  405
LchHSP47     363  MRNPKLFYVDHPFVFLIKDNKTNSILFIGRLVKPKGEKMRDEL  405
AmeHSP47_1   366  LRNPKLFYADHPFIFVVKDNQTNSILYIGRLVKPKGDKMRDEL  408
LocHSP47_1   373  LRNPKLFYADHPFIFVIKDNKTNSILYIGRLVRPKGDKMRDEL  415
DreHSP47_1   363  MRNPKLFYADHPFIFLVKDNKTNSILFIGRLVRPKGDKMRDEL  405
GacHSP47_1   363  LTNPRLFYADHPFVFLVKDNKTNSILYIGRVVKPKGDKMRDEL  405
GmoHSP47_1   364  LRNPRLFYVDHPFIFLVKDNKSGAIMYIGRMVKPNGDKMRDEL  406
OlaHSP47_1   363  LRNPKLFYVDHPFIFLVKDNKTNSILYIGRVVRPKGEKMRDEL  405
OniHSP47_1   363  LRNPKLFYVDHPFIFLVKDNKTNSILYIGRVVKPKGDKMRDEL  405
PfoHSP47_1   363  LRNPKLFYVDHPFIFLVKDNKTNSILYIGRVVRPKGDKMRDEL  405
TruHSP47_1   375  LKNPKLFYVDHPFIFLVKDNKTNSIMYIGRVVKPKGDKMRDEL  417
XmaHSP47_1   363  LKNPKLFYVDHPFIFLVKDNKTNSILYIGRVVRPKGDKMRDEL  405
DreHSP47_2   361  LKNPKLFYADHPFVFLVKDNKTNSILFMGRLIRPKGDKMRDEL  403
OniHSP47_2   368  LKNPKLFYADHPFIFLVKDQKTSSILFIGRMVRPKGEKMRDEL  410
GmoHSP47_2   368  LKNPKLFYADHPFLFLVKDLKTKSILYMGRMVRPKGDKIRDEL  410
XmaHSP47_2   368  LKNPRLFYADHPFIFLIKDKKTNSLLFIGRMVRPKGEKMRDEL  410
GacHSP47_2   368  LKDPKLFYADHPFIFLVKDQKTNSILFIGRMVRPKGDKMKDEL  410
PfoHSP47_2   369  LKTPKLFYADHPFVFFIKDKKTNSLLFIGRMVRPKGEKMRDEL  411
AmeHSP47_2   361  LKNPKLFYADHPFIFLVKDNKTKSILYIGRLVRPKGDKMRDEL  403
LocHSP47_2   364  MRSPKLFYVDHPFIFLIQDKKTNSILLIGRLVKPNGDGNHDEL  406
AmeHSP47_3   376  LDKPKLFYADHSFVILVKENSTGALVLLGALDMAEGAALHDEL  418
DreHSP47_3   372  VKKPKIFYADHSFIILVRDNSTGALLMIGALDHTDGPAIHDEL  414
OniHSP47_3   384  IDRPKLFYADHPFILFVRDSATGALLLMGALDHAEGEPLHDEL  426
OlaHSP47_2   335  VGRPKLFYADHPFLVLVRDNATGALLLMGALDHAEGELLHDEL  377
TruHSP47_2   376  IEKPKMFYADHPFVFLVRDNATGALLLMGALDHVEGEAVHDEL  418
TniHSP47      61  IEAPKLFYADHPFVFLVRDNATGALLLMGALDHVEGEAVHDEL  103
XmaHSP47_3   375  IERPKLFYADHPFIICVRDNTTGALLLMGALDNVEGDLLHDEL  417
LocHSP47_3   359  LQNTRLFYADHPFVLLVRDNQTGALLLMGALDNAQGSALHDEL  401
PfoHSP47_3   366  TERPKLFYADHPFIVFVRDDTTGALLLMGALDNVEGELLHDEL  408
PfoHSP47_4   314  -------------------QVGAPMLAA---------------  322
PmaHSP47     393  MRNPHLFYIDHPFFFLVRDARSGATLLIGRCMRPMGSGRHDEL  435
LjaHSP47     428  MRNPHLFYVDHPFFFLVRDARSGATLLIGRCMRPVGSGRHDEL  470
                  ===> ==>    ==s4B==>   ====s5B==>
                       s1C
```

Motif 3

Fig S3. Summary of sequence analyses of different HSP47/SERPINH1.

A. Set I-III of HSP47/SERPINH1 shares different sequence identity ranges with HsaHSP47/SERPINH1. It hints for recent duplication of sets I and II being very close and set III being diverged.

B. Sequence logo of the reactive center loops of three sets of HSP47/SERPINH1 depicts non-inhibitory nature and differences with loss of two residues in the set III.

C. The C-terminal ends of different HSP47/SERPINH1 proteins depicts that ER-retention signal has different in the set III with R being replaced by H.

