I

HPV and Animal PV Nucleic Acid Sequences

Sequences

Two complete genomes and nine new partial sequences of HPVs have been released since the 1995 HPV compendium was released. These sequences are published in full herein, beginning on page I-13, and have been added to the list and cross reference of all HPV and animal PV sequences presented in Table I-1 (page I-2). The table is ordered by HPV type, with viruses of uncertain or probable "new" type listed last. Included in Table I-1 are the viral TYPE, the LOCUS names we use, the GROUP designation as used in the 1994 compendium, the equivalent new GROUP designation [1], the original GenBank LOCUS name, the GenBank ACCESSION NUMBER, the REGION of the genome sequenced, and the page number on which the sequence is located. The page number is preceded by a (94), (95), or (96) indicating the year of the compendium in which the sequence was published. Several animal papilloma virus sequences (e.g., MMPV) that are only distantly related to other PVs probably represent taxa at the "supergroup" level. These are indicated in the fourth column of the table by the letter S.

Variants

Starting on page I-43 is a comprehensive survey of papillomavirus variant sequences. In this section variant nucleotide positions and their concomitant amino acid changes are tabulated for fourteen different PV types. The variant analysis began with alignments of all variants to their reference sequence. These alignments are available to investigators wishing to compare their new variant sequences to a reference sequence on our World Wide Web site at http://hpv-web.lanl.gov.

References

[1] Chan, S-Y, Delius, H., Halpern, A. L., and Bernard, H-U: Analysis of Genomic Sequences of 95 Papillomavirus Types: Uniting Typing, Phylogeny, and Taxonomy, *Journal of Virology* 1995;**69**:5, 3074–3083.

Table I-1 Sequence List and Cross Reference for HPV Database

❶ HUMAN PAPILLOMAVIRUSES

Type	Locus Name	"Old" Group	"New" Group	GenBank Locus Name	GenBank Accession	Region Sequenced	Page No.
HPV1a	HPV1a	G	E1	PAPAPI	V01116	Complete	(94) I-G-3
HPV2	HPV2a	F	A4	PAHPV2A	X55964	Complete	(94) I-F-4
HPV3	HPV3	F	A2	HPV3	X74462	Complete	(94) I-F-8
HPV4	HPV4	G	B2	PAPPH4	X70827	Complete	(94) I-G-8
HPV5	HPV5	H	B1	PPH5CG	M17463	Complete	(94) I-H-4
HPV5	HPV5b	H	B1	PPH5BCG	D90252	Complete	(94) I-H-8
HPV5	HPV5d	H	B1	PPHDELCG	M22961	Complete	(94) I-H-12
HPV6	HPV6b	B	A10	PAPA6B	X00203	Complete	(94) I-B-5
HPV7	HPV7	F	A8	HPV7	X74463	Complete	(94) I-F-12
HPV8	HPV8	H	B1	PPH8CG	M12737	Complete	(94) I-H-16
HPV9	HPV9	H	B1	HPV9	X74464	Complete	(94) I-H-20
HPV10	HPV10	F	A2	HPV10	X74465	Complete	(94) I-F-16
HPV11	HPV11	B	A10	PPH11	M14119	Complete	(94) I-B-10
HPV12	HPV12	H	B1	HPV12	X74466	Complete	(94) I-H-24
HPV13	HPV13	B	A10	HPVT13DNA	X62843	Complete	(94) I-B-14
HPV14	HPV14d	H	B1	HPV14D	X74467	Complete	(94) I-H-28
HPV15	HPV15	H	B1	HPV15	X74468	Complete	(94) I-H-32
HPV16	HPV16	A	A9	PPH16	K02718	Complete	(94) I-A-3
HPV16	HPV16R	A	A9	?	?	Complete	(95) I-A9-56
HPV17	HPV17	H	B1	HPV17	X74469	Complete	(94) I-H-36
HPV18	HPV18	C	A7	PAPHPV18	X05015	Complete	(94) I-C-4
HPV19	HPV19	H	B1	HPV19	X74470	Complete	(94) I-H-40
HPV20	HPV20	H	B1	HPU31778	U31778	Complete	(95) I-B1-174
HPV20	HPV20E6	H	B1	PPH20E6	D90261	E6	(94) I-H-44
HPV20	HPV20E7	H	B1	PPHC7C	D50547	E7	
HPV20	HPV20My911	H	B1	PPHL1AB	L38910	L1	
HPV21	HPV21	H	B1	HPU31779	U31779	Complete	(95) I-B1-178
HPV21	HPV21E6	H	B1	PPH21E6	D90263	E6	(94) I-H-46
HPV21	HPV21E7	H	B1	PPHE7D	D50548	E7	
HPV21	HPV21My911	H	B1	PPHL1AC	L38911	L1	
HPV22	HPV22	H	B1	HPU31780	U31780	Complete	(95) I-B1-182
HPV22	HPV22My911	H	B1	PPHL1AD	L38912	L1	
HPV23	HPV23	H	B1	HPU31781	U31781	Complete	(95) I-B1-186
HPV23	HPV23My911	H	B1	PPHL1AE	L38913	L1	
HPV24	HPV24	H	B1	HPU31782	U31782	Complete	(95) I-B1-190
HPV24	HPV24My911	H	B1	PPHL1AP	L38924	L1	
HPV25	HPV25	H	B1	HPV25	X74471	Complete	(94) I-H-48
HPV26	HPV26	D	A5	HPV26	X74472	Complete	(94) I-D-3
HPV27	HPV27	F	A4	HPV27	X74473	Complete	(94) I-F-20
HPV28	HPV28	F	A2	HPU31783	U31783	Complete	(95) I-A2-15
HPV28	HPV28MY911	F	A2	HPU1250211	U12502	L1	(94) I-F-24
HPV29	HPV29	F	A2	HPU31784	U31784	Complete	(95) I-A2-19
HPV29	HPV29MY911	F	A2	HPU1250311	U12503	L1	(94) I-F-25
HPV30	HPV30	D	A6	HPV30	X74474	Complete	(94) I-D-7
HPV31	HPV31	A	A9	PPH31A	J04353	Complete	(94) I-A-9
HPV32	HPV32	F	A1	HPV32	X74475	Complete	(94) I-F-26
HPV33	HPV33	A	A9	PPH33CG	M12732	Complete	(94) I-A-14

Table I-1 (cont.) Sequence List and Cross Reference for HPV Database

❶ HUMAN PAPILLOMAVIRUSES (cont.)

Type	Locus Name	"Old" Group	"New" Group	GenBank Locus Name	GenBank Accession	Region Sequenced	Page No.
HPV34	HPV34	B	A11	HPV34	X74476	Complete	(94) I-B-19
HPV35	HPV35	A	A9	PPH35CG	M74117	Complete	(94) I-A-19
HPV35	HPV35h	A	A9	HPV35H	X74477	Complete	(94) I-A-24
HPV36	HPV36	H	B1	HPU31785	U31785	Complete	(95) I-B1-194
HPV36	HPV36LCR	H	B1	HPVLCR4	X52061	LCR	
HPV36	HPV36My911	H	B1	PPHL1AG	L38915	L1	
HPV37	HPV37	H	B1	HPU31786	U31786	Complete	(95) I-B1-198
HPV38	HPV38	H	B1	HPU31787	U31787	Complete	(95) I-B1-202
HPV38	HPV38My911	H	B1	PPHL1AI	L38917	L1	
HPV39	HPV39	C	A7	PPHT39	M62849	Complete	(94) I-C-8
HPV40	HPV40	F	A8	HPV40	X74478	Complete	(94) I-F-30
HPV41	HPV41	G	E	PAP41CG	X56147	Complete	(94) I-G-12
HPV42	HPV42	F	A1	PPHPAPV42A	M73236	Complete	(94) I-F-34
HPV43	HPV43E6	F	A8	PPH43E6A	M27022	E6	(94) I-F-38
HPV43	HPV43MY911	F	A8	HPU1250411	U12504	L1	(94) I-F-39
HPV44	HPV44	B	A10	HPU31788	U31788	Complete	(95) I-A10-154
HPV44	HPV44E6	B	A10	PPH44E6A	M27023	E6	(94) I-B-23
HPV44	HPV44MY911	B	A10	HPU1249311	U12493	L1	(94) I-B-24
HPV45	HPV45	C	A7	HPV45	X74479	Complete	(94) I-C-12
HPV47	HPV47	H	B1	PPH47CG	M32305	Complete	(94) I-H-52
HPV48	HPV48	G	B2	HPU31789	U31789	Complete	(95) I-B2-224
HPV49	HPV49	H	B1	HPV49	X74480	Complete	(94) I-H-56
HPV50	HPV50	G	B2	HPU31790	U31790	Complete	(95) I-B2-227
HPV51	HPV51	D	A5	PPHDNA	M62877	Complete	(94) I-D-11
HPV52	HPV52	A	A9	HPV52	X74481	Complete	(94) I-A-29
HPV53	HPV53	D	A6	HPV53	X74482	Complete	(94) I-D-15
HPV54	HPV54	F	A	HPU37488	U37488	Complete	(95) I-A-164
HPV54	HPV54MY911	F	A	HPU1250111	U12501	L1	(94) I-F-40
HPV55	HPV55	B	A10	HPU31791	U31791	Complete	(95) I-A10-158
HPV56	HPV56	D	A6	HPV56	X74483	Complete	(94) I-D-19
HPV57	HPV57	F	A4	PAHPV57	X55965	Complete	(94) I-F-41
HPV58	HPV58	A	A9	PPH58	D90400	Complete	(94) I-A-33
HPV59	HPV59	C	A7	HPV59VG	X77858	Complete	(95) I-A7-43
HPV59	HPV59MY911	C	A7	HPU1249611	U12496	L1	(94) I-C-16
HPV59	HPV59X03	C	A7	S42987	S42987	L1	
HPV60	HPV60	G	B2	HPU31792	U31792	Complete	(95) I-B1-230
HPV61	HPV61	E	A3	HPU31793	U31793	Complete	(95) I-A3-25
HPV61	HPV61L1AE4	E	A3	HPU01534	U01534	L1	(94) I-E-2
HPV61	HPV61MY911	E	A3	HPU1250011	U12500	L1	(94) I-E-3
HPV62	HPV62MY911	E	A3	HPU1249911	U12499	L1	(94) I-E-4
HPV63	HPV63	G	E1	PAPPH63	X70828	Complete	(94) I-G-16
HPV64	HPV64MY911	B	A11	HPU1249511	U12495	L1	(94) I-B-26
HPV65	HPV65	G	B2	PAPPH65	X70829	Complete	(94) I-G-20
HPV66	HPV66	D	A6	HPU31794	U31794	Complete	(95) I-A6-36
HPV66	HPV66L1AE3	D	A6	HPU01533	U01533	L1	(94) I-D-23
HPV66	HPV66MY911	D	A6	HPU1249811	U12498	L1	(94) I-D-24
HPV66	HPV66E6E7	D	A6	PPHE6E7GEN	M75123	LCR,E6,E7	

Table I-1 (cont.) Sequence List and Cross Reference for HPV Database

❶ HUMAN PAPILLOMAVIRUSES (cont.)

