Human gammaherpesvirus 4, complete genome

NCBI Reference Sequence: NC_007605.1

FASTA Graphics

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LOCUS       NC_007605             171823 bp    DNA     circular VRL 13-AUG-2018
DEFINITION  Human gammaherpesvirus 4, complete genome.
ACCESSION   NC_007605
VERSION     NC_007605.1
DBLINK      BioProject: PRJNA485481
KEYWORDS    RefSeq; complete genome.
SOURCE      Human gammaherpesvirus 4 (Epstein-Barr virus)
  ORGANISM  Human gammaherpesvirus 4
            Viruses; Herpesvirales; Herpesviridae; Gammaherpesvirinae;
            Lymphocryptovirus.
REFERENCE   1  (bases 1 to 171823)
  AUTHORS   de Jesus,O., Smith,P.R., Spender,L.C., Elgueta Karstegl,C.,
            Niller,H.H., Huang,D. and Farrell,P.J.
  TITLE     Updated Epstein-Barr virus (EBV) DNA sequence and analysis of a
            promoter for the BART (CST, BARF0) RNAs of EBV
  JOURNAL   J. Gen. Virol. 84 (PT 6), 1443-1450 (2003)
   PUBMED   12771413
REFERENCE   2  (bases 1 to 171823)
  AUTHORS   Parker,B.D., Bankier,A., Satchwell,S., Barrell,B. and
Farrell,P.J.
  TITLE     Sequence and transcription of Raji Epstein-Barr virus DNA spanning
            the B95-8 deletion region
  JOURNAL   Virology 179 (1), 339-346 (1990)
   PUBMED   2171209
REFERENCE   3  (sites)
  AUTHORS   Hatfull,G., Bankier,A.T., Barrell,B.G. and Farrell,P.J.
  TITLE     Sequence analysis of Raji Epstein-Barr virus DNA
  JOURNAL   Virology 164 (2), 334-340 (1988)
   PUBMED   2835854
REFERENCE   4  (bases 1 to 171823)
  AUTHORS   Baer,R., Bankier,A.T., Biggin,M.D., Deininger,P.L., Farrell,P.J.,
            Gibson,T.J., Hatfull,G., Hudson,G.S., Satchwell,S.C., Seguin,C.,
            Tuffnell,P.S. and Barrell,B.G.
  TITLE     DNA sequence and expression of the B95-8 Epstein-Barr virus genome
  JOURNAL   Nature 310 (5974), 207-211 (1984)
   PUBMED   6087149
REFERENCE   5  (sites)
  AUTHORS   Jones,M.D., Foster,L., Sheedy,T. and Griffin,B.E.
  TITLE     The EB virus genome in Daudi Burkitt's lymphoma cells has a
            deletion similar to that observed in a non-transforming strain
            (P3HR-1) of the virus
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  JOURNAL   EMBO J. 3 (4), 813-821 (1984)
   PUBMED   6327290
REFERENCE   6  (sites)
  AUTHORS   Jeang,K.T. and Hayward,S.D.
  TITLE     Organization of the Epstein-Barr virus DNA molecule. III. Location
            of the P3HR-1 deletion junction and characterization of the NotI
            repeat units that form part of the template for an abundant
            12-O-tetradecanoylphorbol-13-acetate-induced mRNA transcript
  JOURNAL   J. Virol. 48 (1), 135-148 (1983)
   PUBMED   6310141
REFERENCE   7  (bases 1 to 171823)
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (10-NOV-2005) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   8  (bases 1 to 171823)
  AUTHORS   Farrell,P.J. and Davison,A.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-NOV-2005) Department of Virology, Ludwig Institute
            for Cancer Research, Faculty of Medicine, Imperial College, St
            Mary's Campus, Norfolk Place, London W2 1PG, UK
COMMENT     VALIDATED REFSEQ: This record has undergone validation or
            preliminary review. This record has been curated by Drs. Andrew
            Davison (Institute of Virology, Glasgow, UK) and Paul Farrell
            (Imperial College School of Medicine, London, UK). The reference
            sequence was derived from AJ507799.
            CONSTRUCTION: This sequence was assembled from data for the B95-8
            (V01555) and Raji (M35547) strains with corrections. The number of
            IR1 (W) repeats in V01555 has been reduced from 11.6 to a more
            typical 7.6, and the missing B95-8 sequence has been restored to
            give a sequence more representative of wild type EBV.
            NUMBERING: Like the modified B95-8 sequence in V01555, this
            sequence starts 1 bp to the left of the EcoRI site separating
EcoRI
            Dhet from EcoRI I (i.e. the first A of AGAATTC).
            TRANSCRIPTION: Long-range splicing of the EBNA and BART genes
            generates multiple, complex mRNAs. A single mRNA structure is
shown
            for each gene, but alternatives may initiate at other promoters
and
            may involve various exon combinations. TATA and polyA signals are
            shown as non-experimental where predicted or as experimental where
            supporting data are available. Predictions of TATA or polyA
signals
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          are not made for some genes.
          NOMENCLATURE: The original gene nomenclature has been retained.
          Genes presumably inherited from the common ancestor of alpha-,
          beta- and gammaherpesviruses (core genes), from the common
ancestor
          of beta- and gammaherpesviruses (betagamma genes), or from the
          common ancestor of gammaherpesviruses (gamma genes) are indicated.
          A standard protein nomenclature has been applied so that orthologs
          have the same name in all herpesviruses.
          CONFIDENCE: Evidence for encoded protein functions is more
          convincing for some ORFs than others, and rests on a combination
of
          factors, including evolutionary conservation, expression and
          functional data. The most questionable ORFs are annotated as such.
          COMPLETENESS: full length.
