

Figure 1A**A C-terminally truncated HPV16 L1**

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1 MSLWLPSEAT VYLPPVPVSK VVSTDEYVAR TNIYYHAGTS RLLAVGHPYF
51 PIKKPNNNKI LVPKVSGLQY RVFRIHLPDP NKFGFPDTSF YNPDTQRLVW
101 ACVGVEVGRG QPLGVGISGH PLLNKLDDTE NASAYAANAG VDNRECISMD
151 YKQTQLCLIG CKPPIGEHWG KGSPCTNVAV NPGDCPPLEL INTVIQDGDM
201 VDTGFGAMDF TTLQANKSEV PLDICTSICK YPDYIKMVSE PYGDSLFFYL
251 RREQMFVRHL FNRAGAVGEN VPDDLYIKGS GSTANLASSN YFPTPSGSMV
301 TSDAQIFNKP YWLQRAQGHN NGICWGNQLF VTVVDTTTRST NMSLCAAIST
351 SETTYKNTNF KEYLRHGEEY DLQFIFQLCK ITLTADVMTY IHSMNSTILE
401 DWNFGQLPPP GGTLEDTYRF VTSQAIACQK HTPPAPKEDP LKKYTFWEVN
451 LKEKFSADLD QFPLGRKFLL Q

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Figure 1B**A C-terminally truncated HPV18 L1**

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1 MALWRPSDNT VYLPPPSVAR VVNTDDYVTR TSIFYHAGSS RLLTVGNPYF
51 RVPAGGGNKQ DIPKVSAYQY RVFRVQLPDP NKFGLPDINSI YNPETQRLVW
101 ACVGVEIGRG QPLGVGLSGH PFYNKLDDTE SSHAATSNVS EDVRDNVSVD
151 YKQTQLCILG CAPAIGEHWA KGTRACKSRPL SQGDCPPLEL KNTVLEDGDM
201 VDTGYGAMDF STLQDTKCEV PLDICQSICK YPDYLQMSAD PYGDSMFFCL
251 RREQLFARHF WNRAGTMGDT VPPSLYIKGT GMRASPGSCV YSPSPSGSIV
301 TSDSQLFNKP YWLHKAQGHN NGVCWHNQLF VTVVDTTTRST NLTICASTQS
351 PVPQQYDATK FKQYSRHVEE YDLQFIFQLC TITLTADVMS YIHSMNSSIL
401 EDWNFGVPPP PTTSLVDTYR FVQSVAITCQ KDAAPAENKD PYDKLKFWNV
451 DLKEKFSLDL DQYPLGRKFLL VQ

