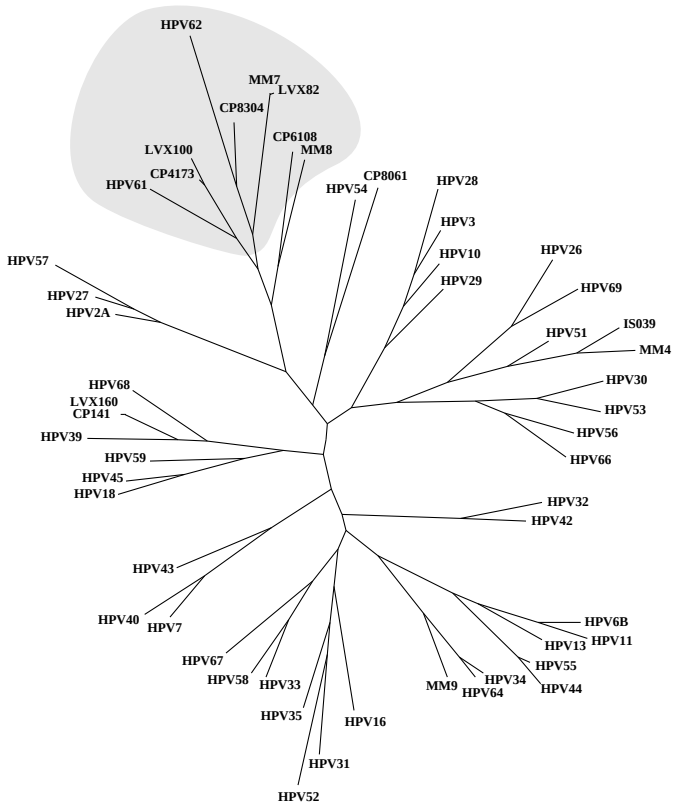
Group E Sequences

HPV61	**HPV62**
HPVCP4173	**HPVCP6108**
HPVCP8304	**HPVLVX100**
HPVLVX82	**HPVMM7**
HPVMM8	



INTRODUCTION

Group E consists of the novel HPV sequences CP4173, CP6108, CP8304, LVX100, LVX82, MM7, and MM8, and the previously characterized types HPV-61 and HPV-62. Viruses in this group primarily infect anogenital tissue and have relatively unknown oncogenic potential and prevalence.

CP4173, CP6108 and CP8304 were obtained through clinical studies conducted in the state of New Mexico among a tri-ethnic population [1]. LVX100 and LVX82 were isolated from the Amazonian Indian population [2]. MM7 and MM8 were identified through studies conducted in the state of California: initial prevalence data for MM7 and MM8 are similar to that obtained for characterized "intermediate risk" viruses [3]. All samples were obtained from cervical lavages or genital swabs (CP6108 and CP4173 were isolated from normal cervices).

The previously characterized HPV types HPV-61 and HPV-62 have been isolated from tissues with at least some degree of dysplasia. Both HPV-61 and HPV-62 have been derived from vulvar intraepithelial neoplasias [4].

All of the members of Group E have currently been sequenced only over the My09-My11 fragment of L1. Phylogenetic analysis of the L1 region categorizes the group E viruses as a distinct group (Part III). The comparatively small L1 region of the group E viruses makes it difficult, however, to assess the members of the group in terms of "close types" or potentially problematic members. The following sequence pairs, sequenced by different groups, differ by only a few nucleotides: HPVMM7 and HPVLVX82; HPVLVX160 and HPVCP141; HPVLVX100 and HPVCP4173; HPV66MY911 and HPV66L1AE4.

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[1] Peyton,C.L. and Wheeler,C.M. Identification of five novel human papillomaviruses in the New Mexico triethnic population. *J. Infect. Dis*. (1994) In press

[2] Ong,C.-K., Bernard,H.-U. and Villa,L.L. Identification of genomic sequences of three novel human papillomaviruses in cervical smears of Amazonian Indians. *J. Infect. Dis*. (1994) In press

[3] Manos,M.M., Waldman,J., Zhang,T. Greer,C., Eichinger, G.,Schiffmann,M., and Wheeler, C. Epidemiology and partial nucleotide sequence of four novel genital human papillomaviruses. *J. Infect. Dis*. (1994) In press