FEATURES           Location/Qualifiers
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                  /mol_type="genomic DNA"
                  /strain="B95-8"
                  /strain="Raji"
                  /host="Homo sapiens"
                  /db_xref="taxon:10376"
                  /type="1"
                  /common="Epstein-Barr virus"
                  /acronym="EBV"
                  /acronym="HHV-4"
    source         join(1..139723,151555..171823)
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                  /mol_type="genomic DNA"
                  /strain="B95-8"
                  /host="Homo sapiens"
                  /db_xref="taxon:10376"
                  /type="1"
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                  /mol_type="genomic DNA"
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                     /db_xref="GeneID:3783751"
mRNA                  join(166040..166458,58..272,360..458,540..788,871..951,
                     1026..1196,1280..1495,1574..1682,5408..5856)
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                     /locus_tag="HHV4_LMP-2A"
                     /db_xref="GeneID:3783751"
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                     /note="type 3 membrane protein; role in intracellular
                     signalling"
                     /codon_start=1
                     /product="membrane protein LMP-2A"
                     /protein_id="YP_401631.1"
                     /db_xref="UniProtKB/TrEMBL:Q777H4"
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                     PNDEERESNEEPPPPYEDPYWGNGDRHSDYQPLGTQDQSLYLGLQHDGNDGLPPPPYS
                     PRDDSSQHIYEEAGRGSMNPVCLPVIVAPYLFWLAAIAASCFTASVSTVVTATGLALS
                     LLLLAAVASSYAAAQRKLLTPVTVLTAVVTFFAICLTWRIEDPPFNSLLFALLAAAGG
                     LQGIYVLVMLVLLILAYRRRWRRLTVCGGIMFLACVLVLIVDAVLQLSPLLGAVTVVS
                     MTLLLLAFVLWLSSPGGLGTLGAALLTLAAALALLASLILGTLNLTTMFLLMLLWTLV
                     VLLICSSCSSCPLSKILLARLFLYALALLLLASALIAGGSILQTNFKSLSSTEFIPNL
                     FCMLLLIVAGILFILAILTEWGSGNRTYGPVFMCLGGLLTMVAGAVWLTVMSNTLLSA
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gene                  join(169294..171823,1..5856)
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                     /note="LMP-2 family"
                     /db_xref="GeneID:3783760"
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CDS                   join(59..272,360..458,540..788,871..951,1026..1196,
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              /product="membrane protein LMP-2B"
              /protein_id="YP_401632.1"
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              IYVLVMLVLLILAYRRRWRRLTVCGGIMFLACVLVLIVDAVLQLSPLLGAVTVVSMTL
              LLLAFVLWLSSPGGLGTLGAALLTLAAALALLASLILGTLNLTTMFLLMLLWTLVVLL
              ICSSCSSCPLSKILLARLFLYALALLLLASALIAGGSILQTNFKSLSSTEFIPNLFCM
              LLLIVAGILFILAILTEWGSGNRTYGPVFMCLGGLLTMVAGAVWLTVMSNTLLSAWIL
              TAGFLIFLIGFALFGVIRCCRYCCYYCLTLESEERPPTPYRNTV"
gene           1691..5856
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              /note="gamma gene; FGARAT family"
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              /regulatory_class="TATA_box"
              /gene="BNRF1"
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              /experiment="experimental evidence, no additional details
              recorded"
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              RPSFRQFQAINHLVLFDNALRKYDSGQVAAGFQRALLVAGPETADTRPDLRKLNEWVF
              GGRAAGGRQLADELKIVSALRDTYSGHLVLQPTETLDTWKVLSRDTRTAHSLEHGFIH
              AAGTIQANCPQLFMRRQHPGLFPFVNAIASSLGWYYQTATGPGADARAAARRQQAFQT
              RAAAECHAKSGVPVVAGFYRTINATLKGGEGLQPTMFNGELGAIKHQALDTVRYDYGH
              YLIMLGPFQPWSGLTAPPCPYAESSWAQAAVQTALELFSALYPAPCISGYARPPGPSA
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                     DPEDVLLTLHLHLDPRRADNSAVMEAMTAASDYARGLGVKLTFGSASCPETGSSASNF
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                     PEALSLKNLFRAVQQLVKSGIVLSGHDISDGGLVTCLVEMALAGQRGVTITMPVASDY
                     LPEMFAEHPGLVFEVEERSVGEVLQTLRSMNMYPAVLGRVGEQGPDQMFEVQHGPETV
                     LRQSLRLLLGTWSSFASEQYECLRPDRINRSMHVSDYGYNEALAVSPLTGKNLSPRRL
                     VTEPDPRCQVAVLCAPGTRGHESLLAAFTNAGCLCRRVFFREVRDNTFLDKYVGLAIG
                     GVHGARDSALAGRATVALINRFPALRDAILKFLNRPDTFSVALGELGVQVLAGLGAVG
                     STDNPPAPGVEVNVQRSPLILAPNASGMFESRWLNISIPATTSSVMLRGLRGCVLPCW
                     VQGSCLGLQFTNLGMPYVLQNAHQIACHFHSNGTDAWRFAMNYPRNPTEQGNIAGLCS
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     misc_RNA        6956..7128
                     /product="EBER-2 (pol III transcript)"
     rep_origin      7315..9312
                     /note="region containing oriP, the latent cycle origin of
                     DNA replication"
     repeat_region   7421..8042
                     /note="binding sites for EBNA-1 (site I, family of
                     repeats, FR); also functions as a cell type-specific
                     enhancer"
                     /rpt_type=direct
                     /rpt_unit_range=7421..7450
     repeat_region   9021..9135
                     /note="dyad symmetry, binding site for EBNA-1 (site II)"
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                     /gene="BCRF1"
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                 23770..23835,23917..24048,26842..26907,26989..27120,
                 29914..29979,30061..30192,32986..33051,33133..33264,
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                     PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
                     HRDPSGPDPPTGPSLCPPAPLQPSLHPRPQLLASPGPPGQPEGPRQPGRVAFPLPWPL
                     LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
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     regulatory      14352..14357
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                     /experiment="experimental evidence, no additional details
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                     /note="repetitive sequence results in variable size; role
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                     RRHRSPSPTRGGQEPRRVRRRVLVQQEEEVVSGSPSGPRGDRSEGPGPTRPGPPGIGP
                     EGPLGQLLRRHRSPSPTRGGQEPRRVRRRVLVQQEEEVVSGSPSGPRGDRSEGPGPTR
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                     SEGPGPTRPGPPGIGPEGPLGQLLRRHRSPSPTRGGQEPRRVRRRVLVQQEEEVVSGS
