Supplementary Materials

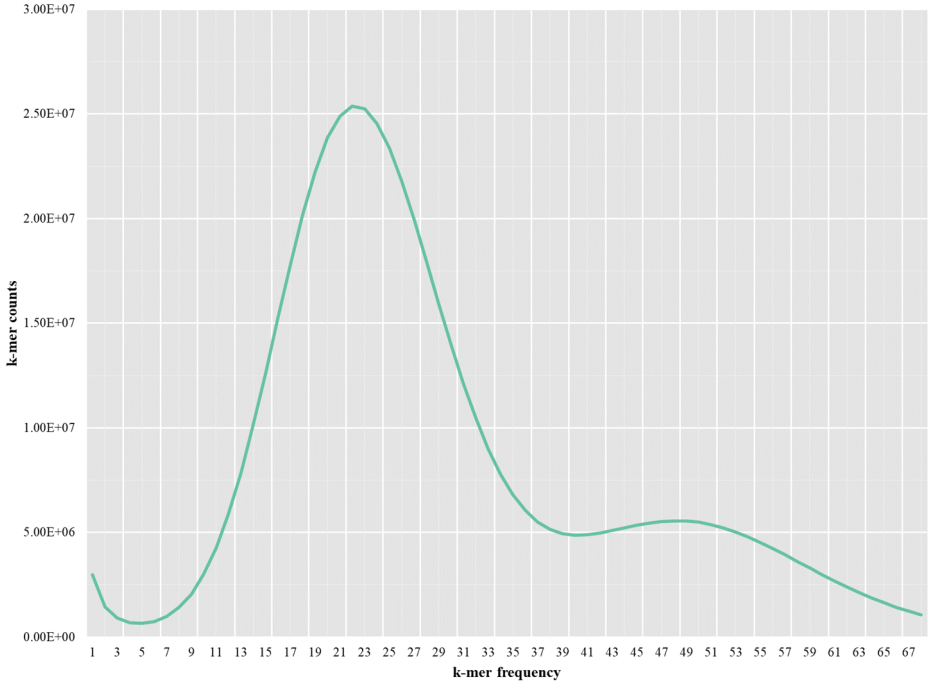
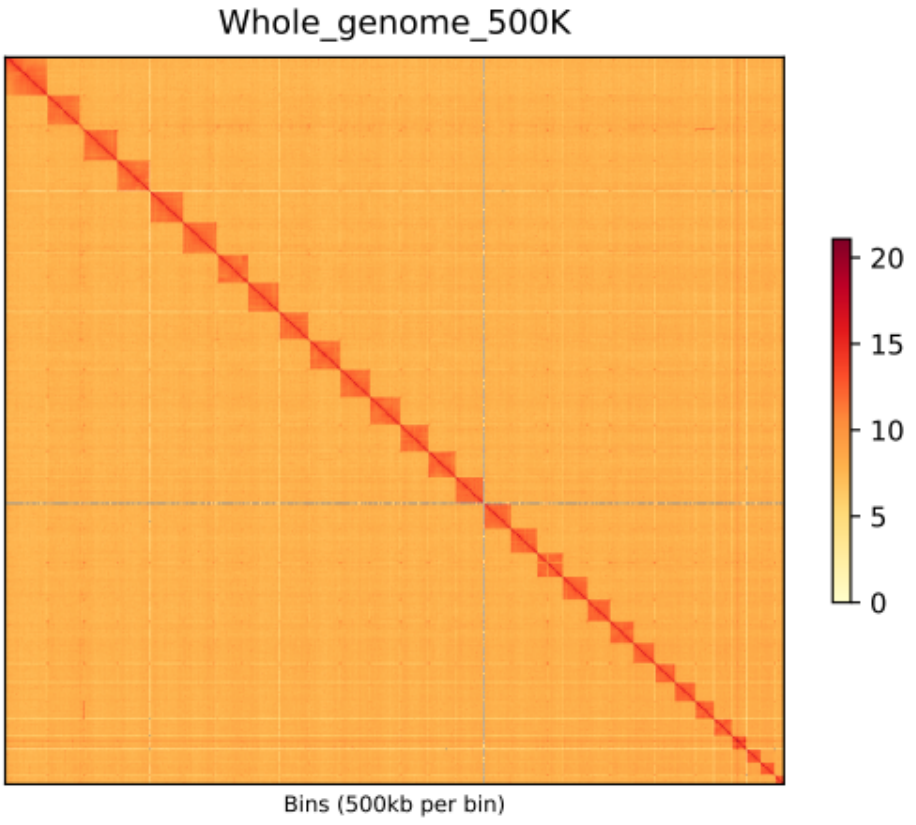


Figure S1 The genome size estimated based on the k-mer analysis.



