

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
CDS	complement(742..3330) /gene="ORF1L" /codon_start=1 /product="ORF1" /protein_id="AAA88104.1" /translation="MDGLKEITAAVASLGGTTDLSTYMNFDLGDMMDSAGVVIDDV HPPVEGASVDSAMDVDAESEDEKDEEPTGRDEPEVESEADEDPDEVEDAIPAAVPST IPLSTTIRGFGADLGLGKNLTPADLAGNGLGKYAATLFSKTLPTLAAVEQKGAIDPG SSVAKSIVTLLSSELGNALGIFSRPRTREQNKMAAVMILMKVLGRTALPPLTKTDEGV LSAINLVFSGAKRKVLVSTHSDITKFIIFNDDGTIPTLGVDTVAPLMKYDPRKLTT LVLIKNLGNNGTVEVKRRSKGKTLVMRERIPVECFLFRAFPVTESSDNIYATLDFVKR LLKGVSTQSSYVYVKNPKSIGDDFLNTKNTSLTLGDAPLTVKLSFRKPTNATSQSGFK RWLLICKWLARGRIELGPKSTLRSKGHEEESLEEEVNTGCIRSMASLTRLASRAWSPK"

NILKVNDRPVMTPSILNEIPDFVHRGNTLPiWLLFAASLRDLIVAVKEWLSTEGGDPR
SIDVAKLTYHQYLFLRLSSDAGIAKKGLSKLLTATNNWLITEMSFIVMYKGSYGVNPT
VLSTISDNNVPNLPIFSWIGEIPLWSTSGIVEKVKIVHTNSSLSVRMMLLSDVTEVAK
VHAIAKAVRAEQKASKESAKGEDAAKKAPKRKREAEAGTETPKKKQKEEKSEKPKKTG
KAEKSTGTAKVTKKEKTEKKTPQTKSTNKKNVKSVSAEAGTAVTPDEANGKKKSTQVK
KKESAGQHTTEKKKRTAAKKKTVDRPSGHRPSSKKEYRSQEFVSSDDSSDEEVISKPR
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KTLLLS"

[gene](#)

3502..6272
/gene="ORF2L"

[CDS](#)

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KPVPAKGLWGVVQVESTVTGIPKMIHVCLDRSLGVGYKCSFAKLWKKTIEELLGTGVG
TTNPHCWFTRTIHSDAIQASFDGLNMI FELFGGRVRTGRVSP EGERRVFHTRCLGDDS
FNALFAATVHDPTVSRVFEARVRTVQTSYPAWYTFGDMWTPAPNNVGWVTTPEGSWC
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TSGDSVELHAPLLPL"

[gene](#)

4886..6272
/gene="ORF3L"

[CDS](#)

4886..5794
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PWSPVRGSLLPKSGSPTYWNPPPPSPSDDTTCEIPSLPSSLVSSPVNPAPMYSVPVSD
APLNTPSFNMMITPTHPLARLLDTPPTPLDADLGDAVDWLYAPQLGDQLRIESGSS
PGKRPLDDPDEVPSKRGPSRRALLN"

[repeat_region](#)

5668..5956
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[repeat_region](#)

6084..6241
/rpt_type=direct

[regulatory](#)

6118..6123
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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      6234..6239
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        /note="ORF2, ORF3"
regulatory      6267..6272
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        /note="ORF2, ORF3"
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CDS             7960..8499
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RVVVHYVPSPEREDPESPTRGVDEVDGACSEPPTPRPEPRFRAIEEMGKIVVLVSVCP
LRPALQHRWVGAPARRHRSDSVARRARFEPWRGRASRPVLTTPASGSDDDVDTRTFGC
GCGPGHPPVDCMCDRQDWL"
regulatory      8557..8562
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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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        /note="deoxyribonucleoside kinase; counterpart in CyHV-3
perhaps acquired independently"
        /codon_start=1
        /product="ORF5"
        /protein_id="AAA88108.1"
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MSATRVFCVNGSRGVIPATALPGMAARGEAVMRTIATRPVVFVYLELPPEECLRRMRR
RDRTG EAGVGLDYLRLLHERYEAWLSSAEDVERVDASRSREEIVDRVIEILCRRHPRL
RAPLTRKSQL"