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                     HRDPSGPDPPTGPSLCPPAPLQPSLHPRPQLLASPGPPGQPEGPRQPGRVAFPLPWPL
                     LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
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                     /experiment="experimental evidence, no additional details
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                     infection"
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                     /experiment="experimental evidence, no additional details
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                     infection"
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                     TSGTPEPLGPASRRPPGLRSPLSPVKPKECLRGATLGAQAPESRGQGHLRVPPRVPGQ
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     CDS             <27901..29052
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                     /locus_tag="HHV4_BWRF1.6"
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                     /citation=[6]
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                     KTQGQSRGQSRGRGRGRGRGRGKGKSRDKQRKPGGPWRPEPNTSSPSMPELSPVLGLH
                     QGQGAGDSPTPGPSNAAPVCRNSHTATPNVSPIHEPESHNSPEAPILFPDDWYPPSID
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                     NPGCPRTWRRRSGAQRGHPPPGAGQRPSGPTGGRPAAPGAPGTPAAPGPGGGAAVPSG
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     rep_origin      40301..41293
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                     of DNA replication"
     repeat_region   40366..41409
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                     /note="Bcl-2 family; can also be expressed from Cp or Wp
                     type of spliced RNA"
                     /db_xref="GeneID:3783706"
     regulatory      41471..41476
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                     /db_xref="GeneID:3783706"
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                  /note="core gene"
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CDS                complement(43691..44647)
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                  /locus_tag="HHV4_BFLF2"
                  /note="interacts with nuclear egress type 2 membrane
                  protein; role in nuclear egress"
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                  /product="nuclear egress lamina protein"
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                  /db_xref="GeneID:3783698"
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                  REMNTPIHVSEAVFLPLSLCTLSPGRCLRLSPFGHSLTLGSHCEICINRSQVHVPQEF
                  SSTQLSFFNNVHKIIPNKTFYVSLLSSSPSAVKAGLSQPSLLYAYLVTGHFCGTICPI
                  FSTNGKGRLIMHLLLQGTSLHIPETCLKLLCENIGPTYELAVDLVGDAFCIKVSPRDT
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regulatory          complement(43697..43702)
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                  /note="role in DNA encapsidation; role possibly in capsid
                  transport"
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                  /product="DNA packaging protein UL32"
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                  /db_xref="GeneID:3783697"
                  /translation="MAHKVTSANEPNPLTGKRLSSCPLTRSGVTEVAQIAGRTPKMED
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                  MPSRILAIDIQLHFYICRCFLPVSSSDMIRNANLGYYKLEFLKSILTGQSPANFCFKS
                  MWPRTTPTFLTLPGPRTCKDSQDVPGDVGRGLYTALCCHLPTRNRVQHPFLRAEKGGL
                  SPEITTKADYCGLLLGTWQGTDLLGGPGHHAIGLNAEYSGDELAELALAITRPEAGDH
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                     /note="interacts with DNA packaging terminase subunit 2;
                     role in DNA encapsidation"
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                     /locus_tag="HHV4_BFLF1"
                     /experiment="experimental evidence, no additional details
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                     /note="core gene"
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                     /experiment="experimental evidence, no additional details
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                     /locus_tag="HHV4_BFRF3"
                     /note="located externally on capsid hexons; role in capsid
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                     /codon_start=1
                     /product="small capsid protein"
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                     /db_xref="UniProtKB/TrEMBL:Q777G5"
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                     /locus_tag="HHV4_BPLF1"
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                     cycle, some spliced to EBNA-1"
     gene            50134..97654
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                     /note="latency I"
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                     /gene="EBNA-1"
                     /locus_tag="HHV4_EBNA-1.2"
                     /product="EBNA-1, QUK transcript"
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     gene             68491..69916
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             /note="type 3 membrane protein; role possibly in membrane
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             /locus_tag="HHV4_EBNA-1.2"
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gene          complement(70454..74593)
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             /locus_tag="HHV4_BSLF1"
             /note="core gene"
             /db_xref="GeneID:3783730"
gene          complement(70454..72068)
             /gene="BSLF2/BMLF1"
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                     /inference="non-experimental evidence, no additional
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                     /note="BSLF1 and BSLF2/BMLF1"
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                     /locus_tag="HHV4_BSLF2/BMLF1"
                     /note="RNA-binding protein; shuttles between nucleus and
                     cytoplasm; inhibits pre-mRNA splicing; exports virus mRNA
                     from nucleus; exerts most effects post-transcriptionally;
                     role in gene regulation; role in RNA metabolism and
                     transport"
                     /codon_start=1