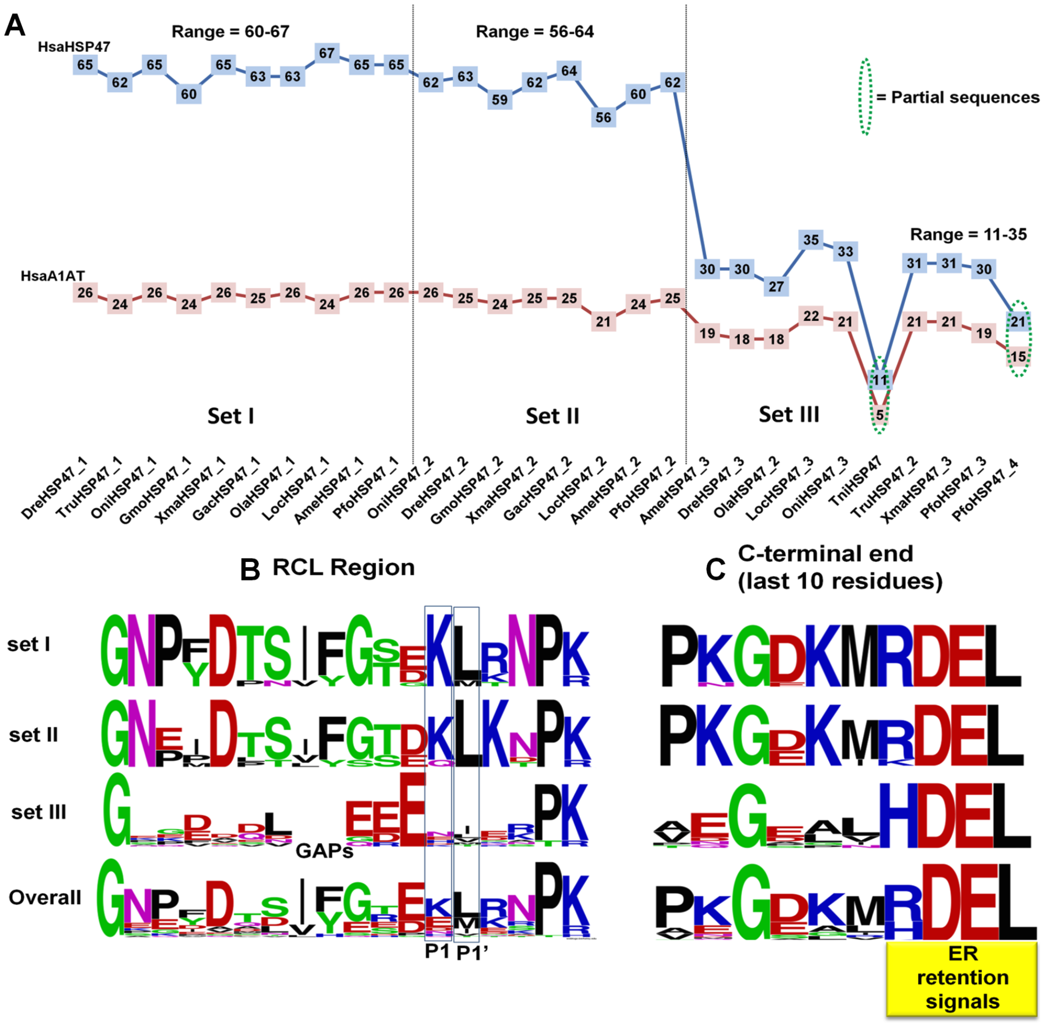

Table S1. Overview of HSP47 genes from 61 vertebrate genomes, their assemblies and genomic localization.

Species	**Genome assembly**	**Accession id**	**Genomic localization**
Ailuropoda melanoleuca	ailMel1 (GCA_000004335.1)	ENSAMEG00000017004	Scaffold GL192425.1: 1,119,608-1,124,040
Anas platyrhynchos	BGI_duck_1.0 (GCA_000355885.1)	ENSAPLG00000014348	Scaffold KB743381.1: 113,502-116,434
Anolis carolinensis	AnoCar2.0 (GCA_000090745.1)	ENSACAG00000002229	Scaffold GL343298.1: 714,401-718,931
Astyanax mexicanus	AstMex102 (GCA_000372685.1)	ENSAMXG00000000056	Scaffold KB871604.1: 223,363-229,678
Astyanax mexicanus	AstMex102 (GCA_000372685.1)	ENSAMXG00000006432	Scaffold KB882085.1: 1,768,034-1,776,194
Astyanax mexicanus	AstMex102 (GCA_000372685.1)	ENSAMXG00000003269	Scaffold KB882131.1: 359,489-395,080
Bos taurus	UMD3.1 (GCA_000003055.3)	ENSBTAG00000001027	Chromosome 15: 55,514,945-55,525,175
Callithrix jacchus	C_jacchus3.2.1 (GCA_000004665.1)	ENSCJAG00000015377	Chromosome 11: 63,119,525-63,130,780
Canis lupus familiaris	CanFam3.1 (GCA_000002285.2)	ENSCAFG00000005386	Chromosome 21: 23,033,455-23,042,446
Cavia porcellus	cavPor3	ENSCPOG00000022994	scaffold_103: 114,481-117,787
Chlorocebus sabaeus	ChlSab1.1 (GCA_000409795.2)	ENSCSAG00000003909	Chromosome 1: 66,788,240-66,799,072
Danio rerio	Zv9 (GCA_000002035.2)	ENSDARG00000019949	Chromosome 15: 28,732,298-28,736,597
Danio rerio	Zv9 (GCA_000002035.2)	ENSDARG00000075954	Chromosome 10: 39,878,541-39,887,981
Danio rerio	Zv9 (GCA_000002035.2)	ENSDARG00000036445	Chromosome 7: 22,441,345-22,478,600
Dasypus novemcinctus	Dasnov3.0 (GCA_000208655.2)	ENSDNOG00000019034	Scaffold JH568609.1: 111,384-121,357
Dipodomys ordii	dipOrd1	ENSDORG00000002978	GeneScaffold_4955: 160,144-165,399
Echinops telfairi	TENREC	ENSETEG00000017520	scaffold_303682: 3,151-7,601
Equus caballus	Equ Cab 2 (GCA_000002305.1)	ENSECAG00000004871	Chromosome 7: 68,605,995-68,611,500
Erinaceus europaeus	eriEur1	ENSEEUG00000003946	GeneScaffold_511: 19,319-22,838
Felis catus	Felis_catus_6.2 (GCA_000181335.2)	ENSFCAG00000011944	Chromosome D1: 59,000,253-59,009,974
Ficedula albicollis	FicAlb_1.4 (GCA_000247815.1)	ENSFALG00000006601	Scaffold JH603425.1: 18,154-20,583
Gadus morhua	gadMor1 (GCA_000231765.1)	ENSGMOG00000001309	GeneScaffold_1352: 269,125-271,324
Gadus morhua	gadMor1 (GCA_000231765.1)	ENSGMOG00000007382	GeneScaffold_4231: 9,838-13,332
Gallus gallus	Galgal4 (GCA_000002315.2)	ENSGALG00000011214	Chromosome 1: 194,288,921-194,295,617
Gasterosteus aculeatus	BROADS1	ENSGACG00000006375	groupI: 3,124,210-3,127,693
Gasterosteus aculeatus	BROADS1	ENSGACG00000020152	groupVII: 12,211,634-12,215,855
Gorilla gorilla gorilla	gorGor3.1 (GCA_000151905.1)	ENSGGOG00000005397	Chromosome 11: 72,594,231-72,604,934
Homo sapiens	GRCh37 (GCA_000001405.13)	ENSG00000149257	Chromosome 11: 75,273,101-75,283,828
Ictidomys tridecemlineatus	spetri2 (GCA_000236235.1)	ENSSTOG00000027738	Scaffold JH393308.1: 4,265,158-4,350,937
Latimeria chalumnae	LatCha1 (GCA_000225785.1)	ENSLACG00000006746	Scaffold JH129193.1: 234,078-249,245

Poecilia formosa	Poecilia_formosa-5.1.2 (GCA_000485575.1)	ENSPFOG00000013710	Scaffold AYCK01029354.1: 5,404-12,214
Pongo abelii	PPYG2 (GCA_000001545.1)	ENSPPYG00000003691	Chromosome 11: 71,005,958-71,015,006
Procavia capensis	proCap1	ENSPCAG00000010663	GeneScaffold_4297: 70,366-73,898
Pteropus vampyrus	pteVam1	ENSPVAG00000011278	GeneScaffold_1708: 259,301-263,374
Rattus norvegicus	Rnor_5.0 (GCA_000001895.3)	ENSRNOG00000016831	Chromosome 1: 170,503,596-170,510,775
Sarcophilus harrisii	Devil_ref v7.0 (GCA_000189315.1)	ENSSHAG00000009364	Scaffold GL849728.1: 535,612-545,598