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CDS 9535..9951
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 ALLTLMTIPIIGLFGIYVRTRASIEEMRGILMQIHLRLITGDQRSNRGDVELGAGAS
 LLTISSQPPSYAEALLMEPVEPQQQEGVPLEAEIRV"
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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repeat_region 10420..10614
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CDS 10863..11285
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 MTPEADDLTRPPLGHGRQIPVLRMRMVLDRDLRIDYSI"
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regulatory 11499..11504
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repeat_region 11658..11751
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repeat_region 11767..11898
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gene 12462..13781
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CDS 12462..13160

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ETPTPEPSRDGGSTPEVLHVVTGPVVRPRDRDPILERLAEILAETHSLHQLLTPGTGPR
EDEDEVFARALAAAEIAIGSVADRVMMWKATLSCMLVVTSLVFAGVALWVIVARHGHFR
VIPHERSRDWSPGL"
gene      13197..13781
/ gene="ORF9L"
CDS      13197..13673
/ gene="ORF9L"
/ note="RING-finger protein; member of RING gene family"
/ codon_start=1
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/ protein_id="AAA88112.1"
/ translation="MATRPKVRPDRALYVPPKVDRIKRVIFACGHRKRCEIGYRPLG
DSGNCGPCGARRDVFPDLYGSGPLPPCPVCGRAVVGPTVREACGHVTCNACETEACA
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
NELAGDEDEVGRLSDAGAANLTGLLRGLILDHLNRSSGLVAADALYERVLTRLRLDI
FVFNGLVAAFNGFWLSFIIMYTCARTVRSGKKVAPAPIHSPPTMMSPYI"
gene      14539..16334
/ gene="ORF11L"
CDS      14539..15384
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/ note="RING-finger protein; tegument protein; member of
RING gene family"

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PRVVLEDLLTAVIITVGALVETRGAPEGAVRVRARGKWEAIALPLPLDDLVELGG
AIEAAGGKVAVGGFLVRTLYELVVRyhDTLAKTFPVMAPRFGSLGALKELLSRFRIpG
YFGSGTPRYDGLLGHIACEIRKCCDPPGIGFPNPFRAFLNRKNRHKRTGGATGSPFTD
PPTGH"

gene      15391..16334
/gene="ORF12L"

CDS      15391..16290
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/translation="MTSPREEITVRLSCGHPLRVPDGEFCFGDGAYCCDCDERAVFFA
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DGALGNVfVDLVTGISAVIADRAEKPIDLVDIVLNPdWSPVPCTIPYRLFRLLVKANA
EMGVHDWSDLVTLGAWNILVEYGAVPGLDRSRLLEFLRYLVIPGFDGAETFPALTETf
LSILAECTWVGDSRCGYRDACSR"

regulatory 16329..16334
/regulatory_class="polyA_signal_sequence"
/note="ORF10, ORF11, ORF12"

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/gene="ORF13L"

CDS      16354..16602
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/note="contains predicted signal peptide"
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repeat region 16665..16716
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regulatory 16740..16745
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regulatory 16744..16749

