

Ictalurid herpesvirus 1 strain Auburn 1, complete genome

GenBank: M75136.2

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LOCUS IH1CG 134226 bp DNA linear VRL 29-AUG-2013

DEFINITION Ictalurid herpesvirus 1 strain Auburn 1, complete genome.

ACCESSION M75136

VERSION M75136.2

KEYWORDS .

SOURCE Ictalurid herpesvirus 1 (IcHV-1)

ORGANISM [Ictalurid herpesvirus 1](#)

Viruses; Duplodnaviria; Heunggongvirae; Pelloviricota;

Herviviricetes; Herpesvirales; Alloherpesviridae; Ictalurivirus.

REFERENCE 1 (bases 1 to 134226)

AUTHORS Davison,A.J.

TITLE Channel catfish virus: a new type of herpesvirus

JOURNAL Virology 186 (1), 9-14 (1992)

PUBMED [1727613](#)

REFERENCE 2 (bases 1 to 134226)

AUTHORS Davison,A.J.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1993) MRC Virology Unit, Church Street, Glasgow
G11 5JR, UK

REFERENCE 3 (bases 1 to 134226)

AUTHORS Davison,A.J.

TITLE Direct Submission

JOURNAL Submitted (28-APR-2006) MRC Virology Unit, Church Street, Glasgow
G11 5JR, UK

REMARK Amino acid sequence updated by submitter

REFERENCE 4 (bases 1 to 134226)

AUTHORS Davison,A.J.

TITLE Direct Submission

JOURNAL Submitted (02-JUL-2013) MRC Virology Unit, Church Street, Glasgow
G11 5JR, UK

REMARK Sequence update by submitter

COMMENT On Jul 2, 2013 this sequence version replaced [M75136.1](#).

1. Data were derived from shotgun sequencing of genome DNA. 2. Predicted coding regions generally start at the first in-frame ATG codon. Where there is supporting evidence, subsequent ATG codons are used instead. Such evidence emerged from alignment with

related

proteins, codon preference or bias, presence of a predicted signal peptide or location of a potential TATA signal. 3. Predicted polyA signals are annotated for each coding region. Alternative

predictions are possible in some cases. PolyA signals are not predicted for a few ORFs where no good candidates are available.

4. The location of the 5'-nucleotide at each genome terminus was determined.

FEATURES	Location/Qualifiers
source	1..134226 /organism="Ictalurid herpesvirus 1" /mol_type="genomic DNA" /strain="Auburn 1" /host="Ictalurus punctatus" /db_xref="ATCC:VR-665" /db_xref="taxon:10401" /clone="A" /tissue_lib="ATCC VR-665" /note="isolated from virus passaged in the ATCC CCL-159 (BB brown bullhead) cell line"
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repeat_region	63..273 /rpt_type=direct
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regulatory	complement(467..472) /regulatory_class="polyA_signal_sequence" /gene="ORF1L"
regulatory	complement(583..588) /regulatory_class="polyA_signal_sequence" /gene="ORF1L"
repeat_region	609..748 /rpt_type=direct
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NILKVNDRPVMTPSILNEIPDFVHRGNTLPiWLLFAASLRDLIVAVKEWLSTEGGDPR
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VLSTISDNNVPNLPIFSWIGEIPLWSTSGIVEKVKIVHTNSSLSVRMMLLSDVTEVAK
VHAIAKAVRAEQKASKESAKGEDAAKKAPKRKREAEAGTETPKKKQKEEKSEKPKKTG
KAEKSTGTAKVTKKEKTEKKTPQTKSTNKKNVKSVSAEAGTAVTPDEANGKKKSTQVK
KKESAGQHTTEKKKRTAAKKKTVDRPSGHRPSSKKEYRSQEFVSSDDSSDEEVISKPR
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[gene](#)

3502..6272
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[CDS](#)

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KPVPAKGLWGVVQVESTVTGIPKMIHVCLDRSLGVGYKCSFAKLWKKTIEELLGTGVG
TTNPHCWFTRTIHSDAIQASFDGLNMI FELFGGRVRTGRVSP EGERRVFHTRCLGDDS
FNALFAATVHDPTVSRVFEARVRTVQTSYPAWYTFGDMWTPAPNNVGWVTTPEGSWC
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[gene](#)