Sus scrofa	Sscrofa10.2 (GCA_000003025.4)	ENSSSCG00000014859	Chromosome 9: 10,972,133-10,976,532
Taeniopygia guttata	taeGut3.2.4	ENSTGUG00000013481	Chromosome 1: 99,126,385-99,128,353
Takifugu rubripes	FUGU4	ENSTRUG00000001559	scaffold_131: 112,128-113,986
Takifugu rubripes	FUGU4	ENSTRUG00000004704	Scaffold_186: 231,121-242,595
Tarsius syrichta	tarSyr1	ENSTSYG00000007354	GeneScaffold_4812: 539-2,737
Tetraodon nigroviridis	TETRAODON8	ENSTNIG00000004097	Chromosome Un_random: 493,910-494,221
Tupaia belangeri	tupBel1	ENSTBEG00000001023	GeneScaffold_3565: 125,861-130,281
Tursiops truncatus	turTru1	ENSTTRG00000012009	scaffold_112285: 165,941-171,301
Xenopus tropicalis	JGI 4.2 (GCA_000004195.1)	ENSXETG00000010725	Scaffold GL172913.1: 1,301,229-1,303,075
Xiphophorus maculatus	Xipmac4.4.2 (GCA_000241075.1)	ENSXMAG00000001370	Scaffold AGAJ01049567.1: 337-4,406
Xiphophorus maculatus	Xipmac4.4.2 (GCA_000241075.1)	ENSXMAG00000014013	Scaffold JH556831.1: 757,758-762,448
Xiphophorus maculatus	Xipmac4.4.2 (GCA_000241075.1)	ENSXMAG00000013925	Scaffold JH557141.1: 97,083-122,348

*From webpage of the Japanese lamprey genome project (http://jlampreygenome.imcb.a-star.edu.sg/)

Lepisosteus oculatus	LepOcu1 (GCA_000242695.1)	ENSLOCG00000000987	Chromosome LG3: 474,771-481,123
Lepisosteus oculatus	LepOcu1 (GCA_000242695.1)	ENSLOCG00000014734	Chromosome LG7: 41,901,506-41,905,696
Lepisosteus oculatus	LepOcu1 (GCA_000242695.1)	ENSLOCG00000013424	Chromosome LG2: 58,538,944-58,547,367
Lethenteron japonicum	LetJap1.0 (APJL00000000.1)	JL8319	Scaffold00131: 1482314-1484962
Loxodonta africana	Loxafr3.0 (GCA_000001905.1)	ENSLAFG00000003780	SuperContig scaffold_79: 1,878,003-1,881,599
Macaca mulatta	MMUL 1.0	ENSMMUG00000007675	Chromosome 14: 73,742,253-73,752,788
Macropus eugenii	Meug_1.0 (GCA_000004035.1)	ENSMEUG00000008709	GeneScaffold_5800: 3,692-18,612
Meleagris gallopavo	UMD2 (GCA_000146605.1)	ENSMGAG00000015291	Chromosome 1: 203,021,087-203,026,274
Microcebus murinus	micMur1	ENSMICG00000015249	GeneScaffold_2542: 23,359-28,326
Monodelphis domestica	monDom5 (GCF_000002295.2)	ENSMODG00000006814	Chromosome 4: 342,820,867-342,826,459
Mus musculus	GRCm38 (GCA_000001635.3)	ENSMUSG00000070436	Chromosome 7: 99,345,375-99,353,230
Mustela putorius furo	MusPutFur1.0 (GCA_000215625.1)	ENSMPUG00000009062	Scaffold GL897030.1: 1,507,718-1,515,757
Myotis lucifugus	Myoluc2.0 (GCA_000147115.1)	ENSMLUG00000004105	Scaffold GL430204: 307,832-312,479
Nomascus leucogenys	Nleu1.0 (GCA_000146795.1)	ENSNLEG00000016882	SuperContig GL397264.1: 14,732,258-14,742,905
Ochotona princeps	OchPri2.0	ENSOPRG00000007518	GeneScaffold_3741: 324,406-328,787
Oreochromis niloticus	Orenil1.0 (GCA_000188235.1)	ENSONIG00000005220	Scaffold GL831147.1: 2,758,965-2,761,367
Oreochromis niloticus	Orenil1.0 (GCA_000188235.1)	ENSONIG00000015878	Scaffold GL831214.1: 2,676,278-2,680,779
Oreochromis niloticus	Orenil1.0 (GCA_000188235.1)	ENSONIG00000019907	Scaffold GL831388.1: 444,615-464,598
Oryctolagus cuniculus	OryCun2.0 (GCA_000003625.1)	ENSOCUG00000026029	Chromosome 1: 141,174,524-141,175,285
Oryzias latipes	MEDAKA1	ENSORLG00000014312	Chromosome 13: 27,993,919-27,996,591
Oryzias latipes	MEDAKA1	ENSORLT00000004598	Chromosome 18: 5,866,958-5,900,935
Otolemur garnettii	OtoGar3 (GCA_000181295.3)	ENSOGAG00000032244	Scaffold GL873520.1: 26,857,182-26,863,215
Ovis aries	Oar_v3.1 (GCA_000298735.1)	ENSOARG00000011824	Chromosome 15: 52,925,655-52,931,691
Pan troglodytes	CHIMP2.1.4 (GCA_000001515.4)	ENSPTRG00000004083	Chromosome 11: 73,325,614-73,336,379
Papio anubis	PapAnu2.0 (GCA_000264685.1)	ENSPANG00000015277	Chromosome 14: 65,410,443-65,424,007
Pelodiscus sinensis	PelSin_1.0 (GCA_000230535.1)	ENSPSIG00000008216	Scaffold JH210954.1: 315,916-321,989