Type	Locus Name	"Old" Group	"New" Group	GenBank Locus Name	GenBank Accession	Region Sequenced	Page No.
HPV67	HPV67MY911	A	A9	HPU1249211	U12492	L1	(94) I-A-37
HPV68	HPV68ME180	C	A7	HUMHPVME18	M73258	LCR,E6,E7,E1,L1,L2	(94) I-C-17
HPV69	HPV69MY911	D	A5	HPU1249711	U12497	L1	(94) I-D-25
HPV70	HPV70	C	A7	HPU21941	U21941	Complete	(95) I-A7-47
HPV70	HPV70CP141	C	A7	HPU12476	U12476	L1	(94) I-C-20
HPV70	HPVL1AE1	C	A7	HPU01535	U01535	L1	(94) I-C-22
HPV70	HPV70LVX160	C	A7	HPU124860	U12486	L1	(94) I-C-23
HPV70	HPV70X11	C	A7	S42991	S42991	L1	
HPV72	HPV72	E	A3	HPVT72ELG	X94164	Complete	(96) I-15
HPV72	HPV72CP4173	E	A3	HPU124773	U12477	L1	(94) I-E-5
HPV72	HPV72LVX100	E	A3	HPU124850	U12485	L1	(94) I-E-11
HPV73	HPV73	B	A11	HPVT73ELG	X94165	Complete	(96) I-22
HPV73	HPVMM9	B	A11	HPU12491	U12491	L1	(94) I-B-27
HPV75	HPV75L1	H	B1	HPVS407	X79942	L1	(95) I-B1-214
HPV76	HPV76L1	H	B1	HPCR148	X79948	L1	(95) I-B1-215
HPV77	HPV77L1	F	A2	HPVS931	X79947	L1	(95) I-A2-23
?	HPVCP6108	E	A3	HPU124788	U12478	L1	(94) I-E-7
?	HPVCP8061	F	A	HPU124791	U12479	L1	(94) I-F-45
?	HPVCP8304	E	A3	HPU124804	U12480	L1	(94) I-E-9
?	HPVICPX1	H	B1	PPHL1AF	L38914	L1	(95) I-B1-206
?	HPVIS039	D	A5	HPU12481	U12481	L1	(94) I-D-26
?	HPVL1AE2	D	A5	HPU01532	U01532	L1	(94) I-D-27
?	HPVLVX82	E	A	HPU12487	U12487	L1	(94) I-E-12
?	HPVMM4	D	A5	HPU12488	U12488	L1	(94) I-D-28
?	HPVMM7	E	A	HPU12489	U12489	L1	(94) I-E-13
?	HPVMM8	E	A3	HPU12490	U12490	L1	(94) I-E-14
?	HPVRTRX1	H	B1	PPHL1AJ	L38918	L1	(95) I-B1-207
?	HPVRTRX2	H	B1	PPHL1AK	L38919	L1	(95) I-B1-208
?	HPVRTRX3	H	B1	PPHL1AL	L38920	L1	(95) I-B1-209
?	HPVRTRX4	H	B1	PPHL1AM	L38921	L1	(95) I-B1-210
?	HPVRTRX5	H	B1	PPHL1AN	L38922	L1	(95) I-B1-211
?	HPVRTRX6	H	B1	PPHL1AO	L38923	L1	(95) I-B1-212
?	HPVTogawa	H	B1	PPHL1FR	L38388	L1	(95) I-B1-213
?	HPVVS19L1	G	B2	HPDNACP1	X89876	L1	(96) I-21
?	HPVVS20L1	H	B1	HPVS204	X79941	L1	(95) I-B1-216
?	HPVVS42L1	H	B1	HPVS421	X79943	L1	(95) I-B1-217
?	HPVVS73L1	H	B1	HPVS731	X79944	L1	(95) I-B1-218
?	HPVVS75L1	H	B1	HPVS753	X79945	L1	(95) I-B1-219
?	HPVVS92L1	H	B1	HPVS921	X79949	L1	(95) I-B1-220
?	HPVVS102L1	H	B1	HPVS1024	X79946	L1	(95) I-B1-221
?	HPVVS200L1	H	B1	HPDNACP2	X89877	L1	(96) I-18
?	HPVVS201L1	G	B2	HPDNACP3	X89878	L1	(96) I-22
?	HPVVS202L1	G	B2	HPDNACP4	X89879	L1	(96) I-23
?	HPVVS203L1	G	B2	HPDNACP5	X89880	L1	(96) I-24
?	HPVVS204L1	G	B2	HPDNACP6	X89881	L1	(96) I-25
?	HPVVS205L1	G	B2	HPDNACP7	X89882	L1	(96) I-26
?	HPVVS206L1	G	B2	HPDNACP8	X89883	L1	(96) I-27
?	HPVVS207L1	G	B2	HPDNACP9	X89884	L1	(96) I-28
?	HPVX06	E	A3	S42984	S42984	L1	(95) I-A3-29

Table I-1 (cont.) Sequence List and Cross Reference for HPV Database

❷ ANIMAL PAPILLOMAVIRUSES

Type	Locus Name	"Old" Group	"New" Group	GenBank Locus Name	GenBank Accession	Region Sequenced	Page No.
BPV1	BPV1L1	I	C1	BPU23379	U23379	L1	
BPV1	BPV1R	I	C1	?	?	Complete	(95) I-C1-235
BPV1	BPV1	I	C1	PPBCG	J02044	Complete	(94) I-I-23
BPV2	BPV2	I	C1	PPB2CG	M20219	Complete	(94) I-I-28
BPV3	BPV3	I	D1	BP3ORF	X59062	L1,E8,E7,E1	
BPV3	BPV3L1	I	D1	BPU21862	U21862	L1	(95) I-D1-248
BPV4	BPV4	I	D1	PABPV4XX	X05817	Complete	(94) I-I-32
BPV5	BPV5L1	I	C	BPU21863	U21863	L1	(95) I-C-246
BPV6	BPV6	I	D1	BP6ORF	X59064	L1,E8,E7,E1	
BPV6	BPV6L1	I	D1	BPU21864	U21864	L1	(95) I-D1-249
CgPV1	CgPV1E1	I	A	MPAWART1	M64365	E1	(95) I-A-167
CgPV1	CgPV1L1	I	A	MPAWART2	M64366	L1	(95) I-A-168
COPV	COPV	I	E	PPHCG	L22695	Complete	(94) I-I-5
CRPV	CRPV	I	E	RAPRBFCG	K02708	Complete	(94) I-I-9
CRPV	PSU09494	I	E	PSU09494	U09494	E7	
DPV	DPV	I	C2	PPDCG	M11910	Complete	(94) I-I-18
EEPV	EEPV	I	C2	PPECG	M15953	Complete	(94) I-I-13
FPV1	FPV1L1	I	S	PPA12	K02020	L1	(95) I-S-257
FPV1	FPV1E1	I	S	PPA11	K02019	E1	(95) I-S-256
MmPV	MMPVE6	I	S	MMPVE6	X65200	E6	(95) I-S-258
MnPV	MnPV	I	S	U01834	U01834	Complete	(94) I-I-42
OvPV	OvPV	I	C2	OPU21861	U21861	L1	(95) I-C2-241
PCPV1	PCPV1	I	A10	PCPVT1DNA	X62844	Complete	(94) I-I-37
RhPV1	RhPV1	I	A9	RPLCG	M60184	Complete	(94) I-I-46
ROPV	ROPVL2	I	E	RAP02	M19498	L2	
ROPV	ROPVE2L2	I	E	RAP01	M19497	E2,E4,L2	
RPV	RPVE5E9	I	C2	S74218	S74218	E9	(95) I-C2-244
RPV	RPVE5	I	C2	PPRE5A	M18176	E5	(95) I-C2-243
RPV	RPVE5B	I	C2	PPRE5A	M18176	E5	
RPV	RPVE1L1	I	C2	PPRE5GA	M18175	E1,L1	(95) I-C2-242

Contents of Part I of *Human Papillomaviruses 1996*

PART I HPV Nucleotide Sequences and Some Variants

Contents of Part I of *Human Papillomaviruses 1995*

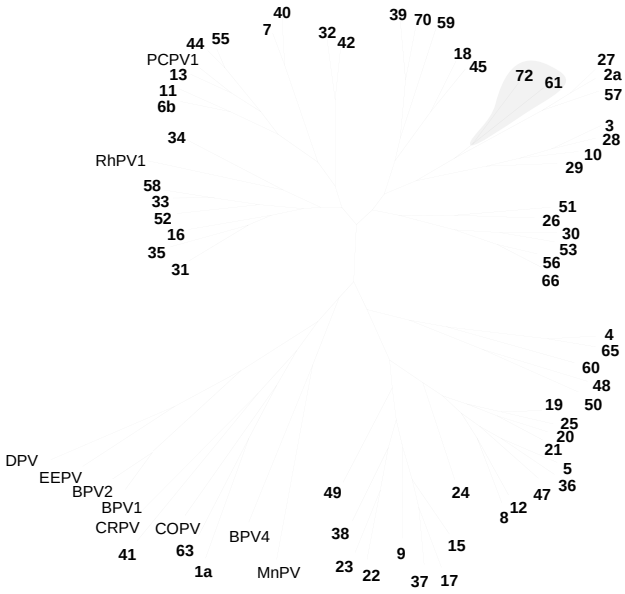
PART I HPV and Animal PV Nucleotide Sequences

PART I HPV and Animal PV Nucleotide Sequences

Group I Sequences

Group A3 Sequences

HPV61	**HPV62**
HPV72	**HPVCP4173**
HPVCP6108	**HPVCP8304**
HPVLVX100	**HPVMM8**
HPVX06	



INTRODUCTION

Group A3 comprises sequences CP6108, CP8304, MM8, HPVX06, and the types HPV61, HPV62 and HPV72. These viruses formed group E in the old classification. CP4173 and LVX100 are variants of type HPV72, based on their similarity over the My09-My11 region. HPVX06, an L1 fragment, is very similar, but not identical to HPV61 over this region. Viruses in this group primarily infect anogenital tissue, although the reference isolate of HPV72 was taken from an oral lesion [1], and have relatively unknown oncogenic potential and prevalence.

The reference isolate of HPV72 was obtained from an oral wart with atypia from an HIV positive patient in a study of 67 oral lesions from 58 patients [1].

Types HPV61 and HPV62 have been isolated from tissues with at least some degree of dysplasia. Both HPV61 and HPV62 have been derived from vulvar intraepithelial neoplasias [2].

The remaining isolates were obtained from cervical samples, with little information regarding relative risk/grade (or presence) of lesions available. CP4173, CP6108 and CP8304 were obtained through clinical studies conducted in the state of New Mexico among a tri-ethnic population [3]. LVX100 and LVX82 were isolated from an Amazonian Indian population [4]. MM8 was identified through studies conducted in the state of California. Initial prevalence data for MM8 are similar to that obtained for characterized "intermediate risk" viruses [5]. All samples were obtained from cervical lavages or genital swabs (CP6108 and CP4173 were isolated from normal cervices).

With the exception of HPV61 and HPV72, the members of Group A3 have been sequenced only over the My09-My11 fragment of L1. Phylogenetic analysis of the L1 region categorizes the group A3 viruses as a distinct group.

What's new?

The complete genomic sequence of HPV72 is presented on the following pages. HPV61 and HPVX06 were presented in *Human Papillomaviruses (HPV) 1995*, pp. I-A3-25 et seq. The sequences of the other members of this group were published in *HPV 1994*, pp. I-E-2 et seq.

References

[1] Volter, C., He, Y., Delius, H., Roy-Burman, A., Greenspan, J.S., Greenspan, D., and de Villiers,E.M. Novel HPV types present in oral papillomatous lesions from patients with HIV infection. *Int J Cancer* **66**(4):453–456 (1996)

[2] 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)

[3] Peyton,C.L. and Wheeler,C.M. Identification of five novel human papillomaviruses in the New Mexico triethnic population. *J. Infect. Dis*. **170**:1089–92 (1994)

[4] 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*. **170**:1086–8 (1994)

[5] 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* **170**:1096–99 (1994)

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LOCUS       HPV72        7988 bp    DNA             VRL       14-AUG-1996
DEFINITION  Human papillomavirus type 72 E6, E7, E1A, E1B, E2, E4, L2, and L1
            genes.
ACCESSION   X94164
NID         g1491683
KEYWORDS    E1A gene; E1B gene; E2 gene; E4 gene; E6 gene; E7 gene;
            early gene; L1 gene; L2 gene; late gene.
SOURCE      Human papillomavirus type 72.
  ORGANISM  Human papillomavirus type 72
            Viridae; ds-DNA nonenveloped viruses; Papovaviridae;
            Papillomavirus.
REFERENCE   1  (bases 1 to 7988)
  AUTHORS   Volter,C., He,Y., Delius,H., Roy-Burman,A., Greenspan,J.S.,
            Greenspan,D. and de Villiers,E.M.
  TITLE     Novel HPV types present in oral papillomatous lesions from patients
            with HIV infection
  JOURNAL   Int. J. Cancer 66 (4), 453-456 (1996)
  MEDLINE   96213783
REFERENCE   2  (bases 1 to 7988)
  AUTHORS   Delius,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-DEC-1995) H. Delius, Deutsches Kerbsforschungzentrum,
            Abt. ATV - 0686, Im Neuenheimer Feld 506, 69120 Heidelberg, FRG
COMMENT     The complete genome of HPV72 was isolated from a wart with atypia
            taken from an HIV positive patient in a study of oral lesions [1].
            The sequence of the E1 region below appears to contain a
            frame-shift mutation, leading to the identification of two ORFS,
            designated E1a and E1b by the authors [1].