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Figure 2A

HPV16 and -18 L1 Loop DE

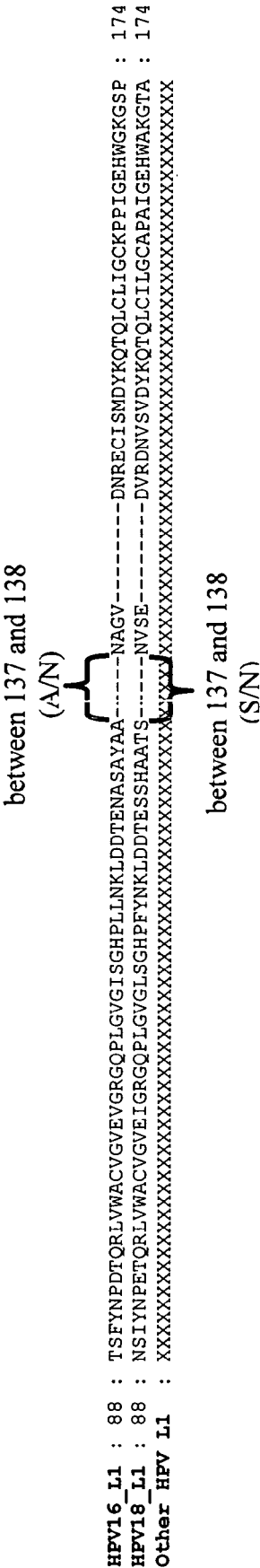


Figure 2B

HPV16 and -18 L1 Loop FG

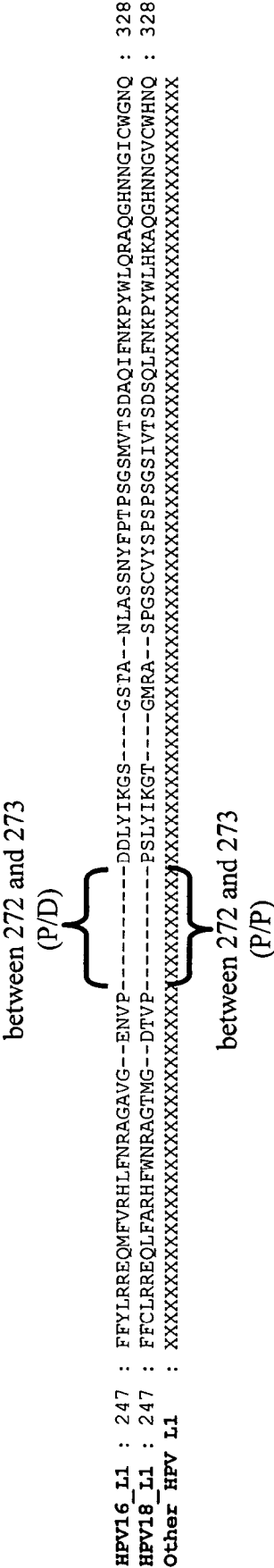


Figure 2C

HPV16 -18 L1 Loop HI

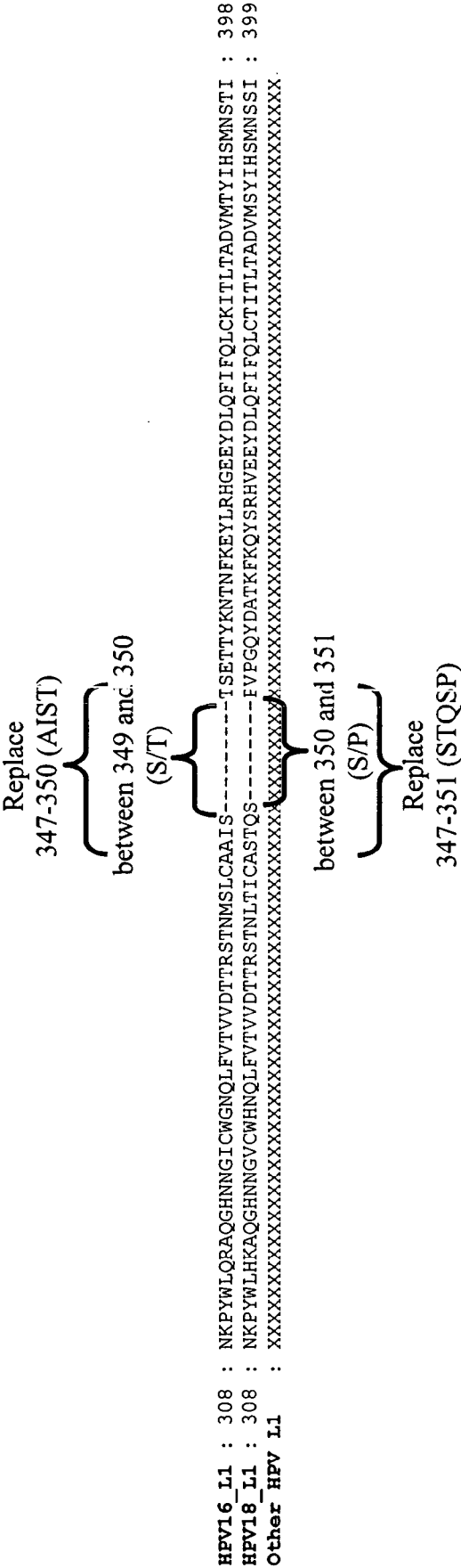


Figure 3A

HPV16 and -18 L1 Loop BC

HPV16_L1	1	-----MSLWLPSEATVYLLPPV-PVSKVSTDEYVARTNIYYHAGTSRLAVGHPYFPIKKPN--N-NKILVPKVSGLOQYRVFRIHLDPDNKGFPP	87
HPV18_L1	1	-----MALWRPSDNTVYLLPP-PVSRVNTDDYVTRTISIFHAGSSRLTVGNPYFR-VPAG--GGHKQDIPKVSAYQYRVFVQVLPDNKFGFLP	87
HPV31_L1		-----MSLRSEATVYLLPPV-PVSKVSTDEYVTRTNIYYHAGSARLLTVGHPYYSIKPSD--NPKIIVPKVSGLOQYRVFVRLPDPNKGFLP	88
HPV35_L1		-----MSLRSEATVYLLPPV-SVSKVSTDEYVTRTNIYYHAGSARLLAVGHPYAIKKQD--S-HKIAVPKVSGLOQYRVFVRLPDPNKGFLP	87
HPV52_L1		-----VNVFHFLOMSVWRPSEATVYLLPPV-PVSKVSTDEYVSRISIIYAGSRLTVGHPYFSIKNTSSNGHKVLLPKVSGLOQYRVFRIKLPDPNKGFLP	116
HPV53_L1		-----MSVWRPSEATVYLLPPV-PVSKVSTDEYVSRISIIYAGSRLTVGHPYFSIKNPT--NAIKLLVPKVSGLOQYRVFVRLPDPNKGFLP	88
HPV58_L1		-----VNVFHFLOMSVWRPSEATVYLLPPV-PVSKVSTDEYVSRISIIYAGSRLTVGHPYFSIKNPN--NKKVILVPKVSGLOQYRVFVRLPDPNKGFLP	114
HPV67_L1		-----VNGFHFLOMSVWRPSEATVYLLPPV-PVSKVSTDEYVSRISIIYAGSRLTVGHPYFSIPNPS--NTIKVILVPKVSGLOQYRVFVRLPDPNKGFLP	117
HPV34_L1		-----VNVCHIF--LQWRPTEAKVYLLPPV-SVSKVSTDEYVTRTNIYYHAGSRLTVGHPYFPIKDTN--GKIKIAPKVSGLQYRVFRIRLPDPNKGFLP	112
HPV32_L1		-----MSVWRPSDNKVYLLPP-PVSKVSTDEYVQRTNIFHAGSRLTVGHPYFPIKTP--NRTSI PKVSGLOQYRVFVRLPDPNKFPLP	86
HPV54_L1		-----MWRESENKVYLLPP-PVSKVSTDEYVTRTNIYYHAGSRLTVGHPYFVKQTN----HKQSI PKVSGLOQYRVFVRLPDPNKGFLP	84
HPV11_L1		-----MWRESDSTVYVPPNPVSKVATDAYVTRTNIYYHAGSRLTVGHPYFSIKKVN----KTVVPKVSGYQYRVFVRLPDPNKGFLP	84
HPV13_L1		-----MWRESDNKLYVPPNPVSKVATDAYVTRTNIYYHAGSRLTVGHPYFPIKKQN----KTVVPKVSGYQYRVFVRLPDPNKGFLP	84
HPV6B_L1		-----MWRESDSTVYVPPNPVSKVATDAYVTRTNIYYHAGSRLTVGHPYFSIKRAN----KTVVPKVSGYQYRVFVRLPDPNKGFLP	84
HPV6A_L1		-----MWRESDSTVYVPPNPVSKVATDAYVTRTNIYYHAGSRLTVGHPYFSIKRAN----KTVVPKVSGYQYRVFVRLPDPNKGFLP	84
HPV42_L1		-----MSVWRPSDNKVYLLPP-PVSKVSTDEYVQRTNIFHAGSRLTVGHPYFSIKRAN----KTVVPKVSGYQYRVFVRLPDPNKGFLP	86
HPV10_L1		-----VNVSHIFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--SNKKVDPKVSFAQYRVFVRLPDPNKGFLP	115
HPV55_L1		-----MWRESENQVYVPPNPVSKVLTDAYVTRTNIYYHAGSRLTVGHPYFAIRPAN----KTLVPKVSGYQYRVFVRLPDPNKGFLP	87
HPV28_L1		-----MALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	84
HPV03_L1		-----VNVSHIFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFA-IPKS--SNKMDIPKVSFAQYRVFVRLPDPNKGFLP	115
HPV07_L1		-----MWQLENOQVYVPPNPVSKVLTDAYVTRTNIYYHAGSRLTVGHPYFSIKRAN----KTVVPKVSGYQYRVFVRLPDPNKGFLP	85
HPV40_L1		-----MWQLENOQVYVPPNPVSKVLTDAYVTRTNIYYHAGSRLTVGHPYFSIKRAN----KTVVPKVSGYQYRVFVRLPDPNKGFLP	85
HPV29_L1		-----MALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFSIPKS--SGNKVDVPKVSFAQYRVFVRLPDPNKGFLP	87
HPV44_L1		-----MWRESENQVYVPPNPVSKVLTDAYVTRTNIYYHAGSRLTVGHPYFAIRPAN----KTLVPKVSGYQYRVFVRLPDPNKGFLP	84
HPV27_L1		-----VNVSTISLOMALWRNESKVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFSIKKQ--SNRLAVPKVSGYQYRVFVRLPDPNKGFLP	196
HPV57_L1		-----VNVCHISLOMALWRNESKVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFSIKKQ--SNRLAVPKVSGYQYRVFVRLPDPNKGFLP	103
HPV2A_L1		-----VNVSTISLOMALWRNESKVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFSIKKQ--SNRLAVPKVSGYQYRVFVRLPDPNKGFLP	102
HPV43_L1		-----VNAFHIFLOQITWRLNDNKVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPLKNS--GKITVPKVSGYQYRVFVRLPDPNKGFLP	113
HPV30_L1		-----MWRESENQVYVPPNPVSKVLTDAYVTRTNIYYHAGSRLTVGHPYFSIPKS--SGNKVDVPKVSFAQYRVFVRLPDPNKGFLP	87
HPV45_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV51_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV66_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV61_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV82_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV56_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV62_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV39_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV70_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV69_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV68_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV38_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV20_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV14_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV21_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV25_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV63_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV17_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV19_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115
HPV09_L1		-----VNVFHFLOMALWRSNDLVYLLPP-PVSKVSTDDYVTRTNIYYHAGSRLTVGHPYFPIKPS--STKADVPKVSFAQYRVFVRLPDPNKGFLP	115