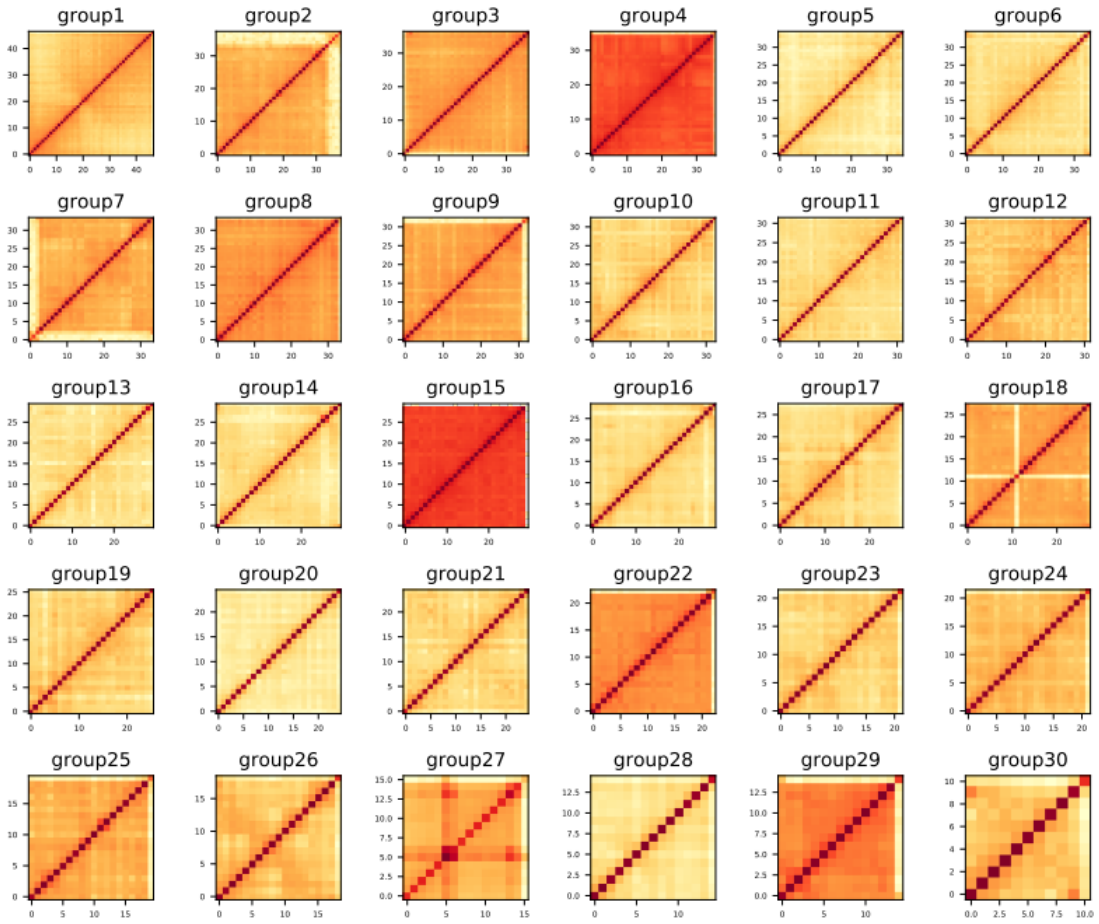


Figure S2 The Hi-C chromatin interaction map of *H. assimilis.*

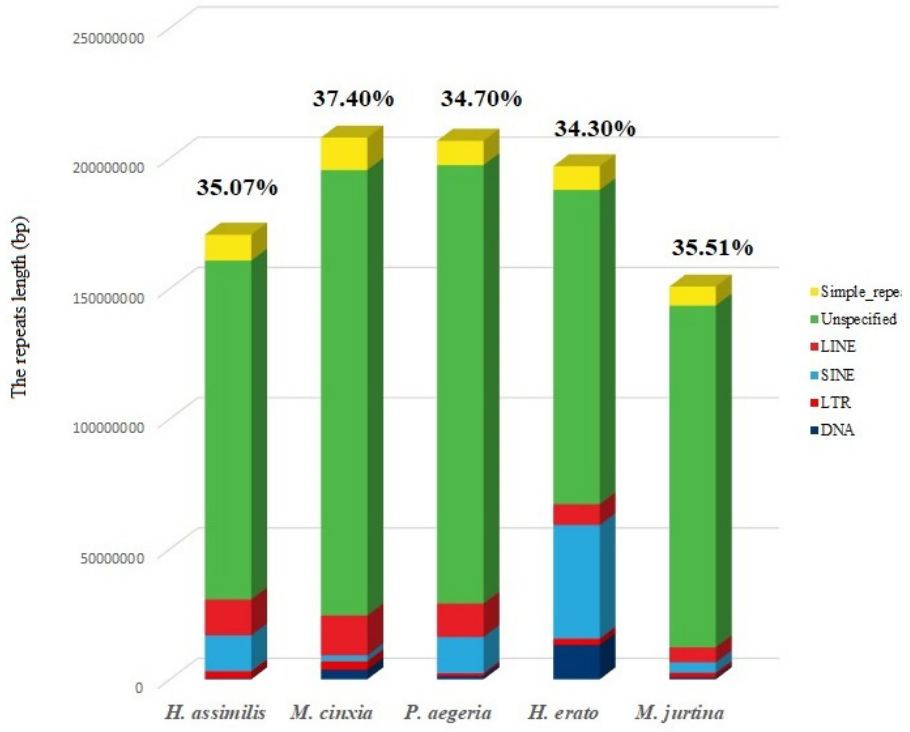


Figure S3 Proportion of each repeat class in the genomes surveyed. Numbers above

the bar plot correspond to total repeat length percentage in each species. The repeats length ranges from 35.07% in the genomes of *H. assimilis* to 37.4% in the genome of *Melitaea cinxia* are shown.