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regulatory      complement(17076..17081)
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        /gene="ORF14L"
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SYLHLFVPLRHRTRGNIFFGFSPLSATGMAVLKIKTFHGGTQAPDRPGVPMEVYAWETA
HFLDAAPKLIWEVSGTRENKSAQMTVFSECGLYGSMEGYFYRERATVDICATILAD
LTGKLLALIRKGIYHGDLKSENIIMSRSGPGKLIDFEHSHGPGETMTSFWYPDRTF
WNPIGTEAYAPPERSRGRGRNAGVPGIVFQIGLIALNIMVERMERVFVNHTWIKGDGY
RAHVLKVIKARGTLDLRGGARTLARVDELIGLVARCLERDPAMRPSLETILVDEFSKI"
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CDS complement(18866..20008)
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 LFGFSPLSRTGMATLKTA PVFRGGYAPAAPGIPMQVYAWEMACKIDAAPRLFKWELIV
 GEYFVRLATLSECSAGGDVGAYIRGGRPISIEAAVKTRELASTLYLLAQNNVYHGDV
 KIAN TVITEPHGRLGLIDFEMAHPD MTMSGLREGLEVPIKWD MVCTDEYRAPEGHGP
 FPDILSAEAQLVWQVGLFMLDVIGIEIIENRNQGLWEQPDFPGLAAREVGIGRSLAC
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gene complement(20123..21334)
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regulatory complement(20123..20128)
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repeat_region 20139..20161
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CDS complement(20171..21334)
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 EECILFGFSPLSSTGMAALK AIDL VYGGYAPAAPGIPMEVYAWEMAYKIGAAPRLLRW
 VLIEGEGIEQFATLAESGLRGSLRDYIGTHPSGCKTPMDLGLVVKNVHGLVAALGMLM
 DSNIYHGD LKIDNLT VTEPGGPYKLIDFEFAHPFEARMRPMIEARGPITWLM PGTPAC
 NPPEHDEETPCRDRRMKELGVTWQLGLIMLETIVLDEALVRDENMEWKRPDFKRLVSA
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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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 MLAEATEDIKRERLTKALSTFTILAASRAPINTWTTTRPRERFDALTGIPARWDDALCE
 MEFDRTCGSGERGLHALHALSGVIVGELERLLVEGHVSTDLAQVYLTMLIVTLFRDDE
 FGRALLKVDSIILALESRIDTVRLEEIQRVMCASVTRFHGVRPGFETEAFAKMHDAIN
 RCGLYGTARGEPESEVEEPGSTV"

gene 23762..24753
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CDS 23762..24718
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 QRVTEWLATLSPEEKTTVRILNWSGTTFEDQLELTERVLRSWADFSEYQLPSRHLSEF
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gene 24842..25457
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CDS 24842..25456
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 VLIITACLTIIYIIAKVRSRCRRPIERTPKDPDPERVRLYLDSVRRRYWPCSGTEGDE
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regulatory 25452..25457
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RFRCPRCETILWRFPPLGETVTPDEMNIIRRAWNHVALIQNECRSPETQIMCIHFLVDPE
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gene 26089..27104
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CDS 26089..26979
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gene complement (27145..32537)
/gene="ORF23"
gene complement (27145..31357)
/gene="ORF22"
regulatory complement (27145..27150)
/regulatory_class="polyA_signal_sequence"
/note="ORF22, ORF23"
CDS complement (27146..31357)
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/note="contains myosin-like domain; probably conserved in
RaHV-1, RaHV-2 and CyHV-3"

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KVKDIFGNCSVTWIADVKAADRAVTA AVTGT VHAVTGGMGAMWGTLDRAMIDLKLDLV
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VFLEQNDILNKAVQAISVSYTAMNSNFQAGLAKYKPPRVPTADGALTARGIAPDRPRQ
AKYETVKTYATNMGFDVLIGGKVP GSKGDIESLVSGILLAGKSLDELGALVGGIGSDG
AIVSRDQMDQVRSLIDSLVKIIYDTRDRFIAMTGVHVITEYANDLLRVLDLIAQKYG
EFQRTISGLEPSWATIVSNTEGLIPLYAERAAYAAERAVIIDEFQKMAMDHANNVKEV
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ESLKGT LKGETTLGTTVMDLSKANRQLES RVAELQGKLG IQENEAKLRDEQHKAQAEQ
IANLHRDLRVATERLHKKDTKILETGINTGVSTARVRELEQ RVKELVAEKKSIRHENR
MARRKMDPTEAAAKGGPRQSERPRSQTAVHAHCALIRKNLHDTNKRLLTRNTRLEKSI
SSKEELISSLTIKGNALSSQLADAREQHAVLKREYDALRAERGGTARTKKDALEALQS
KLTQSESQ LAIEKLVMELEAAAKRLGKSSVT KSEVETVEVRVNL LTEELARTKKTVD
ELRKLNNAYLTAKDRLQARVEALT TDNQSMKLLVGNGGTLDEANKRITTLTQRLATVS
GELVTATETLAFVRGSLKRVNHQRDELAKESAATKKSCEAQIRALTDRHATEMRTAAG
ARDGLEAELGRVKRTLVD TETKLAGVERDRVVL RDELTRMQKASHIGADRQLTHAEKV
AHDMGVLNAGLTLARTELREIQREL VHEKNKSRDAEQ RHVASEAALREQIRTLTDERD
RLLATGVADLQRENAELHAAITEAANTCADTKIQLENITADYNGLLAEYERRLGRRPP
GPVDP PATTEEPIAGYGGGNWDTGSGAARAPIDHDMFGISSLLGESQGGLSDYHGSY
AGGRELSSEESGDDESVD PVPDSNGTRGDGVCREEDEEDRQGGETESGEEEESEES
EESEDEDPPSAGGPLELIGVPAGGIGADPEPARVPSRRPVTL LERRGAHVAEPKPTPR
VRGKRPAARHSHKRVHLSITRET LRLALAAGPEMSAEEIFQRLNTDMETSSLINSLTV
TAADI PRGQLAVLN RDTAVEYATPGTPVSDRDHQRVELSMKAILLIMICAKHGIMNHE
EFTDGDLSWFKSYDNNLSVTGSDSE"
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[CDS](#)