4886..6272
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[CDS](#)

4886..5794
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PWSPVRGSLLPKSGSPTYWNPPPPSPSDDTTCEIPSLPSSLVSSPVNPAPMYSVPVSD
APLNTPSFNMMITPTHPLARLLDTPPTPLDADLG DWAVDWLYAPQLGDQLRIESGSS
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[repeat_region](#)

6084..6241
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[regulatory](#)

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/note="ORF2, ORF3"

[regulatory](#)

6158..6163

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        /note="ORF2, ORF3"
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        /note="ORF2, ORF3"
regulatory      6267..6272
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        /note="ORF2, ORF3"
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GCGPGHPPVDCMCDRQDWL"
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regulatory      8642..8647
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        /gene="ORF4L"
gene            8785..10048
        /gene="ORF5L"
CDS             8785..9471
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perhaps acquired independently"
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        /product="ORF5"
        /protein_id="AAA88108.1"
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VNVVEEPVDQWVNHNGKNYLELSYTDPTGYAVPFQNLVFD SYVNVQRLQNPDIMERSP
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RAPLTRKSQL"

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CDS 9535..9951
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 ALLTLMTIPIIGLFGIYVRTRASIEEMRGILMQIHLRLITGDQRSNRGDVELGAGAS
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regulatory 10043..10048
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 /note="ORF5, ORF6"
repeat_region 10248..10267
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repeat_region 10298..10326
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CDS 10863..11285
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 MTPEADDLTRPPLGHGRQIPVLRRLMVLDRLRIDYSI"
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regulatory 11499..11504
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repeat_region 11658..11751
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CDS 12462..13160

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ETPTPEPSRDGGSTPEVLHVVTGPVRPRDRDPILERLAEILAETHSLHQLLTPGTGPR
EDEDEVFARALAAAEIAIGSVADRVMMWKATLSCMLVVTSLVFAGVALWVIVARHGHFR
VIPHERSRDWSPGL"
gene      13197..13781
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CDS      13197..13673
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/ note="RING-finger protein; member of RING gene family"
/ codon_start=1
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DSGNCGPCGARRDVFAFDLYGSGPLPPCPVCGRAVVGPTVREACGHVTCNACETEACA
VDRLCIGGGRRLLVAICDPYPPYPGPRWRGPRPTRPEAHEAVQSRSGSSEDACTCAP"
repeat_region 13714..13733
/ gene="ORF9L"
/ rpt_type=direct
regulatory 13776..13781
/ regulatory_class="polyA_signal_sequence"
/ note="ORF8, ORF9"
gene      14076..16334
/ gene="ORF10L"
CDS      14076..14531
/ gene="ORF10L"
/ note="membrane glycoprotein"
/ codon_start=1
/ product="ORF10"
/ protein_id="AAA88113.1"
/ translation="MTVKGCLCLAFGVTLIVIVGVVAMGVALSKGRAPGDDLVTAL
NELAGDEDEVGRLSDAGAANLTGLLRGLILDHLSRNSSGLVAADALYERVLTRLRLDI
FVFNGLVAAFNGFWLSFIIMYTCARTVRSGKKVAPAPIHSPPTMMSPYI"
gene      14539..16334
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/ note="RING-finger protein; tegument protein; member of
RING gene family"

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AIEAAGGKVAVGGFLVRTLYELVRYHDTLAKTFPVMAPRFGSLGALKELLSRFRIPIG
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PPTGH"
gene      15391..16334
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DGALGNVFDLVTGISAVIADRAEKPIDLVDIVLNPDWSPVPCTIPYRLFRLLVKANA
EMGVHDWSDLVTLGAWNILVEYGAVPGLDRSRLLEFLRYLVIPGFDGAETFPALTETF
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/note="ORF10, ORF11, ORF12"
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CDS       16354..16602
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regulatory 16744..16749