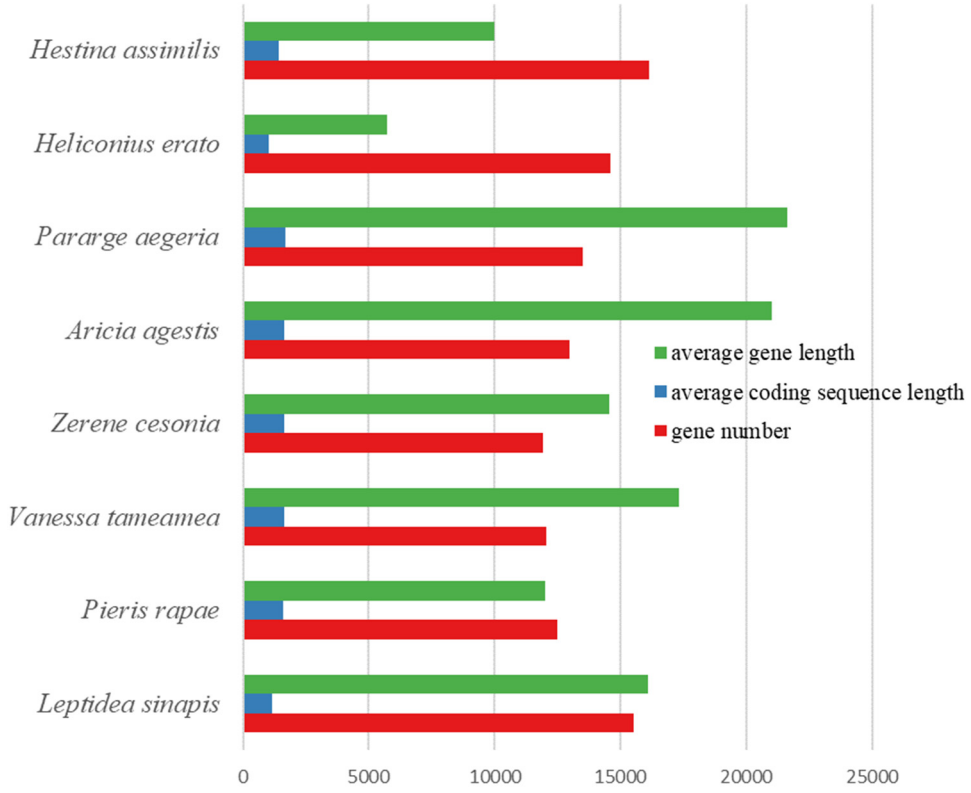


Figure S4 The comparison of gene number, average coding sequence length, and average gene length with other lepidoptera species.

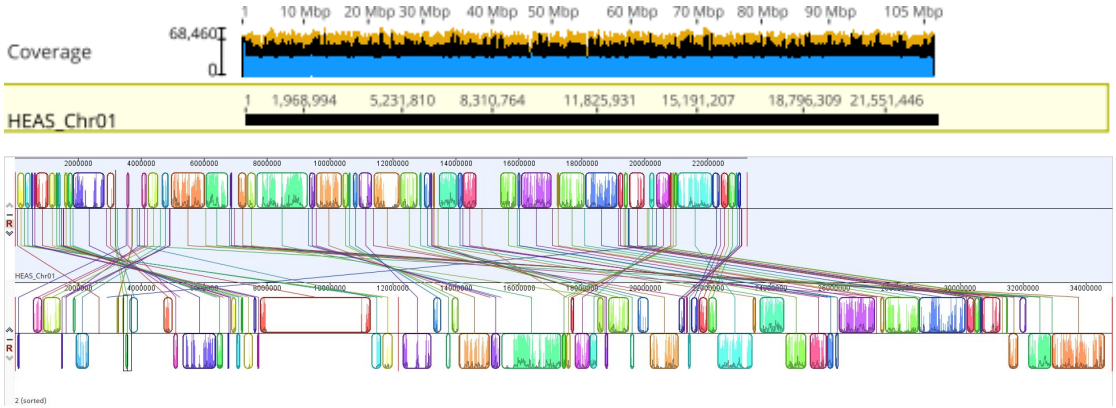


Figure S5 Normalized male coverage along the length of chimeric scaffolds for chromosome 1 of *H. assimilis*. Coverages are plotted as sliding windows (width = 64 kbp, step = 10 kbp) of median base pair values.

Table S8 Amino acid sequences of cytochrome P450 in *H. assimilis*.

Cytochrome P450

>HaCYP1
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AYALMSLKTSLAHILRNYKLQGDHTKLELDLDIVLKPVSGHHISIQRRK
>HaCYP80
MIENSEKTDTGYTQEELREEALVLLIAGTDTTATAICFIFVLLAHHQDVQEKIY
KELVEILGDTNKPIEIEDLVKLRYMEAVIKETLRLYSPVPVTARNSKSDFMLPSG
LTVPKGCDVIIQIAGIHHNPRYWGADVEDFKPERFLKDEKPDAFVAFSNGPRN
CVGFCFFYNLLLRVSRGSESDRMKM

Table S9 Amino acid sequences of olfactory receptor (OR), gustatory receptor (GR), and odorant binding protein (OBP) in *H. assimilis*.