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complement(31281..32537)
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/note="positional counterpart in RaHV-1, RaHV-2 and
CyHV-3"
/codon_start=1
/product="ORF23"
/protein_id="AAA88126.1"
/translation="MYIRINESRGESTSLDNRLISASRVPSVSSSARFLSTCAESSRL
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YEWLCV LASTAGVLS PMPDPPMPSLLDRFTDSDELEIFVHLGRNIEINGATALWDRTVR
YAFVPPSIELRFKNVWNAILKGGDPRSVMDRAVTVCSTVGADALVVLPRGDGDDEV
PVVAVRNADRYLEELSERSTNRTVT EILAAPTPPFP IPNFGIGVLTDRVKGLCEVFII
IKDSDRWMFDRYTFALNTCMIGNVISNGLGIYETTLAGLERTLQPPAPTSRPRFVCVV
RDGSHTEAGQPVGALGKCQAKPRNLW"
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[gene](#)

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32293..36040
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[CDS](#)

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32293..33294  
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/note="probably conserved in RaHV-1, RaHV-2 and CyHV-3"  
/codon_start=1  
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/protein_id="AAA88127.1"  
/translation="MTSSIPAIIVYTNGTAAISRELTAKRERDELRRREVETLNLELSA  
QVDKNRALEETLGTDAEISRLSKLVDSPRDSLIRMYITKNQTLAQRVKLEHRLARE  
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ILDYVRGGVVTPEFYTVLFSASAIFFVGVWFDQRQFSVSTGHDLDFCWKLVALRVTTQ  
YLTLNLTFSDSAQLALKTHVNQRQLFQTTQFLRVQQQFVDLVNIRSDELGEVYTSAP  
PLDEYTKKRANLIAEAGDEDLDKLLILADDPIIRVPAEKNRKRRAIGGSEELTACVE"
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[gene](#)

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33342..36040
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[CDS](#)

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33342..34838  
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/translation="MDVEIKEYAGFVQNEWVRGVASLWMTHPGDGAIVLSGDAGCGKS  
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KCLFDARHRQAIEMWDRIVSNRTGLAAVKKKGHSCVTLMRCPVCVATIHESIRCTDKP  
YPYFIARTMFIIDEYGILSELKILYALSKFKLPGQGYILVFTGVSQQLPSPEHPQ  
IWQTPLLRDMIINTYSLFINFRVEDAAYAEAINLFQFNVITRPAVEMLNARVIGANAV  
DAEYCDVTRIFNGNRERDAYNTRHTMVMMEGRGAGRVDLTPVIEHVGSASCRFGALI  
EYMCSTVPKIFNKATKGKRTVYEGGYVFLPTQERYTFFGLDDVNTAVVGREDGRLYL  
ERQITKYKGWTVSFFPIFPVAAINTYSAQGETLDRVIYAPPEKNYSMSSIRASAYVAC  
TRVRTRTAIELSCNSFAKSVGRTNMFPEKLLNHKKSVMEMGYVPRECPY"
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[gene](#)

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34727..36040
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[CDS](#)