Petromyzon Marinus	Pmarinus_7.0 (GCA_000148955.1)	ENSPMAG00000007485	Scaffold GL481971: 179,843-181,907
Poecilia formosa	Poecilia_formosa-5.1.2 (GCA_000485575.1)	ENSPFOG00000005984	Scaffold KI519751.1: 1,375,174-1,379,276
Poecilia formosa	Poecilia_formosa-5.1.2 (GCA_000485575.1)	ENSPFOG00000001716	Scaffold KI520426.1: 60,059-64,596
Poecilia formosa	Poecilia_formosa-5.1.2 (GCA_000485575.1)	ENSPFOG00000001241	Scaffold KI519773.1: 208,366-229,202

Table S2. Summary of 15 genes flanking on the each side of Human HSP47.

Gene	Description	Chromosomal Location	Strand
KCNE3	potassium channel, voltage gated subfamily E regulatory beta subunit 3	11 : 74,454,841 - 74,467,729	minus
LIPT2	lipoyl(octanoyl) transferase 2 (putative)	11 : 74,491,712 - 74,493,733	minus
POLD3	polymerase (DNA-directed), delta 3, accessory subunit	11 : 74,493,851 - 74,669,117	plus
CHRDL2	chordin-like 2	11 : 74,696,429 - 74,731,385	minus
RNF169	ring finger protein 169	11 : 74,748,868 - 74,842,413	plus
XRRA1	X-ray radiation resistance associated 1	11 : 74,807,739 - 74,949,200	minus
SPCS2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	11 : 74,949,247 - 74,979,031	plus
NEU3	sialidase 3 (membrane sialidase)	11 : 74,988,134 - 75,018,893	plus
OR2AT4	olfactory receptor, family 2, subfamily AT, member 4	11 : 75,088,713 - 75,089,754	minus
SLCO2B1	solute carrier organic anion transporter family, member 2B1	11 : 75,100,563 - 75,206,549	plus
TPBGL	trophoblast glycoprotein-like	11 : 75,240,905 - 75,243,697	plus
ARRB1	*arrestin, beta 1*	*11 : 75,264,182 - 75,351,705*	*minus*
RPS3	*ribosomal protein S3*	*11 : 75,399,486 - 75,422,280*	*plus*
KLHL35	*kelch-like family member 35*	*11 : 75,422,394 - 75,430,629*	*minus*
GDPD5	*glycerophosphodiester phosphodiesterase domain containing 5*	*11 : 75,434,640 - 75,525,903*	*minus*
HSP47	***Heat Shock protein 47 kDA, HSP47, SERPINH1***	***11 : 75,562,056 - 75,572,783***	***plus***
MAP6	*microtubule-associated protein 6*	*11 : 75,586,918 - 75,669,120*	*minus*
MOGAT2	*monoacylglycerol O-acyltransferase 2*	*11 : 75,717,819 - 75,732,958*	*plus*
DGAT2	*diacylglycerol O-acyltransferase 2*	*11 : 75,759,512 - 75,801,535*	*plus*
UVRAG	*UV radiation resistance associated*	*11 : 75,815,167 - 76,143,195*	*plus*
WNT11	*wingless-type MMTV integration site family, member 11*	*11 : 76,186,325 - 76,210,736*	*minus*
PRKRIR	*protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)*	*11 : 76,349,956 - 76,380,971*	*minus*
RP11-111M22.2	RP11-111M22.2	11 : 76,381,313 - 76,414,619	plus
C11orf30	chromosome 11 open reading frame 30	11 : 76,444,923 - 76,553,025	plus
LRRC32	*leucine rich repeat containing 32*	*11: 76,657,524 - 76,670,747*	*minus*

TSKU	*tsukushi, small leucine rich proteoglycan*	*11 : 76,782,251 - 76,798,154*	*plus*
ACER3	*alkaline ceramidase 3*	*11 : 76,860,867 - 77,026,797*	*plus*
B3GNT6	*UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6*	*11 : 77,034,398 - 77,041,973*	*plus*
CAPN5	*calpain 5*	*11 : 77,066,932 - 77,126,155*	*plus*
OMP	*olfactory marker protein*	*11 : 77,102,840 - 77,103,331*	*plus*
MYO7A	*myosin VIIA*	*11 : 77,128,264 - 77,215,239*	*plus*

Table S3. Detailed overview of gene annotation for the flanking genes on the ancestral locus of HSP47/SERPINH1 on the scaffold00131 from Japanese lamprey genome, A total 45 genes are residing on this locus of size 1 Mb. The gene g32.t1 is LjaHSP47/SERPINH1 and the g19.t1 is P2RY6-like GPCR (also known as lysophosphatic acid receptor, LPA6R) and these two genes are conserved in several vertebrate genomes (**Fig. 3**) and hence marked in red color. Gene annotation was performed using BLAST2GO 3.0 [8] and INTERPRO (www.ebi.ac.uk/**interpro**).