OR
>HaOR1
MFLMYYKKKPGMDIINNIDSDYLSYNNLPQKYKLIVNKNIDNSLFYSEKCWA

LTVFIGVLIFPLMATVSTVDSFLIKGESTKYMIHDLVIPFMDPEDRFKSPIFEIMF
AYTLYACMWYFVSFFGYDGFFGVCINHACLKMALYCQAFDDALKEVNEKAM
HKKIVEVIHEQNNLKRFVDLIQETFNFWLGVILIATITQTDRVYTRFIDTYKIITF
AMGVGMIYPNPKTNKRRIVCILMVLVSVMPFALMMLIDIYNSWKRRDILNILR
HTTIVGPFLGLFFKMFLMYYKKRPGMDIINKIDSDYLSYNNLRQNYKFIVNRSI
DNSLFYSEKCWGVSVFIAVLIFPFMATVSTVDSFLIKGESTKYMIHDLVIPFMD
PEDRFKSPIFEIMFTYTLYASLWYIFSFLGYDGFFGLCINHACLKMAVYCKAFE
DALKEVNEKTMHSKIVEVIQEQNDYTRFVDLIQDTFNIWLGLIVVATMIQIGTV
LYLISEGYGLDLRYIIFLAGTTLHIYIPCRYSAKLKYKASYIYFIISECVLLLGLL
ALTASCEFSRDSYANLLRGMGKCNLDEYSENCSNYDR
>HaOR2
MWLAFRKFGLDYDDFSTMIENVSILMIVLTINIYKNSTKRLEPMFESPNFEIATL
IFMLGICFGVVTLANVLAYIIVIVGYIESQMRALSEELRNIWDDSQHFYNNVKH
KVTDKINIMYYKEKIVDEFIKQSLRRIVKFHIANINLSHEVDQNFRPSLALEFSI
MAFAIIAELLGGLDKTYLEIPFTLSQIFMNCFIGQRLIDACCDFENSLYSFWFVFI
RCPQTGDYVSASVELSLAMCNGASILKFIYLKIYRKEVTNLIDQYLECHARVDI
KSRFYESLEKYLRGVKRRALMTWGALVLNGTIYISYGFLKPGRHLSEDLYVIY
GLEPMFESPNFEMAVVLMTISVVFGVITLANYRLLITVTIGYVEAQLLALSEDL
RKLWDDSETFYENYSEKELDIIKHVSPYDIKNVYIKHRLREIVKFHITGITLQHF
VENKFRFIYVLEFLFAAIGIVTELLGGLENTYLELPYSLNQVFLDCLIGQRLIDA
GNVFEDAIYDSQWENYNAENQRTVALMLENAQKTLTLSAGGLSPLSFMCLM
SVIRCTYSTYTALHSTVK
>HaOR3
MEVCKIYPKIKQICLMNSGREDCDIVDIYSEAVNVIKPKDRKTSIYVLPAIYQH
DLVGYCNIIINYRCPRSRDKVRVHIPFSFKAQASRRTSPLLKDYIGNNKFMKCE
SDDQNSLDNCSPTDCDLKYQGQRPFYEMNLQTCIEAPLCFADEDKELPNVVIV
PEINICKDLGVPLSIQDIYSLSTGLGTVTKILTKRDHVKLIVTIIRRNEMQAIFDG
INADYDKFNNLPEDYKEIVFDTIKKTKGLEKAWVIMVAITAGSYPGLAGICTIY
SSMFSDNPRRYMIHELALPFLTEEEKYESPYYELFAVYSIFIVWVIFVGFTGYDG
MFSVCILHVSLKIKIFSQNLKYLFVDTTDLSKIKRNLAEFVKDHCEVVRLIGEI
QKCFEVWLVGIFLNAVLQIGMALIQITSNNESDINAMYYLFALATVVHIYLPCY
LTSDVTHNAAEIANVAYSCSWELVQDKEIRKSIAIIISKAQNPIHFRALGMLTFN
MELFVSILQTSYSMYTLLRS
>HaOR4
MMTKTKTQGLVSDLMPNIKLMQLAGHFLFNYHSDNAGMTTLLRKVYSCVH
AILIIVNYVCMAVNMAKYSDEVNELTANTITVLFFAHTIIKLIFFAITSKNFYRTL
AVWNQSNSHPLFTESDARYHQLALTKMRRLLYFICGMTIFSVTCWVTITFFGD
SVRLLMDKETNETLTEPVPRLPLKAWYPFNAMSGTMYIVAFVFQIYWLLFAM
SIANLMDVMFCSWLIFACEQLQHLKAIMKPLMELSASLDTYRPNTAELFKVSS
SEKSEKIPDPIDMDIRGIYSTQQDFGMTLRGAGGRLQTFGQQNPNGLTQKQEM
LARSAIKYWVERHKHIVRLVSSIGDTYGTALLFHMLVSTITLTLLAYQATKING
LNVYAFSTIGYLCYTLGQVFHFCIFGNRLIEESSSVMEAAYSCQWYDGSEEAK
TFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTYFMVLVQLK
>HaOR5