            The isolates CP4173 (Peyton and Wheeler, J Inf Dis 170(5) 1089-92)
            and LVX100 (Ong, Bernard and Villa, J Inf Dis 170(5):1086-8),
            obtained from cervical samples, are variants of HPV72, as
            indicated by their MY09-MY11 sequences.

FEATURES             Location/Qualifiers
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     CDS             join(832..2142,2142..2783)
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                     GAVQEAEEERVGGDGEAQCSAQTQQTPERAADVLEIFKVSNLRVTLLHKFKELFGLAY
                     GDLVRQFKSDKSICGDWVVCAFGVYHAVAEAVKTLIQPICLYAHIQIQTCQWGMVILM
                     LVRYKCGKSRETVAHSMSTLLNIPEKQMLIEPPKIRSGPCALYWYRTAMGNGSEVYGE
                     TPEWIVRQTVVGHAMQETQFSLSTLVQWAYDNDITDESELAYDYAMLGNEDPNAAAFL
                     ASNCQAKYIKDAITMCKHYKRAEQARMSMTQWIAHRGRKVADSGDLREIVKYLRYQRV
                     EFVTFMGALKLFLKGVPKKSCMVFYGPSDTGKSLFCMSLLKYLGGAVISYVNSGSHFW
                     LSPLVDAKVGLLDDATYQCWQYIDTYLRTVLDGNAISIDRKHRNLTQLKCPPLMITTN
                     INPLEDQAFKYLHSRIVLFKFMHKCPLKSNGDPVYTLNNENWKSFFQRSWARIEGPDE
                     QEEEEDEDGSTSRPFRCVPGEIARPL"
exon                 832..2142
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mRNA                 832..2142
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                     /note="putative"
mRNA                 2142..2783
                     /partial
                     /gene="E1B"
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                     /gene="E1B"
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                     LYYEFQGQKQYYVTFGHEARKYGDTNTWEVHVGSTVIYEPCASVSSTQDTVREVPTVE
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                     TVHL"
CDS                  4409..5809
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                     LFTEPSIIEPPQAGDLSGHVFTSTPTSGSHSFEEIPMHTFATHSSTSTDPFSSTPLPG
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                     RKRVPYSFADGFVAAW"
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                     TSLLVADNSDSRDNVSVDYKQTQLLIIGCKPPIGEHWTKGTPCAGSNSQPTDCPPLEF
                     TNSTIQDGDMVETGYGAIDFATLQENKSEVPLDICTTTCKYPDYLQMAAEPYGDCMFF
                     CLRREQMFARHFFNRQGTMGEALPASLYLKGASGSDRVTPGSYIYSPTPSGSMVSSDA
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                     YLRHTEEFDLQFIFQLCKIHLTPEIMAYLHNMNKALLDDWNFGVVPPPSTSLDDTYRF
                     LQSRAITCQKGAATPPPKEDPYANLSFWTVDLKDKFSTDLDQFPLGRKFLLQVGSRAV
                     SVSRKRAAPPSSTSTPAPTKRKKRKK"
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                     VGHPYCAIPLNGQGKKNTIPKVSGYQYRVFRVKLPDPNKFALPDGTLYNPDTERLVWA
                     CRGIEVGRGQPLGVGTSGHPLYNRLDDTENTSLLVADNSDSRDNVSVDYKQTQLLIIG
                     CKPPIGEHWTKGTPCAGSNSQPTDCPPLEFTNSTIQDGDMVETGYGAIDFATLQENKS
                     EVPLDICTTTCKYPDYLQMAAEPYGDCMFFCLRREQMFARHFFNRQGTMGEALPASLY
                     LKGASGSDRVTPGSYIYSPTPSGSMVSSDAQLFNKPYWLQRAQGHNNGICWFNELFVT
                     VVDTTRSTNVTICTATASSVSEYTASNFREYLRHTEEFDLQFIFQLCKIHLTPEIMAY
                     LHNMNKALLDDWNFGVVPPPSTSLDDTYRFLQSRAITCQKGAATPPPKEDPYANLSFW
                     TVDLKDKFSTDLDQFPLGRKFLLQVGSRAVSVSRKRAAPPSSTSTPAPTKRKKRKK"
     misc_feature    832..2783
                     /gene="E1A and E1B"
BASE COUNT     2136 a   1705 c   1942 g   2205 t
ORIGIN
        1 attactaaca ataatacatg taaaaaagta agacaagACC GAAAACGGTc cgACCGACAT
                                        E2 bind  ->      E2 bind  ->
       61 AGGTacatat aTAAgggaac tgtgaactca gcaaatcagc aATGcctatg ggactgcaca
                         -> E6 ORF start               -> E6 cds start
      121 atccaactaa tatttggttg ctgtgcaagg aaattgaggt ggacctagaa gatttacgga
      181 ttacctgcat attttgcaaa aatgaattaa caacagaaga attgctggcg attgcaataa
      241 aggagctgca gattgtgtgg cgggacaact ggccatttgg agtctgcgca ccatgccttg
      301 caagagcaac taaagtgagg gagctacgat actggacgta ttcgggctac ggacccactg
      361 tggaacagga aacaggcaaa tcattagcag aactatatat aaggtgccat gcatgctgca
      421 aacccctaag ctgtcaggaa aaggaatatc aggtgcagac aggaatccac ttccacaaga
      481 taagcggact gtggacggga aggtgctgcc agtgTAGagg ggcATGcacg gccaggtggc
                                     E7 ORF start ->     -> E7 cds start
      541 aaccaTAAag gacattgtcc ttcaggaact tcctgatgtg gttgacctac actgcaatga
    E6 cds stop <-
      601 gcagttacta gacagctcag agtcagagtc agaggatgag agggacggtg ttggtgtgca
      661 ggagcaactt gtagaacaag cacagcaggc ctacggggtg gttactacct gtggcaggtg
      721 ctaccgtcca gtTAGgctgg tggtggagtg cagagacgca gacgtgaagg cgctacaaca
                          -> E1a ORF start
```

```
 781 actactgctg gacaatttgt ccatagtgtg tcctcgctgc gcataaggga cATGGCCAAc
                                                E1a cds start ->
                                                     NF1 bind ->
 841 tgcgaaggta ctgaacgggg ggatggggac gaggatgcga atcgcgcggg cggatggttt
 901 ttggttgagg ccatagtgga gcaaaccaca gggtaccaag agtccagtga tgaggacgaa
 961 aacagtgagg acaggggaga agatctggta gactttatag acacaagatc cttaggggat
1021 gggcaggaag tgccgttaga tttgttcgtg caacaaaatg cacgggatga cgctgcaacc
1081 gtgcaggccc taaaacgaaa gtatacatgt agcccagcaa gcagctcgtg tgtgtctttg
1141 gtggacagtg agttaagtcc ccgactggac gccataagca taaaccgggg acacgacagg
1201 gctagaagaa ggctgtttga ccaagacagt ggctatggcc atacgcaggt ggatattgga
1261 gcaccagaaa gccaggtatc ggggggtaca cagcatacaa agggggggagg cggcgccgtt
1321 caggaagcgg aagaggagcg tgtgggggggg gatggtgagg cgcagtgtag tgcacagaca
1381 cagcaaacgc cagagagagc agcagacgta ctagaaatat ttaaggttag taatttgcgt
1441 gtcacattac tgcataaatt taaagagcta tttggactag catatgggga tctggtaaga
1501 caatttaaaa gcgataaatc aatatgtggg gattgggtag tatgtgcatt tggggtatat
1561 catgcagtgg cagaggcagt aaagacgtta atacaaccca tatgtctgta tgcacatata
1621 caaatacaga cgtgtcaatg ggggatggta attttaatgc tggtgcggta taaatgtggc
1681 aagagtaggg agacagtggc acacagcatg agcacgctgc taaatatacc tgaaaagcaa
1741 atgcttattg aaccaccaaa aattagaagt ggaccatgtg ccctatactg gtatagaaca
1801 gcaatgggaa atggcagcga ggtgtacggg gaaaccccag aatggatagt aagacaaaca
1861 gtagtggggc atgcaatgca agagacacag tttagccttt ctaccttagt acagtgggca
1921 tatgacaatg acataacaga tgagagcgag ctagcatatg actacgcaat gctaggtaat
1981 gaggacccaa atgcagcagc atttttagca agcaactgcc aggcaaagta tattaaggat
2041 gcaattacaa tgtgcaaaca ttataaacgt gcagaacagg cacgaatgtc tatgacacag
2101 tggatagcac atagggggcg caaggtggca gattcaggTG AcTGAgagaa atagtaaaat
                                       E1a cds stop <-
                                                  -> E1b ORF start
2161 atttaagata tcaaagggtt gaatttgtaa catttatggg agcattaaag ctatttttaa
2221 aaggggtacc aaaaaaaagc tgtatggtat tctatggGCC AAgtgacacc ggaaagtcat
                                    NF1 bind ->
2281 tgttttgtat gagtttactt aagtatttag ggggagcagt aatttcatat gtaaattcag
2341 gaagccattt ttggttatca ccactggtag acGCCAAagt agggttgtta gatgatgcaa
                                NF1 bind ->
2401 cataccagtg ctggcaatat atagatacat acctacgaac agtgttagat ggaaatgcta
2461 taagcataga tagaaaacat agaaatttaa cacagttgaa gtgtccacca cttatgataa
2521 caacaaatat aaatccattg gaagaccagg catttaaata tttgcacagt agaatagtgt
2581 tgtttaaatt tatgcataag tgcccattaa aaagcaacgg tgatcccgta tataccctaa
2641 ataatgaaaa ttggaaatcg tttttccaaa ggtcctgggc acgtaTAGag ggacctgacg
                                                          -> E2 ORF start
2701 aacaggagga ggaggaggAT Gaggatggaa gcacTAGccg accgtttaga tgcgtgccag
                               E1b ORF stop <-
                          -> E2 cds start
2761 gagaaattgc tagaccttta tgaaaaagat agcgacaagc ttgaggacca aatattgcat
2821 tggcactatg tgcgtctgga acatgcaatg ttatttaagg cacgacaagc aggacttacc
2881 catgtaggcc accaggtggt accaacactt agtgttacaa aaggcaaagc acatcaggca
2941 attgaagtgc acctgtcact gcaagggttg caaaacagtg cgtatgcgca agaaccatgg
3001 acattacaga acacctcact ggaaatgtgg aatgcacACC CACAACGGTg ttggaagaaa
                                    E2 bind ->
3061 aaaggacgca caataacagt taaatttgat tgcgaggacc taaaagcagt ggagtatgtg
3121 agctgggggt gtatttatgt gcaaagtaca gaggacgaac agtggtataa agtacaagga
3181 catgtgtcat atcatgggct atattatgaa tttcagggtc agaaacagta ctatgtaaca
3241 tttggacacg aagccagaaa atatggggac acaaacacat gggaggtaca tgtgggaagt
3301 acagTGAttt ATGaaccctg cgcctctgta tctagcaccc aggacaccgt gcgagaagta
            -> E4 ORF start
                -> E4 cds start
3361 cccactgttg aaactgttgg gcgactgcca gacgccacca aatccaccgc caccgccacg
3421 tgcgtgggcc ccgcccagac atcctcctca gtgcagacgc cgccttgtaa gcgacagcga
3481 ctccacagag acggattgca gcagcagccc gactctacgg aaagagacat ctgcaggcaa
3541 cggcgtgaca gtgctgacca gtgggtcaac cgtgacagtg actgcacaca acaagcaagg
```