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HFLDAAPKLIWEVSGTRENKSAQMVT FSECGLYGSMEGYFYRERATVDICATILAD
LTGKLLALIRKGIYHGDLKSENIIMSRSGPGKLIDFEHSHGPGETMTSFWYPDRTF
WNPIGTEAYAPPERSRGRGRNAGVPGIVFQIGLIALNIMVERMERVFVNHTWIKGDGY
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misc_feature     18557..115670
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gene            complement(18768..20008)
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regulatory complement(18854..18859)
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CDS complement(18866..20008)
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 GEYFVRLATLSECSAGGDVGAYIRGGRPISIEAAVKTRELASTLYLLAQNNVYHGDV
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 FPDILSAEQLVWQVGLFMDVIGIEIIENRNQGLWEQPDFPGLAAREVGIGRSLAC
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regulatory complement(20123..20128)
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repeat_region 20139..20161
 /rpt_type=direct

CDS complement(20171..21334)
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 EECILFGFSPLSSTGMAALKALDLVYGGYAPAAPGIPMEVYAWEMAYKIGAAPRLLRW
 VLIEGEGIEQFATLAESGLRGSLRDYIGTHPSGCKTPMDLGLVVKNVHGLVAALGMLM
 DSNIYHGDLDKIDNLTVTEPGGPYKLIDFEFAHPFEARMRPMIEARGPITWLMPGTPAC
 NPPEHDEETPCRDRMKELGVTWQLGLIMLETIVLDEALVRDENMEWKRPDFKRLVSA
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gene complement(22737..23728)
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regulatory complement(22737..22742)
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 /gene="ORF17"

CDS complement (22832..23728)
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 MEFDRTCGSGERGLHALHALSGVIVGELERLLVEGHVSTDLAQVYLTMLIVTLFRDDE
 FGRALLKVDSIILALESRIDTVRLEEIQRVMCASVTRFHGVRPGFETEAFAMHDAIN
 RCGLYGTARGEPESEVEEPGSTV"

gene 23762..24753
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CDS 23762..24718
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 QRVTEWLATLSPEEKTTVRILNWSGTTFEDQLELTERVLRSWADFSEYQLPSRHLSEF
 VTLKDSLRYGTDSSGHQYYHAKMDSVDETGVVYRVNLTRASIPRRFTLIVCHGTAVAT
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gene 24842..25457
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CDS 24842..25456
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 VLIITACLTIIYIIAKVRSRCRRPIERTPDKPDPERVRLYLDSVRRRYWPCSGTEGDED
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regulatory 25452..25457
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CDS         complement(25576..25884)
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gene      26089..27104
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gene          complement(27145..32537)
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gene          complement(27145..31357)
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regulatory    complement(27145..27150)
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              /note="ORF22, ORF23"
CDS           complement(27146..31357)
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RaHV-1, RaHV-2 and CyHV-3"

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KVKDIFGNCSVTWIADVKAADRAVTA AVTGT VHAVTGGMGAMWGTLDRAMIDLKLDLV
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VFLEQNDILNKAVQAISVSYTAMNSNFQAGLAKYKPPRVPTADGALTARGIAPDRPRQ
AKYETVKTYATNMGFDVLIGGKVP GSKGDIESLVSGILLAGKSLDELGALVGGIGSDG
AIVSRDQMDQVRSLIDSLVKIIYDTRDRFIAMTGVHVITEYANDLLRVLDLIAQKYG
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IANLHRDLRVATERLHKKDTKILETGINTGVSTARVRELEQ RVKELVAEKKSIRHENR
MARRKMDPTEAAAKGGPRQSERPRSQTAVHAHCALIRKNLHDTNKRLLTRNTRLEKSI
SSKEELISSLTIKGNALSSQLADAREQHAVLKREYDALRAERGGTARTKKDALEALQS
KLTQSESQ LAIEKLK VMELEAAAKRLGKSSVT KSEVETVEVRVNL LTEELARTKKTVD
ELRKLNNAYLTAKDRLQARVEALT TDNQSMKLLVGNGGTLDEANKRITTLTQRLATVS
GELVTATETLAFVRGSLKRVNHQRDELAKESAATKKSCEAQIRALTDRHATEMRTAAG
ARDGLEAELGRVKRTLVD TETKLAGVERDRVVL RDELTRMQKASHIGADRQLTHAEKV
AHDMGVLNAGLTLARTELREIQREL VHEKNKSRDAEQ RHVASEAALREQIRTLTDERD
RLLATGVADLQRENAELHAAITEAANTCADTKIQLENITADYNGLLAEYERRLGRRPP
GPVDP PATTEEPIAGYGGGNWDTGSGAARAPIDHDMFGISSLLGESQGGLS DYHGSY
AGGRELSSEESGDDESVD PVPDSNGTRGDGVCREEDEEDRQGGETESGEEEESEES
EESEDEDPPSAGGPLELIGVPAGGIGADPEPARVPSRRPVTLLERRGAHVAEPKPTPR
VRGKRPAARHSHKRVHLSITRETLRLALAAGPEMSAEEIFQRLNTDMETSSLINSLTV
TAADI PRGQLAVLN RDTAVEYATPGTPVSDRDHQRVELSMKAILLIMICAKHGIMNHE
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[CDS](#)