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/gene="ORF26"  
34727..35146  
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/note="positional counterpart in RaHV-1 and RaHV-2"  
/codon_start=1  
/product="ORF26"  
/protein_id="AAA88129.1"  
/translation="MQLVREKRGAHQHVPRKTTEPQKVRGDGICPERMSLLMMINWPF  
VDSTVHLETVDALMRYEGVQPPFPDNDSSRKYIMDRWIPWFVTNCRPSNTELYTL  
VSKIREDIVFGASIVTTLTHLVPQREVRNKCRLKII"
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[gene](#)

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35148..36040
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[CDS](#)

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/gene="ORF27"  
35148..36014
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/gene="ORF27"
/note="capsid triplex protein 2; conserved in RaHV-1,
RaHV-2 and CyHV-3"
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/protein_id="AAA88130.1"
/translation="MASITGQLSPMYINNVNTRSAYQPYIPVLERFDPRDLEVPKGVE
VPLSGAMYFPTVHGMSLPQRRPLGLVQTGGLMSEPMTVDVVPGKLYTVLNTGCDTLRV
GDHFMVQFPQPEDTDAQLRASKKPGTRRICNAASFNRMLPLWGGFMAVKKIDPIVPRE
LMHQLTRDVVTARSELLYGLAGVYDLVEKTSAAARGVFKDIAEKKAVTKEEVVAAMT
ADQVDIFRKIVDEFSTMLNCVNFATIGMYHSSTLANPTPSLSQNQVWCNTDGVTEPGL
QFHAFIKQFSGV"
regulatory      35991..35996
/regulatory_class="polyA_signal_sequence"
/note="ORF24, ORF25, ORF26, ORF27"
regulatory      36035..36040
/regulatory_class="polyA_signal_sequence"
/note="ORF24, ORF25, ORF26, ORF27"
gene            complement(36075..38499)
/gene="ORF29"
gene            complement(36075..37874)
/gene="ORF28"
regulatory      complement(36075..36080)
/regulatory_class="polyA_signal_sequence"
/note="ORF28, ORF29"
CDS             complement(36102..37874)
/gene="ORF28"
/note="putative capsid maturational protease; conserved in
RaHV-1, RaHV-2 and CyHV-3"
/codon_start=1
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/translation="MSLPGGRGTVKIE TRERIWVRRVNGETGVYDTRAGSFETVSCQE
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KRCVETFTADIPCALSLGTLDVGLNEVILECSVVVIPARRGCHAKLFTRD TVSDGLE
KFCFQSHATLPPTLLASFGSTSESPERKTFYEAHVDALNNYIKLLRTIYSHKGETEIE
QYLIEGSKLYSELIGEPSRVLDATMKAAQIAEPQTH TGGADRQRPQRPDGI PYSVPDR
FPMTGYPFAPQFCGDPGLVSHYNPFVPPQSFGQGYGP ERVGGYYPQPPNPVYLPISYG
QQPYPGHPQPHGHHQQRSGGGDLKAELIETLGLAPKTN AVQESLSKSFISEILESELKN
CGIKRAAGNIERNCDVDEEPPRTKRARPEPKTAVEAIV RAPYGD FDFSTALTTKIGQVS
DTVEKLNKVIETLLTQSSAQPAPLSTPAQAAPVQPSLPQ PVPEPLAPQEPPPPGTSAP
TLEASLPQQKPVVSKGAFETLMNL"
CDS             complement(37738..38499)

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

gene      38368..39015
/ gene="ORF30"

CDS      38368..38994
/ gene="ORF30"
/ codon_start=1
/ product="ORF30"
/ protein_id="AAA88133.1"
/ translation="MMDIFNSVSESINILNNSVAPMDHREEHEGAPSDKPWGVNFSGH
DFLVNSTSRSDIITSVEQVDRTGSCPICASKNDQGTSLAEAMESMVATRQLDSAMSFL
SMVRPDLANWDVINYHFSHGKDPKIEKLEYQIDTMIDVHYRAGMAIGRDFAMMVTANG
SQFVSPNEKNKICLSSLTTGLTKLIQVRGDIRKMTTSKKNKRGTAAPL"