MPVSVDIAPRRYFYVQYILLRFLGLGWWHHPDEGNTDNFPGLYIYYAIVTEIF
WVAGFVGLETIDPFIGEKDLDRFMFSLSFVITHDLTIIKLYIFFFKNQDIQEIVRIL
EIDLQQFYQNIEKNRRTIRITKILTASFIFFGWMTIGNTNVYGIVQDLRWRGEVA
LLNGSDKIPPRTLPQPIYIPWKYQSDVSYISTFLLETIGLLWTGHIVMTIDTFIGS
LLLHMSSQFAILREAITTAYDRTIIFLNNNISNNDDTVIEGFTNMGLGSYYERIV
RRYYTEEDIEKALESTLKNCFRQHQMLISCVEKFAKTYSYGFMTQLVSSMAAI
CVVMVQISQDASSFKSIRLVTSLAFFMVMIIQLALQCFTGNELTRQAGLVSEAV
MQCKWERMPPRLRRSLIITMMRAQRPLHLTAAGFAKMDNDCFLRVSVTFHR
KNVARILSLCTML
>HaOR6
MALRSQCGAFRKIVMHCVHGKPYLGKKWLRLTEDILRTNTSLNIRSLVSVLGP
GVAFKANRPNYNINSERNWLSSYDHTVGYSTYSTIVKSLLILLGCGELWSFFSS
NWSLDGITDGLNVILIQFGALYKYKVVMRHKKEFRELASSMESENFDLSTRR
RKMILEVWTKRNDSTLKLMLGLGTCTVIVWHIYPLMDDLDYNLMVAIRLPFD
YKTPTLYAVTYICTLIVFSYISYFVMANDLIVQAHLMHLLCQFAVLNDCFKNIL
RDCQSNFKDIDTRYLHLNQNFTKVYKNRLGKLVEQHQLILNNTMKLRNLMST
PMLIQLAVSTALICSIGFQIATSLNVNMTKGLMSLFYLGYNMFVLYILCRWCEE
IKIQSQKIGDALYSSGWENGIVMVPGVRTSILLILARANKPTSLSAGGMYELSL
EAYSNMVKTSYSALTVLLRLR
>HaOR7
MLFFPQPASASSVLLVHLGAVGALASGAALCGGGGTCACGALLHALHPLQLW
TVCGLHADRAAAIAAPLHYAAIVSAKKVVICVASGWIGLAALLAPLAAAQPP
LTYSIGLGSCAPDCGAGPGALGFCLIYTLLTLLLPTALVLLCSLKILRIARYHRH
RIAAAIYEVTLSAQVTVTHQRNPFSPPPPPRRRALSAVIQPLGSLAILYFPYYCV
LMWPAIAEPPQLLAAFSAVLLAAAPPVNGILYGIRSRAFKDSLRNYRRKRMTK
SEVTQEIQARTPSACGSRRPSLSAGSGCIRPLTTRRLSDAAAMGSRGSERPAQR
AASCNMLQDCQEVDTPKSRASAIPLIRAPPHVVLGRALGLEEGVNRERRRRQ
SPRIMVTRAMSDECESPSRRPLCRQHSRSSGALLGNMTYSPALLEKVNDNKA
DEQLLLSWPQRSQVTKNDVL
>HaOR8
MKLNKSKSTVNNEGVSSYTHFLEIPLKSVGCWDWYEKPKKLYEIFINNIYLCV
VLFVLLNVLLSLTVHLYTEWTDIMSSLDIIADGLPLLTSVLIVSYFAINKDELYS
LTKFMNANFKWHSARGLTNMTMMNSYKTAVNFSFFYTACTLFSVTMYVLMP
VIVHLWTKQPLQHWIYMDVTYTSYIVLIFLRQCLAQVFVALALGQLGVFFAC
NSILLCGQLDLLCCGLRNTRYTALLKGGVDHAALFNQYKGIEEDEKHNYLYN
KSEMIDSEYHYDDKVRNNFMGKKTQYDIYNKAYDKATSDALRECARVCQVI
NEYKDRFEKFVSPLLVLRVVQVTLYLCTLLYAATLKFDMITVEYLGAVALDIY
VYCHFGNQIILQADRVSTAAYQSAWPTMGVEPRRLLLNILLANLRPVVVRAG
RFLPMNLHTFVVVCLLM
>HaOR9
MLKFLRVTEEEYEKCAKGIINPELFYKNFYLLLKWFQVLDGPIPKWTTYAKIF
MTLCAITAQILLSLSIYHGVDNFDIPIMTEAGTYFIVMSYELLILSCTKLNIVDY
HKLQHSLKEDFLYVCNKGGKYREIFFYNQIETRKISMLAMIFIGNFGVCMIVTA
VSSLLYHLATHGPNEGKRPLLFPFWAFETDFGMTPTYEIAFIFSNICVTAYAFSY