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complement(31281..32537)
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CyHV-3"
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RVSTSLRSSRSRLFASVNSREIAAVPFVYTIAGMEDVIITLGIDDTVYFLEWAILSIN
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YEWLCV LASTAGVLS PMPDPPMPSLLDRFTDSDELEIFVHLGRNIEINGATALWDRTVR
YAFVPPSIELRFKNVWNAILKGGDPRSVMDRAVTVCSTVGADALVVLPRGDGDDEV
PVVAVRNADRYLEELSERSTNRTVTETILAAPTPPFPINFGIGVLTDRVKGLCEVFII
IKDSDRWMFDRYTFALNTCMIGNVISNGLGIYETTLAGLERTLQPPAPTSRPRFVCVV
RDGSHTEAGQPVGALGKCQAKPRNLW"
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[gene](#)

32293..36040

[CDS](#) /gene="ORF24"
32293..33294
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/note="probably conserved in RaHV-1, RaHV-2 and CyHV-3"
/codon_start=1
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/translation="MTSSIPAIIVYTNGTAAISRELTAKRERDELRRREVETLNLELSA
QVDKNRALEETLGTDAEISRLSKLVDSPRDSLIRMYITKNQTLAQRVKLEHRLARE
TKKGSRAGPVATGTGVYGPYPYPRVPIPVADYPIMYSRVGFPEYVLTMYAAYGKCQKN
ILDYVRGGVVTPEFYTVLFSASAIFFVGWFDQRQFSVSTGHDLDFCWKLVALRVTTQ
YLTLNNTFSDSAQLALKTHVNQRQLFQTTQFLRVQQQFVDLVNIRSaelGEVYTSAP
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[gene](#) 33342..36040
/gene="ORF25"

[CDS](#) 33342..34838
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/note="helicase; conserved in RaHV-1, RaHV-2 and CyHV-3"
/codon_start=1
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/protein_id="[AAA88128.1](#)"
/translation="MDVEIKEYAGFVQNEWVRGVASLWMTHPGDGAIVLSGDAGCGKS
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KCLFDARHRQAIEMWDRIVSNRTGLAAVKKGHSCVTINMRCPVCVATIHEsirCTDKP
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IWQTPLLRDMIINTYSLFINFRVEDAAYAEAINLFQFNVITRPAVEMLNARVIGANAV
DAEYCDVTRIFNGNRERDAYNTRHTMVMMEGRGAGRVDLTPVIEHVGSASCRFGALI
EYMCSTVPKIFNKATKGKRTVYEGGYVFLPTQERYTFFGLDDVNTAVVGREDGRLYL
ERQITKYKGWTVSFFPIFPVAAINTYSAQGETLDRVIYAPPEKNYSMSSIRASAYVAC
TRVRTRTAIELSCNSFAKSVGRTNMFPEKLLNHKKSVMEMGYVPRECPY"