```
3601 gacatctgta acagtcacgg tgcacctaTA Atacatttaa aaggtgaacc aaataagtta
                         E4 cds stop <-
3661 aagtgttttc ggtataggct tcagcagtca gtgcctaact tgtttttaaa agcatcctct
3721 acatggcatt gggcctgtgg gggtgacaca acaaaatgtg catttgtaac actgtggtat
3781 gtggatactg accaacggac acaattttta agtcgtgtga acattccaaa ggggatacaa
3841 gccactgctg gctatatgtc aatgtgtata TAAtgtttgt tgcgatggca accagtgtat
                           E2 cds stop <-
3901 agaaccacac ctgcaacatt atgtaaggca gaagcaatcc tggatatact tgtgtgtttg
3961 atatctgggt ggtgtactgt gctgttgctg cttattattt tctggctttc ctatctttct
4021 gcactaagtg ctttttggt gtttgtgtgt gttatatatc taggattgtt ttgtatatat
4081 atgcaggtga tgtggtacat aggtgactta taatccaccc agccattaca tgctgctatt
4141 gtgtaaatag tgttccttgt gtatcttgta tgtaatatgt atcctgttgt agtgggcaat
4201 acggatgggg gtgcattaat tgtactacga gacgataatt gtggattgtg gttcttcttg
4261 tgtatgttaa taatcattgt agtgttgcta tataggttgc tacactgatc ccttcctttt
4321 gtgtattccc acctcctttt tatttttgtt ttgttttgtt tttgtttttt atttttttgc
4381 atttttataa TAAacattat ctGCCAAaAT Gacccaagct gtaaggcgtc gcaaacgtgc
                   -> L2 ORF start -> L2 cds start
                    NF1 bind ->
4441 ctctgcaacg gacctgtatc gcacatgcaa acaggcgggt acctgccctc ctgatgttat
4501 accaaaggtg gagggtgaca cccttgctga taggttcctg aagtgggcca gtttaggggt
4561 gttctttggt gggttaggca taggcacggg ttcaggcacc ggtgggcgca ctggctatgt
4621 gcctataggt actcgccctc ccactgttgt ggatataggc cctacaacac gcccgcctgt
4681 tgttattgag cccgtggggg ccgcagaccc ttccatagtc acccttgtgg aagaatccag
4741 cgttgtggaa gccggtgcca ccgttcccac ttttactggg tctggtggct ttgaggttac
4801 cacgtcctca actactaccc ctgctgtttt agacattaca ccctctggag cgtctgtcca
4861 agttagcagt agtagcttta caaatccctt atttactgaa ccgtccatta ttgaacctcc
4921 acaggccggg gacctttcag gccatgtatt cactagcaca cccacatctg ggtcgcatag
4981 ctttgaggaa atacccatgc acacatttgc aactcatagc agtactagca cagacccctt
5041 tagtagtacc cctttgcctg gtgttcgtcg ccttgcacag ccccgcttag gattgtatag
5101 caaggctaat caacaggtta gggttactaa ccctgccttt ttgtctcgac cccagtctct
5161 tgttacttat gacaaccctg tgtatgatcc agaggaaact attatttttg agcatcctag
5221 tatatatacc cctcctgatc ctgacttttt ggatattatt tccttacata ggcctgccct
5281 tacagcccgc cagggtacag tacgggtcag ccggttgggt caacgtgcta ccttgcgtac
5341 acgtagtggc aaacgcattg gcgctcgggt acacttttat caggacatta gccccatttc
5401 atctgatact attgaaatgc aatccttggc ctcctctacg cagccagaca taacatatga
5461 catttatgct gaccctgatt taggggaacc cccgccgcgt gcttctgtgt cttctacatc
5521 attgcacagc ccgtccctgt ctgcagcgtc tgctgtttct GCCAAgtatg acaatgtaac
                                        NF1 bind ->
5581 agttcccttg tcctTAGggc cacacatccc tgcctcctct ggccctgaca ttgatttgtc
                        -> L1 ORF start
5641 ctttgctcct gcccctgtac ctacaatgcc tcttgtaccc tctacgcatc cacattctat
5701 ttATGttgag ggctttgatt tttatttgtt gcctgcatat atctttttc ctaaacgtcg
       -> first ATG of L1 ORF
5761 taaacgtgtg ccctattctt ttgcagATGg ctttgtggcg gcctggTGAc ggcaaggtat
                                             L2 cds stop <-
                                   -> second ATG of L1 ORF
5821 acctgcctcc caatcctgtt tctaaggttc tcagtactga tcgctatgtc caacgcacca
5881 acctctatta ttatggtggc agttctcgtc tactaactgt aggacatcct tactgtgcca
5941 tacctctcaa cggacagggc aaaaaaaaca ccattcctaa ggtttcgggg tatcaataca
6001 gggtgtttag agtaaaactt cctgatccca ataaatttgc tttgcctgat ggcacacttt
6061 acaatccaga tactgaacgg ctggtatggg cctgtcgtgg cattgaggtt ggtaggggcc
6121 agccccttgg tgttggcact agcggtcacc ccttgtataa tcgcttggat gacactgaaa
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6241 aacagaccca attgcttatt atagggtgca agcctcccat tggtgagcat tggaccaagg
6301 gcactccttg tgcaggctct aattctcaGC CAActgactg ccccccttta gaatttacaa
                          NF1 bind ->
6361 attccactat acaggatggt gacatggtgg aaacaggcta tggtgccata gattttgcta
6421 cccttcagga aaataaatca gaagtgcctt tggatatttg caccaccacc tgcaaatatc
6481 ctgactattt gcaaatggct gctgaaccat atggtgattg tatgtttttt tgtcttcgca
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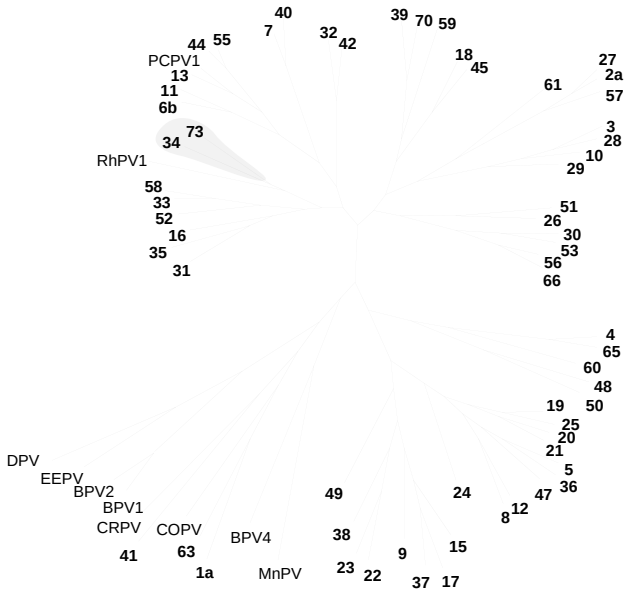
HPV72

```
      6541 gggaacaaat gtttgcacgc cattttttta ataggcaggg cacaatgggt gaggcactac
      6601 cagccagttt atatcttaaa ggtgcctcgg gtagcgacag ggtgacacct ggtagttata
      6661 tttattctcc cacccccagc ggctctatgg tgtcctctga tgcacaatta tttaataagc
      6721 cctattggct acagcgcgcc cagggtcaca acaatggcat ctgttggttt aatgagcttt
      6781 ttgtgacagt tgtagatact actcgcagta ctaatgtaac tatttgtact gccacagcgt
      6841 cctctgtatc agaatataca gcttctaatt ttcgtgagta tcttcgccac actgaggaat
      6901 ttgatttgca gtttatattt caactgtgta aaattcactt aactcctgaa attatggcct
      6961 acttgcacaa tatgaataag gccttattgg atgactggaa ttttggtgtg gtgcctcctc
      7021 cttctaccag tttggatgat acctataggt ttttgcagtc tcgtgccatt acctgtcaaa
      7081 agggggctgc cacccctcct cctaaagaag atccatatgc taacttatcc ttttggactg
      7141 tggatttaaa ggacaaattt tccactgact tggatcagtt tcctttaggg cgcaagtttc
      7201 tgttacaggt tggttctagg gctgtttcag tgtcacgcaa acgtgctgcc ccaccaagct
      7261 ctacctcgac ccccgcccct actaaacgta aaaagcgcaa aaagTAAcat gtcatactgt
                                              L1 cds stop <-
      7321 ttgtgtggtg tatgtgtgta tgtgtgcaat gcatgcatgt gtgtttctgt tgttgtttgt
      7381 gtgtacatgt ttgtactatg ttatgttgtt gtatgttttt tgtatggccc ctgcccccgt
      7441 gttgtgtatg tatgtggaat gtgtgttatg tgttgtgcat taataaagcg tgtgtcatgt
      7501 gtgtgtgtgt gtccggtgaa ccctgtgagt aagtgtgtgt ttgcacgttg tcctacttcc
      7561 tacactttgt tttgtgtcac ctttgtatgc cctttactgt actccatttt atattttctc
      7621 cattttgtat tcgcgACCGT TTTCGGTctc ccgccttttc ggtcgtggcg ccgtgccact
                  E2 bind ->
      7681 gtacatagaa actatgcatt gtgctttcct cccacatcct gtttcaacaa accttatcca
      7741 catctgggtg tgcctgacag gtttctggca catacatttt ccatagttat gtgtttcctg
      7801 actcatttta caatagatat gcttttaggc acatatttta tgctgactac tttctcctaa
      7861 ttgctgtttt ggctACCTTT CTAGGTgttg taGCCAAgta tgtgtcttgc aactatgggc
                 E2 bind ->        NF1 bind ->
      7921 aagcccttta caaacgtgtt aaaacattct actccggtcg ctcccctatg tctcatggtt
      7981 ttatagtt
//
```

Group A11 Sequences

HPV34 HPV64
HPV73/MM9



INTRODUCTION

Group A11 is made up of three viruses (HPVs 34, 64, and 73) formerly placed in old Group B; the sequence HPVMM9 has been found to be a variant of HPV73. The group is primarily associated with orogenital lesions of low oncogenic potential.

These viruses have been predominantly linked to anogenital lesions. HPV34 was initially isolated and cloned from a squamous cell carcinoma of Bowen's type and subsequently detected in a genital intraepithelial neoplasia and periungual Bowen's disease [1]. A study which probed lesions with Bowen's disease and squamous cell carcinomas for HPV34 DNA, reported only one case of positive hybridization, indicating that HPV34 infection of this nature is relatively rare [1]. HPV64, a recently identified virus, was cloned and isolated from a vulvar intraepithelial neoplasia [2]. MM9 was derived from a genital swab specimen. Initial prevalence data for MM9 is similar to that obtained for characterized "intermediate-risk" viruses [3]. It was observed in 6 cancers (0.6%) in the IBSCC study [4], where it is referred to as PAP 238a. The reference isolate of HPV73 was obtained from an oral wart with atypia from an HIV positive patient in a study of 67 oral lesions from 58 patients [5].

What's new?

The complete genome of HPV73 is presented on the following pages. The sequences of other members of this group were published in *Human Papillomaviruses 1994* pp. I-B-19, 26, 27, and I-I-37.