Figure 3B

HPV16 and -18 L1 Loop BC-continued

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HPV08_L1 : -----MAVWQATGKVLPPSTPVARVQSTDEYIORTNIYYHANTDRLLTVGHPIYFNVY--NN--NGDTLQVPKVSQNGHRVFRLLKLPDPNRFALAD : 88
HPV15_L1 : -----MTLWLETTGKVLPPSTPVARVQSTDEYVTRTNFYHMSDRLLTVGHPIYFNVY--SV--NGGSIIEVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV1A_L1 : ---MYNVFQMAVWLPQAKKEYLPPQ-PIITRILSTDEYVTRTNFYHATSERLLLVGHPLSEIS-----SNQVTYTI PKVSQNGYRFRVTFPPDPNRFALAD : 91
HPV65_L1 : -----MASWLSAKGKVLPPSTPVARVQSTDEYITGTSIFHAGTERLLTVGHPIYFNVY--DQRKVLVPKVSQNGYRFRVTFPPDPNRFALAD : 89
HPV49_L1 : -----MTSLWLPATGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--DNRKVLVPKVSQNGYRFRVTFPPDPNRFALAD : 90
HPV37_L1 : -----MTLWLPATGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--SS--DGLKIEVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV04_L1 : -----MSSWLSSTGKVLPPSTPVARVQSTDEYITGTSIFHAGTERLLTVGHPIYFNVY--EPH KVLVPKVSQNGYRFRVTFPPDPNRFALAD : 89
HPV24_L1 : -----MSVWLPASGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--NN--DGTVLEVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV12_L1 : -----MAVWQAAHGKVLPPSTPVARVQSTDEYIORTNIYYHANTDRLLTVGHPIYFNVY--DN--TGKLEVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV23_L1 : -----MTLWLPASGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--SP--DGSKIDVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV05_L1 : -----MAVWHSANGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--NI--NGDKLEVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV47_L1 : -----MAVWHSANGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--NN--NGTTLEVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV22_L1 : -----MTLWLPSTGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--SS--DGAKIEVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV36_L1 : -----MAVWHSANGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--DI--TGNKLEVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV5B_L1 : -----MAVWHSANGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--NI--TGKLEVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV60_L1 : -----MALWLOTAGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--DI--TGNKLEVPKVSQNGYRFRVTFPPDPNRFALAD : 88
HPV48_L1 : -----MALWSAVPGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--DI--TGNKLEVPKVSQNGYRFRVTFPPDPNRFALAD : 86
HPV50_L1 : -----MAHWSSTGKVLPPSTPVARVQSTDEYIORTNIYYHANSRDLTVGHPIYFNVY--DI--TGNKLEVPKVSQNGYRFRVTFPPDPNRFALAD : 86
HPV41_L1 : -----KNAVVFIFQMAVWLPQAKKEYLPPQ-PIQRTLNTEEVYRRTSTFLHAATDRLLTVGHPIYFNVY--GKE--VVPKVSQNGYRFRVTFPPDPNRFALAD : 107
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Figure 3C