[gene](#) 34727..36040
/gene="ORF26"

[CDS](#) 34727..35146
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/note="positional counterpart in RaHV-1 and RaHV-2"
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/protein_id="[AAA88129.1](#)"
/translation="MQLVREKRGahQHVPRKTTEPQKVRGDGICPERMSLLMMINWPF
VDSTVHLETVDALMRYEGVQPPFPDNDSSRKYIMDRWIPWFVTNCRPSNTELYTL
VSKIREDaIVFGASIVTTLTHLVPQREVRNKCRLKII"

[gene](#) 35148..36040
/gene="ORF27"

[CDS](#) 35148..36014

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RaHV-2 and CyHV-3"
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GDHFMVQFPQPEDTDAQLRASKKPGTRRICNAASFNRMLPLWGGFMAVKKIDPIVPRE
LMHQLTRDVVTARSELLYGLAGVYDLVEKTSAAARGVFKDIAEKKAVTKEEVVAAMT
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regulatory      35991..35996
/regulatory_class="polyA_signal_sequence"
/note="ORF24, ORF25, ORF26, ORF27"
regulatory      36035..36040
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/note="ORF24, ORF25, ORF26, ORF27"
gene            complement(36075..38499)
/gene="ORF29"
gene            complement(36075..37874)
/gene="ORF28"
regulatory      complement(36075..36080)
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/note="ORF28, ORF29"
CDS             complement(36102..37874)
/gene="ORF28"
/note="putative capsid maturational protease; conserved in
RaHV-1, RaHV-2 and CyHV-3"
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KRCVETFTADIPCALSLGTLDVGLNEVILECSVVVIPARRGCHAKLFTRD TVSDGLE
KFCFQSHATLPPTLLASFGSTSESPERKTFYEAHVDALNNYIKLLRTIYSHKGETEIE
QYLIEGSKLYSELIGEPSRVLDATMKAAQIAEPQTH TGGADRQRPQRPDGI PYSVPDR
FPMTGYPFAPQFCGDPGLVSHYNPFVPPQSFGQGYGP ERVGGYYPQPPNPVYLPISYG
QQPYPGHPQPHGHHQQRSGGGDLKAELIETLGLAPKTN AVQESLSKSFISEILESELKN
CGIKRAAGNIERNCDVDEEPRTKRARPEPKTAVEAIV RAPYGD FDSALTTKIGQVS
DTVEKLNKVIETLLTQSSAQPAPLSTPAQAAPVQPSLPQPVPEPLAPQEPPPPGTSAP
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CDS             complement(37738..38499)

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/ gene="ORF29"
/ note="contains predicted signal peptide"
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/ protein_id="AAA88132.1"
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RSQESREMQLNQDIFDGVQLTILLDGLVGDGKCLSLVPGVRGLLLHDKKCGICTRTK
PDRGLFTAYFGGLPEEDHIRSRHFQFFNDYGYLLRSMDLDAYTAPIIAPIVPGVVDCV
VIYNKVHHIPIPALKPLLALNVQYEWNTVTQQLRIRTPKIRSNSYSVRDVTTRRKRYR
EDRDSGEDLGAESKRNGSVRYTGREL RDSIMSRI"

gene      38368..39015
/ gene="ORF30"

CDS       38368..38994
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/ codon_start=1
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/ protein_id="AAA88133.1"
/ translation="MMDIFNSVSESINILNNSVAPMDHREEHEGAPSDKPWGVNFSGH
DFLVNSTSRSDIITSVEQVDRGTGSCPICASKNDQGTSLAEAMESMVATRQLDSAMSFL
SMVRPDLANWDVINYHFSHGKDPKIEKLEYQIDTMIDVHYRAGMAIGRDFAMMVTANG
SQFVSPNEKNIKCLSSLTTGLTKLIQVRGDIRKMTTSKKNKRGTAAPL"

regulatory 39010..39015
/ regulatory_class="polyA_signal_sequence"
/ gene="ORF30"

gene      complement(39052..39301)
/ gene="ORF31"

regulatory complement(39052..39057)
/ regulatory_class="polyA_signal_sequence"
/ gene="ORF31"