References

[1] Kawashima,M., Jablonska,S., Favre,M., Obalek,S., Croissant,O., and Orth,G. Characterization of a new type of human papillomavirus found in a lesion of Bowen's disease of the skin. *J Virol* **57**:688–92 (1986)

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

[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* **170**:1096–99 (1994)

[4] Bosch, F.X., Manos, M.M., Munoz, N., Sherman, M., Jansen, A.M., Peto, J., Schiffman, M.H., Moreno, V., Kurman, R., Shah, K.V., International Biological Study on Cervical Cancer (IBSCC) Study Group. Prevalence of human papillomavirus in cervical cancer: a worldwide perspective. *J Natl Cancer Inst* **87**:796–801 (1995)

[5] Volter, C., He, Y., Delius, H., Roy-Burman, A., Greenspan, J.S., Greenspan, D., and de Villiers,E.M. Novel HPV types present in oral papillomatous lesions from patients with HIV infection. *Int J Cancer* **66**(4):453–456 (1996)

```
LOCUS       HPV73        7700 bp    DNA             VRL       14-AUG-1996
DEFINITION  Human papillomavirus type 73 E6, E7, E1, E2, E4, L2, and L1 genes.
ACCESSION   X94165
NID         g1491692
KEYWORDS    E1 gene; E2 gene; E4 gene; E6 gene; E7 gene; early gene; L1 gene;
            L2 gene; late gene.
SOURCE      Human papillomavirus type 73.
  ORGANISM  Human papillomavirus type 73
            Viridae; ds-DNA nonenveloped viruses; Papovaviridae;
            Papillomavirus.
REFERENCE   1  (bases 1 to 7700)
  AUTHORS   Volter,C., He,Y., Delius,H., Roy-Burman,A., Greenspan,J.S.,
            Greenspan,D. and de Villiers,E.M.
  TITLE     Novel HPV types present in oral papillomatous lesions from patients
            with HIV infection
  JOURNAL   Int. J. Cancer 66 (4), 453-456 (1996)
  MEDLINE   96213783
REFERENCE   2  (bases 1 to 7700)
  AUTHORS   Delius,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-DEC-1995) H. Delius, Deutsches Kerbsforschungzentrum,
            Abt. ATV - 0686, Im Neuenheimer Feld 506, 69120 Heidelberg, FRG
COMMENT     The complete genome of HPV73 was isolated from an oral wart with
            atypia taken from an HIV positive patient in a study of 67 oral
            lesions from 58 patients [1].

            The isolate MM9 (Manos et al, J Inf Dis 170(5) 1096-9), obtained
            from a cervical sample, is a variant of HPV73, as indicated by its
            MY09-MY11 sequence.

FEATURES             Location/Qualifiers
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                     /note="early gene, putative"
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                     /db_xref="PID:g1491693"
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                     LVLVRFKCNKNRLTVQKLLSSLLNVTQERMLIEPPRLRSTPCALYWYRTSLSNISEIV
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BASE COUNT     2570 a   1269 c   1522 g   2339 t
ORIGIN
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       1 actataatgt actattaaaa aaaagggtgT AACCGAAAAC GGTttcaACC GAAATCGGTg
                                         -> E2 bind        -> E2 bind
                                           -> E6 ORF start
      61 catataaaag taggaaagca aaaaacgcta cagattggga aATGctgttt cccaattcag
                                                      -> E6 cds start
     121 aagaacgacc atacaagcta caagcgttat gtgacgaagt gaatatttct atacatgata
     181 taaacctgga ctgtgtgttt tGCCAAcgtg gactgtacag atctgaggta tatgattttg
                               -> NF1 bind
     241 catttagtga tttgtgtatt gtatatagaa aggataaacc atatggtgta tgtcaaccgt
     301 gtttaaaatt ttattctaaa attagagagt ataggcgata tagacaatca gtatatggca
     361 ctacgttaga aaatttaact aacaaacagt tatgtaatat tttaataagg tgcggaaaat
     421 GCCAAaaacc attatgtcca ctggaaaagc aaaagcatgt agatgaaaaa aaacggtttc
         -> NF1 bind
     481 atcaaaTAGc agaacagtgg accggacgct gtacacggtg ctggagacca tctgcaactg
                 -> E7 ORF start
     541 tggtgTAAgA TGcatggaaa aaaaacaacc ttgcaggaca ttactttaga cctgaaacca
 E6 cds stop  <- -> E7 cds start
     601 acaaccgaaa ttgaccttac atgttacgag tcattggaca actcagagga tgaggatgaa
     661 acagacagcc atctagacag acaagctgaa cgagagtgtt acagaatagt tactgactgc
     721 acgaagtgtc agtgcacagt atgccttgcc attgaaagca acaaagctga tttaagagtg
     781 atagaagagt tgcttatggg tacactaggt attgtgtgcc ccaactgttc cagaaaccta
     841 TAAaagaagA TGgctgattc aggtaattgg gaagggaggt gtacgggatg gtttaatgta
          <-      -> E1 cds start
E7 cds stop
           -> E1 ORF start
     901 gaagccattg tagaaagaaa aacaggggat ccaattccag aggatgaaaa ttatgatgga
     961 ggggatacag atgagtcgga aatgggggat tttattgata atgcacatat accaaatata
    1021 tatgcacaac aggaaattgc acaggcattg tatcagtcac agcaagcaaa tgcagacaat
    1081 gaggctatac gtgttctaaa acgaaagttt acaggtagtc ctggcggtag cccagatatg
    1141 aaaagagatg aattcataga caaacagctt agtccacaaa taaatgtatt gtcaataagt
    1201 agcggtagaa gtacatctaa acgaagactg tttgaggagc aggacagtgg atatggcaat
    1261 actgaagtgg aaacttacga gacagaggta ccgggacttg gggcaggggt agggtgttta
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    1381 agtagcattt caaatatgga tatagaaaca gagagcacac ctataacaga tattacaaat
    1441 ttattacaaa ggaataatgc aaaagcagca ttgctagcaa aatttaaaga agtatatggg
    1501 ttaagttata tggaattagt tagaccatat aaaagtgata aaacacattG CCAAgattgg
                                                            -> NF1 bind
    1561 gtgtgtgctg tgtttggtgt aataccctca cttgcagaaa gtttaaaatc cttactaaca
    1621 cagtattgta tgtatataca tttgcagtgt ttaacatgta catggggcat aatagtgtta
    1681 gtattagtaa gatttaagtg caataaaaat agactaacag tgcaaaaatt attaagtagt
    1741 ttattaaatg taacacaaga acgcatgtta attgaacctc caagactacg aagtacacca
    1801 tgtgcattat attggtatag aactagttta tcaaatatta gtgaaatagt aggagacaca
    1861 cctgagtgga ttaaaagaca aacgttagtg cagcatagtt tagatgatag tcaatttgac
    1921 ctatctcaaa tgatacagtg ggcatttgat aatgatataa cagacgactg tgaaatagca
    1981 tataaatatg cattattagg caatgtagac agtaatgcag ctgcattttt aaaaagtaat
    2041 gcacaagcaa aatatgtaaa agactgtggt acaatgtgca gacattataa agcagcagaa
    2101 cgtaaacaaa tgtcaatggc acaatggata caacatagat gtgatttaac taatgatggt
    2161 ggtaattgga aagatattgt gctattccta agatatcaaa atgtagaatt tatgcctttt
    2221 ttaattacat taaaacaatt tttaaaaggt attcccaaac aaaactgtat agtattatat
    2281 ggaccgccag atacaggaaa atcacatttt ggaatgagtt taattaaatt tatacaaggt
    2341 gtagttattt cgtatgtaaa ttcaactagt cattttggt tatcaccctt agctgatgca
    2401 aaaatggcat tattagatga tgcaacacct ggatgctgga cgtacataga caaatattta
    2461 agaaatgcat tagatggtaa tcctatatgt ttagatagaa aacataaaaa tttattacaa
    2521 gttaaatgcc ctccattact gataacatca aatacaaatc ctaaagcaga tgatacttgg
    2581 aaatatttac atagtagaat taaggtgttt actttttaa atccatttcc atttgacagt
    2641 aatgggaacc cactatacca acttactaat gaaaactgga aagcattttt tacaaaaacg
    2701 tggtcaaaac tagattTAAc agaggacgac gacaaggaaa ATGatggaga cactgtgcaa
                           -> E2 ORF start         -> E2 cds start
    2761 acgtttaagt gcgtgtcagg acgcaatcct agaactgtaT GAacgtgaca gtgtacacct
```

```
                                    E1 cds stop <-
2821 aagtgatcat attgatcatt ggaaacacgt gcgacatgaa aatgtattat tacataaagc
2881 acgtgaaatg ggactgcaaa ctgttaacaa tcaagcggtG CCAAgccttg cagtatcacg
                                                -> NF1 bind
2941 atccaaaggg tataatgcaa ttgaaatgca aatagcacta gaaagtttaa atgaatcttt
3001 gtataacaca gaggaatgga cattgcaaca tacaagttgg gaactgtggg ttacagaacc
3061 taaacaatgt tttaaaaagg atggaaaaac agtagaggtt agatatgact gtgaaaagga
3121 caatagcatg caatatgtat tttggacaca tatatattgt tggtatgaag gggggtgggc
3181 aaaggtaggt agcaaaatag attataatgg tatatattat gaaacagatg atgaggaaaa
3241 ggtatactat acaagatttg atacagatgc aaaacggtac ggggtaaaag gcatatggga
3301 agtacatatg ggtggtcagg TAAtatgttg tgctcctgta tctagcgcct gtgaagtatc
                               -> E4 ORF start
3361 cattcctgaa attgttaacc cactgcacac cacaaccacc aacaccacca ccacctgcac
3421 caacgttgac accggtgtgc catcacggaa acggcaaaga cagtgtgact cggaccagag
3481 gcccctggat tgtttgcata acctacatcc caccacagag tcctgtaccc agtgtactac
3541 acataatgtt gcGCCAATAG tgcatttaaa aggtgacaaa aacagcttaa aatgttttag
                  -> NF1 bind
            E4 ORF stop <-
3601 atatagattg cataaaggct attcacattt atttaaaaat gtaacaacaa catggcattg
3661 gaccaatact acaaatagta aatgtggtgt aataacatta atgtttacaa ctgtattgca
3721 acaacaacat tttttacaac atgtaaaaat accacaaact attgtagtta catcaggata
3781 catgtctttg TAAcattggt tacacagtat atatgattct ttgtatattt gtatttttgt
     E2 cds stop <-
3841 tttgtgttgg cttttgtttg tgcttgtgtg tgtcgcttgc agtgtctgtg tatatttacc
3901 catggttatt ggtattgatt ataataacct ttatacatgt atcacaatca ttgttaaaag
3961 tatttttttt atatgttttg gtatttata ttcctatggc acttgtacat taccatgcta
4021 cattacaaat aacataaaca attttacata tataataaac tgcctaatat tttTAGtgta
                                                                    ->
                                                                  L2 ORF start
4081 ccATGcgtcg caagcgtgac acacacatac gaaaaaaacg tgcatctgca acacaattat
       -> L2 cds start
4141 ataaaacatg taaacaagca ggtacgtgcc ctcctgatgt aattcccaag gttgaaggta
4201 gtactatagc tgataatata ttaaaatatg gtagtattgg agttttttt gggggattgg
4261 gaataggtag tgggtctgga tcaggggggc gtactggata cgttccatta tctacaggca
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4381 ttgggccttc agattcttct attgtttcat tagtggaaga atcaagtttt atagagtcag
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5161 atgatgggtt atatgatgtg tttttagaca atgatgtaga agagactgta ctacaacaaa
5221 catatacacc tacaagtata catagtaata gtttagttag tagtgatatt tctactgcaa
5281 ctgcaaatac aactattcct tttagtactg ggttagacac acatcctggt ccagatattg
5341 ctttaccact accttctaca gaaactattt ttacaccaat agtgccatta cagcctgctg
5401 gtcctatata tatttatggg tcaggtttta tattacaccc tagttattat ttgtTAAagc
                                                                      ->
                                                                    L1 ORF start
5461 gcaaacgtaa acgtctgtca tattctttta cagATGtggc gacctacTGA tgcaaaggta
                                                L2 cds stop <-
                                           -> L1 cds start
5521 tacctgcccc ctgtgtctgt gtctaaggtt gtaagcacag atgaatatgt aacaagaaca
```

```
5581 aatatatatt attatgcagg tagcacacgt ttgttggctg tgggacaccc atattttcct
5641 atcaaggatt ctcaaaaacg taaaaccata gttcctaaag tttcaggttt gcaatacagg
5701 gtgtttaggc ttcgtttacc agatcctaat aaatttggat ttccagatgc atccttttat
5761 aatcctgata aggagcgcct agtatgggcc tgttctggtg tggaggttgg acgtggacaa
5821 cccttaggta taggtactag tggcaatcca tttatgaata aattagatga tactgaaaat
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6361 tatcctacac ctagtggttc catggtttct tcagatgcac agttgtttaa taaaccttat
6421 tggttgcaaa aggcacaggg acaaaataat ggtatttgtt ggcataatca attattttta
6481 actgttgtag atactactag aagcactaat ttttctgtat gtgtaggtac acaggctagt
6541 agctctacta caacgtatGC CAActctaat tttaaggaat atttaagaca tgcagaagag
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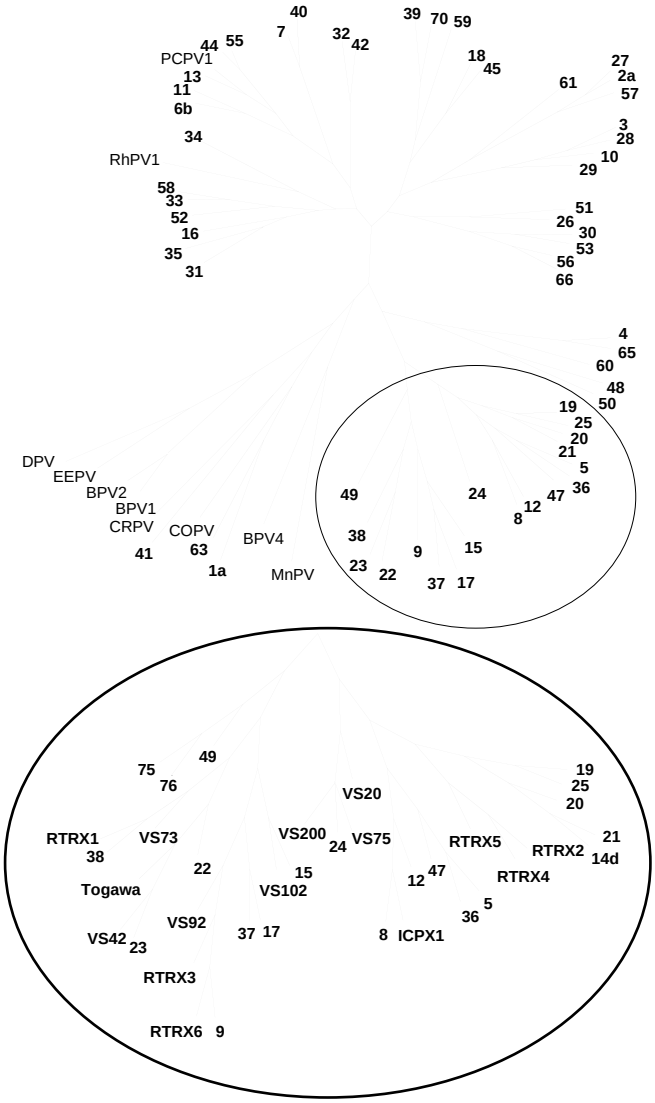
6601 tttgatttac agtttgtttt tcagttatgt aaaattagtt taactactga ggtaatgaca
6661 tatatacatt ctatgaattc tactatattg gaagagtgga attttggtct taccccacca
6721 ccgtcaggta ctttagagga aacatataga tatgtaacat cacaggctat tagttGCCAA
                                                                -> NF1 bind
6781 cgtcctcaac ctcctaaaga aacagaggac ccatatGCCA Agctatcctt ttgggatgta
                                             -> NF1 bind
6841 gatcttaagg aaaagttttc tgcagaatta gaccagtttc ctttgggaag aaaatttta
6901 ttacaacttg gtatgcgtgc acgtcctaag ttacaagctt ctaaacgttc tgcatctgct
6961 accacaagtg ccacacctaa gaaaaaacgt gctaaacgta ttTAAtaagt gtaatgtgta
                                       L1 cds stop <-
7021 tgtgttgttt gttgtatgtt acatgtgttt tgtatgtttg tttgttgtat gttaactgtt
7081 tactaatact gtgtgtatgt ttatgtacat gtgtataact gtttgtttat atatatgtat
7141 gtatttgtgt gtatgtgtat gtgtatgtgt atgtgtagta atgtttgtat gtatgtttaa
7201 taaagtttat atgtgtgttg tgtgggtggt ttacttgact actgtgcttc cattttgtat
7261 agtcgccatt ttacatgcat taaggtaaaa agggcaACCG ATTTCGGTtg cacagtaaaa
                                             -> E2 bind
7321 catgttttaa tgtgttttgc tgttgtagca aaatagttgt actgtttttg gcttcctgca
7381 ggcaacttgg cagggtttgt ttccttaaca tgttcatccc acgcaaggtt ataaaggtaa
7441 aaggcgccac ctggcagtta ctcatttgtc tgcaattatt taaacaatgt cttgcacaca
7501 catttttac ccaccctatc ataaaattgc ttttaagcac atacctatac tatgtacaca
7561 gtgtactctt ggcagaacat tgtttttttaa atGCCAAgta attgttttat aaatgagtaa
                                       -> NF1 bind
7621 taacgtgtta ctcatactgc acctaaaaag ttaaacctat ttggatcaca caaatGCCAA
                                                                -> NF1 bind
7681 tttatttctt attacaaata
//
```