HPV16 and -18 L1 Loop DE

HPV16_L1	: 88	: TSFYNPDTQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NAGV-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 174
HPV18_L1	: 88	: NSIYNPDTQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NVSE-----	DVRDNVSDYKOTQQLCI GCPAIPGEHWKGS	: 174
HPV31_L1	: 175	: TSFYNPETQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----GPGT-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 175
HPV35_L1	: 174	: TSFYNPASQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NSGT-----	DNRECI SMDYKOTQQLCI GCRPPIGEHWKGS	: 174
HPV52_L1	: 203	: TSFYNPETQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----KPGI-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 203
HPV53_L1	: 175	: TSFYNPETQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----QPGS-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 175
HPV58_L1	: 201	: TSFYNPETQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----QPGS-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 201
HPV67_L1	: 204	: TSFYNPETQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----QPGT-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 204
HPV34_L1	: 173	: ASFYNPDKERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----GNTA-----	DSRECK SVDYKOTQQLCI GCPAIPGEHWKGS	: 173
HPV32_L1	: 170	: PSLYNPETQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----AGA-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 170
HPV54_L1	: 171	: SSLEFPTQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NPGQ-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 171
HPV13_L1	: 171	: TSIFDSTQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NPGQ-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 171
HPV68_L1	: 170	: SSLEFPTQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NPGQ-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 170
HPV6A_L1	: 170	: SSLEFPTQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NPGQ-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 170
HPV42_L1	: 173	: ARIYNPDAERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----GPGT-----	DNRECI SMDYKOTQQLCI GCKPPIGEHWKGS	: 173
HPV10_L1	: 202	: TSIDYPTQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----PIGQ-----	DSRDNI SVDYKOTQQLCI GCTPPMGEHWKGS	: 202
HPV55_L1	: 171	: ARIYNPDAERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----PIGQ-----	DSRDNI SVDYKOTQQLCI GCTPPMGEHWKGS	: 171
HPV28_L1	: 174	: ARIYNPDAERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----DIGQ-----	DSRDNI SVDYKOTQQLCI GCTPPMGEHWKGS	: 174
HPV03_L1	: 202	: TSLEFSETQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----VPGQ-----	DSRDNI SVDYKOTQQLCI GCTPPMGEHWKGS	: 202
HPV07_L1	: 172	: TSLEFSETQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----VPGQ-----	DSRDNI SVDYKOTQQLCI GCTPPMGEHWKGS	: 172
HPV40_L1	: 174	: ARIYNPDAERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----GPGQ-----	DSRDNI SVDYKOTQQLCI GCTPPMGEHWKGS	: 174
HPV29_L1	: 171	: TSIDYPTQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----GPGQ-----	DSRDNI SVDYKOTQQLCI GCTPPMGEHWKGS	: 171
HPV44_L1	: 188	: ADLYDPDQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----AB-----	DGRENI SMDYKOTQQLCI GCTPPMGEHWKGS	: 188
HPV27_L1	: 187	: ADLYDPDQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----AD-----	DGRENI SMDYKOTQQLCI GCTPPMGEHWKGS	: 187
HPV57_L1	: 173	: TLVTSDTQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NADT-----	DNRECI SMDYKOTQQLCI GCTPPMGEHWKGS	: 173
HPV2A_L1	: 200	: TNVFNPEQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----SPGQ-----	DNRECI SMDYKOTQQLCI GCTPPMGEHWKGS	: 200
HPV53_L1	: 172	: TNVFNPEQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----DTAQ-----	DSRDNI SVDYKOTQQLCI GCTPPMGEHWKGS	: 172
HPV45_L1	: 201	: STIYNPQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----DTAQ-----	DSRDNI SVDYKOTQQLCI GCTPPMGEHWKGS	: 201
HPV51_L1	: 173	: PSFYNPQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----VITQ-----	DVRDNVSDYKOTQQLCI GCPAIPGEHWKGS	: 173
HPV66_L1	: 173	: PSFYNPQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NAQ-----	DVRDNVSDYKOTQQLCI GCPAIPGEHWKGS	: 173
HPV82_L1	: 175	: PNLNPDTRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----ESS-----	DSRDNI SVDYKOTQQLCI GCPAIPGEHWKGS	: 175
HPV56_L1	: 173	: PNLNPDTRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NDQ-----	DVRDNVSDYKOTQQLCI GCPAIPGEHWKGS	: 173
HPV62_L1	: 208	: ATLYNPQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NVIE-----	DSRDNI SVDYKOTQQLCI GCPAIPGEHWKGS	: 208
HPV39_L1	: 173	: ASLYNPQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----AND-----	DSRDNI SVDYKOTQQLCI GCPAIPGEHWKGS	: 173
HPV70_L1	: 174	: PSLYNPQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----TN-K-----	DSRDNI SVDYKOTQQLCI GCPAIPGEHWKGS	: 174
HPV69_L1	: 174	: PSLYNPQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----VSTQ-----	DSRDNI SVDYKOTQQLCI GCPAIPGEHWKGS	: 174
HPV68_L1	: 172	: STLYNPQRLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----NADT-----	DNRECI SMDYKOTQQLCI GCTPPMGEHWKGS	: 172
HPV38_L1	: 174	: MSVYNPDKERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----KNPK-----	DSRDNI SVDYKOTQQLCI GCTPPMGEHWKGS	: 174
HPV14_L1	: 176	: MSVYNPDKERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----GNST-----	DRQNV SFDPKQVQMFII GCAFCI GEHWKGS	: 176
HPV21_L1	: 176	: MSVYNPDKERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----ANST-----	DRQNV SFDPKQVQMFII GCAFCI GEHWKGS	: 176
HPV25_L1	: 175	: MSVYNPDKERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----PNST-----	DRQNV SFDPKQVQMFII GCAFCI GEHWKGS	: 175
HPV63_L1	: 174	: KDI FPDTERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----ASTD-----	DRQNV SFDPKQVQMFII GCAFCI GEHWKGS	: 174
HPV17_L1	: 203	: MSVYNPDKERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----THAT-----	DRQNV SFDPKQVQMFII GCAFCI GEHWKGS	: 203
HPV19_L1	: 174	: MSVYNPDKERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----GSTD-----	DRQNV SFDPKQVQMFII GCAFCI GEHWKGS	: 174
HPV09_L1	: 174	: MSVYNPDKERLVWACVGVGVEGRGQPLGVGIGSGHPLLNKLDLTENASVAA	-----GSTD-----	DRQNV SFDPKQVQMFII GCAFCI GEHWKGS	: 174
			-----TTMD-----	DRQNT SFDPKQVQMFII GCAFCI GEHWKGS	: 174