                     /product="multifunctional expression regulator"
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                     VSKITFVTLPSPLASLTLEPIQDPFLQSMLAVAAHPEIGAWQKVQPRHELRRSYKTLR
                     EFFTKSTNKDTWLDARMQAIQNAGLCTLVAMLEETIFWLQEITYHGDLPLAPAEDILL
                     ACAMSLSKVILTKLKELAPCFLPNTRDYNFVKQLFYITCATARQNKVVETLSSSYVKQ
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                     KIRMEPPAPYTWDPDPDDGLMRAWAGLSVDVARELVELARWHADEGPTYPPTLQGFLC
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                     /db_xref="GeneID:3783731"
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                     /inference="non-experimental evidence, no additional
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                     /note="core gene; DURP family"
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                     /note="role in nucleotide metabolism"
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                     IPHHRPTIFGRSGLAMQGILVKPCRWRRGGVDVSLTNFSDQTVFLNKYRRFCQLVYLH
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             /note="type 1 membrane protein; complexed with envelope
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             membrane fusion"
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             "
gene          76575..77129
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             /locus_tag="HHV4_BLRF2"
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                     /locus_tag="HHV4_BLLF1"
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                     /note="BLLF1 and BLLF2"
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                     /note="type 1 membrane protein; binds to cell surface
                     receptor CD21; role in cell attachment"
                     /codon_start=1
                     /product="glycoprotein 350"
                     /protein_id="YP_401667.1"
                     /db_xref="UniProtKB/TrEMBL:Q777F0"
                     /db_xref="GeneID:3783713"
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                     KWDNCNSTNITAVVRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEI
                     SQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLG
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                     MVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASNRTFDIT
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                     STHVPTNLTAPASTGPTVSTADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTS
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              WRLQTLAAGWPMGYQAYSSWMYSYTDHQTTPTFVHLQATLGCTGGRRCHVTFSAGTFK
              LPRCTPGDRQWLYVQSSVGNIVQSCNPRYSIFFDYMAIHRSLTKIWEEVLTPDQRVSF
              MEFLGFLQRTDLSYIKSFVSDALGTTSIQTPWIDDNPSTETAQAWNAGFLRGRAYGID
              LLRTEGEHVEGATGETREESEDTESDGDDEDLPCIVSRGGPKVKRPPIFIRRLHRLLL
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              LAAQGMAYPLHEQHGMAPCPVAQAPPTPLPPVSPGDQLPGVFSDGRVACAPVPAPAGP
              IVRPWEPSLTQAAGQAFAPVRPQHMPVEPVPVPTVALERPVYPKPVRPAPPKIAMQGP
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repeat_region   81920..81989
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repeat_region   82361..82431
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              /rpt_family="type D"
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                     /note="role in latency"
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                     CPSMPFASDYSQGAFTPLDINATTPKRPRVEESSHGPARCSQATAEAQEILSDNSEIS
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                93838..93893))
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                /locus_tag="HHV4_BRLF1"
                /db_xref="GeneID:3783727"
gene             complement(89838..90943)
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                /locus_tag="HHV4_BZLF1"
                /note="gamma gene"
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                /db_xref="GeneID:3783744"
regulatory        complement(89863..89868)
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             /note="for BRLF1 and BZLF1"
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             /gene="BZLF2"
             /locus_tag="HHV4_BZLF2"
             /inference="non-experimental evidence, no additional
             details recorded"
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             /gene="BZLF1"
             /locus_tag="HHV4_BZLF1"
             /note="ZEBRA, Zta, Z; bZIP protein; role in gene
             regulation"
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             /product="protein Zta"
             /protein_id="YP_401673.1"
             /db_xref="UniProtKB/TrEMBL:Q777E5"
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             PCVLWPVLPEPLPQGQLTAYHVSTAPTGSWFSAPQPAPENAYQAYAAPQLFPVSDITQ
             NQQTNQAGGEAPQPGDNSTVQTAAAVVFACPGANQGQQLADIGVPQPAPVAAPARRTR
             KPQQPESLEECDSELEIKRYKNRVASRKCRAKFKQLLQHYREVAAAKSSENDRLRLLL
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repeat_region   90293..90364
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CDS             complement(91078..92895)
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             /locus_tag="HHV4_BRLF1"
             /note="role in gene regulation; role in latency"
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             /product="protein Rta"
             /protein_id="YP_401674.1"
             /db_xref="UniProtKB/TrEMBL:Q777E4"
             /db_xref="GeneID:3783727"
             /translation="MRPKKDGLEDFLRLTPEIKKQLGSLVSDYCNVLNKEFTAGSVEI
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              CPIVMRYVLDHLIVVTDRFFIQAPSNRVMIPATIGTAMYKLLKHSRVRAYTYSKVLGV
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              ELMGNDGGASHTEARYSESGQFHAFTDELESLPSPTMPLKPGAQSADCGDSSSSSSDS
              GNSDTEQSEREEARAEAPRLRAPKSRRTSRPNRGQTPCPSNAAEPEQPWIAAVHQESD
              ERPIFPHPSKPTFLPPVKRKKGLRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRP
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              DEETSQAVKALREMADTVIPQKEEAAICGQMDLSHPPPRGHLDELTTTLESMTEDLNL
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exon           complement(92638..92897)
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              /note="part of fused transcript from BRLF1 and BZLF1"
gene           92728..93827
              /gene="BRRF1"
              /locus_tag="HHV4_BRRF1"