[4] de Villiers,E.M. Human pathogenic papillomavirus types: an update. in *Human pathogenic papillomaviruses*, edited by Harald zur Hausen, Springer-Verlag, Heidelberg, pp 1–12 (1994)

HPV61L1AE4

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LOCUS       HPV61L1AE4    415 bp    DNA             VRL       25-MAY-1994
DEFINITION  Human papillomavirus type 61, partial L1 cds, My09/My11
            region.
ACCESSION   U01534
SOURCE      Human papillomavirus type 61 DNA, PCR amplified clone AE4
REFERENCE   1  (bases 1 to 415)
  AUTHORS   Tachezy,R., Van Ranst,M.A., Cruz,Y. and Burk,R.D.
  TITLE     Consensus primer mediated PCR allows identification of novel human
            papillomavirus PCR-types in cervicovaginal lavages
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 415)
  AUTHORS   Van Ranst,M.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-SEP-1993) Marc A. Van Ranst, Albert Einstein College
            of Medicine, Dept. of Microbiology & Immunology, 1300 Morris Park
            Avenue, Bronx, NY 10461, USA
COMMENT     Isolate AE4 is a variant of HPV type 61 identified in a study
            conducted to screen cervical lavages from over 500 women for novel
            HPV types.  All women involved in the study were seen by physicians
            from clinics or private practices in the Bronx, N.Y. area.  Derived
            sequences are PCR products amplified over the My09/My11 primer
            region of L1.
BASE COUNT      109 a     88 c     84 g    134 t
ORIGIN
        1 tatttgttgg tttaatgaat tgtttgtaac cgtcgtggat accacccgca gtactaatgt
       61 aaccatttgt actgctacat ccccccctgt atctgaatat aaagccacaa gctttaggga
      121 atatttgcgc catacagtgg agtttgattt gcaatttatt tttcagttat gtaaaataca
      181 tttaacccct gaaattatgg cctacctaca taatatgaat aaggccttgt tggatgactg
      241 gaactttggt gtggtaccac caccctctac cagtttagaa gacacatata ggtttttgca
      301 gtccagagct attacatgtc agaagggtgc tgctgccccg ccgcccaagg aggatcgcta
      361 tgccaagtta tccttttgga ctgttgattt acgagacaag ttttccactg atttg
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LOCUS       HPV61MY911    455 bp ds-DNA             VRL       16-OCT-1994
DEFINITION  Human papillomavirus type 61 (HPV-61), partial L1 cds, My09/My11
            region.
ACCESSION   U12500
SOURCE      Human papillomavirus type 61 DNA recovered from a patient with
            vulvar intraepithelial neoplasia (VaIN).
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Bernard,H.-U., Chan,S.-Y., Manos,M.M., Ong,C.-K., Villa,L.L.,
            Delius,H., Peyton,C.L., Bauer,H.M., and Wheeler,C.M.
  TITLE     Identification and assessment of known and novel human
            papillomaviruses by PCR amplification, restriction fragment
            length polymorphisms, nucleotide sequence, and phylogenetic
            algorithms
  JOURNAL   J. Infect. Dis. (1994) In press
COMMENT     HPV-64 has recently been characterized and isolated from a vulvar
            intraepithelial neoplasia by Dr. T. Matsukura.  The cloned DNA
            was subsequently sequenced by Dr. H. Delius over the L1 MY09/MY11
            segment.  HPV-64 and the several other types recently sequenced
            over the MY09/MY11 primer region by Dr. Delius were used as
            type-specific probes to screen DNA for novel genital HPV types.
            The screened DNA was obtained from four recent epidemiological
            studies.  Similar to sequence with accession number U01534.
            Primer regions are annotated in the sequence; information in this
            region is not accurate due to primer degeneracy.
BASE COUNT      116 a     99 c     96 g    144 t
ORIGIN
        1 gcccagggcc acaacaatgg tatttgttgg tttaatgaat tgtttgtaac cgttgtggat
  L1 cds ->
          -> MY11 PCR primer <-
       61 accacccgca gtactaattt aaccatttgt actgctacat ccccccctgt atctgaatat
      121 aaagccacaa gctttaggga atatttgcgc catacagagg agtttgattt gccatttatt
      181 tttcagttat gtaaaataca tttaacccct gaaattatgg cctacctaca taatatgaat
      241 aaggccttgt tggatgactg gaactttggt gtggtaccac caccctctac cagtttagaa
      301 gacacatata ggtttttgca gtccagagct attacatgtc tgaagggtgc tgctgccccg
      361 ccgcccaagg aggatcgcta tgccaagtta tccttttgga ctgttgattt acgagacaag
      421 ttttccactg atttggatca gtttcctttg gggcg
                                        L1 cds ->
                        -> MY09 PCR primer  <-
```

HPV62MY911