Gene ID	Gene Annotation	Protein Length	e-Value	sim mean	#GO	GO Names list	Enzyme Codes list	InterPro IDs
g1.t1	diacylglycerol kinase partial	99	5,40E-57	96%	22	C:cytosol; C:cytoskeleton; C:plasma membrane; C:cytoplasmic membrane-bounded vesicle; C:nuclear speck; F:diacylglycerol kinase activity; F:ATP binding; F:kinase binding; F:activating transcription factor binding; F:protein homodimerization activity; F:phospholipase binding; F:metal ion binding; F:protein heterodimerization activity; P:regulation of transcription from RNA polymerase II promoter; P:protein kinase C-activating G-protein coupled receptor signaling pathway; P:phosphorylation; P:cAMP-mediated signaling; P:response to ATP; P:diacylglycerol metabolic process; P:protein	EC:2.7.1.107	IPR001206 (SMART); IPR001206 (PFAM); PTHR11255 (PANTHER); PTHR11255:SF30 (PANTHER); IPR001206 (PROSITE_PROFILES); IPR016064 (SUPERFAMILY)

						homooligomerization; P:thrombin receptor signaling pathway; P:protein kinase C signaling		
g2.t1	---NA---	109	-	-		-	-	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
g3.t1	---NA---	108	-	-		-	-	Coil (COILS)
g4.t1	phosphatidylinositol-glycan biosynthesis class f protein	207	2,10E-33	76,05 %	5	C:endoplasmic reticulum membrane; C:integral component of membrane; F:ethanolaminephosphotransferase activity; P:C-terminal protein lipidation; P:preassembly of GPI anchor in ER membrane	EC:2.7.8.1	IPR009580 (PFAM); IPR009580 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE

								(PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
g5.t1	ovotransferrin-like	794	0,00E+00	58,80%	7	C:extracellular space; C:intracellular; F:GTP binding; F:metal ion binding; P:ion transport; P:small GTPase mediated signal transduction; P:iron ion homeostasis	-	IPR001156 (PRINTS); IPR001156 (SMART); IPR001156 (PFAM); G3DSA:3.40.190.10 (GENE3D); G3DSA:3.40.190.10 (GENE3D); IPR016357 (PIRSF); G3DSA:3.40.190.10 (GENE3D); G3DSA:3.40.190.10 (GENE3D); PTHR11485 (PANTHER); IPR018195 (PROSITE_PATTERNS); IPR018195 (PROSITE_PATTERNS); IPR001156 (PROSITE_PROFILES); IPR001156 (PROSITE_PROFILES); SSF53850 (SUPERFAMILY); SSF53850 (SUPERFAMILY)
g6.t1	conserved oligomeric golgi complex subunit 3	913	0,00E+00	74,25%	13	C:nucleoplasm; C:cis-Golgi network; C:plasma membrane; C:Golgi transport complex; F:protein transporter activity; P:retrograde	-	-

						transport, vesicle recycling within Golgi; P:protein glycosylation; P:intracellular protein transport; P:ER to Golgi vesicle-mediated transport; P:retrograde vesicle-mediated transport, Golgi to ER; P:Golgi organization; P:protein localization to organelle; P:protein stabilization		
g7.t1	hypothetical chloroplast rf2	813	2,70E-18	50,30 %	6	C:microtubule; C:chloroplast stroma; F:calmodulin binding; F:ATP binding; F:microtubule binding; P:microtubule cytoskeleton organization	-	Coil (COILS); IPR029281 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011044 (SUPERFAMILY); SSF58113 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
g8.t1	glypican- partial	202	3,80E-07	68,55 %	4	C:proteinaceous extracellular matrix; C:plasma membrane;	-	IPR001863 (PFAM); IPR001863 (PANTHER); IPR031188

						C:anchored component of membrane; F:heparan sulfate proteoglycan binding		(PTHR10822:PANTHER)
g9.t1	glypican-5 isoform x25	537	1,40E-101	60,35%	4	C:proteinaceous extracellular matrix; C:plasma membrane; C:anchored component of membrane; F:heparan sulfate proteoglycan binding	-	IPR001863 (PFAM); IPR031188 (PTHR10822:PANTHER); IPR001863 (PANTHER); IPR001863 (PANTHER)
g10.t1	endoplasmic reticulum-golgi intermediate compartment protein partial	161	1,20E-86	88,15%	5	C:endoplasmic reticulum membrane; C:Golgi apparatus; C:integral component of membrane; C:endoplasmic reticulum-Golgi intermediate compartment membrane; P:vesicle-mediated transport	-	IPR012936 (PFAM); PTHR10984 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
g11.t1	endoplasmic reticulum-golgi intermediate compartment protein 3 isoform x1	266	2,50E-89	76,95%	5	C:endoplasmic reticulum membrane; C:Golgi apparatus; C:integral component of membrane; C:endoplasmic reticulum-Golgi intermediate compartment membrane; P:vesicle-mediated transport	-	PF13850 (PFAM); IPR012936 (PFAM); PTHR10984 (PANTHER); PTHR10984:SF25 (PANTHER)
g12.t1	progestin and adipoq receptor family member 9	354	4,10E-74	59,30%	2	C:integral component of membrane; F:receptor activity	-	IPR004254 (PFAM); PTHR20855:SF29 (PANTHER); PTHR20855:SF29 (PANTHER); IPR004254 (PANTHER); IPR004254 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN

								(PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
g13.t1	procollagen c-endopeptidase	389	3,10E-64	52,75 %	5	C:extracellular exosome; F:collagen binding; F:heparin binding;	-	IPR000859 (SMART); G3DSA:2.40.50.120 (GENE3D);

	enhancer 2					F:peptidase activator activity; P:positive regulation of peptidase activity		IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127:SF40 (PANTHER); PTHR10127 (PANTHER); PTHR10127:SF40 (PANTHER); PTHR10127 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); IPR008993 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); TMhelix (TMHMM)