              /note="gamma gene"
              /db_xref="GeneID:3783728"
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              /note="cooperates with protein Rta; role in gene
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              /db_xref="GeneID:3783728"
              /translation="MASSNRGNARPLKSFLHELYLKHYPEVGDVVHLLNTIGVDCDLP
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              MRKVIADVCRSGYASMPSMTATHNLSHQLLMASGPSEEPCAWRGFFNQVLLWTVALCK
              FRRCIYYNYIQGSIATISQLLHLEIKALCSWIISQDGMRLFQHSRPLLTLWESVAANQ
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             /locus_tag="HHV4_BRRF2"
             /note="gamma gene"
             /db_xref="GeneID:3783729"
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             QCSPVNLLNMLVHKLVALRGHVQLAYDARVLTPDFHEIPDLDDSDAVFARTLLAALFH
             LNMFFILKDYITQDSMSLKQALSGHWMSATGNPLPAAPETLRDYLEAFRNSDNHFYLP
             TTGPLNTFQFPEELLGRVVVIDSSLCAASHVQDVITHGVGAGVPRPRFSALPPAPSRE
             PQQTCSQLTSRGNESSRRNLGQPGGTSPAVPPVCPIVSLTASGAKQNRGGMGSLHLAK
             PEETSPAVSPVCPIASPAASRSKQHCGVTGSSQAAPSFSSVAPVASLSGDLEEEEEGS
             RESPSLPSSKKGDEEFEAWLEAQDANLEDVQREFSGLRVIGDEDEDGSEDGEFSDLDL
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             /locus_tag="HHV4_BRRF2"
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               SPPRRPPPGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPSTGP
               RGQGDGGRRKKGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWVAGVF
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repeat_region   95929..96636
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               /rpt_type=direct
gene            97617..99504
               /gene="BKRF2"
               /locus_tag="HHV4_BKRF2"
               /note="core gene"
               /db_xref="GeneID:3783710"
regulatory      97617..97622
               /regulatory_class="TATA_box"
               /gene="BKRF2"
               /locus_tag="HHV4_BKRF2"
               /experiment="experimental evidence, no additional details
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regulatory      97649..97654
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               /gene="EBNA-1"
               /locus_tag="HHV4_EBNA-1.1"
               /experiment="experimental evidence, no additional details
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CDS             97670..98083
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                     /function="virion glycoprotein gL"
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                     glycoprotein H; role in cell entry; role in cell-to-cell
                     spread"
                     /codon_start=1
                     /product="envelope glycoprotein L"
                     /protein_id="YP_401678.1"
                     /db_xref="UniProtKB/TrEMBL:Q777E0"
                     /db_xref="GeneID:3783710"
                     /translation="MRAVGVFLAICLVTIFVLPTWGNWAYPCCHVTQLRAQHLLALEN
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                     HLRELLTTLETLYGSFSVEDLFGANLNRYAWHRGG"
     gene            98065..99504
                     /gene="BKRF3"
                     /locus_tag="HHV4_BKRF3"
                     /note="core gene"
                     /db_xref="GeneID:3783711"
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                     /locus_tag="HHV4_BKRF3"
                     /EC_number="3.2.2.3"
                     /note="role in DNA repair"
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                     /db_xref="UniProtKB/TrEMBL:Q777D9"
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                     QRKLAAVIACVRRLRTQATVYPEEDMCMAWARFCDPSDIKVVILGQDPYHGGQANGLA
                     FSVAYGFPVPPSLRNIYAELHRSLPEFSPPDHGCLDAWASQGVLLLNTILTVQKGKPG
                     SHADIGWAWFTDHVISLLSERLKACVFMLWGAKAGDKASLINSKKHLVLTSQHPSPLA
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     gene            98846..99504
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                     /locus_tag="HHV4_BKRF4"
                     /note="gamma gene"
                     /db_xref="GeneID:3783712"
     CDS             98846..99499
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             TPGSQASRSSRVSPSTQQSSGLTPTPSFSRPRTRAPPRPPAPAPVRGRASAPPRPPAP
             VQQSTKDKGPHRPTRPVLRGPAPRRPPPPSSPNTYNKHMMETTPPIKGNNNYNWPWL"
regulatory     99499..99504
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             /inference="non-experimental evidence, no additional
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             /gene="BBLF4"
             /locus_tag="HHV4_BBLF4"
             /note="core gene"
             /db_xref="GeneID:3783685"
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             /inference="non-experimental evidence, no additional
             details recorded"
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             /locus_tag="HHV4_BBLF4"
             /note="role in DNA replication"
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             /product="helicase-primase helicase subunit"
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             /db_xref="UniProtKB/TrEMBL:Q777D7"
             /db_xref="GeneID:3783685"
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             IAAEFRRTKPRGLYSGVSGPAFEVLRDMHQGQLWTTNVIVVDEAGTLSVHILTAVVFC
             YWFFNAWLRTPLYRRGRIPCIVCVGSPTQTDAFQSSFSHETQVNKIRECDNILTFLVG
             NPRAATYVDVARNWALFINNKRCTDVQFGHLMKTLEYGLELSPDILAYVDRFVVPRAA
             IMDPAQYVGWTRLFLSHAEVKTFLTTLHATLKTAGQGRAARGTGGDGGGVTMFTCPVE
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             TYNVTYVKHSSVSVNCKTKKSICGYTGTFGDFMDTLEADSFVEAHGHEQPEYVYSFLA
             RLIYGGIYAFSHGGHSLCENGEYVAELGAVPLPGRTWDPEVTAGMELGELPLEVAWDG
             ERSPAAVFYARVLAPPAANSAPLCSLLNIYNDLRAYFRQCLDVAVRYGGREFRDLPFC
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                SSRMPRLMVKDEAGFVCCLEHNTNKLYETIEDKSLNLCSIRDYGISSKLAMTIAKAQG
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gene             101588..104502
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                /note="core gene"
                /db_xref="GeneID:3783764"
regulatory       101588..101593
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                /gene="BBRF1"
                /locus_tag="HHV4_BBRF1"
                /inference="non-experimental evidence, no additional
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                EEFITDASNNLVDRNRLFGQPGETAAQGLKKKVSNTVVKCLTDQINEQFDQINGLEKE