Figure 3D

HPV16 and -18 L1 Loop DE-continued

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HPV08_L1 : MSVYNPDKERLVWACRGLEISRGQPLGVGSGTGHPYFNKVKDTENSNSYTT-----TSTD-----DRQNTSFDPKQIQMFIVGCTPCIGEHWEKAIP : 174
HPV15_L1 : MSVYNPEKERLVWACVGLIEIGRGQPLGVGSGTGHPYFNKVKDTENSNSYQG-----NSTD-----DRQNTSFDPKQIQMFIVGCTPCIGEHWDRAIV : 174
HPV1A_L1 : KALFNPETERLVWGLRGIEIGRGQPLGIGITGHPYFNKVKDTENSNSYTTIN-----THANG-----DSRQNTAFDAKQIQMFIVGCTPASGEHWTSSR- : 178
HPV65_L1 : NGFYDSHERLVWRLRGIEIGRGQPLGIGITGHPYFNKKGDSSENPNYR-----KQSD-----DNRODVSLDPKQIQMFIIIGCTPAIGEHWDKAEP : 175
HPV49_L1 : MNIYNPEKERLVWACRGLEIGRGQPLGVGTTGHPYFNKVKDTENNANNIV-----TSKD-----DRQNTSFDPKQIQMFIIIGCTPCMGGEYWDAAKP : 176
HPV37_L1 : MSVYNPEKERLVWACAGLEIGRGQPLGVGTTGHPYFNKLRDTENSNNYQG-----GSRD-----DRQNTSFDPKQIQMFIVGCTPCMGGEHWDKAPV : 174
HPV04_L1 : NGFYDSHERLVWKLRGIEIGRGQPLGIGITGHPYFNKKGDTENPNYK-----KQSD-----DNRODVSLDPKQIQMFIIIGCTPAIGEHWDKAEP : 175
HPV24_L1 : MSVYNPEKERLVWGCGRGVEIGRGQPLGVGSGTGHPYFNKVDNTENPVSYRTQ-----ASSTD-----DRQNTSFDPKQIQMFIIIGCAPCIGEHWEVAER : 176
HPV12_L1 : MSVYNPDRERLVWACRGLEISRGQPLGVGSGTGHPYFNKIKDTENSNNYAT-----GSKD-----DRQNTSFDPKQIQMFIVGCTPCVGEHWEKALP : 174
HPV23_L1 : MTLYPDKYRLVWACAGLEIGRGQPLGVGSGTGHPYFNKLRDAENSERQE-----GTVD-----DRQNTSFDPKQIQMFIIIGCTPCIGEHWDTPAV : 174
HPV05_L1 : MSVYNPEKERLVWACRGLEIGRGQPLGVGRSTGHPYFNKVKDTENSNAVIT-----FSKD-----DRQNTSFDPKQIQMFIVGCTPCIGEHWDKAVP : 174
HPV47_L1 : MSVYNPDKERLVWACRGLEIGRGQPLGVGSGTGHPYFNKVKDTENSNSYIT-----NSKD-----DRQNTSFDPKQIQMFIVGCTPCIGEHWDKAEP : 174
HPV22_L1 : MTLHPERYLVWACRGLEIGRGQPLGVGTTGHPYFNKLRHDTENPTEQE-----GTSN-----DRNTSFDPKQIQMFIIIGCTPCIGEHWDKAPV : 174
HPV36_L1 : MSVYNPDKERLVWACRGLEIGRGQPLGVGSGTGHPYFNKLRHDTENSNSYIK-----SSKD-----DRQNTSFDPKQIQMFIVGCTPCIGEHWDKAIP : 174
HPV5B_L1 : MSVYNPDKERLVWACRGLEIGRGQPLGVGSGTGHPYFNKVKDTENSNAVIT-----FSKD-----DRQNTSFDPKQIQMFIIIGCTPCIGEHWDKAIP : 183
HPV60_L1 : RAVFNPERERLVWRLGLEIGRGQPLGIGITGHPYFNKKGDTENPAAVPL-----KQNGD-----DNRMVSMDPKQIQMFIVGCTPCIGEHWDKAIP : 177
HPV48_L1 : KNLNSDKERLVWKLVLGVGRGGPLGVGSGTGHPYFNKIKGDTENPSFYL-----EQTK-----DERQNTSMDPKQIQMFIVGCTPCIGEHWDKAIP : 173
HPV50_L1 : TTLNSDTERLVWKLVLGVGRGGPLGVGSGTGHPYFNKKGDTENPSFYL-----PQEK-----DERQNTSMDPKQIQMFIVGCTPCIGEHWDKAIP : 173
HPV41_L1 : KSLFNPDKERLVWGIKRGIEVSRGQPLGIGITGHPYFNKKGDTENPYNKNNITDQGS-----DSRLSIAFDPKQIQMFIVGCTPCIGEHWDKAIP : 199

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HPV16 and -18 L1 Loop EF

[illegible]