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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/ product="ORF31"
/ protein_id="AAA88134.1"
/ translation="MYLQMNFFPCPSPSFHLGESVMVVVDRGTGRCTHRHGRCITV
IQSAGNPVHATDYEAYWLRERLMGMRIGRLVILYTS GK"

gene      39359..42955
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CDS      39359..39763
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/ codon_start=1
/ product="ORF32"
/ protein_id="AAA88135.1"
/ translation="MRGATTDD SITSSVRALPAVVPGSGLFLPMVLHVSSLLSLDQLM

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GSKSDDRPRLIGIGSVTRVTPDPTRPAMAHTPSVFLGTRSDLIMFSPHNLKNSSVLQ
PGNDLSSFLLSFSSSVPRNPDNFSASIAIVS"

gene      39821..42955
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CDS       39821..40693
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          /codon_start=1
          /product="ORF33"
          /protein_id="AAA88136.1"
          /translation="MEPISYVTITDYTAFANWLLSTTTVTDVRFWDRIIGFFNLTSN
GRLLDLSRRAYVHWNLRVHGHFSELCTVGGGVERTPLFRALTLRAWNSEPERVLRITIR
ELRTEKLHERGDYWGRNLEYMCTNILAETPEPIFRTLCHTRIIPELKRLVTTWKVYIT
AMYAGRHDDLVLQVTFYFIRRSIEVDRPLLEFIGELKHSCSLPISRKMTTDKTFHVS GF
ITTTCTKELDRDDTARLVHRNGTG FETVVDRIWVGATMWWYRRTYRAVESYDEFWYKY
CGWMDTPTGELPDE"

gene      40536..42955
          /gene="ORF34"

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

gene      41707..42955
          /gene="ORF35"

CDS       41707..42423
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          /note="probably conserved in RaHV-1 and RaHV-2"
          /codon_start=1
          /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
 /gene="ORF36"
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 /protein_id="[AAA88139.1](#)"
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 PCDEFRASLKKNGISSLLTTRGPVTCIKFQIPEDKVISLETTLACLEGTIKVVGDYCYI
 TVTTGDTVLEPPTPSQPAPTPEPAVKPQPIATRKRSGLSALLWPF"
gene complement(42925..45027)
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regulatory complement(42925..42930)
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 /gene="ORF37"
regulatory 42950..42995
 /regulatory_class="polyA_signal_sequence"
 /note="ORF32, ORF33, ORF34, ORF35, ORF36"
regulatory complement(42990..42995)
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 /gene="ORF37"
CDS complement(43015..45027)
 /gene="ORF37"
 /note="conserved in RaHV-1, RaHV-2 and CyHV-3"
 /codon_start=1
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 TETFKRHMLWSVLTNFSPVAYYPAADIARADEACDLVTRATVDRLRKTEETVLADERF
 RGLLGPEMVARLLKVIPGIPPDARSIGLVFDNIRPKLSTEAARTLGGM LIETLRQY
 SGYLPVAPLVDLTETVMVYVHEVDTCLLMDKRGVFRALGEPISRSQPLSSPVARTSE
 STMKFQALFDDYMRAASMAKRTVVTAPQTVAAQESRNPFTRELD SGQLSRATFENLI
 QLTGQLNYHQRTAIAESSGLVANPTMVSPTNTALAHMLRTNGAAIQESMLDDLNSRIN
 DLTDQSRRFTDLKRVIGLLQSRDFETLAVHVGELHPDDRELVLHALGPSTRSAAQIDP
 PEIHRLPENTKLLCSFTTSINLPEIEELLHLWTITWETVFCGRNLFTRRKHALQYTTT
 GRHDNEPSQSIQFMFVDSL NAPGVLM DRLYPSKVTKLTFTELMVLSEKVETVTLPEIF
 AAQIGLNPSEVRLKNRDACEPPREIVTGVNHEL GVDGRFRVAMEDV"
gene 44891..48750
 /gene="ORF38"
CDS 44891..45256
 /gene="ORF38"