                RELYLKKIRSMESQLQASLGPGGNNPAASAPAAVAAEAASVDILTGSTASAIEKLFNS
                PSASLGARVSGHNESILNSFVSQYIPPSREMTKDLTELWESELFNTFKLTPVVDNQGQ
                RLYVRYSSDTISILLGPFTYLVAELSPVELVTDVYATLGIVEIIDELYRSSRLAIYIE
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gene             103660..104502
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                /locus_tag="HHV4_BBRF2"
                /note="core gene"
                /db_xref="GeneID:3783686"
CDS              103660..104496
                /gene="BBRF2"
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                /note="role in virion morphogenesis"
                /codon_start=1
                /product="tegument protein UL7"
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              LYKPNNVNLMEMCALLSMIENAKSPSIGLCREVLGRLTLLHSKCNNLDSLFLYNGART
              LLSTLVKYHDLEEGAATPGPWNEGLSLFKLHKELKRAPSEARDLMQSLFLTSGKMGCL
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              IP"
gene           complement(104403..106750)
              /gene="BBLF2/BBLF3"
              /locus_tag="HHV4_BBLF2/BBLF3"
              /note="core gene"
              /db_xref="GeneID:3783684"
regulatory      complement(104403..104408)
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              /gene="BBLF2/BBLF3"
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              /inference="non-experimental evidence, no additional
              details recorded"
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              /locus_tag="HHV4_BBLF2/BBLF3"
              /note="role in DNA replication"
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              /db_xref="GeneID:3783684"
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              DLSFRTRDRRLLSAARVEDEQGLIFQPLFPAQVVCQSCSGDDGRDQQPPPVDGFGSEM
              EGEQTCPHAQRHSESPGQLDVYIRTPRGDVFTYSTETPDDPSPVPFRDILRPVTYEVD
              LVSSDGATGRGGDARRHRVSLKILEPAGGFESWLVNSWSMAGGGLYAFLRSIYASCYA
              NHRGTKPIFYLLDPELCPGGSDFQPYVPGFPFLPIHYVGRARPAFWHRAPHSEGLLLL
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              DETTVVGRAEATAILEADATWWLYELARCHLSARGAPVGTPDGGGQARDAQTWLRALH
              RYGTSDTRRALGGLYTAVTRVLLHAAADLGLTWAYADEFILGFVAPTSAHPSEEPLAQ
              AFLQGVKDSEDASRLDRDVMGGEATVARRHIRVKARRGPGCLLMAIFQGDLYVGGCRE
              HSGPFLVWHEAFSWTLDQLAARPEADKAPPSHDHLLTLVRDLTRRLAPGRRRNRFWAL
              PRAWLQRLRRAGLRLSGSHVCLLDKDGARPAPCQTATEHGLSPTAYFREIMAFLLDVI
              SALHPGYTIPMEITRETDLLMTVLSLF"
regulatory      104497..104502
              /regulatory_class="polyA_signal_sequence"
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             details recorded"
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gene          106693..108075
             /gene="BBRF3"
             /locus_tag="HHV4_BBRF3"
             /note="core gene"
             /db_xref="GeneID:3783687"
regulatory     106693..106698
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             /gene="BBRF3"
             /locus_tag="HHV4_BBRF3"
             /experiment="experimental evidence, no additional details
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regulatory     106810..106815
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             /gene="BBRF3"
             /locus_tag="HHV4_BBRF3"
             /inference="non-experimental evidence, no additional
             details recorded"
CDS           106849..108066
             /gene="BBRF3"
             /locus_tag="HHV4_BBRF3"
             /note="type 3 membrane protein; 8 transmembrane domains;
             complexed with envelope glycoprotein N; role in virion
             morphogenesis; role in membrane fusion"
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             /protein_id="YP_401685.1"
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             /db_xref="GeneID:3783687"
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             FLASVLHACACVTRFSPVWVVKAQDNSIPQDTFLWWVVFYLKPVVTNLYLGCLALETL
             VFSLSVFLALGNSFYFMVGDMVLGAVNLFLILPIFWYILTEVWLASFLRHNFGFYCGM
             FIASIILILPLVRYEAVFVSAKLHTTVAINVAIIPILCSVAMLIRICRIFKSMRQGTD
             YVPVSETVELELESEPRPRPSRTPSPGRNRRRSSTSSSSSRSTRRQRPVSTQALVSSV
             LPMTTDSEEEIFP"
regulatory     108070..108075
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             /locus_tag="HHV4_BBRF3"
             /experiment="experimental evidence, no additional details
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     gene             complement(108459..112825)
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                     /locus_tag="HHV4_BGLF3"
                     /note="betagamma gene"
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     gene             complement(108459..111829)
                     /gene="BGLF3.5"
                     /locus_tag="HHV4_BGLF3.5"
                     /note="core gene"
                     /db_xref="GeneID:3783766"
     gene             complement(108459..111326)
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                     /locus_tag="HHV4_BGLF4"
                     /note="core gene; PK family"
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     gene             complement(108459..110053)
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                     /locus_tag="HHV4_BGLF5"
                     /note="core gene"
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                     RLPSEGDYLLTQDEAWNLKDVRKRKLGPGHDLVADSLAANRGVESMLYVMTDPSENAG
                     RIGIKDRVPVNIFINPRHNYFYQVLLQYKIVGDYVRHSGGGKPGRDCSPRVNIVTAFF
                     RKRSPLDPATCTLGSDLLLDASVEIPVAVLVTPVVLPDSVIRKTLSTAAGSWKAYADN
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              LYLDVRDWKGEDIAPPFDVSRLNKMAKQLCLLPQEPFCITRVCLLCLLHKQNLNAQYK
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                     HVNILRGWTEDDSPGTSGTCPCLLPCTALNNDYVPITGHRALLGLMFKPEDAPFVVGL
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                     AIRESRALVRGIAHIFSPHALYVVTYPELSAQGRLHRMTAVTHASPATDLAEVSILGA
                     PEREFRFLISVALRISASFREKLAMQAWTAQQEIPVVIPTSYSRIYKNSDLIREAFFT
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                     /gene="BGRF1/BDRF1"
                     /locus_tag="HHV4_BGRF1/BDRF1"
                     /inference="non-experimental evidence, no additional
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                 /gene="BDLF3"
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                     /note="complexed 2:1 with capsid triplex subunit 1 to