CDS       complement(39053..39301)
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/ codon_start=1
/ product="ORF31"
/ protein_id="AAA88134.1"
/ translation="MYLQMNFFPCPSPSFHLGESVMVVVDRGTGRCTHRHGRCITV
IQSAGNPVHATDYEAYWLRERLMGMRIGRLVILYTSBK"

gene      39359..42955
/ gene="ORF32"

CDS       39359..39763
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/ codon_start=1
/ product="ORF32"
/ protein_id="AAA88135.1"
/ translation="MRGATTDDSISSVRALPAVVPGSGLFLPMVLHVSSLLSLDQLM

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gene      39821..42955
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CDS       39821..40693
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          /codon_start=1
          /product="ORF33"
          /protein_id="AAA88136.1"
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GRLLDLSRRAYVHWNLRVHGHFSELCTVGGGVERTPLFRALTLRAWNSEPERVLRITIR
ELRTEKLHERGDYWGRNLEYMCTNILAETPEPIFRTLCHTRIIPELKRLVTTWKVYIT
AMYAGRHDDLVLQVTFIRRSIEVDRPLLEFIGELKHSCSLPISRKMTTDKTFHVS GF
ITTTCTKELDRDDTARLVHRNGTG FETVVDRIWVGATMWYRRTYRAVESYDEFWYKY
CGWMDTPTGELPDE"

gene      40536..42955
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CDS       40536..41861
          /gene="ORF34"
          /note="conserved in RaHV-1 and RaHV-2"
          /codon_start=1
          /product="ORF34"
          /protein_id="AAA88137.1"
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CTIGTHRDVINNLNYTTYLYGVCNPMSTMVDSMKQKNFLTPFFFSSINLAGPIETTNQ
LFISMTINTQKLTHETIYDLGKTLPIYSLLEVDTKFNWFCNMIALFLECFINTPNKI
GMIWMNERYYLENPTENATRSTETWNEYRKYMLEKCAPLLNGFSMAFAQRTGQFVYKN
CEMVHIAPFFVAAALEEAVLSYGSFLLNTRKIKSFKELVMMLSVTPTPDPRLTVTQTDD
RTDVYRTGDRVLTWSHGADFKVGASERLVLGKKINQYIKCKTGHDGDQD"

gene      41707..42955
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CDS       41707..42423
          /gene="ORF35"
          /note="probably conserved in RaHV-1 and RaHV-2"
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          /product="ORF35"
          /protein_id="AAA88138.1"
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EITAIKTENEARAKALRQSLEEDRAFWTNKITALGYKVAKRMMAMVTTEPGESTAPHL
EVVHSDKGLLGLFEISAGDQLLCPSAITPFIRDRGGPGTCPLCLRTFDQKLEGHIYTE
LISSGHGVSRGSDGAWRAHFTGDTPPVLFPRKTLGKERAATLSAAIKQFKCLQVDHCT
LEGIIESLAIAKHKILDICE"

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gene 42425..42955
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CDS 42425..42868
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 PCDEFRASLKKNGISSLLTTRGPVTCIKFQIPEDKVISLETTLACLEGTIKVVGDYCYI
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gene complement (42925..45027)
 /gene="ORF37"
regulatory complement (42925..42930)
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regulatory 42950..42995
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 TETFKRHMLWSVLTNFSPVAYYPAADIARADEACDLVTRATVDRLRKTEETVLADERF
 RGLLGPEMVARLLKVIPGIPPDARSIGLVFDNIRPKLSTEAARTLGGM LIETLRQY
 SGYLPVAPLVDLTETVMVYVHEVDTCLLMDKRGVFRALGEPISRSQPLSSPVARTSE
 STMKFQALFDDYMRAASMAKRTVVTPQTVAQAQESRNPFTRELD SGQLSRATFENLI
 QLTGQLNYHQRTAIAESSGLVANPTMVSPTNTALAHMLRTNGAAIQESMLDDLNSRIN
 DLTDQSRRFTDLKRVIGLLQSRDFETLAVHVGELHPDDRELVLHALGPSTRSAAQIDP
 PEIHRLPENTKLLCSFTTSINLPEIEELLHLWTITWETVFCGRNLFTRRKHALQYTTT
 GRHDNEPSQSIQFMFVDSL NAGVLM DRLYPSKVTKLTFTELMVLSEKVETVTLPEIF
 AAQIGLNPSEVRLKNRDACEPPREIVTGVNHELGV DGRFRVAMEDV"
gene 44891..48750
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CDS 44891..45256
 /gene="ORF38"