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CyHV-3"
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/feature "protein_id" "AAA88141.1"
/feature "translation" "MSVLGTCCCWCPCNLYIAMMGFFRRRFTKTQVYDILSANDPNLTP
DISMRAVDHYRQAARLTSICAQHPAVMGTRDICALKRAATNIAAGNALMDQLNKWTM
DRAENSTTNLVGIINDINS"
gene 45306..48750
/feature "gene" "ORF39"
CDS 45306..48677
/feature "gene" "ORF39"
/feature "note" "major capsid protein; conserved in RaHV-1, RaHV-2
and CyHV-3"
/feature "codon_start" 1
/feature "product" "ORF39"
/feature "protein_id" "AAA88142.1"
/feature "translation" "MEAIARLDSNALAKIGSGGTPFDGLHSGVKWFDNALRLREQF
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KPASLPQAQTEFHMLFDITEQORVAQTGNLQTVGGGSTTTTYDIVMSLERKIVTTEIDS
LELFYTNDPLVIAESITRELESMQTALDLSVILEHAKFCARQPLLGEMCGLREARQN
DLTDGAIIRACQLENIVCGSLNRSKPNLVSLHTALKILDISPKDAAVTTNTVTFQNS
SLDRRLVESQVGGSDDEVYIYSVNGAVGMQPIAKFGKTVPPGEGLRAFNAPVEVSPGV
ARSAYGGLKSVDDVMAIHLGNNETIPVIPLDSTKFSVYGNTSVETAMTQECIKRLFFT
VGTCPCNIYDSLEPGSFFGPGSSGTGEEITPAMVAMRSRSTYIMDLDRGDRVQEITLRQ
LHRVFLDGNKDAFDTSFGFARKIARLLEALEKFNEAEVANLFLEPEWERKMADPGSIFE
FDPRQMLIEIPDAEADDVLVVGVDTMNDRAYAAVPRTCMYNSSSLSMKHNMIGVLSS
MLQLVGQSSAITNYCQLVQTALSDTSAEGVEAVNNIRHMDLTGATPPLTRVMVDKITL
RGGRYLPLSDPYCQLAIKIFYDDPAAITDVGNRVDVVQTVVNTIRAGFDAIVNVFKTI
FDEPDFSIFSNNMPKSICVTQALTATENLFMNIAYAAILPIFTDTLASMGGMGTVD
ETNFNGMVFPVYRNACFIGSGATLPNQVKLWELTGVTPELLVRAVWKCRTEIMKTFG
GQNPFMGFLYHLHLSTLIDKTVILKHFDVKYYSYSGFSYLCVTRTTRFTGHGLSVLPRKSA
RFITGNMYAGMPISEGTGKHAWTQCMELAVGPAGLDRLGLYIPNIFCTDIHGMGVDFN
PRDYMAYIAIFDAYNGFTPETKTTASPTNIALSGRVRVEGLGAPDPVTGLYSQCPTL
VAGLGAGFDRLRSLVHRLNLPCHAYAMILAAVDRGNVFETLPVIFS NVEYMRDLELL
KRTVDATPADRNLYRET MGLIFADNYVIGKNGEHVFRANTKTVPTTIAALSPKVLGES
LYNGAIYGDLEYGFS LKLAKYTGVTTS LRIDLNAV"
regulatory 48745..48750
/feature "regulatory_class" "polyA_signal_sequence"
/feature "note" "ORF38, ORF39"
gene complement(48788..49290)
/feature "gene" "ORF40"
regulatory complement(48788..48793)
/feature "regulatory_class" "polyA_signal_sequence"

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[CDS](#) /note="ORF40, ORF41"
 complement(48880..49290)
 /gene="ORF40"
 /codon_start=1
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 /protein_id="[AAA88143.1](#)"
 /translation="MTPVPPSSLRSIAPLSTVFLFTDNVRSNSWVCKIVYRCLSPRR
 IISPSICTAFSCWANHGLRLSSTAAMRRSSSTFLFMASTRMSSSTFVCFIFVFCVSR
 TAMVFWSFSESTSLWCIISSSMRLCFSITSGST"

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

[CDS](#) complement(49423..50325)
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 /codon_start=1
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 /protein_id="[AAA88144.1](#)"
 /translation="MYLRDFHELAPSQTGKGYEVFFVVGFTKAGLKLGRLLVFNKRYL
 IQKKGCVTIPNKWMYWDPFQAFVVDREYLQIFFRSLPEVIVNQLCLTHRFPQVSGSF
 TREICGFATDWIRNLVVSIDPRSEARLGLQQRLSLVDHLKTTFPDDYDLRQLPPSTG
 GLYTTVSTAEMFNPTGTPDFLAAFDALFEEGGGTHKPPIQFPTVRFDKCEGTCEAADH
 IHELTRRIIGEVRRVYISNATGKVIPLLVLTAVITAENRGVEVPERVGARPIHATGN
 IHFDTVLSYVVQMMYLGKVRVCAP"