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regulatory      complement(125417..125422)
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                     ANTRRTIRDILEIPVTVLSSLQLSPTKSILKKAPEPPPPEPQATFDATPYARIFYDIG
                     RQVPKLGNAPAAQVSNVLIANRSHNSLRLVPNPDLLPLQHLYLKHVVLKSLNLENIVQ
                     DFEAIFTSPSDTISEAETKAFEKLVEQAKNTVENIVFCLNSICSTSTLPDVVPDVNNP
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gene                  complement(128608..132846)
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regulatory             complement(128608..128613)
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                     /experiment="experimental evidence, no additional details
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                     complexed with envelope glycoprotein L; role in cell
                     entry; role in cell-to-cell spread"
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                    DASKVHPGVISGLNSPACMLSAPLEKQLFYYIGTMLPNTRPHSYVFYQLRCHLSYVAL
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                    AQSGDYSLVIVTTFVHYANFHNYFVPNLKDMFSRAVTMTAASYARYVLQKLVLLEMKG
                    GCREPELDTETLTTMFEVSVAFFKVGHAVGETGNGCVDLRWLAKSFFELTVLKDIIGI
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                    IGGATSVLLSAYNRHPLFQPLHTVMRETLFIGSHVVLRELRLNVTTQGPNLALYQLLS
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                    AVDGFLGRLSLEREDRDAWHLPAYKCVDRLDKVLMIIPLINVTFIISSDREVRGSALY
                    EASTTYLSSSLFLSPVIMNKCSQGAVAGEPRQIPKIQNFTRTQKSCIFCGFALLSYDE
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                    SRSFMYQKGFEEGLAGLGLDDKSDCESEDESNFRRPSSHSALKQKNGGKGKPSGLFEH
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                    KNVTRARHGREDTSAEVLACQMKFTTPFRVLASRKRSLLVTESGARSVAPLDCWILHD
                    RHLLSASVVFPLMLLRSQLLSYSDFIQVLATFTADPGDTIVWMKLNVEENMRRLKKRG
                    RKHESGLDAGYLKSVNDAYHAVYCAWLLTQYFAPEDIVKVCAGLTTITTVCHQSHTPI
                    IRSGVAEKLYKNSIFSVLKEVIQPFRADAVLLEVCLAFTRTLAYLQFVLVDLSEFQDD
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regulatory            complement(131016..131021)
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                     EFPALGQKTLPTSTTGLLNLLSRWQDGALRARLDRPRPTAQGHRPRTHVGPKPSQLTA
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                     /locus_tag="HHV4_BXLF1"
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                     /locus_tag="HHV4_BVRF1"
                     /note="located on capsid near vertices; possibly
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                     stabilizes the capsid and retains the genome; role in DNA
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                     /codon_start=1
                     /product="DNA packaging tegument protein UL25"
                     /protein_id="YP_401703.1"
                     /db_xref="UniProtKB/TrEMBL:Q777B7"
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                     GNINQWVPSFGPWYRTMSANAMQRRVFPKQLRGNLNFTNSVSLKLMTEVVAVLEGTTQ
                     DFFSDVRHLPDLQAALILSVAYLLLQGGSSHQQRPLPASREELLELGPESLEKIIADL
                     KAKSPGGNFMILTSGNKEARQSIAPLNRQAAYPPGTFADNKIYNLFVGAGLLPTTAAL
                     NVPGAAGRDRDLVYRIANQIFGEDVPPFSSHQWNLRVGLAALEALMLVYTLCETANLA
                     EAATRRLHLSSLLPQAMQRRKPAMASAGMPGAYPVQTLFRHGELFRFIWAHYVRPTVA
                     ADPQASISSLFPGLVLLALELKLMDGQAPSHYAINLTGQKFDTLFEIINQKLLFHDPA
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                     /inference="non-experimental evidence, no additional
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                     /note="required for expression of late genes; role in
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                     /db_xref="GeneID:3783771"
                     /translation="MLMGLGVRGDDARMTPGIHGLLLKMLKNWPLCALREDELRFLHL
                     SLTKLLTLSVNFYLWREAVINTGNRTNRVLARKVPDEYWYLLYRALARVGFPAEALRP
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                     LVVGVLYCLVHWGADEHETRVRARLRPLFVAFLCLAGYLLLDRAILSDAHDYEGLWHA
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                     /locus_tag="HHV4_BVRF2"
                     /EC_number="3.4.21.97"
                     /note="serine protease (N-terminal region); minor scaffold
                     protein (remainder of protein, clipped near C terminus);
                     role in capsid morphogenesis"
                     /codon_start=1
                     /product="capsid maturation protease"
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                     /db_xref="UniProtKB/TrEMBL:Q777B6"
                     /db_xref="GeneID:3783733"
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                     WVLKHFSDLEPSIAAQIENDANAAKRESGCPEDHPLPLTKLIAKAIDAGFLRNRVETL
                     RQDRGVANIPAESYLKASDAPDLQKPDKALQSPPPASTDPATMLSGNAGEGATACGGS
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                     AVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAYFGLPGLFGPPPPV
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                     QHTLQALRRETLSYGHTGVGYCPQQGPCYTHSGPYGFQPHQSYEVPRYVPHPPPPPTS
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                     QASASGVAQSKEPTTPKAKSVSAHLKSIFCEELLNKRVA"
gene                  136331..137455
                     /gene="BdRF1"
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                     /db_xref="GeneID:3783696"
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                     /db_xref="UniProtKB/TrEMBL:Q66541"
                     /db_xref="GeneID:3783696"
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                     DEEGGGLFPGEDATLYRKDIAGLSKSVNELQHTLQALRRETLSYGHTGVGYCPQQGPC
                     YTHSGPYGFQPHQSYEVPRYVPHPPPPPTSHQAAQAQPPPPGTQAPEAHCVAESTIPE
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                     IAPTTLVSHTTSTSHRPHRRPVSKRPTHKPVTLGPFPIDPWRPKTTWVHWALLLITCA
                     VVAPVLLIIIISCLGWLAGWGRRRKGWIPL"
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                     150237..150348,155267..156737,156846..156928,
                     158625..160531)
                     /gene="RPMS1"
                     /locus_tag="HHV4_RPMS1"
                     /note="BART mRNAS, of which RMPS1 and part of A73 are
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                     transcripts"