Group B1 Sequences

HPV5	**HPV8**
HPV9	**HPV12**
HPV14d	**HPV15**
HPV17	**HPV19**
HPV20	**HPV21**
HPV22	**HPV23**
HPV24	**HPV25**
HPV36	**HPV37**
HPV38	**HPV47**
HPV49	**HPV75 (VS40)**
HPV76 (CR148)	**HPVICPX1**
HPVRTRX1	**HPVRTRX2**
HPVRTRX3	**HPVRTRX4**
HPVRTRX5	**HPVRTRX6**
HPVVS20	**HPVVS42**
HPVVS73	**HPVVS75**
HPVVS92	**HPVVS102**
HPVVS200	**HPVTogawa**



What's new?

The sequence of a putative new type, HPVVS200, is presented following this introductory material. VS200 was isolated from a non-immunocompromised patient in a study of non-melanoma carcinomas of the skin [5a]. More details on the study are given in the introduction to group B2 on page I-33.

INTRODUCTION

Group B1 viruses composed the old group H and are primarily associated with the multifactorial disease Epidermodysplasia Verruciformis (EV). Recent work suggests they are also commonly associated with immunosuppressed renal transplant recipients [1,2]. Several isolates which appear to constitute new types have been found in skin lesions of renal transplant patients [5,6]. Association of EV-related HPV types with squamous cell carcinomas (SCC) of the skin, and with SCCs of the esophagus has recently been suggested [3,4,5,7,27]. Two potential new types have been isolated from immunocompetent patients [5,5a].

Patients with EV tend to have depressed cell-mediated immunity [8]. In roughly one-third of EV-associated HPV infection, the sun-exposed flat wart-like or macular lesions transform into malignant squamous cell carcinomas [9]. Benign wart scrapings tend to be multiply-infected, with as many as six different viral types. However, in contrast, EV carcinomas tend to harbor only a few types, specifically HPV-5 and HPV-8, and less frequently HPV-14, HPV-17, HPV-20 and HPV-47 [9,10]. These types are rarely detected in lesions afflicting the general population. A key to host restriction of these viruses may be in part due to the unusual organization of the LCR in these viruses. The LCR of these viruses is short compared to the viruses in other groups; most of the types in this group also contain two EV-specific regulatory regions: M33 and M29, both shown to be involved in protein binding [10,11,12]. Study of variants of HPV5 and HPV8 has revealed a higher level of sequence diversity within these types [13,14,15] than has been observed in primarily mucosal types such as HPVs 6, 11, 16 and 18 [16,17,18], suggesting that the EV-related types may accumulate mutations at a higher rate.

One possible explanation for this is that the cutaneous tropism of the EV types could lead to additional mutations through UV-induced DNA damage; however, sequencing of variants of primarily cutaneous HPV2 show levels of variability comparable with that seen in the mucosal types [19].

This group forms two major branches based on phylogenetic analysis, each of which can be subdivided into two minor branches. These clusters have been designated as a_1, a_2, b_1, and b_2. This phylogenetic classification is compatible with other classifications based on hybridization [21], transforming activity of the E6 gene [20], and conservation of the M33 and M29 regions and E2 binding sites in the LCR [11]. In addition, HPV-24, HPV-49, and several of the new sequences seem to form isolated branches, which may be related with their detection in immunosuppressed, non-EV patients.

Cluster a_1 consists of HPV-5, HPV-8, HPV-12, HPV-36 and HPV-47; the available sequence of HPVICPX1 suggests that it too is a member of this cluster. Both HPV-5 and HPV-8 are associated with macular lesions which frequently progress to malignancy [22,23,24]. Yabe et al. studied the characteristics of HPV-5 in lesions of differing severity. In a primary carcinoma, HPV-5 was present in an episomal state with a 40% subgenomic segment amplified. In the metastatic tumor, only the 40% subgenomic region was present, but integrated into the host genome [24]. The segment was determined to be the entire sequences of E6, E7, and the noncoding region and portions of E1 and L1, with no mutations present [25]. In addition, amplifications of the LCR have been reported in HPV-5 associated carcinomas [26]. HPV-5 and HPV-8 have also been found in significant numbers in squamous cell carcinomas of renal allograft patients. Barr et al. detected either HPV-5 or HPV-8 in nearly 60% of the cases surveyed in Scotland [27]. HPV-47 is primarily associated with benign lesions; however, it has also been detected in cases of malignancy [20]. HPV-12 induces benign macular and flat wart-like lesions [28]. HPV36 was isolated from two patients with actinic keratosis. HPVICPX1 was isolated from an immunocompetent patient [5]; other information is not currently available.

Cluster a_2 consists of HPV-14, HPV-19, HPV-20, HPV-21 and HPV-25. HPV types forming this cluster produce benign macular or flat wart-like lesions and malignant lesions in isolated cases. Both HPV-19 and HPV-25 induce macular lesions, which are benign in character [21,20,29]. HPV-14, HPV-20 and HPV-21 induce flat-wartlike lesions; HPV-20 and HPV-14 have been detected in carcinomas [20,29].

Cluster b_1 includes of HPV-9, HPV-15, HPV-17, and HPV-37; available sequence indicates that HPVRTRX3, HPVVS92 and HPVVS102 are also members of this cluster [5,6]. HPV-15 was isolated from a benign flat wart-like lesion [29]. HPV-17 was isolated from benign macules and subsequently from squamous cell carcinomas and the malignant melanoma of an immunosuppressed patient [29,30]. HPV 9 DNA induces both macular and flat wart-like lesions, however it has also been identified in a keratoacanthoma [28,31]; HPV-37 was found in the same keratoacanthoma. HPVRTRX3, HPVVS92, and HPVVS102 were isolated from a squamous cell carcinoma, skin wart, and dysplastic wart respectively in renal transplant patients [5,6]. Also possibly belonging to this cluster is HPVRTRX6, although its position in phylogenetic trees is rather unstable. HPVRTRX6 was isolated from an SCC in one renal transplant patient [5].

Cluster b_2 includes HPV-22, HPV-23, and HPV-38; available sequence indicates that HPVRTRX1, the Togawa isolate, HPVVS42 and HPVVS73 are also members of this cluster. HPV-22 and HPV-23 were isolated from macules of EV patients [29]. HPV-38 was isolated, along with HPV17a, from a superficial spreading melanoma in an immunocompromised patient [31]. The Togawa isolate was found in multiple SCCs of the esophagus in nonimmunocompromised patients [7]. HPVRTRX1, HPVVS42 and HPVVS73 were isolated from an SCC, a verrucous biopsy and a skin wart biopsy in renal transplant patients [5,6].

Isolated types Several EV-related types or potential new types seem to be relatively unrelated to the clusters defined above, and, for the most part, to each other. HPV-49 was isolated from the flat warts of a Polish renal transplant patient. Favre et al. screened benign and malignant lesions from the general population, EV patients and transplant patients for the presence of HPV-49. In the survey, HPV-49 was not detected in any of the patients with EV but was detected in two additional cases of flat warts in renal transplant patients [32]. Related to HPV49 are HPV-75 (VS40) and HPV-76 (CR148), from a dysplastic wart biopsy and a skin wart biopsy, respectively, from renal transplant patients [6].

HPV-24 was isolated from macules in an EV patient [29]. HPVVS75 and HPVVS20 appear to be relatively closely related to HPV24, and were isolated from skin wart biopsies of renal transplant patients [6]. HPVVS200, isolated from a basal cell carcinoma of a nonimmunosuppressed patient [5a], is most similar to HPVVS75 and HPV-24.

HPVRTRX2, HPVRTRX4, and HPVRTRX5 appear to form their own cluster, and were all isolated from cutaneous SCCs of renal transplant patients [5]. HPVRTRX2 and HPVRTRX5 were each isolated from one SCC in each of two patients, and HPVRTRX4 was isolated once, out of 53 SCCs from 26 renal transplant patients.