```
LOCUS       HPV62MY911    449 bp ds-DNA             VRL       16-OCT-1994
DEFINITION  Human papillomavirus type 62 (HPV-62), partial L1 cds, My09/My11
            region.
ACCESSION   U12499
SOURCE      Human papillomavirus type 62 DNA isolated from a patient with
            vulvar intraepithelial neoplasia (VaIN).
REFERENCE   1  (bases 1 to 449)
  AUTHORS   Bernard,H.-U., Chan,S.-Y., Manos,M.M., Ong,C.-K., Villa,L.L.,
            Delius,H., Peyton,C.L., Bauer,H.M., and Wheeler,C.M.
  TITLE     Identification and assessment of known and novel human
            papillomaviruses by PCR amplification, restriction fragment
            length polymorphisms, nucleotide sequence, and phylogenetic
            algorithms
  JOURNAL   J. Infect. Dis. (1994) In press
COMMENT     HPV-62 has recently been characterized and isolated from a vulvar
            intraepithelial neoplasia by Dr. T. Matsukura.  The cloned DNA
            was subsequently sequenced by Dr. H. Delius over the L1 MY09/MY11
            segment.  HPV-62 and the several other types recently sequenced
            over this region by Dr. Delius were used as type-specific probes to
            screen DNA for novel genital HPV types.  The screened DNA was
            obtained from four recent epidemiological studies. Primer regions
            are annotated in the sequence; information in this region is not
            accurate due to primer degeneracy.

BASE COUNT      116 a     92 c     99 g    142 t
ORIGIN
        1 gcacagggtc ataataatgg tatttgttgg tttaatgaac tgtttgttac tgtggtggat
  L1 cds ->
          -> MY11 PCR primer <-
       61 actaccagaa gtactaattt tactatttgt accgcctcca ctgctgcagc agaatacacg
      121 gctaccaact ttagggaatt tttgcgacac acggaggaat ttgatttgca atttatattt
      181 caattgtgca aaatacagtt aacccccgaa attatggcct acctgcataa tatgaacaag
      241 gacctttggg atgactggaa ctttggggtt ttacctcccc cttccactag tttagatgag
      301 acatatcact atttcgagtc tcgggctatt acatgtcaaa gggggctgcc tacccgtccc
      361 aaggtggacc cgtatgcgca aatgacattt tggactgtgg atcttaagga caagttgtct
      421 actgatttgg atcagtttcc cttgggttg
                                 L1 cds ->
                  -> MY09 PCR primer  <-
```

LOCUS HPVCP4173 455 bp ds-DNA VRL 16-OCT-1994
DEFINITION Human papillomavirus, isolate CP4173, partial L1 cds, My09/My11 region.
ACCESSION U12477
SOURCE Human papillomavirus DNA derived from a cytologically normal cervical sample from a non-Hispanic white woman, 18 years of age, isolate CP4173.
REFERENCE 1 (bases 1 to 455)
AUTHORS Peyton,C.L. and Wheeler,C.M.
TITLE Identification of five novel human papillomaviruses in the New Mexico triethnic population
JOURNAL J. Infect. Dis. (1994) In press
COMMENT Data kindly provided prior to publication by Dr. C. Wheeler, University of New Mexico, School of Medicine, New Mexico Tumor Registry, 900 Camino del Salad NE, Albuquerque, NM, 87131-5306.

Five novel HPV sequences were identified in a study in which 3655 cervical specimens were screened against known genital HPV DNA [1]. The specimens were obtained from clinical investigations conducted at the University of New Mexico. The study subjects included Native Indians, Hispanics, and non-Hispanic whites. CP4173 was derived from a cytologically normal cervical sample from a non-Hispanic white woman, 18 years of age. The viral DNA was PCR amplified using the L1 consensus primer MY09/MY11 pair, which can hybridize to a broad spectrum of HPV types. Resultant fragments range from 449 to 458 nucleotides in length. The amplification products were initially screened against 2 sets of type-specific probes and a generic probe. If hybridization to the generic probe and not to the type-specific probes ocurred, the samples were further analyzed by restriction fragment length polymorphisms. RFLP patterns which did not match reference patterns were considered to be derived from novel HPVs. The five novel samples which were were identified in this study include CP8304, CP6108, CP8061, CP141, CP4173. Peyton et al. also identified two HPV45 subtypes and one HPV56 subtype. They conclude that since the existence of subtypes appears to be relatively rare, it suggests that HPV45 and HPV56 are more divergent than many HPV types. It should be noted that CP141 (U12476) is almost identical to LVX160 (U12486) and HPVL1AE1 (U01535) and that CP4173 (U12477) is almost identical to LVX100 (U12485). Both LVX160 and LVX100 were identified by Ong et al. in a 1994 study which examined Amazonian Indian subjects (Ong et al., J. Infect. Dis., 1994, in press). Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy.

In a subsequent study Bernard et al. evaluated ten novel genital HPV types, including the five identified in the Peyton et al. study, and other known genital types to determine phylogenetic relationships. They observed that the genital types CP6108, CP8304, CP4173 and CP8061 form a branch with HPV types 61 and 62. This emergent minor branch is positioned between two others which contain cutaneous types. Bernard et al. speculate as to whether other low-risk genital types have escaped detection because of considerable sequence divergence from the common genital types (Bernard et al., J. Infect. Dis., 1994, in press).

Bernard et al. also assessed the linear correlation coefficients for the MY9/MY11 fragments against the rest of L1 (.851) and against the E6 gene (.888). Since these values are close, the authors suggest that the evolutionary distance information obtained for the primer pair region should be comparable to that available from the other regions of the genome (Bernard et al., J. Infect. Dis., 1994, in press).

BASE COUNT 117 a 95 c 85 g 158 t