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ncRNA          139351..139374
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misc_feature    139724..151554
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ncRNA          139795..139818
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                     /product="ebv-miR-BART6-5p"
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                     /gene="LF3"
                     /locus_tag="HHV4_LF3"
                     /db_xref="GeneID:3783749"
     CDS              complement(140570..143344)
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                     /locus_tag="HHV4_LF3"
                     /note="questionable whether a protein function is encoded"
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                     LQPATPRRSGAADPADPVGHPAAPRAPGPEPRTRLQPATPRRSGAADPADPVGHPAAP
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     rep_origin      143207..144444
                     /note="region containing oriLyt, core lytic cycle origin
                     of DNA replication"
     repeat_region   143272..144328
                     /note="DRright, similar to 40366..41409"
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ncRNA         147203..147225
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ncRNA         147321..147342
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             /locus_tag="HHV4_RPMS1"
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ncRNA         147356..147378
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ncRNA         147537..147560
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ncRNA         147936..147957
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             /note="betagamma gene; DURP family"
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gene          complement(149025..150417)
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             /inference="non-experimental evidence, no additional
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             RIHTFPGKVCPVNAIRRGKGYVRVSVDTPDLKREGPLNVKVGMTLLDDVIIAFRYNPY
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CDS           complement(150285..151694)
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             /locus_tag="HHV4_LF1"
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                SPTSLSLAFPYAGPPPVAWYRHSINLTRSEGVGIGKDCAQDHACPVPPQGHASSAADQ
                AGVPERGRKRAHEGPGAGEAASAGRGDVALSQSRALLWRGLGWDTGRGRLAPGLAMSR
                DAASGSVHLDIQVDRAEEGWVCDVLLEPGPPTAREGCSLSMDPGLVTLKDAWTLFPLH
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CDS              join(150323..150348,155267..155552)
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                /inference="non-experimental evidence, no additional
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                /note="core gene"
                /db_xref="GeneID:3783681"
CDS              complement(151703..152641)
                /gene="BILF1"
                /locus_tag="HHV4_BILF1"
                /note="type 3 membrane protein; 7 transmembrane domains;
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                /codon_start=1
                /product="membrane protein BILF1"
                /protein_id="YP_401711.1"
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                     MGPDANLNRGPNMCREGPTKGMHTAVQGLKAGCYLLAAVLIVLLTVIIIWKLLRTKFG
                     RKPRLICNVTFTGLICAFSWFMLSLPLLFLGEAGSLGFDCTESLVARYYPGPAACLAL
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                     DLSVRREDSSWPSYQALAFDIECLGEEGFPTATNEADLILQISCVLWSTGEEAGRYRR
                     ILLTLGTCEDIEGVEVYEFPSELDMLYAFFQLIRDLSVEIVTGYNVANFDWPYILDRA
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                     TVIQPLSGFYNSPVLVVDFASLYPSIIQAHNLCYSTMITPGEEHRLAGLRPGEDYESF
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     mRNA            join(<155549..156737,156846..156928,158625..158751,
                     159781..160531)
                     /gene="A73"
                     /locus_tag="HHV4_A73"
                     /note="BART mRNAS, of which RMPS1 and part of A73 are
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                     transcripts"
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     gene            complement(156244..160908)
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                     /gene="BALF4"
                     /locus_tag="HHV4_BALF4"
                     /note="type 1 membrane protein; possible membrane fusogen;
                     binds cell surface heparan sulphate; role in cell entry;
                     role in cell-to-cell spread"
                     /codon_start=1
                     /product="envelope glycoprotein B"
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                     TYEGQLGTDNEIFLTKKMTEVCQATSQYYFQSGNEIHVYNDYHHFKTIELDGIATLQT
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     CDS              complement(158851..160908)
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                     IPDPRLYITSVPCWRCVGELMVLPNHGNPSTAEGTHVSCNHLAVPVNPEPVSGLFENE
                     VRQAGLGHLLEAEEKARPGGPEEGAVPGPGRPEAEGATRALDTYNVFSTVPPEVAELS
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                     VAPGATERLFCGGVYSSSGDAVEALKADCAAAFTAHPQYRAILQKRNELYTRLNRAMQ
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             AFLTSLIWPGIEPSDWIETSFNSFYSVPGGSLASSQQILCRALREAVLTVSLYNKTWG
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             /experiment="experimental evidence, no additional details
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             /locus_tag="HHV4_BARF0"
             /trans_splicing
             /note="it is questionable whether a protein function is
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regulatory     160508..160513
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gene          complement(160550..164356)
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             /locus_tag="HHV4_BALF2"
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                     role possibly in gene regulation"
                     /codon_start=1
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                     /protein_id="YP_401717.1"
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                     RDDAEYLLGRFSVLADSVLETLATIASSGIEWTAEAARDFLEGVWGGPGAAQDNFISV
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                     /gene="BALF2"
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