HPV-5, HPV36 and HPV-47 are close enough to each other to be considered "close types"—sequences that qualify to be distinct types under the criterion of ten percent dissimilarity at the nucleotide level, but between which most of these changes are "silent", causing no difference at the amino acid level (Part III). Also qualifying as close types are HPV-19 and HPV-25, and HPV-14d, HPV-20f and HPV-21.

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HPVVS200L1

```
LOCUS       HPVVS200L1    422 bp    DNA             VRL       30-APR-1996
DEFINITION  Human papillomavirus DNA for capsid protein L1 gene (clone
            vs200-1).
ACCESSION   X89877
NID         g1296539
KEYWORDS    capsid protein L1.
SOURCE      Human papillomavirus.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   Shamanin,V., Zur Hausen,H., Lavergne,D., Proby,C., Leigh,I.,
            Neumann,C., Hamm,H., Goos,M., Haustein,U.F., Jung,E., Plewig,G.,
            Wolff,H. and de Villiers,E.M.
  TITLE     HPV infections in non-melanoma skin cancers from renal transplant
            recipients and non-immunosuppressed patients
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 422)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1995) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 422)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1996) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
COMMENT     The partial sequence of clone vs200-1 suggests that
            it constitutes a previously unidentified HPV type. Its
            sequence is most similar to those of HPVVS75 and HPV24, making it
            a new member of group B1.  It was isolated from a basal cell
            carcinoma of a nonimmunosuppressed patient as part of a study
            of nonmelanoma carcinomas of the skin.

            NCBI gi: 1296539
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  L1 cds ->
         <-    PCR primer   ->
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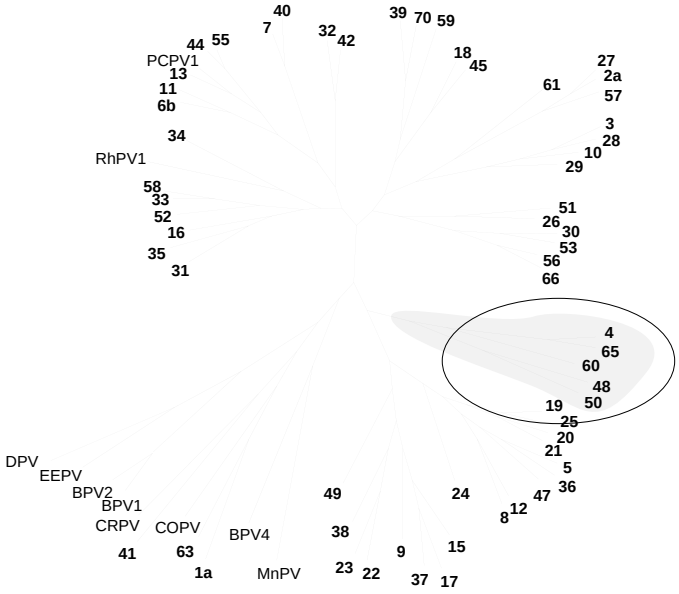
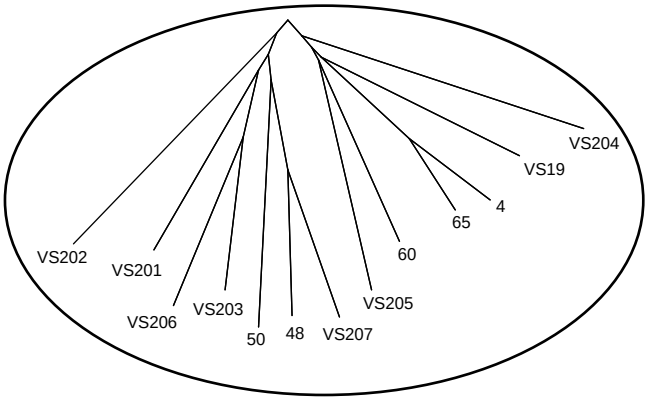
      121 ttgaagatgc aaaatgatgt ttatggagac tcctgtttct tttttgctcg tagagagcaa
      181 tgttatgcca gacacttttt tgtaagaggt ggcaacgtag gggatgacat tcctggtgaa
      241 caaatagacg caggcacata taaaaatgat ttttacattc caggagcatc aggtcagaca
      301 caaaataaaa taggtaactc catgtatttc ccaacagtta gtggctcatt agtgtctagt
      361 gatgctcagc tgtttaatag gccctactgg ctccaacgcg cacagggcca caacaacggc
      421 gt                                                 <-   PCR primer
           ->
     L1 cds ->
//
```

Group B2 Sequences

HPV4	**HPV48**
HPV50	**HPV60**
HPV65	**HPVVS19**
HPVVS201	**HPVVS202**
HPVVS203	**HPVVS204**
HPVVS205	**HPVVS206**
HPVVS207	





INTRODUCTION

Group B2 is equivalent to part of the old group G. It consists of the human papillomaviruses HPV-4, HPV-48, HPV-50, HPV-60, and HPV-65, a group primarily associated with the benign cutaneous lesions, commonly seen in the general population. HPV-50 is the only member of this group associated with EV lesions. A number of apparent new types belonging to this group have recently been isolated [1], and partial sequences are presented below.

HPV-4, in conjunction with HPV-1 (group E1) and HPV-2, (group A4) are the major etiological agents of benign cutaneous papillomas in the general population. HPV-1 is primarily associated with deep palmoplantar warts, while HPV-4 has been correlated with common warts and keratotic flat lesions on the hands and feet [2,3]. HPV-4 is also frequently present in hand warts of meat handlers [4]. HPV-65 has been linked to pigmented common warts and keratotic flat lesions [3].

HPV-4 and HPV-65 produce homogeneous intracytoplasmic inclusion bodies in most infected epidermal cells. The inclusion bodies primarily contain E4 proteins that can be used to histologically identify these viruses.

The primary target tissue of the Group B2 viruses is the epithelium, however rare mucosal infection has been reported for HPV-4, which has been identified in isolated cases of both normal and malignant oral lesions [5].

What's new?

Partial L1 sequences for VS19, VS201, VS202, VS203, VS204, VS205, VS206, and VS207 are given on the following pages. These putative new types were isolated as part of a a study of nonmelanoma carcinomas of the skin, involving samples from 20 squamous cell carcinomas (SCC), 5 basal cell carcinomas (BCC), and 4 carcinomas in situ (CIS) from 11, 4 and 4 renal allograft recipients (RARs) respectively, as well as an additional 26 SCC, 11 BCC and 4 karatoakanthoma from 19, 9 and 4 nonimmunosuppressed patients. Specimens were subjected to degenerate primer PCR as well as PCR with several less degenerate sets of primers. The more degenerate primer system led to the isolation of HPV DNA from many of the RAR samples (8/20 SCC; 1/4 CIS); the remaining samples gave faint signals or none at all. The less degenerate primers led to the isolation of HPV DNA in an additional 5 SCC samples (for a total of 13/20), 3 BCCs (for 3/5), and an additional 2 CIS (3/4). Faint signals were found in the remaining 7 SCCs and 2 BCCs, reflecting either very weak amplification of distantly related HPVs or nonspecific amplification of cellular sequences. The less-degenerate primer systems

also led to isolation of HPV DNA in 8/25 SCCs and 4/11 BCCs taken from the nonimmunosuppressed patients, with an additional 8 SCCs yielding an unidentified DNA which hybridizes with HPV DNA. The prevalence and quantity of HPV DNA, as well as the types of isolated HPV DNA, differed between RAR and immunocompentent patients. See the following pages for details of the sources of individual isolates.

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LOCUS       HPVVS19L1     407 bp    DNA             VRL       30-APR-1996
DEFINITION  Human papillomavirus DNA for capsid protein L1 gene (clone vs19-6).
ACCESSION   X89876
NID         g1296535
KEYWORDS    capsid protein L1.
SOURCE      Human papillomavirus.
REFERENCE   1  (bases 1 to 407)
  AUTHORS   Shamanin,V., Zur Hausen,H., Lavergne,D., Proby,C., Leigh,I.,
            Neumann,C., Hamm,H., Goos,M., Haustein,U.F., Jung,E., Plewig,G.,
            Wolff,H. and de Villiers,E.M.
  TITLE     HPV infections in non-melanoma skin cancers from renal transplant
            recipients and non-immunosuppressed patients
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 407)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1995) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 407)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1996) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
COMMENT     The partial sequence of clone vs19-6 suggests that
            it constitutes a previously unidentified HPV type. Its
            sequence is most similar to that of HPV65, making it a new
            member of group B2.  It was isolated from a carcinoma in situ
            and a squamous cell carcinoma on the hands of an immuno-
            suppressed patient as part of a study of non-melanoma
            carcinomas of the skin.

            NCBI gi: 1296535
BASE COUNT      120 a     73 c     92 g    122 t
ORIGIN
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         <-    PCR primer   ->
       61 caagataggt caggtgttcc tttagatata gtagatagta cttgcaagta tccagacttt
      121 ttgaaaatga caaaagacaa gtatggtgat gaatgcttct tttttggtcg tcgagagcag
      181 ttgtatgcaa ggcattattt taccagagca ggcacaatag gtgattctat tccaacgcca
      241 tatcaggaat ctgaatttta cagatctcca caggatagcc aggctcagaa taatgtggat
      301 tctcacattt atgtagccac tcctagtggt tctttaacta gcagtgatgc tcagctgttt
      361 aacagacctt attggctcca aaatgctcaa ggtaccaata acggaat
                                                  L1 cds ->
                                      <-     PCR primer     ->
//
```

```
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DEFINITION  Human papillomavirus DNA for capsid protein L1 gene (clone
            vs201-1).
ACCESSION   X89878
NID         g1296541
KEYWORDS    capsid protein L1.
SOURCE      Human papillomavirus.
REFERENCE   1  (bases 1 to 398)
  AUTHORS   Shamanin,V., Zur Hausen,H., Lavergne,D., Proby,C., Leigh,I.,
            Neumann,C., Hamm,H., Goos,M., Haustein,U.F., Jung,E., Plewig,G.,
            Wolff,H. and de Villiers,E.M.
  TITLE     HPV infections in non-melanoma skin cancers from renal transplant
            recipients and non-immunosuppressed patients
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 398)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1995) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 398)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1996) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
COMMENT     The partial sequence of clone vs201-1 suggests that it
            constitutes a previously unidentified HPV type. Its sequence is
            most similar to that of HPV48, making it a new member of group B2.
            It was isolated from a squamous cell carcinoma of an immuno-
            suppressed patient as part of a study of non-melanoma carcinomas
            of the skin.

            NCBI gi: 1296541
BASE COUNT      114 a     65 c     95 g    124 t
ORIGIN
        1 ctagaggatg gtgatatggg tgatatagga tttgggcatg ctaattttag ccgtttacaa
  L1 cds ->
         <-    PCR primer   ->
       61 gaagataaag caggtgtgcc attagaatta gtggacactt ttagtatatg gcctgacttt
      121 ttacgcatga ccagtgatat atatggagat gctgtgtttt tttggggaaa gcgagaacat
      181 atgtttgcca gacatttatg ggcaagagct ggaactatgg gcgacgctat tccagataat
      241 aatgcagagt tttttctgca tcccaatggt gcacctcaaa ataagttagc ctcatttgct
      301 tattttccaa cacctagtgg ttctcttaat accagtgata atcaattgtt taataagccg
      361 tattggttgc gaaaagctca gggcaccaac aatgggat
                                           L1 cds ->
                             <-     PCR primer     ->
//
```

```
LOCUS       HPVVS202L1    425 bp    DNA             VRL       30-APR-1996
DEFINITION  Human papillomavirus DNA for capsid protein L1 gene (clone
            vs202-8).
ACCESSION   X89879
NID         g1296543
KEYWORDS    capsid protein L1.
SOURCE      Human papillomavirus.
REFERENCE   1  (bases 1 to 425)
  AUTHORS   Shamanin,V., Zur Hausen,H., Lavergne,D., Proby,C., Leigh,I.,
            Neumann,C., Hamm,H., Goos,M., Haustein,U.F., Jung,E., Plewig,G.,
            Wolff,H. and de Villiers,E.M.
  TITLE     HPV infections in non-melanoma skin cancers from renal transplant
            recipients and non-immunosuppressed patients
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 425)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1995) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 425)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1996) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
COMMENT     The partial sequence of clone vs202-8 suggests that it
            constitutes a previously unidentified HPV type. Its sequence is
            most similar to that of HPV48, making it a new member of group B2.
            It was isolated from a carcinoma in situ on the hand of an
            immunosuppressed patient as part of a study of non-melanoma
            carcinomas of the skin.