IFMVVTQIVWIREIAIKADIVKLCIQDLMNGIHPTSDKERKNYFDFLIKYRMKE
IIQQHQSMYSLMGHYANVYKKLVLFEQKVSAPVVCLSAYSATQKLETGELNAI
LIILCIGAVTLLFIPSYLCTYLSIKVSSICYACWDIPFWNANRVIRPYLVLIMQRSL
RPLPLIAPGFDEVSVQTFSNKMASAYSFFNMLRQANI
>HaOR10
MIQNISKSFKRLEDPKYPLLGPNVTGLYWFGLWQCGNKYRDGFFNFIHFCSLL
FVISEFVELYFMRNDLMKVLFNISVTALSLVSISKTMFFIFYLPYWKTLIENISRE
EISGLQDKNLKVVDIMNQYKTYSRIITYSFWSVILLTNLVTILSPFLKYVTTETY
REMIKNGTEPYPQILSSWFPFDKTKFPGYLVAVAVHIIMTTQGAGVVAVYDSNA
VAIMSFLKGQMQILRYKCQLIFGDEKSIPKEDVLENIKEQYKTFNSIISPVMCV
YVLVCSIMICCSVVQLSLGEITVSQKLWVMEYTTALAVQLFLYCWHSNEIAYE
SLGVDQGVYSSNWWRADVQVRRQVLLLAGKLAPTFILDAGPFAKFSMSTFID
VSIFHNNYGLTIFEVITSYGRISRFVK
>HaOR11
MLKIFTCLEDPAHPLLGPTLWGLQKWGMWQPNKGISRIVYNVIHVLAIIFVVT
QYIELWHIRSNLEMALRNLSVTMLSTVCVVKAGTFIIWQEPWNFIFEYISSLER
DQLSNRSAVTKKIIKKYTGYSRTVTYFYWCLVTATVFTVIFAPLALYLSSFQRR
EEIKAGTEAYPEIMSSWVPFEKTRGFGYWSLVLVHTLICFYGGGIVANYDSNA
VVLMSFFTGQLELLKSDCERLFGDGIEFICYEEAVKRIRNCHQHHVELIRYSKV
LNSLLSPVMFLYIIICSLMICASAVQLTSDGTTRMQQVWIAEYLVALVAQLFLYC
WHSNQVLYMSLKVDEGVYASAWWSQCVRIRRSVALLGGQLNRPIMFSAGPF
TQLTVATFVGILKGSYSYYTLLSKK
>HaOR12
MRNYYILKGFCKRIFLVRSGNFWYEEGVMGDDNCISYKISKYILFSVYGFVTL
LEIMAALIGDFPEDEKRDSVTFAVSHTIVMIKIFSVISNKGLIKKLIYDLIKVCEI
HEEEVLMKEKYRIMKINVLAYFITVYGSAACFVFEGLRKMFEGSHFVTVVTY
YPNFEDNSVIATVVRIFTTIVLFVMMLTMIVSVDCFTVIHIIMLKYKFITLRNYF
EKLSDGFEHEIKIKNSQISATKLTKGLIEGIKMHKELLRLTKEIDKAFGTVMAL
QLCQSSGSAVSLLLQIALSDQLTFVAGMKIFFFVVALFFLLGLFLCNAGEITYQA
SLLSDSIFYCGWHLCPSQHSQQRNLGRLVLLACAQAQRPLVMKAFKMLELTY
GTFLLILERGLLERIAA
>HaOR13
MPEKKFKSFNETFPHCAFALAIALLYPNRANLNKRKILFAIVIVVNSLILFWFLL
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MANDMEKEYQEIFEYYIKIGKLGQTCWIIIPILLSSQFPIYAGACMIYENLKSDV
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NHLRLKLKLLAHKVCKAFKIAKSRHELESMVKEAIRDHQEALIFHKDLQEIYG
GWLLMVFLLSSLLISLNLFQLYLSQRIDPKYTIFAISGVIHMFTPCYFASNLMKT
SEELSWDLYSAAWEKWADPAVTKLLIFMIAKSQQTLILTGKGMVYFNMQLFIS
VLQTSYSFFTLISS
>HaOR14
MSFLKSITYDIVNKDLFEFNIKYLTLVGLWTNKDWSTNKLRLYKLYEVVLHILS
FVFIIVTGIGTYQHKENIPIFTSSLGKCLAAYNFVSKIFFFVMKRKQLSNLIHEIR
SSGDEVSVGKRQLMVIHVIMITTISTVLATAFSILSLLKGEMTIEAWMPFDPMK