Figure 3F

HPV16 and -18 L1 Loop EF-continued

HPV08_L1	: FDPKQIQMFIVGCTPCIGEHWEKAI	FCAD	-Q-QQ-GLCPP	IELKNTVIEDGM	ADIGFGNN	FKTLQQR	SDVSLD	IVNEICKYPDFL	MQNDVYGDAC	: 245	
HPV15_L1	: FDPKQIQMFVVGCVPCIGEHWDRA	LVCFSE	-RNOAG	KCPPIELKNTVIEDGM	DFDIGFGN	TNNKALSVTK	SDVSLD	IVNETCKYPDFL	TWANDVYGDAC	: 247	
HPV1A_L1	: FDKAQIQMFIVGCTPASGEHWTSS	R-CPGE	--QVXLG	DCPRVOMIES	IEDGM	MDIGFGAD	FAALQQR	SDVPLDVV	QATCKYPDYIR	250	
HPV65_L1	: LDPKQIQMFIIIGCTPAIGEHWDK	AEFCAP	-V-PQGGC	PPPIELNTVIEDGM	CDIGFGAF	NKALQQR	SSAPLDV	ATMKWPDFL	MSKDYGD	247	
HPV49_L1	: FDPKQIQMFIIIGCTPCMGGEYD	AAKPCD	A-R--GGG	KCPPIELINS	VIQDGM	TDIGFGN	TNNKTL	SVNRSDVSLD	IVNDICKYPDFL	247	
HPV37_L1	: FDPKQIQMFVVGCVPCMGGEHWD	KAPVCASE	-ENNOT	GQCPPPIELKNTVIEDGM	FDIGFGN	TNNKVLSTNK	SDVSLD	IVNEICKYPDFL	TWANDVYGDAC	: 247	
HPV04_L1	: LDPKQIQMFIIIGCTPAIGEHWD	KAEFCPS	-A-PQGGC	PPPIELNSYIQDGM	CDIGFGAF	NKALQQR	SSAPLDV	ATVKWPDFL	MGKDIYGD	247	
HPV24_L1	: FDPKQIQMFIIIGCAPCIGEHWE	VAERCA	D-N-NDAG	RCPPIKLVNSYIQDGM	ADIGYGN	LNFRTLQQR	SDVSLD	IVNETCKYPDFL	MQNDVYGD	248	
HPV12_L1	: FDPKQIQMFIVGCTPCVGEHWE	KALPCG	DA-P-AENG	VCPPIELKNTVIEDGM	ADIGFGN	NFKTLQQR	SDVSLD	IVNETCKYPDFL	MQNDVYGD	: 246	
HPV23_L1	: FDPKQIQMFIIIGCTPCGGEYD	TAPVCK	DA-G-SQL	GLCPPPIELKNSYIEDGM	FDIGFGN	TNNKTL	SVNRSDVSLD	IVNEICKYPDFL	MSNDVYGD	: 246	
HPV05_L1	: FDPKQIQMFIVGCTPCIGEHWD	KAVPCA	EN-O-QOT	GLCPPPIELKNTVIEDGM	ADIGFGN	NFKALQDR	SDVSLD	IVNETCKYPDFL	MQNDIYGD	: 246	
HPV47_L1	: FDPKQIQMFIVGCTPCIGEHWD	KAEPCGE	---QOT	GLCPPPIELKNTVIEDGM	ADIGFGN	INFKALQHSR	SDVSLD	IVNETCKYPDFL	MQNDVYGD	: 244	
HPV22_L1	: FDPKQIQMFIIIGCIPCLGEYD	KAPVCE	DA-G-SQV	GLCPPPIELKNGYIEDGM	FDIGFGN	TNNKTL	SVNRSDVSLD	IVNEICKYPDFL	MSNDVYGD	: 246	
HPV36_L1	: FDPKQIQMFIVGCTPCIGEHWD	KAI	PCEKE	-R-QDN	RCPPIELKNTVIEDGM	ADIGFGN	LNFKNLQESR	SDVSLD	IVNETCKYPDFL	MQNDVYGD	: 246
HPV58_L1	: FDPKQIQMFIVGCTPCIGEHWD	KAVPCA	KN-D-QOT	GLCPPPIELKNTVIEDGM	ADIGFGN	NFKALQDR	SDVSLD	IVNETCKYPDFL	MQNDIYGD	: 255	
HPV60_L1	: MDPKQIQMFIVGCTPCIGEHWD	KIAKPC	DP--A-PAR	GSCPPPIKLTQSI	IQDGM	CDTGF	GNANFTLQED	K3GVPLDITNEICKYPD	LLKMTKDIYGD	: 248	
HPV48_L1	: MDPKQIQMFIVGCTPCIGEHWD	KAPVCK	EN--D-L	ENGA	APPIQLVNTVIEDGM	GDIGFGA	NFKLMQDR	AGVPLELID	SIISIPDFL	243	
HPV50_L1	: FDPKQIQMFIVGCTPCIGEHWD	KAEPCD	KN-S-LN	GKCPPIQLVNSYIQDGM	GDIGFGA	NFKLMQDR	AGVPLELID	SIISIPDFL	LLKMTKDIYGD	: 245	
HPV41_L1	: FDPKQIQMFIVGCTPCIGEHWD	KAEPCD	KN-S-LN	GKCPPIQLVNSYIEDGM	ADISYIEDA	MSDI	GLGNLNFSTLQQR	NK3DAPLDIV	SDISICKYPDY	273	