            NCBI gi: 1296543
BASE COUNT      133 a     67 c     89 g    136 t
ORIGIN
        1 attgaggatg cggatatgag tgatatagga tttggagctg tgaattttag cactttctct
  L1 cds ->
         <-    PCR primer   ->
       61 gaaagccggg ctgatgcacc tttagaatta atcaattcta ttagtaaatg gcctgatttt
      121 attcaaatgt ctaaggatat ttatggcgat agaatgtttt tctttggaaa acgtgagcag
      181 atgtatgcaa gacacacatt ttgtaaagat ggtgctgtgg gagatgctat tccagaaaat
      241 ttaaataatg atgaggatgt tcatcatagg tttttattaa atcctaagcc tgacgcacca
      301 ccatattcaa acttaggaaa cagtacttac tttcctatgc caagtggttc attagttagt
      361 agtgaaactc aattatttaa cagaccattt tggctacatc gagcacaggg caccaataac
                                                          <-     PCR primer
      421 ggcat
              ->
        L1 cds ->
//
```

```
LOCUS       HPVVS203L1    404 bp    DNA             VRL       30-APR-1996
DEFINITION  Human papillomavirus DNA for capsid protein L1 gene (clone
            vs203-2).
ACCESSION   X89880
NID         g1296545
KEYWORDS    capsid protein L1.
SOURCE      Human papillomavirus.
REFERENCE   1  (bases 1 to 404)
  AUTHORS   Shamanin,V., Zur Hausen,H., Lavergne,D., Proby,C., Leigh,I.,
            Neumann,C., Hamm,H., Goos,M., Haustein,U.F., Jung,E., Plewig,G.,
            Wolff,H. and de Villiers,E.M.
  TITLE     HPV infections in non-melanoma skin cancers from renal transplant
            recipients and non-immunosuppressed patients
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 404)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1995) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 404)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1996) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
COMMENT     The partial sequence of clone vs203-2 suggests that it
            constitutes a previously unidentified HPV type. Its sequence is
            most similar to that of HPV65, making it a new member of group B2.
            It was isolated from a carcinoma in situ from an immuno-
            suppressed patient as part of a study of non-melanoma
            carcinomas of the skin.

            NCBI gi: 1296545
BASE COUNT      120 a     65 c     94 g    125 t
ORIGIN
        1 atggaggatg gtgaaatggg cgacataggc tttggagcct ttaattttaa agccctacag
  L1 cds ->
         <-    PCR primer   ->
       61 aaagatcgtg ctggtgttag tttagattta gttgatacat tcagtatatg gccagacttt
      121 ttaaaaatga ctaatgatat atatggtgac agtatctttt tttatggtaa aagagaacag
      181 ctatttagta gacacttgtg ggcccgcgca ggaacggctg gagatgccat tccatctcct
      241 gataacaaaa atctaatatt tcagggtgat gatgcagtgc cacaaaagac tgctgggtct
      301 tttacttatt ttagtgcccc tagtgggtca ttaacaacta gtgattctca gttatttaat
      361 aggccatatt ggttaagaag agctcaaggt accaacaacg gtgt
                                                 L1 cds ->
                                    <-     PCR primer     ->
//
```

```
LOCUS       HPVVS204L     401 bp    DNA             VRL       30-APR-1996
DEFINITION  Human papillomavirus DNA for capsid protein L1 gene (clone
            vs204-4).
ACCESSION   X89881
NID         g1296547
KEYWORDS    capsid protein L1.
SOURCE      Human papillomavirus.
REFERENCE   1  (bases 1 to 401)
  AUTHORS   Shamanin,V., Zur Hausen,H., Lavergne,D., Proby,C., Leigh,I.,
            Neumann,C., Hamm,H., Goos,M., Haustein,U.F., Jung,E., Plewig,G.,
            Wolff,H. and de Villiers,E.M.
  TITLE     HPV infections in non-melanoma skin cancers from renal transplant
            recipients and non-immunosuppressed patients
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 401)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1995) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 401)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1996) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
COMMENT     The partial sequence of clone vs204-4 suggests that it
            constitutes a previously unidentified HPV type. Its sequence is
            most similar to that of HPV65, making it a new member of group B2.
            It was isolated from a carcinoma in situ and a basal cell carcinoma
            from an immuno-suppressed patient as part of a study of non-melanoma
            carcinomas of the skin.

            NCBI gi: 1296547
BASE COUNT      128 a     64 c     84 g    125 t
ORIGIN
        1 atggaggacg gtgagatgag tgatacaggt tttggtgcta tgaattttga taatctatgc
  L1 cds ->
         <-    PCR primer   ->
       61 gaggacagag cttcatttcc tttagacatt ataaatgaga cctccaagtg gcctgatttt
      121 ctaaaaatga ataaagatcc ttatggagat catatatttt tctttggttt acgagagcag
      181 ttatattcca gacatcatgg tgctcgggga ggaaaaatgg gagatactat tccagaaaat
      241 acagcaggcg aatattatta tcctcctact gatggtgctc agcaaaatat aggttcacat
      301 atttatttca atactgttag tggatcttta acatcttcag aaactcagat atttaatagg
      361 ccatattttt tacaacgtgc acagggcaca aacaacggag t
                                                 L1 cds ->
                                <-     PCR primer     ->
//
```

HPVVS205L1

```
LOCUS       HPVVS205L1    416 bp    DNA             VRL       30-APR-1996
DEFINITION  Human papillomavirus DNA for capsid protein L1 gene (clone
            vs205-1).
ACCESSION   X89882
NID         g1296549
KEYWORDS    capsid protein L1.
SOURCE      Human papillomavirus.
REFERENCE   1  (bases 1 to 416)
  AUTHORS   Shamanin,V., Zur Hausen,H., Lavergne,D., Proby,C., Leigh,I.,
            Neumann,C., Hamm,H., Goos,M., Haustein,U.F., Jung,E., Plewig,G.,
            Wolff,H. and de Villiers,E.M.
  TITLE     HPV infections in non-melanoma skin cancers from renal transplant
            recipients and non-immunosuppressed patients
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 416)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1995) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 416)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1996) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
COMMENT     The partial sequence of clone vs205-1 suggests that it
            constitutes a previously unidentified HPV type. Its sequence is
            most similar to that of HPV4, making it a new member of group B2.
            It was isolated from a squamous cell carcinoma from an immuno-
            suppressed patient as part of a study of non-melanoma
            carcinomas of the skin.

            NCBI gi: 1296549
BASE COUNT      132 a     65 c     90 g    129 t
ORIGIN
        1 attcaagatg gggatatgtg cgatattggc tttggagcag ccaattttaa agcattacag
  L1 cds ->
         <-    PCR primer   ->
       61 caagataaat caggtgttcc tttagatatt gttgacagta tatgtaaatg gccagatatt
      121 attaaaatgg agcaagaaat atatggagac agattatttt tctttactaa acgtgagcaa
      181 gcttatgcca ggcattattt cgctcgtgca ggaattaatg gtgattcttt accagatgca
      241 atgaaaccag gagaatatta tctctctcct aagttgggag atgagcaagt accccagaaa
      301 gacttaggat cgcatattta ttttcctaca gttagtggtt ctttggtttc tagtgaaaat
      361 cagttattta acagaccata ttggttgcag aaatctcagg gcacaaacaa cggcgt
                                                              L1 cds ->
                                                 <-     PCR primer     ->
//
```

```
LOCUS       HPVVS206L1    404 bp    DNA             VRL       30-APR-1996
DEFINITION  Human papillomavirus DNA for capsid protein L1 gene (clone
            vs206-2).
ACCESSION   X89883
NID         g1296551
KEYWORDS    capsid protein L1.
SOURCE      Human papillomavirus.
REFERENCE   1  (bases 1 to 404)
  AUTHORS   Shamanin,V., Zur Hausen,H., Lavergne,D., Proby,C., Leigh,I.,
            Neumann,C., Hamm,H., Goos,M., Haustein,U.F., Jung,E., Plewig,G.,
            Wolff,H. and de Villiers,E.M.
  TITLE     HPV infections in non-melanoma skin cancers from renal transplant
            recipients and non-immunosuppressed patients
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 404)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1995) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 404)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1996) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
COMMENT     The partial sequence of clone vs206-2 suggests that it
            constitutes a previously unidentified HPV type. Its sequence is
            most similar to that of HPV50, making it a new member of group B2.
            It was isolated from a squamous cell carcinoma and a basal cell
            carcinoma from one immuno-suppressed patient and a carcinoma in
            situ from another as part of a study of non-melanoma carcinomas of
            the skin.

            NCBI gi: 1296551
BASE COUNT      123 a     72 c     89 g    120 t
ORIGIN
        1 ctggaagatg gtgaaatggg agatattggg tttggtgcag caaattttaa aacgttacaa
  L1 cds ->
         <-    PCR primer   ->
       61 aaggacagag ccggagtcag cttagattta gtagacactt ttagcatttg gcctgacttt
      121 ttaaaaatga ctaatgatat ttacggagat agtatgtttt tctttggaaa acgtgagcag
      181 ctctttggca gacatctttg gacaagagca ggtactcccg gcgatgcaat tcctactcca
      241 gaaaatataa acttaatatt tccagctgat gatggcacta gtcaaaagga tgcagggtct
      301 ttcacttact ttacttcagc tagtggatct cttaatacta gcgattcaca attatttaat
      361 agaccttact ggcttcgacg tgcacaaggc acaaacaatg gcgt
                                                    L1 cds ->
                                    <-     PCR primer     ->
//
```

HPVVS207L1

```
LOCUS       HPVVS207L1    413 bp    DNA             VRL       30-APR-1996
DEFINITION  Human papillomavirus DNA for capsid protein L1 gene (clone
            vs207-22).
ACCESSION   X89884
NID         g1296553
KEYWORDS    capsid protein L1.
SOURCE      Human papillomavirus.
REFERENCE   1  (bases 1 to 413)
  AUTHORS   Shamanin,V., Zur Hausen,H., Lavergne,D., Proby,C., Leigh,I.,
            Neumann,C., Hamm,H., Goos,M., Haustein,U.F., Jung,E., Plewig,G.,
            Wolff,H. and de Villiers,E.M.
  TITLE     HPV infections in non-melanoma skin cancers from renal transplant
            recipients and non-immunosuppressed patients
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 413)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1995) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 413)
  AUTHORS   Shamanin,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1996) V.A. Shamanin, Deutsches
            Krebsforschungszentrum, Im Neuenheimer Feld 242, D- 69120
            Heidelberg, FRG
COMMENT     The partial sequence of clone vs207-22 suggests that it
            constitutes a previously unidentified HPV type. Its sequence is
            most similar to that of HPV48, making it a new member of group B2.
            It was isolated from a squamous cell carcinoma from an immuno-
            suppressed patient as part of a study of non-melanoma
            carcinomas of the skin.

            NCBI gi: 1296553
BASE COUNT      131 a     68 c     95 g    119 t
ORIGIN
        1 ctagaggatg gggagatggg tgatatagga tttggtgctg ctaattttgc taagcttatg
  L1 cds ->
         <-    PCR primer   ->
       61 caagatagag ctggtgtacc tctggaatta atagatagta ttagtatatg gccagatttt
      121 ctaaaaatga caaaggatat ttatggaaat gaagtatttt tctttggaaa acgcgagcaa
      181 tgttatgctc gccatttatt tgccagagct ggtactatgg gagaaccagt acctaatgag
      241 actaatggag taaattttat aaatgcaaaa ccaggagatc caaatcccag gagcgctcat
      301 atgggttctt cagtatactt tgcaacacct agtggctccc ttaataccag tgattcacaa
      361 atatttaaca gaccttattg gttacgacgg gctcaaggaa cgaacaacgg cat
                                                          L1 cds ->
                                            <-     PCR primer     ->
//
```