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/note="positional counterpart in RaHV-1, RaHV-2 and
CyHV-3"
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DISMRAVDHYRQAARLTSICAQHPAVMGTRDICALKRAATNIAAGNALMDQLNKWTM
DRAENSTTNLVGIINDINS"
gene      45306..48750
/gene="ORF39"
CDS       45306..48677
/gene="ORF39"
/note="major capsid protein; conserved in RaHV-1, RaHV-2
and CyHV-3"
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/protein_id="AAA88142.1"
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DLTDGAIIRACQLENIVCGSLNRSKPNLVSLHTALKILDISPKDAAVTTNTVFNQNS
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ARSAYGGLKSVDDVMAIHLGNNETIPVIPLDSTKFSVYGNTSVETAMTQECIKRLFFT
VGTCPNIYDSLEPGSFFGPSSGTGEEITPAMVAMRSPRSTYIMDLDRGDRVQEITLRQ
LHRVFLDGNKDAFDTSFGFARKIARLTEALEKFNEAEVANLFLEPEWERKMADPGSIFE
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MLQLVGQSSAITNYCQLVQTALSDTSAEGVEAVNNIRHMDLTGATPPLTRVMVDKITL
RGGRYLPLSDPYCQLAIKIFYDDPAAITDVGNRVDVVQTVVNTIRAGFDAIVNVFKTI
FDEPDFSIFSNNMPKSICVTQALTATENLFMNIAYAAILPIFTDTLASMGGGMTVDT
ETNFNGMVFPVYRNACFIGSGATLPNQVKLWELTGVTPELLVRVWKCRTREIMKTFG
GQNPFMGFLYHLHLSTLIDKTVILKHFDVKYYSGFSYLCVTRTTRFTGHGLSVLPRKSA
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PRDMYAIAIFDAYNGFTPETKTTASPTNIALSGRVRVEGLGAPDPVTGLYSQCPTL
VAGLGAGFDRLRSLVHRLNLPCHAYAMILAAVDRGNVFETLPVIFS NVEYMRDLELL
KRTVDATPADRNLYRETMGILFADNYVIGKNGEHVFRANTKTVPTIAALSPKVLGES
LYNGAIYGDLEYGFSCLKAKYTGVTTSRLRIDLNAV"
regulatory 48745..48750
/regulatory_class="polyA_signal_sequence"
/note="ORF38, ORF39"
gene      complement(48788..49290)
/gene="ORF40"
regulatory complement(48788..48793)
/regulatory_class="polyA_signal_sequence"

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[CDS](#) /note="ORF40, ORF41"
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 /protein_id="AAA88143.1"
 /translation="MTPVPPSSLRSIAPLSTVFLETDNVRNSWVFCVIRCLSPRR
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 TAMVFWSFSESTSLWCIISSSMRLCFSITSGST"

[gene](#) complement(49423..50325)
 /gene="ORF41"

[CDS](#) complement(49423..50325)
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 GLYTTVSTAEMFNPTGTPDFLAAFDALFEEGGGTHKPPIQFPTVRFDKCEGTCEAADH
 IHELTRRIIGEVRRVYISNATGKVIPLLVLTAVITAENRGVEVPERVGARPIHATGN
 IHFDTVLSYVVQMMYLGKVRVCAP"

[gene](#) 50324..50752
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[CDS](#) 50324..50713
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 /codon_start=1
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 /protein_id="AAA88145.1"
 /translation="MASFGERSRAYWTMSMGMECYKASTSSDESCQRRGVRDDTGTQP
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[regulatory](#) 50747..50752
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[gene](#) complement(50977..53707)
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[regulatory](#) complement(50977..50982)
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[CDS](#) complement(51032..53707)
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 /note="conserved in RaHV-1 and RaHV-2"
 /codon_start=1