g14.t1	short transient receptor potential channel 1	497	0,00E+00	84,20%	16	C:cytosol; C:integral component of plasma membrane; C:basolateral plasma membrane; C:sarcomere; C:costamere; C:receptor complex; C:membrane raft; F:store-operated calcium channel activity; F:ion channel binding; F:inositol 1,4,5	-	IPR002153 (PRINTS); IPR005457 (PRINTS); IPR005821 (PFAM); IPR002153 (PANTHER); IPR005457 (PTHR10117:PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS);

						trisphosphate binding; P:manganese ion transport; P:saliva secretion; P:positive regulation of release of sequestered calcium ion into cytosol; P:cytosolic calcium ion homeostasis; P:response to calcium ion; P:calcium ion transmembrane transport		NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-TM

								(SIGNALP_EUK); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
g15.t1	inhibitor of nuclear factor kappa-b kinase-interacting protein isoform x1	254	5,30E-04	47,44%	2	C:endoplasmic reticulum membrane; C:integral component of membrane	-	Coil (COILS)
g16.t1	ninein-like protein	366	4,70E-12	48,70%	1	F:calcium ion binding	-	Coil (COILS); Coil (COILS); PTHR18905 (PANTHER)
g17.t1	nucleoredoxin-like protein 2	128	2,00E-15	55,45%	3	P:visual perception; P:sensory perception of smell; P:photoreceptor cell maintenance	-	IPR012336 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR029519 (PTHR13871:PANTHER); PTHR13871 (PANTHER); IPR012336 (SUPERFAMILY)
g18.t1	---NA---	169	-	-		-	-	IPR029242 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
g19.t1	**lysophosphatidic acid receptor 6, P2RY6-like GPCR**	**404**	**2,60E-54**	**57,85%**	**4**	**C:plasma membrane; C:integral component of membrane; F:G-protein coupled receptor activity; P:G-protein coupled receptor signaling pathway**	**-**	**IPR023242 (PRINTS); IPR000276 (PFAM); IPR022533 (PFAM); G3DSA:1.20.1070.10 (GENE3D); PTHR24232 (PANTHER); IPR000276 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN**

								(PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017452 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
g20.t1	ef-hand calcium-binding domain-containing protein 2	82	5,50E-26	85,10 %	1	F:calcium ion binding	-	IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); PTHR23050

								(PANTHER); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)
g21.t1	---NA---	70	-	-		-	-	SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); TMhelix (TMHMM)
g22.t1	coiled-coil domain-containing protein 160	326	7,20E-17	47,40%	10	C:nucleoplasm; C:nucleolus; F:zinc ion binding; F:tubulin binding; F:histone binding; F:histone deacetylase binding; F:ribonucleoprotein complex binding; F:poly(A) RNA binding; F:phosphoprotein binding; F:scaffold protein binding	-	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS)
g23.t1	low quality protein: wd repeat-containing protein 78	665	0,00E+00	59,65%	1	P:hematopoietic progenitor cell differentiation	-	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR12442 (PANTHER); PTHR12442 (PANTHER); PTHR12442:SF12

								(PANTHER); PTHR12442:SF12 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
g24.t1	growth hormone secretagogue receptor type 1	260	4,60E-54	67,65 %	21	C:cell surface; C:integral component of membrane; C:neuron projection; C:membrane raft; F:growth hormone secretagogue receptor activity; F:growth hormone-releasing hormone receptor activity; P:G-protein coupled receptor signaling pathway; P:actin polymerization or depolymerization; P:adult feeding behavior; P:hormone-mediated signaling pathway; P:growth hormone secretion; P:response to food; P:positive regulation of appetite; P:negative regulation of interleukin-1 beta production; P:cellular response to insulin stimulus; P:positive regulation of multicellular organism growth; P:negative regulation of tumor necrosis factor biosynthetic process; P:positive regulation of insulin-like growth factor receptor signaling pathway; P:negative regulation of interleukin-6	-	IPR000276 (PRINTS); IPR000276 (PFAM); G3DSA:1.20.1070.10 (GENE3D); PTHR24243 (PANTHER); PTHR24243:SF3 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR017452 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM);

						biosynthetic process; P:negative regulation of inflammatory response; P:regulation of synapse assembly		TMhelix (TMHMM); TMhelix (TMHMM)
g25.t1	fibronectin type iii domain-containing protein 3b	843	2,00E-152	50,75 %	10	C:endoplasmic reticulum; C:integral component of membrane; F:protein binding; F:poly(A) RNA binding; P:cell migration; P:substrate adhesion-dependent cell spreading; P:positive regulation of fat cell differentiation; P:negative regulation of osteoblast differentiation; P:positive regulation of fibroblast proliferation; P:Type II pneumocyte differentiation	-	Coil (COILS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19900 (PANTHER); PTHR19900 (PANTHER); PTHR19900:SF49 (PANTHER); PTHR19900:SF49 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR003961

								(SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
g26.t1	---NA---	438	-	-		-	-	no IPS match
g27.t1	fibronectin type iii domain-containing protein 3b	94	4,80E-08	70,71 %		-	-	PTHR19900 (PANTHER); PTHR19900:SF54 (PANTHER)