[gene](#) 50324..50752
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[CDS](#) 50324..50713
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 /codon_start=1
 /product="ORF42"
 /protein_id="[AAA88145.1](#)"
 /translation="MASFGERSRAYWTMSMGMECYKASTSSDESCQRRGVRDDTGTQP
 HGLVRPIPPPEMPTTAHHRPVVVEGDRGPPRRPEKEPSTTTTKKKGPPATAATRTTSKKI
 VKNKASMDLAGTEKELEDECSFLFLEM"

[regulatory](#) 50747..50752
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 /gene="ORF42"

[gene](#) complement(50977..53707)
 /gene="ORF43"

[regulatory](#) complement(50977..50982)
 /regulatory_class="polyA_signal_sequence"
 /gene="ORF43"

[CDS](#) complement(51032..53707)
 /gene="ORF43"
 /note="conserved in RaHV-1 and RaHV-2"
 /codon_start=1

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/product="ORF43"
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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 SVTISPTNTHFTLPLAPIFNKWDQHKVYGIILEMNTNVYSQ
ATRGTWTATGGGQFFGADV GIDSLMSSLLSQVSEDEPVTSELINMFSLDKVRY
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gene 53657..55365
/gene="ORF44"

CDS 53657..54664
/gene="ORF44"
/note="conserved in RaHV-1 and RaHV-2"
/codon_start=1
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/translation="MGTADEIHDPVLAECIHFAHKKINGLITQNEKKRAVFKSLLK
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SLTPEYNLKLQVVVDIMRRYTVEDPLDLLVTIYPEFTETLEELAKVKRGAANLE
HMG LIYHVLNAHINWFAFNRHQFLNPGITLPSS ELSQEALGMAYDLRCSGCWR
LLSIRSLRKTGNPKNMKIYYSTD SHGLISSCKASVLKAPLSIGKTALVINTPFK
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gene 54642..55365
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CDS 54642..55364
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SEWCEPPTVSAPPPPSQFSDEPTSP ELAPAVPKIDIHEAPVATVSSPTSPRPIT
TESSRVSPSTKEKWGRKRVHKKTHAEATWIPQILKRGMSLSSLLPAAARGQ
RS AVRRRVTF TNSKDVLYYD"

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KYSAPVMIQGNTVYVEKTFSDK"

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)
 /gene="ORF46"
 /note="membrane glycoprotein; conserved in RaHV-1, RaHV-2
 and CyHV-3"
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gene 59469..60776
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CDS 59469..60584
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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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CDS complement(64574..65038)
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gene 65102..66058
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CDS 65102..66058
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regulatory complement(65812..65817)
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/gene="ORF53"

CDS       complement(66033..66959)
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RaHV-2 and CyHV-3"
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CDS       66952..68775
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FTGSKHRETIIPSELIDYIVQYYQYVDHVGVDYVIDPARTQALRLTVYAHMARLGREIQ
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regulatory      70082..70087
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CDS             complement(70265..73804)
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FGPGFINIPGIGTRFTHSRAAMYALGDEIKLKARAGIPADHTEWEYKHAESVYREYM
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[gene](#)

73958..78608

/gene="ORF57"

[CDS](#)

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

/gene="ORF57"

/EC_number="[2.7.7.7](#)"

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

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CDS complement(78703..79740)
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RaHV-2 and IchV-3"
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MRKWNYPARA"

gene 79779..81078
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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)
/ gene="ORF62"
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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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regulatory complement(86254..86259)
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CDS       complement(86367..90671)

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[CDS](#)

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repeat_region 91672..91693

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CDS 91887..96557

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/gene="ORF68"

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gene 100000..104536
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regulatory 104246..104251
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regulatory 104322..104327
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[CDS](#) 119172..120395

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[gene](#) 120556..121942

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[CDS](#) 120556..121464

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ORIGIN

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