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HNAFLELAQLYTTVYRNFYGLGDFLALVATSLHLDNIWPLAVTRKITTPLFVDTVK
QEEVE MEVNGEQMVLVSQKYVTFKAFKGFVLETDSEGGLES DAADDPFLAESITL
KLEKNQMT KMMDRDLMLKTAILSIRDENPRIKRAKNNIKLVDEFFMGIDRMAQPA
FVKLAKKLMGS AHMVAILQSTLRSSILSWGLNDVAGTNTTMSDPELLNKLRRQT
YVRMLADLSLLKVSRTPMGMFSVKDVSVKLDDRYWQGKKDATADQDKILQFYNQ
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GKGATQSGTKHNSCSDLSDLGKFRYVVRATPGTPPASILGLMHLIRTALFGVVC
VSIHMAGEFFAEENLDLELNSNNKAA TTVMRKMGDQFFRGYFFNLGNDDKKV
KSSFDMIFRVFGAKGRALLSRKDGNPNLRRS NAFNGLEWLRKKVKARPELAN
NMRRAIRNLLERYDVQAMILDQAETRSLYYLRPFMT PFKTELQASTIISKKADF
NNAPTLLHVNLT SVTISPTNTHFTLPLAPIFNKWDQHKVY GIILEMNTNVYSQ
ATRGTWTATGGGQFFGADV GIDSLMSSLLSQVSEDEPVTSELINM FSLDKVRY
DTVVERLKALSRYEETEPVYGEDLVLSRELEQSDELDCGTENNEPLVLQ PFEK
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gene      53657..55365
CDS       /gene="ORF44"
          53657..54664
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          /protein_id="AAA88147.1"
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ICKKTPSLTPEYNLKLQVVVDIMRRYTVEDPLDLLVTIYPEFTETLEELAKVKR
GAANLEHMG LIYHVLNAHINWFAFNRHQFLNPGITLPSSSELSQEALGMAYDLR
CSGCWRLLSIRS LRKTGNPKNMKIYYSTD SHGLISSCKASVLKAPLSIGKTALV
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gene      54642..55365
CDS       /gene="ORF45"
          54642..55364
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regulatory 55360..55365
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 /note="ORF44, ORF45"

gene complement(55397..59494)
 /gene="ORF46"

regulatory complement(55397..55402)
 /regulatory_class="polyA_signal_sequence"
 /gene="ORF46"

CDS complement(55427..59494)
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 /note="membrane glycoprotein; conserved in RaHV-1, RaHV-2
 and CyHV-3"
 /codon_start=1
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 /protein_id="[AAA88149.1](#)"
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gene 59469..60776
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CDS 59469..60584
 /gene="ORF47"

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CDS complement(61678..62244)

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and CyHV-3 perhaps acquired independently"
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CDS complement(62436..64448)
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gene 65102..66058
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CDS      complement(66033..66959)
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RaHV-2 and CyHV-3"
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[gene](#)

73958..78608

/gene="ORF57"

[CDS](#)

join(73958..76759,76872..78608)

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/EC_number="[2.7.7.7](#)"

/note="DNA polymerase catalytic subunit; conserved in
RaHV-1, RaHV-2 and CyHV-3"

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regulatory complement(78633..78638)
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CDS complement(78703..79740)
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RaHV-2 and IchV-3"
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CDS 79779..80960
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gene complement(80525..81891)

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CDS join(81869..82717,97459..98016,98746..99543)
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RaHV-1, RaHV-2 and CyHV-3"
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CDS 82758..84746

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CDS      84664..86208
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CDS      complement(86367..90671)

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[repeat_region](#) 87758..88025

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CDS 91887..96557

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[regulatory](#) 104322..104327
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regulatory complement(111526..111531)
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[gene](#) 120556..121942

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[CDS](#) 120556..121464

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ORIGIN

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