NRMSLLLAAQILVVYFVVPCVYRAYAIQGIVCSIVMYFCDQLVELQQRLKNLS
YSKERERIMREEFKEIVKKHIRIMRYSNILKNIFKEFFLIQNLAVTMELCLNALM
VTVIRLEEKTLLASFLGYLGLALMNAYIFCYLGNELIIQSTGLAQAAYEASWTS
WPVDLQKDLLLVIRVAQKPLTLSAGGITNMCIKTYSEALYNAYSIFAVLSDFVD
>HaOR15
MSTKYFDKSIEKVQFIFLCSGLTLQSKKLTTIKKLKSRLFYLINFFWLNSDVLG
AIFWFIEGIKNGRTFVELTYVAPCITFSFMANLKAIYLIHYEDKISDLIDKLRDLE
ASDVIIDKSRDDIRKTDSIFLHLVLKCSNILNIVLLVTFIVSPFILIAIKYVQTNKV
DLILPFLIVYPFDSHDIKYWPFVYVHQFWSVSIVLANICGADYFLYICCTYLRT
QFRLLQHDFTNIIKKNRHLSDFDLGRFDLEFIKLVKWHQELIRLSDILELINAKP
TLFNFVSSSILICLTGFNVIAIENVAFAVTFLVFLTASLLQIYLLCFFGDLLMKSS
MEVSDAVYNCKWYNLNAKSRKNLIIVLTR
>HaOR16
MTDDSREESFDLDFENVFGVMTSAMRMNRSHPDIKRNIKWVFQFGVMHGVF
SLMFGGLVYSIIFHDLKNNDYTQACANGILCVIFNVVTFSYILMLWHQNIFKD
MIAKINRDYELAKHFTKDEQNIIKTFAGKGQRVIKLWLVVGILSAGLFPIKAIV
LMIYYTTVSEFKYVHLFDLTYPDSVEEVKNTLGVFIVLYIYFLYCDLYSTTIYIS
FVPLGPVFMLHACGQVELAKIRVMKVFSENLTIEEKNKRLSDIAKLLDNIYSFV
DKIKTSFKMLYELTLKGTIVIIPISLFQILEGEELHFAVYSCNWEKQWNKKNRSL
VILLLQRTSQPVAIRTLFRDLCLDALTDVRQ
>HaOR17
MNYYFGLLRSAAWRCVAAHTTLLQGAGYMRWRGADKSTSRVHFIYRKIVFAI
TSLYLLQECIYAYRERNDMTKLSKVMFLLLCHITSIAKQLLKCYVSFQDPIYNA
ANPKAQTLLQSTSRGARLLLSAYTGCAVLTCTLWLVFSIMHRVDGHYVEFPF
WTGFNTDPPIVFVVVLIYSFYVTTLVGIANTTMDALMATILYQCKTQMRILRN
DFENLPERAKVICNETGEGYERVLMMLLVRGFQHYRRVIGTAKSLQDIFGVAI
LVQFGIGGWILCIAAYKLVSSERIVCSVYSMQWLKTPPHFKRTLVLLMQFVRR
PLRPAVGRIIPLSLDTFVKILKSSYTFYAVLRQTK
>HaOR18
MRILKSEDLYLNRAKFVMKYLGVWVPRINENKIHKSYRMFMMSLQYLFLIFQ
IVYIVQVWGDLEAVSQSSYLLFTQACLCFKVTVFQVNIDKLKDLLKRMNDGIF
LPQSTEHERILKNQAKRIKRLLLAFMISSQTTCGLWALKPLFDDAGSRKFPFD
MWMPVRPELSPQYELGYAFQLLTICMSAYMYFGVDSVVLSMVIFACAQLEIIK
DKIMNSRNDDNETIDRKNILTENNNKLIECIKQHQAISENLHTVLYNCAWYEQ
DANFKRMICFAMMRMSRPIVLRAGHYISLSRQTFVSILRMSYSYFAVLNQTNL
N
>HaOR19
MIFLENLAAAFGNFPKVEKNSAIMFSAIHNIILVKMFLLFYYKSSIKRINYEMA
SLMKDIEDGDTMIMQKKKVLWGIVFYAITVYLSLIAYGVESLRKFLVEGTPFY
TVVTYLPDYYDVSLVASGFRVFFYLTWLYMMLPMMAADCMPIIHLIIIAYKFIT
LCKHFETIKMEFDRNLLIMSNKKATELLKTGCIKGIKIHQKLIFLAEEIQRIFGVI
MSLQVCESSAVAVLLLLRLAASLLANSIFFCGWHLCAMDKQSHKDIRRIVLVG
CAQAQKPLILKSFGVQDLSYSTFVSVARMTYSVFAVFYQRRD
>HaOR20

MDESSRNKAKLEINESLTLSIFSMRRIGLSFDKPKTSSAYFRQKILFVVSVCGIC
CHVFSEFINIILTFASSPRVEDVVPLFHTFGYGALSIAKVFVLWYKNTVFGELID
ELAGIWPMPPLQEDALVIKEKSLTALRISHRWYFCVNVMGVWFYNLTPIIIYFY
RIWQGRDAEIGYVWESWYPFDKHQPIAHVAVYLFEMFGGVTCVWIMVSSDL
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>HaOR21
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LITVTIGYVEAQLLALSDDLQKLWEDSETFYEKFSKKELDIIKHVSPYDIKNVY
IKHRLREIVKFHITGITLQHFVENKFRFIYVIEFLFAALGIVTELLGGLENTYLEL
PYSLNQVFLDCLIGQRLIDAGNVFENAIYDSQWENYNAKNQRTVALMLQNAQ
KTLTLSAGGLSPLSFMCLMSVIRCTYSTYTALHSTVK
>HaOR22
MDIINEIDNDYSSYNNLPQDYKLIVNKHIDNSLLYSEKSWAITVFITVMIFPFMA
TVSNVKSVLFDSEPTRYMIHDLVIPYTDPEDRFKSPIFEIVFMYMLYACFWYVL
NFLGYDGFFGLCINHACLKMALYCKAFDEALKEVNEKAIHKKIVEVIQEQNN
FKRFMDMIQDTFNIWLGLILVATLTQMGTVMYLISEGYGLDLRYIIFLAGTTLH
IYVPCRYSAKLKHKVGNAPACPLVLQMFLGGDDRLTSVSRDSYAYLLRGMGK
RNFEEYQENCTNYDR
>HaOR23
MATTYSTAFMFTVCTALISYGFDGLVEVIHADGTFTTVITAWPSPLDKSVLANF
VRIINFLVWWAFVIRVSATYVVIITVATALSHQYKNLQSYFYKLNDLFEDAVDD
RTQNENEIKYMKALEVGIKLHSDTLWCKTQFQEICSPVFSGSIMINIFVLCMLM
LQMVNSERTLLNGISTLTTSAAVLLSTGCIMWNAGDVTVEAAVLPSAMYSSG
WENCQDKVSRRIRNLLVVAMQQGQKEVIIRGFGIFEISYQSHLAIVKSSYSTFS
LLY
>HaOR24
MSRLLMIYHAAVGICGVLFTAYPIINKALGDEVYLTGYIPFDTNASPVFEVAAT
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YVDHDAEAKNILHERFVNCIKHYEQIVWYAKEIECIFSEAMVLQLFVVAWVIC
MTMYKIVGLPLFSAEFISMAMYLGCMLAQLFIYCYYGTYLKFESDLINESIYK
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RK
>HaOR25
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VTVTDMERRKSQDKTYQDIIKKFTRYCRSITYWYWFLTYCTVVMTISQPLVK
YLIILYNGNDSDTIPEIVNSWLPVDKHTLPGYLLLMSYQIYAAFYSGGWMTSF
DTNAFSIMIFFQCEIELLRKDGQFLFGTLDNPRSKEEAKMRFAFCSKRHNDLLR
>HaOR26
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LCNDSYSIGDTSANIDLTPSPKTLILTPAQEEQVRIRLRGCVQQHQKALAAAVH