Figure 3G

HPV16 and -18 L1 Loop FG

HPV16_L1 : 247 : FFYLREQMFVRHLFNRAVG--ENVP-----DDLVIKGS-----GSTA--NLASSNYFTPTSGSMVTSDAQLENKPYWLQRAQGHNNGICWGNQ : 328
 HPV18_L1 : 247 : FFCLRREQLFARHFNRACTMG--DTVP-----PSLYIKGT-----GTRA--SGSCVYSPSGSVITSDQLENKPYWLHRAQGHNNGICWHNQ : 328
 HPV31_L1 : FFYLREQMFVRHLFNRACTMG--ESVP-----TDLVIKGS-----GTRA--TLANSTYFTPTSGSMVTSDAQLENKPYWLQRAQGHNNGICWGNQ : 329
 HPV35_L1 : FFYLREQMFVRHLFNRACTMG--ETVP-----ADLYIKG-----TTG--TLPSTYFTPTSGSMVTSDAQLENKPYWLQRAQGHNNGICWGNQ : 326
 HPV52_L1 : FFYLREQMFVRHLFNRACTMG--DPVP-----GDLVIQGN--S-GNTA--TVQSAFAFTPTSGSMVTSSEQLFNKPYWLQRAQGHNNGICWGNQ : 359
 HPV33_L1 : FFYLREQMFVRHLFNRACTMG--EAVP-----DOLVIKGS-----GTTA--SIQSAFAFTPTSGSMVTSSEQLFNKPYWLQRAQGHNNGICWGNQ : 328
 HPV58_L1 : FFYLREQMFVRHLFNRACTMG--EAVP-----DOLVIKGS-----GTTA--SIQSAFAFTPTSGSMVTSSEQLFNKPYWLQRAQGHNNGICWGNQ : 354
 HPV67_L1 : FFYLREQMFVRHLFNRACTMG--EDVP-----TDLVIKGS-----GTTA--SIQSAFAFTPTSGSMVTSSEQLFNKPYWLQRAQGHNNGICWGNQ : 358
 HPV34_L1 : FFYLREQMFVRHLFNRACTMG--DAIP-----DOLVIKGT-----GNTA--SPSSCVYFTPTSGSMVTSSEQLFNKPYWLQRAQGHNNGICWGNQ : 351
 HPV32_L1 : FFYLREQMFVRHLFNRACTMG--EPVP-----EDMYIKASGA--SGRN--NLASSIYFTPTSGSMVTSDAQLENKPYWLQRAQGHNNGICWGNQ : 328
 HPV54_L1 : FFYLREQMFVRHLFNRACTMG--EPVP-----NDLYIKGS-----SG--NLDSIYATPTSGSMVTSSEQLFNKPYWLQRAQGHNNGICWGNQ : 322
 HPV11_L1 : FFYLREQMFVRHLFNRACTMG--EPVP-----DOLVIKGS-----NNRS--SVASSIYVFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNH : 325
 HPV13_L1 : FFYLREQMFVRHLFNRACTMG--EQIP-----AELVIKGS-----N-----TILNSIYVFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNH : 322
 HPV68_L1 : FFYLREQMFVRHLFNRACTMG--EPVP-----DOLVIKGS-----GNT--SVGSSIYVFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 324
 HPV6A_L1 : FFYLREQMFVRHLFNRACTMG--EPVP-----DOLVIKGS-----GNT--SVGSSIYVFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 324
 HPV42_L1 : FFYLREQMFVRHLFNRACTMG--DAIP-----DOLVIKGS-----GNT--SVGSSIYVFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 328
 HPV10_L1 : FFYLREQMFVRHLFNRACTMG--DAIP-----DOLVIKGS-----GNT--SVGSSIYVFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 355
 HPV55_L1 : FFYLREQMFVRHLFNRACTMG--EDIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 324
 HPV28_L1 : FFYLREQMFVRHLFNRACTMG--DTIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 328
 HPV03_L1 : FFYLREQMFVRHLFNRACTMG--DTVP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 358
 HPV44_L1 : FFYLREQMFVRHLFNRACTMG--DKIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 328
 HPV29_L1 : FFYLREQMFVRHLFNRACTMG--DSVP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 328
 HPV07_L1 : FFYLREQMFVRHLFNRACTMG--DSVP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 326
 HPV40_L1 : FFYLREQMFVRHLFNRACTMG--DSVP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 433
 HPV27_L1 : FFYLREQMFVRHLFNRACTMG--DTIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 340
 HPV57_L1 : FFYLREQMFVRHLFNRACTMG--DALP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 339
 HPV2A_L1 : FFYLREQMFVRHLFNRACTMG--DALP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 328
 HPV26_L1 : FFYLREQMFVRHLFNRACTMG--DALP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 354
 HPV43_L1 : FFYLREQMFVRHLFNRACTMG--EQIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 335
 HPV30_L1 : FFYLREQMFVRHLFNRACTMG--EQIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 326
 HPV53_L1 : FFYLREQMFVRHLFNRACTMG--EQIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 357
 HPV45_L1 : FFYLREQMFVRHLFNRACTMG--DTVP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 328
 HPV51_L1 : FFYLREQMFVRHLFNRACTMG--EDIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 327
 HPV66_L1 : FFYLREQMFVRHLFNRACTMG--EALP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 329
 HPV61_L1 : FFYLREQMFVRHLFNRACTMG--EALP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 362
 HPV82_L1 : FFYLREQMFVRHLFNRACTMG--DAIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 328
 HPV36_L1 : FFYLREQMFVRHLFNRACTMG--ETIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 362
 HPV62_L1 : FFYLREQMFVRHLFNRACTMG--EALP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 329
 HPV39_L1 : FFYLREQMFVRHLFNRACTMG--DAIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 327
 HPV70_L1 : FFYLREQMFVRHLFNRACTMG--DTIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 326
 HPV69_L1 : FFYLREQMFVRHLFNRACTMG--DSVP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 329
 HPV68_L1 : FFYLREQMFVRHLFNRACTMG--DTIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 328
 HPV38_L1 : FFYLREQMFVRHLFNRACTMG--DAIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 337
 HPV20_L1 : FFYLREQMFVRHLFNRACTMG--DDIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 340
 HPV14_L1 : FFYLREQMFVRHLFNRACTMG--DDIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 342
 HPV21_L1 : FFYLREQMFVRHLFNRACTMG--DDIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 341
 HPV63_L1 : FFYLREQMFVRHLFNRACTMG--DDIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 333
 HPV17_L1 : FFYLREQMFVRHLFNRACTMG--DDIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 330
 HPV19_L1 : FFYLREQMFVRHLFNRACTMG--DDIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 370
 HPV09_L1 : FFYLREQMFVRHLFNRACTMG--DDIP-----DOLVIKGS-----TKS--TVNATYFTPTSGSLVSSSEQLFNKPYWLQRAQGHNNGICWGNQ : 338