```
ORIGIN
        1 gcacattgtc ataataatgg catctattgg tttaatgagc tttttgtgac agttgtagat
  L1 cds ->
          -> MY11 PCR primer <-
       61 actactcgca gtactaatgt aactatttgt actgccacag cgtcctctgt atcagaatat
      121 acagcttcta attttcgtga gtatcttcgc cacactgagg aatttgattt gcagtttata
      181 tttcaactgt gtaaaattca cttaactcct gaaattatgg cctacttgca caatatgaat
      241 aaggccttat tggatgactg gaattttggt gtggtgcctc ctccttctac cagtttagat
      301 gatacctata ggtttttaca gtctcgtgcc attacctgtc aaaagggggc tgccacccct
      361 cctcctaaag aagatccata tgctaactta tccttttgga ctgtggattt aaaggacaaa
      421 ttttccactg acttggatca gtttcctctt ggacg
                                          L1 cds ->
                          -> MY09 PCR primer  <-
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LOCUS HPVCP6108 452 bp ds-DNA VRL 16-OCT-1994
DEFINITION Human papillomavirus, isolate CP6108, partial L1 cds, My09/My11 region.
ACCESSION U12478
SOURCE Human papillomavirus DNA derived from a cytologically normal cervical sample from a non-Hispanic white woman, 20 years of age, isolate CP6108.
REFERENCE 1 (bases 1 to 452)
AUTHORS Peyton,C.L. and Wheeler,C.M.
TITLE Identification of five novel human papillomaviruses in the New Mexico triethnic population
JOURNAL J. Infect. Dis. (1994) In press
COMMENT Data kindly provided prior to publication by Dr. C. Wheeler, University of New Mexico, School of Medicine, New Mexico Tumor Registry, 900 Camino del Salad NE, Albuquerque, NM, 87131-5306.

Five novel HPV sequences were identified in a study in which 3655 cervical specimens were screened against known genital HPV DNA [1]. The specimens were obtained from clinical investigations conducted at the University of New Mexico. The study subjects included Native Indians, Hispanics, and non-Hispanic whites. CP6108 was derived from a cytologically normal cervical sample from a non-Hispanic white woman, 20 years of age. The viral DNA was PCR amplified using the L1 consensus primer MY09/MY11 pair, which can hybridize to a broad spectrum of HPV types. Resultant fragments range from 449 to 458 nucleotides in length. The amplification products were initially screened against 2 sets of type-specific probes and a generic probe. If hybridization to the generic probe and not to the type-specific probes ocurred, the samples were further analyzed by restriction fragment length polymorphisms. RFLP patterns which did not match reference patterns were considered to be derived from novel HPVs. The five novel samples which were were identified in this study include CP8304, CP6108, CP8061, CP141, CP4173. Peyton et al. also identified two HPV45 subtypes and one HPV56 subtype. They conclude that since the existence of subtypes appears to be relatively rare, it suggests that HPV45 and HPV56 are more divergent than many HPV types. It should be noted that CP141 (U12476) is almost identical to LVX160 (U12486) and HPVL1AE1 (U01535) and that CP4173 (U12477) is almost identical to LVX100 (U12485). Both LVX160 and LVX100 were identified by Ong et al. in a 1994 study which examined Amazonian Indian subjects (Ong et al., J. Infect. Dis., 1994, in press). Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy.