g28.t1	---NA---	201	-	-		-	-	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
g29.t1	---NA---	423	-	-		-	-	no IPS match
g30.t1	glycerol kinase 5	532	9,10E-175	64,60 %	6	C:mitochondrion; F:glycerol kinase activity; P:glycerol metabolic process; P:triglyceride metabolic process; P:phosphorylation; P:glycerol-3-phosphate biosynthetic process	EC:2.7.1.30	G3DSA:3.30.420.40 (GENE3D); IPR018485 (PFAM); G3DSA:3.30.420.40 (GENE3D); IPR018484 (PFAM); PTHR10196:SF54 (PANTHER); PTHR10196 (PANTHER);

								PTHR10196 (PANTHER); PTHR10196:SF54 (PANTHER); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
g31.t1	zinc finger b-box domain-containing protein 1	236	1,70E-14	42,65%	2	C:intracellular; F:zinc ion binding	-	Coil (COILS)
g32.t1	**HSP47/SERPINH1**	**470**	**1,60E-105**	**68,05%**	**14**	**C:collagen trimer; C:extracellular space; C:endoplasmic reticulum; C:endoplasmic reticulum-Golgi intermediate compartment; C:extracellular exosome; F:serine-type endopeptidase inhibitor activity; F:collagen binding; F:poly(A) RNA binding; F:unfolded protein binding; P:chondrocyte development involved in endochondral bone morphogenesis; P:negative regulation of endopeptidase activity; P:collagen fibril organization; P:collagen biosynthetic process; P:protein maturation**	**-**	**IPR023796 (SMART); G3DSA:3.30.497.10 (GENE3D); G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); PTHR11461:SF27 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)**
g33.t1	lysosome-associated membrane glycoprotein 1	380	3,30E-32	40,05%	24	C:multivesicular body; C:integral component of plasma membrane; C:external side of plasma membrane; C:dendrite; C:platelet dense granule membrane; C:late endosome membrane;	-	IPR002000 (PFAM); IPR002000 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE

						C:sarcolemma; C:melanosome; C:neuronal cell body; C:cytolytic granule; C:phagolysosome membrane; C:extracellular exosome; C:alveolar lamellar body; F:enzyme binding; F:protein domain specific binding; P:autophagy; P:granzyme-mediated apoptotic signaling pathway; P:viral process; P:positive regulation of natural killer cell degranulation; P:autophagic cell death; P:protein stabilization; P:establishment of protein localization to organelle; P:Golgi to lysosome transport; P:regulation of organelle transport along microtubule		(PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002000 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM)
g34.t1	haus augmin-like complex subunit partial	355	8,10E-08	63,10 %	4	C:centrosome; C:HAUS complex; P:spindle assembly; P:centrosome organization	-	Coil (COILS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS)
g35.t1	---NA---	225	-	-		-	-	no IPS match
g36.t	adp-ribosylation	208	3,10E-53	67,15	3	C:intracellular; F:GTP binding;	-	IPR006689 (PRINTS); IPR024156

1	factor			%		P:small GTPase mediated signal transduction		(SMART); IPR003579 (SMART); IPR006687 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); IPR005225 (TIGRFAM); PTHR11711 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
g37.t1	rcc1 and btb domain-containing protein 1	531	0,00E+00	83,15%	1	C:cytoplasm	-	IPR000408 (PRINTS); IPR000210 (SMART); IPR009091 (G3DSA:2.130.10.GENE3D); IPR000210 (PFAM); IPR000408 (PFAM); G3DSA:3.30.710.10 (GENE3D); PTHR22870:SF133 (PANTHER); PTHR22870 (PANTHER); IPR000408 (PROSITE_PATTERNS); IPR000408 (PROSITE_PROFILES); IPR000408 (PROSITE_PROFILES); IPR000408 (PROSITE_PROFILES); IPR000210 (PROSITE_PROFILES); IPR000408 (PROSITE_PROFILES); IPR000408 (PROSITE_PROFILES); IPR009091 (SUPERFAMILY); IPR011333 (SUPERFAMILY)
g38.t1	neuroligin-3 isoform x4	656	0,00E+00	66,25%	6	C:integral component of plasma membrane; C:synapse; F:neurexin family protein binding; P:cell adhesion; P:regulation of synaptic transmission; P:synapse	-	IPR000460 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); IPR030025 (PTHR11559:PANTHER); IPR030025 (PTHR11559:PANTHER);

						organization			PTHR11559 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
g39.t1	neuroligin- x-linked-like	187	2,50E-69	70,55 %	42	C:extracellular space; C:integral component of plasma membrane; C:cell surface; C:postsynaptic density; C:cell junction; C:endocytic vesicle; C:postsynaptic membrane; C:excitatory synapse; C:inhibitory synapse; F:receptor activity; F:neurexin family protein binding; F:cell adhesion molecule binding; F:carboxylic ester hydrolase activity; F:scaffold protein binding; P:regulation of respiratory gaseous exchange by neurological system process; P:receptor-mediated endocytosis; P:neuron cell-cell adhesion; P:metabolic process; P:visual learning; P:sensory perception of pain; P:adult behavior; P:positive regulation of synaptic transmission, GABAergic; P:social behavior; P:locomotory exploration behavior; P:axon extension; P:oligodendrocyte	EC:3.1.1.1	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559 (PANTHER); PTHR11559 (PANTHER); IPR030025 (PTHR11559:PANTHER); IPR029058 (SUPERFAMILY)