LQKCFSEPTFAQFTVSLVIICVTAFQLVSSEDVAGAAYDFPWYACSVRIRKSILIL
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>HaOR27
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AHLMYLLCQYTVLANCFEDIINDCLGDENKLNEKHLIMTEQFKRRYLERLNG
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CSGWERGLTAIPGVSASLLIVAIRARKPIVLTAGGLFDLSLASYTTVIMYL
>HaOR28
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FENMAERKRKRDLRKNHGIEDPRSHPIQIIWMAIYLTCMLIEVFILCWFGNELI
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LINWSYKAFAVMRNTKK
>HaOR29
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PIGVNFGSNAVCMCLFFYLPLRECVTFSPVLIYCFLVFFLYCFLCQRLINASEFF
ENAVYSCGWEKFDVKEQKTVYVMLLQAQQPITLLAADIIPVNIYTFATTLQAI
FKFITVVKF
>HaOR30
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QISVIFELIGSQSEKLKDAVYNLHWEHMNQKNKTIVLFFLYKSQTPITLKAMG
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>HaOR31
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NQEDSDHMEYLTDVARYALLILRIDNILALFTCFLWVILPFVLHLQGKPVEFAI
WLPFDVNFEPA
>HaOR32
MNENFLKPYSFICVLDFTTVDALYYIMTTHICSHFTILSNEIQHLDEKTSYRLK
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LFLLSVFIQILMISVFGEHLIQESRKIGEAAFKSKWYNMDQKSKKTILLLMLR
>HaOR33
MYHKEKIVNEFTKQRLKHIVKFHIANINLSHEVDQNFRPSLALEFSIMAFAIIAE
LLGGLDKTYLQFPFTLVQIFMNCFIGQRLIDACDDFENALYSCKWENFNTTNQ
KTVYLMLIMSQKTLTLSAGGVTKLDFNCLMNVLKSAFSVYTTLKSALK
OBP
>HaOBP1
MTKSIVEMSLNKTIAALFLIFTSYCYALTCHSQRGGKENEFKRVINTCLRQMEN
NNSRNSNEDWSDWDNYNQRNQRERDNRHENRENKMGNRDIEKGERDRNK
NKRDGANERHNRQQNRDGVNENISNRMDDGYNSMGARNVNVNMNGPDSG
SGRSRNDMTKNYGKNDQINGRDEFFQSEEFDGDNPTVQQYNYHPSPQPSRRY

RREKRVEMNSGQRSQYNPHSQKSNSHEGNNEKRNSSNSSSNDADRACVLHC
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DKCEFSKNLLTCLLEKGRANCDDWNESTSLLFE
>HaOBP2
MQCSDMSDLLEFNETTFSSVSSRLPARGSMLVQVVLATLLALGAAPCVLQRA
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RLSLAAVLYLLPLRVSQGGEMIAIFVFVMFFGIREIAADCKNCGMLGKDEKAM
FRAHSEACRSHSQVDPKLIESLLNGELVDDPGLRKHVYCVLLKCKVISKDGKL
QKAAVLGKMAARGDGKNVTKVLENCANQPGESPEDLAWNLFRCGYDKKAV
LFGHTRAAPAGNDA
>HaOBP3
MNSNCFILIACAIFSVCNSSYVDKLLKCSVNDEECFKKLLNKFLEDNSDNGIPE
INIPPLDPFELKNVVVTVPDLINATFIDGTVSGAKKCVINSFKIQSDKGFTKVGL
TCDLVLKGTYSLEGTGPLLKNLLGGDFLRGSGNMELKLNKIKMNLGVVYHFI
KKDDGEVYYKCHRDKFQYDCDVGNAHLTSEKIFLGKEDATELVVGFFNQNW
KMLEKSFGKHLFDTALNIFNDVLQKFLESTSVKHFIIEDLSNLVKN
>HaOBP4
MYKSNLSYLFLVPSLPKCHVHDEDCLKSLAQKAITDISNIGVPEMGIRPIDPFQ
LSNVTVSIFDIINITLVDGEAKGIKDCVVDSLVSQVEEGKTKVAYTCDLIIEGKF
NLQAASPLFQNLLGGEKIHGNGNAKVELDKVHMSLEFSFHYIRKEDGNIYTK
FHPEEYEYDYSIGDMRISADNIFLGDKDVSKMIVVWLNENWKYAMQTFGRSF
VDVAMGLFYDILQQIFYATPTKSYIIEDLSSLVKHEE
>HaOBP5
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