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BASE COUNT 122 a 101 c 87 g 142 t

```
ORIGIN
        1 gcacagggtc ataataatgg tatttgttgg tttaatgagt tgtttgttac tgtggtagat
  L1 cds ->
          -> MY11 PCR primer <-
       61 accacccgta gtaccaacct taccatttgt gctgcttccc agtctgccac agaatacagt
      121 tctacacgct ttaaggaata tttaagacac actgaggaat atgacctaca gtttatattc
      181 caactatgta agatacacct aacgcctgag ataatgtcct atttacacga tatgaatgac
      241 acattgttag atgaatggaa ctttggtgtc attccccctc cctccactag tttggatgat
      301 acctatcgct ttcttacctc tcgggccatt acatgtcaaa agggcactgc tgccccagaa
      361 cctaaaaagg atccatatga taagttatcc ttttgggatg tggatcttaa ggaacgtttg
      421 tccactgatc ttgatcagtt tccccttgga cg
                                       L1 cds ->
                        -> MY09 PCR primer  <-
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LOCUS       HPVCP8304     452 bp ds-DNA             VRL       16-OCT-1994
DEFINITION  Human papillomavirus, isolate CP8304, partial L1 cds, My09/My11
            region.
ACCESSION   U12480
SOURCE      Human papillomavirus, isolate CP8304.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Peyton,C.L. and Wheeler,C.M.
  TITLE     Identification of five novel human papillomaviruses in the New
            Mexico triethnic population
  JOURNAL   J. Infect. Dis. (1994) In press
REFERENCE   2
  AUTHORS   Ong,C.-K., Bernard,H.-U. and Villa,L.L.
  TITLE     Identification of genomic sequences of three novel human
            papillomaviruses in cervical smears of Amazonian Indians
  JOURNAL   J. Infect. Dis.  (1994) In press
REFERENCE   3
  AUTHORS   Bernard,H.-U., Chan,S.-Y., Manos,M.M., Ong,C.-K., Villa,L.L.,
            Delius,H., Peyton,C.L., Bauer,H.M., and Wheeler,C.M.
  TITLE     Identification and Assessment of Known and Novel Human
            Papillomaviruses by PCR Amplification, Restriction Fragment
            Polymorphisms, Nucleotide Sequence, and Phylogenetic Algorithms
  JOURNAL   J. Infect. Dis. (1994) In press
COMMENT     Data kindly provided prior to publication by Dr. C. Wheeler,
            University of New Mexico, School of Medicine, New Mexico
            Tumor Registry, 900 Camino del Salad NE, Albuquerque, NM,
            87131-5306.
```

Five novel HPV sequences were identified in a study in which 3655 cervical specimens were screened against known genital HPV DNA [1]. The specimens were obtained from clinical investigations conducted at the University of New Mexico. The study subjects included Native Indians, Hispanics, and non-Hispanic whites. The viral DNA was PCR amplified using the L1 consensus primer MY09/MY11 pair, which can hybridize to a broad spectrum of HPV types. Resultant fragments range from 449 to 458 nucleotides in length. The amplification products were initially screened against 2 sets of type-specific probes and a generic probe. If hybridization to the generic probe and not to the type-specific probes ocurred, the samples were further analyzed by restriction fragment length polymorphisms. RFLP patterns which did not match reference patterns were considered to be derived from novel HPVs. The five novel samples which were were identified in this study include CP8304, CP6108, CP8061, CP141, CP4173. Peyton et al. also identified two HPV45 subtypes and one HPV56 subtype. They conclude that since the existence of subtypes appears to be relatively rare, it suggests that HPV45 and HPV56 are more divergent than many HPV types. It should be noted that CP141 (U12476) is almost identical to LVX160 (U12486) and HPVL1AE1 (U01535) and that CP4173 (U12477) is almost identical to LVX100 (U12485). Both LVX160 and LVX100 were identified by Ong et al. in a 1994 study which examined Amazonian Indian subjects (Ong et al., J. Infect. Dis., 1994, in press). Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy.