						differentiation; P:neuromuscular process controlling balance; P:positive regulation of synapse assembly; P:positive regulation of synaptic transmission, glutamatergic; P:rhythmic synaptic transmission; P:regulation of dendritic spine morphogenesis; P:vocalization behavior; P:postsynaptic membrane assembly; P:presynaptic membrane assembly; P:gephyrin clustering involved in postsynaptic density assembly; P:postsynaptic density protein 95 clustering; P:positive regulation of inhibitory postsynaptic membrane potential; P:regulation of long-term synaptic potentiation; P:regulation of N-methyl-D-aspartate selective glutamate receptor activity; P:regulation of terminal button organization; P:positive regulation of excitatory postsynaptic membrane potential; P:positive regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity		
g40.t	neuroligin-2-like	164	2,50E-57	84,95	53	C:extracellular space; C:Golgi	EC:3.1.1.1	IPR029058

1	isoform x5			%		apparatus; C:external side of plasma membrane; C:N-methyl-D-aspartate selective glutamate receptor complex; C:cell junction; C:filopodium tip; C:dendritic spine; C:postsynaptic membrane; C:excitatory synapse; C:inhibitory synapse; C:neuronal postsynaptic density; F:receptor activity; F:PDZ domain binding; F:neurexin family protein binding; F:protein dimerization activity; F:cell adhesion molecule binding; F:carboxylic ester hydrolase activity; F:scaffold protein binding; P:regulation of respiratory gaseous exchange by neurological system process; P:protein targeting; P:heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules; P:neuron cell-cell adhesion; P:metabolic process; P:positive regulation of circadian sleep/wake cycle, wakefulness; P:synaptic vesicle targeting; P:calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules; P:neuronal signal transduction; P:neuron projection development; P:positive		(G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559:SF176 (PANTHER); PTHR11559 (PANTHER); IPR019819 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR029058 (SUPERFAMILY)

						regulation of synaptic transmission, GABAergic; P:rhythmic process; P:cytoskeletal matrix organization at active zone; P:protein homooligomerization; P:protein heterotetramerization; P:positive regulation of filopodium assembly; P:positive regulation of synapse assembly; P:positive regulation of synaptic transmission, glutamatergic; P:positive regulation of dendritic spine development; P:negative regulation of dendritic spine morphogenesis; P:terminal button organization; P:synaptic vesicle clustering; P:postsynaptic membrane assembly; P:alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor clustering; P:N-methyl-D-aspartate receptor clustering; P:neurexin clustering involved in presynaptic membrane assembly; P:postsynaptic density protein 95 clustering; P:receptor localization to synapse; P:positive regulation of ruffle assembly; P:positive regulation of synaptic vesicle endocytosis; P:positive regulation of intracellular signal		

						transduction; P:positive regulation of synaptic vesicle exocytosis; P:regulation of N-methyl-D-aspartate selective glutamate receptor activity; P:regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity; P:positive regulation of excitatory postsynaptic membrane potential		
g41.t1	---NA---	96	-	-		-	-	no IPS match
g42.t1	protein ect2 isoform x1	368	1,40E-35	55,80%	9	C:nucleus; C:cytoplasm; F:Rho guanyl-nucleotide exchange factor activity; F:GTPase activator activity; P:cell morphogenesis; P:cytokinesis; P:intracellular signal transduction; P:positive regulation of GTPase activity; P:positive regulation of neuron differentiation	-	Coil (COILS); IPR026817 (PANTHER)
g43.t1	hypothetical protein H310_04227	72	7,30E-04	61%		-	-	no IPS match
g44.t1	protein ect2 isoform x1	1002	5,30E-101	73,35%	27	C:cytoplasm; C:bicellular tight junction; C:midbody; C:nuclear membrane; C:cleavage furrow; C:centralspindlin complex; F:signal transducer activity; F:Rho guanyl-nucleotide exchange factor activity; F:GTPase activator activity; F:Rho GTPase binding; F:protein	-	IPR001357 (SMART); IPR000219 (SMART); IPR001357 (G3DSA:3.40.50.GENE3D); IPR000219 (G3DSA:1.20.900.GENE3D); IPR000219 (PFAM); IPR001357 (PFAM); IPR026817 (PANTHER); IPR001331 (PROSITE_PATTERNS);

						homodimerization activity; P:cell morphogenesis; P:cytokinesis; P:activation of protein kinase activity; P:positive regulation of cytokinesis; P:intracellular signal transduction; P:positive regulation of protein import into nucleus; P:positive regulation of apoptotic process; P:positive regulation of I-kappaB kinase/NF-kappaB signaling; P:positive regulation of GTPase activity; P:positive regulation of neuron differentiation; P:protein homooligomerization; P:regulation of attachment of spindle microtubules to kinetochore; P:cellular response to hydrogen peroxide; P:bicellular tight junction assembly; P:cellular response to calcium ion; P:cellular response to ionizing radiation		TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001357 (PROSITE_PROFILES); IPR000219 (PROSITE_PROFILES); IPR001357 (SUPERFAMILY); IPR000219 (SUPERFAMILY); IPR001357 (SUPERFAMILY)
g45.t1	gpalpp motifs-containing protein 1	320	7,90E-56	55,25 %	3	F:molecular_function; P:biological_process; C:cellular_component	-	IPR022226 (PFAM); PTHR15606:SF3 (PANTHER); PTHR15606 (PANTHER)

red - matching to syntenic data in **Fig. 3**