In a subsequent study Bernard et al. evaluated ten novel genital HPV types, including the five identified in the Peyton et al. study, and other known genital types to determine phylogenetic relationships. They observed that the genital types CP6108, CP8304, CP4173 and CP8061 form a branch with HPV types 61 and 62. This emergent minor branch is positioned between two others which contain cutaneous types. Bernard et al. speculate as to whether other low-risk genital types have escaped detection because of considerable sequence divergence from the common genital types (Bernard et al., J. Infect. Dis., 1994, in press).

Bernard et al. also assessed the linear correlation coefficients for the MY9/MY11 fragments against the rest of L1 (.851) and against the E6 gene (.888). Since these values are close, the authors suggest that the evolutionary distance information obtained for the primer pair region should be comparable to that available from the other regions of the genome (Bernard et al., J. Infect. Dis., 1994, in press).

```
BASE COUNT      125 a     93 c     95 g    139 t
ORIGIN
        1 gcacagggac ataataatgg tatttgttgg tttaatgaaa tgtttgttac agtggtggat
  L1 cds ->
          -> MY11 PCR primer <-
       61 actaccagaa gcaccaattt tactatttgc acagctacat ctgctgctgc agaatacaag
      121 gcctctaact ttaaggaatt tctgcgccat acagaggaat atgatttgca gtttattttc
      181 caattatgta aaatacagtt aacaccagaa attatggcct acttacataa tatgaacaag
      241 gcactgttgg atgattggaa ttttggtgtg ttgccacctc cttccaccag tttagatgac
      301 acatatcgct ttttacagtc tcgggccatt acctgtcaaa agggtgctgc tgcccctgcg
      361 cccaaagagg acccttatgc cgacatgtca ttttggacag ttgaccttaa ggacaagttg
      421 tctactgatt tggatcagta tcctctggga cg
                                      L1 cds ->
                      -> MY09 PCR primer  <-
```

```
LOCUS       HPVLVX100     452 bp ds-DNA             VRL       16-OCT-1994
DEFINITION  Human papillomavirus, isolate LVX100, partial L1 cds, My09/My11
            region.
ACCESSION   U12485
SOURCE      Human papillomavirus, isolate LVX100 from cervical smear.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Ong,C.-K., Bernard,H.-U. and Villa,L.L.
  TITLE     Identification of genomic sequences of three novel human
            papillomaviruses in cervical smears of Amazonian Indians
  JOURNAL   J. Infect. Dis. (1994) In press
COMMENT     HPVLVX82, HPVLVX100 and HPVLVX160 were found in cervical smears
            taken from members of isolated Amazonian tribes. The samples were
            PCR-amplified using the MY09/My11 consensus primers, then examined
            in hybridization experiments in order to determine their homology
            with known HPV types. In addition to many previously characterized
            HPV types, these three novel variants were discovered to be more
            than 10% divergent from their closest known relatives, suggesting
            that they may qualify to be considered new types. Although the
            tribes were thought to have been sexually isolated from
            non-Amerindian populations for at least 12,000 years, sequences
            closely related to these novel variants have since been detected in
            other distinct populations.  The authors of [1] state that this may
            be evidence for the hypothesis that papillomavirus types evolved
            before the speciation of Homo sapiens, and consequently before the
            divergence of ethnic groups.  Primer regions are annotated in the
            sequence; information in this region is not accurate due to primer
            degeneracy.  All similarity calculations exclude data from this
            region.

BASE COUNT      116 a     96 c     85 g    155 t
ORIGIN
        1 gcccagggtc ataataatgg catctgttgg tttaatgagc tttttgtgac agttgtagat
  L1 cds ->
          -> MY11 PCR primer <-
       61 actactcgca gtactaatgt aactatttgt actgccacag cgtcctctgt atcagaatat
      121 acagcttcta attttcgtga gtatcttcgc cacactgagg aatttgattt gcagtttata
      181 tttcaactgt gtaaaattca cttaactcct gaaattatgg cctacttgca caatatgaat
      241 aaggccttat tggatgactg gaattttggt gtggtgcctc ctccttctac cagtttagat
      301 gatacctata ggtttttaca gtctcgtgcc attacctgtc aaaaggctgc cacccctcct
      361 cctaaagaag atccatatgc taacttatcc ttttggactg tggatttaaa ggacaaattt
      421 tccactgact tggatcagta tcctcttgga cg
                                    L1 cds ->
                      -> MY09 PCR primer  <-
```

```
LOCUS       HPVLVX82      452 bp ds-DNA             VRL       16-OCT-1994
DEFINITION  Human papillomavirus, isolate LVX82, partial L1 cds, My09/My11
            region.
ACCESSION   U12487
SOURCE      Human papillomavirus, isolate LVX82 from cervical smear.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Ong,C.-K., Bernard,H.-U. and Villa,L.L.
  TITLE     Identification of genomic sequences of three novel human
            papillomaviruses in cervical smears of Amazonian Indians
  JOURNAL   J. Infect. Dis. (1994) In press
COMMENT     HPVLVX82, HPVLVX100 and HPVLVX160 were found in cervical smears
            taken from members of isolated Amazonian tribes. The samples were
            PCR-amplified using the MY09/My11 consensus primers, then examined
            in hybridization experiments in order to determine their homology
            with known HPV types. In addition to many previously characterized
            HPV types, these three novel variants were discovered to be more
            than 10% divergent from their closest known relatives, suggesting
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            tribes were thought to have been sexually isolated from
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            closely related to these novel variants have since been detected in
            other distinct populations.  The authors of [1] state that this may
            be evidence for the hypothesis that papillomavirus types evolved
            before the speciation of Homo sapiens, and consequently before the
            divergence of ethnic groups.  Primer regions are annotated in the
            sequence; information in this region is not accurate due to primer
            degeneracy.  All similarity calculations exclude data from this
            region.

BASE COUNT      123 a    104 c     87 g    138 t
ORIGIN
        1 gcccagggtc ataataatgg catttgttgg tttaatgagt tatttgttac agttgtagat
  L1 cds ->
          -> MY11 PCR primer <-
       61 actacccgca gtaccaatat tactatttca gctgctgcta cacaggctaa tgaatacaca
      121 gcctctaact ttaaggaata cctccgccac accgaggaat atgacttaca ggttatattg
      181 caactttgca aaatacatct tacccctgaa attatggcat acctacatag tatgaatgaa
      241 catttattgg atgagtggaa ttttggcgtg ttaccgcctc cctccaccag ccttgatgat
      301 acctatcgct atttgcagtc ccgtgctatt acctgccaaa agggtccttc cgcccctgcc
      361 cctaaaaagg atccttatga tggccttgta ttttgggagg ttgatttaaa ggacaaacta
      421 tccacagatt tagatcagtt tcctttggga cg
                                      L1 cds ->
                        -> MY09 PCR primer  <-
```

```
LOCUS       HPVMM7        452 bp ds-DNA             VRL       16-OCT-1994
DEFINITION  Human papillomavirus, isolate MM7, partial L1 cds, My09/My11
            region.
ACCESSION   U12489
SOURCE      Human papillomavirus DNA recovered from a genital swab sample,
            isolate MM7.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Manos,M.M., Waldman,J., Zhang,T. Greer,C., Eichinger,G.,
            Schiffmann,M., and Wheeler, C.
  TITLE     Epidemiology and partial nucleotide sequence of four novel genital
            human papillomaviruses
  JOURNAL   J. Infect. Dis. (1994) In press
COMMENT     MM7, also known as PAP291, was isolated from a genital swab sample.
            Samples were obtained from over 500 patients examined at either the
            Shasta/Diablo planned parenthood clinic or at a private practice
            in the state of California over the course of seventeen months.
            Each of the samples were cervical or vulvar/intraoital in origin.
            DNA was PCR amplified over the MY09/MY11 region and subsequently
            sequenced if the HPV digested products yielded unique RFLP patterns.
            This procedure resulted in the identification of four novel HPV
            types: W13B, PAP291, PAP155, and PAP238a, which have subsequently
            been renamed MM4, MM7, MM8, and MM9. Oligonucleotide probes over
            the MY9/MY11 region from these viruses have been reported by
            Hildesheim et al. (J Infect Dis 169: 235-40).   These probes were
            used to determine prevalence in different populations.  Prevalence
            for each of these viruses was similar to that seen in other
            characterized "intermediate risk" viruses probed for in these
            studies.  It should be noted that MM4 is extremely similar (90.8%)
            to novel HPVIS39 (U12481) and MM7 is virtually identical to LVX82
            (U12487).  Primer regions are annotated in the sequence;
            information in this region is not accurate due to primer degeneracy.
            All similarity calculations exclude data from this region.
BASE COUNT      125 a    104 c     87 g    136 t
ORIGIN
        1 gcccagggac ataataatgg catttgttgg tttaatgagt tatttgttac agttgtagat
  L1 cds ->
          -> MY11 PCR primer <-
       61 actacccgca gtaccaatat tactatttca gctgctgcta cacaggctaa tgaatacaca
      121 gcctctaact ttaaggaata cctccgccac accgaggaat atgacttaca ggttatattg
      181 caactttgca aaatacatct tacccctgaa attatggcat acctacatag tatgaatgaa
      241 catttattgg atgagtggaa ttttggcgtg ttaccacctc cttccaccag ccttgatgat
      301 acctatcgct atctgcagtc ccgtgctatt acctgccaaa agggtccttc cgcccctgcc
      361 cctaaaaagg atccttatga tggccttgta ttttgggagg ttgatttaaa ggacaaacta
      421 tccacagatt tggatcagta tcctttggga cg
                                       L1 cds ->
                        -> MY09 PCR primer  <-
```

HPVMM8

```
LOCUS       HPVMM8        452 bp ds-DNA             VRL       16-OCT-1994
DEFINITION  Human papillomavirus, isolate MM8, partial L1 cds, My09/My11
            region.
ACCESSION   U12490
SOURCE      Human papillomavirus DNA recovered from a genital swab sample,
            isolate MM8.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Manos,M.M., Waldman,J., Zhang,T. Greer,C., Eichinger,G.,
            Schiffmann,M., and Wheeler, C.
  TITLE     Epidemiology and partial nucleotide sequence of four novel genital
            human papillomaviruses
  JOURNAL   J. Infect. Dis. (1994) In press
COMMENT     MM8, also known as PAP155, was isolated from a cervical swab sample.
            Samples were obtained from over 500 patients examined at either the
            Shasta/Diablo planned parenthood clinic or at a private practice
            in the state of California over the course of seventeen months.
            Each of the samples were cervical or vulvar/intraoital in origin.
            DNA was PCR amplified over the MY09/MY11 region and subsequently
            sequenced if the HPV digested products yielded unique RFLP patterns.
            This procedure resulted in the identification of four novel HPV
            types: W13B, PAP291, PAP155, and PAP238a, which have subsequently
            been renamed MM4, MM7, MM8, and MM9. Oligonucleotide probes over
            the MY9/MY11 region from these viruses have been reported by
            Hildesheim et al. (J Infect Dis 169: 235-40).   These probes were
            used to determine prevalence in different populations.  Prevalence
            for each of these viruses was similar to that seen in other
            characterized "intermediate risk" viruses probed for in these
            studies.  It should be noted that MM4 is extremely similar (90.8%)
            to novel HPVIS39 (U12481) and MM7 is virtually identical to LVX82
            (U12487).  Primer regions are annotated in the sequence;
            information in this region is not accurate due to primer degeneracy.
            All similarity calculations exclude data from this region.

BASE COUNT      117 a     96 c    102 g    137 t
ORIGIN
        1 gcgcggggtc ataacaatgg tatatgctgg tttaatcaat tgtttgtcac ggtggtggat
  L1 cds ->
          -> MY11 PCR primer <-
       61 accacccgca gcaccaattt tactattagt gctgctacca acaccgaatc agaatataaa
      121 cctaccaatt ttaaggaata cctaagacat gtggaggaat atgatttgca gtttatattc
      181 cagttgtgta aggtccgtct gactccagag gtcatgtcct atttacatac tatgaatgac
      241 tccttattag atgagtggaa ttttggtgtt gtgccccctc cctccacaag tttagatgat
      301 acctataggt acttgcagtc tcgcgccatt acttgccaaa agggggccgc cgccgccaag
      361 cctaaggaag atccttatgc tggcatgtcc ttttgggatg tagatttaaa ggacaagttt
      421 tctactgatt tggatcagta tcctttggga cg
                                       L1 cds ->
                      -> MY09 PCR primer  <-
```