Figure 3H

HPV16 and -18 L1 Loop FG-continued

HPV08_L1 : FFYARREOCYARHFFVRGGKTG--DDIPAAQIDDGMKNQYIPGGQDSQK-----DIGNAMYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGILWANQ : 339
HPV15_L1 : FFYARREOCYARHFFVRGGAVG--DALPDAVNG---DHNEYLPAQSTQQN-----NLANSTYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGILWANQ : 338
HPV1A_L1 : FFYARREOMYTRHFFTRGGSVGDKEAVP-----OSLYLTRADAE--PRTL-----ATTNYVGTSGSMVSSDVQLENRSPYWLQRCQGNNGICWRNQ : 335
HPV65_L1 : FFYGRREQLYARHFFVRAGAMG--DALPEP-----FEVKTDYWIPAQEQDQNT-----LGPHIYIGTTPSGSLVSSSEQLENRPYWLNRQAQGTNNNGICWDNQ : 337
HPV49_L1 : FFYARREOCYARHFFVRGGNVG--DALPNTAVGQ---DNNYILPAASQAQK---TLGSSIYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGICWENQ : 338
HPV37_L1 : FFYARREOCYARHFFVRGGNVG--DALPDGTVNQ---DHKYILPAKSQQQY---LIGNSTYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGILWGNQ : 338
HPV04_L1 : FFFGRREQLYARHFFVRAGTMG--DALPEP-----FEATSDYFPAQNDQDYT-----LGPHIYVGTTPSGSLVSSSEQLENRPFWLNRQAQGTNNNGICWDNQ : 337
HPV24_L1 : FFYARREOCYARHFFVRGGKPG--DDIPGEQIDAGTYKNDFYIPRATQGTOK-----NIGNSMYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGICWANQ : 342
HPV12_L1 : FFYARREOCYARHFFVRGGKTG--DDIPDAQIDDGMKNQYIPGAQDSQK-----DIGNAMYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGILWANQ : 340
HPV23_L1 : FFYARREOCYARHFFVRGGVVG--DAIPDGAQQ---DHKYILPADQ---QN-----TLGNSLYFPTVSGSLVSSSEQLENRPFWLQRAQGHNNGILWNNQ : 334
HPV05_L1 : FFYARREOCYARHFFVRGGKTG--DDIPRAQIDNGTYKNQFYIPGADGQAOK---TIGNSMYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGILWANQ : 340
HPV47_L1 : FFYARREOCYARHFFVRGGKTG--DDIPGAQVGNMKNQFYIPGATGAOK---TIGNAMYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGILWANQ : 338
HPV22_L1 : FFYARREOCYARHFFVRGGVVG--DAIPDDAVQQ---DHKYILPAAS---QT-----ALENSTYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGILWNNQ : 334
HPV36_L1 : FFYARREOCYARHFFVRGGKTG--DDIPDARIDNGTYKNQFYIPGADGQDOK---TIGNAMYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGILWANQ : 340
HPV5B_L1 : FFYARREOCYARHFFVRGGKTG--DDIPGAQIDNGTYKNQFYIPGADGQAOK---TIGNAMYFPTVSGSLVSSDAQLENRPFWLQRAQGHNNGILWANQ : 349
HPV60_L1 : FFFGKREQLYSRHYFVRGGIDG--DPSLP-----DSGY--LAPQTDKPNQ---LGGYSYFPTPSGSAVSSDNQLENRPFYWLHRAQGANNGICWGNQ : 333
HPV48_L1 : FFYAKREOCYARHFFVRAGOMG--EPIPT-----ENGVI--YITPDSADQNRRSHSGSVYFPTPSGSLNISDSQLENRPFYWLHRAQGTNNNGICWNE : 333
HPV50_L1 : FFYVRREALLYARHIMFHAGPIG--EPIPN-----VSGVINYVNPQPEONRKTNIGSYLYFPTPSGSLNISSSQLENRPFYWLHRAQGTNNNGICWNE : 336
HPV41_L1 : FFYVRREALLYARHIMFHAGKMDA-EQFP-----TSLYIDSSVEGEKLS--LQRTDREYFMTPSGSLVATEQQLENRPFWLQRAQGHNNGILWNE : 360

Figure 31

HPV16 and -18 L1 Loop HI

HPV16_L1 : 308 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTSLCAATIS-----TSETTYKNTNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMSTI : 398
 HPV18_L1 : 308 : NKPYWLHKAQGHNGICWGNQLFVTVVDTTRTNNTIICASTOS-----PVPQYDATKFKQYSRHVEV'DLQFI'FOLCKITLTDVMSYIHSNMSSI : 399
 HPV31_L1 : NKPYWMORAGGHNGICWGNQLFVTVVDTTRTNNSVCAAI-----NSDFTFKSSNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 399
 HPV35_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNSVCAV-----SSDSTYKDNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 396
 HPV52_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAEV-----KKESTYKNEFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 428
 HPV33_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCTQV-----TSDSTYKNEFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 397
 HPV38_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCTEV-----TKGETYKDNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 423
 HPV67_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCSVTT-----KSEATYKNEFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 427
 HPV34_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCSVTT-----KSEATYKNEFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 423
 HPV32_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----TSDSTYKNEFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 397
 HPV54_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVSK-----TQDSFNNSDFREYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 391
 HPV11_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVSK-----S--ATYNSDYKVMRHEEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 394
 HPV13_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAATIS-----SLDSTYKATEYKQVMRHEEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 393
 HPV68_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----S--STYNSDYKVMRHEEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 393
 HPV62_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----S--STYNSDYKVMRHEEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 393
 HPV42_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAATIS-----SGDTYKATNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 397
 HPV10_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----SPATYKATNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 393
 HPV55_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAATQ-----SPSTYNSDYKVMRHEEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 426
 HPV28_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----S--ATYNSDYKVMRHEEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 395
 HPV03_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----S--ATYNSDYKVMRHEEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 397
 HPV07_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----S--ATYNSDYKVMRHEEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 427
 HPV40_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----PTPTPYNSKFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 397
 HPV29_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----PTPTPYNSKFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 397
 HPV44_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----QPLTTYDATKIKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 399
 HPV27_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----SPSTYSEYKQVMRHEEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 395
 HPV57_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----DN--TKYATNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 503
 HPV2A_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----E--TKYATNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 409
 HPV26_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----D--TKYATNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 408
 HPV43_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----SASTPFPSDYKQVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 399
 HPV30_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----TPSTYNSKFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 425
 HPV53_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----QTLSTYNSKFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 404
 HPV45_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----OSMSTYNSKFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 395
 HPV51_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----PVSTYDPTKFKQYSRHVEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 428
 HPV66_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----AVSPTFPNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 398
 HPV61_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----STLKYDAREINQVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 396
 HPV82_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----PV--SEYKATNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 399
 HPV56_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----SVAOTFTPANFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 399
 HPV62_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----EOLSKYDARKINQVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 431
 HPV39_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----AA--AEYKATNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 398
 HPV70_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----SIPSTYDPSKFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 398
 HPV69_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----AIPAVSPTFPNFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 397
 HPV68_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----SASTPFPSDYKQVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 400
 HPV38_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----TPAVYDPSKFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 399
 HPV20_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----GGAGEYDANIREYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 408
 HPV14_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----DYSKIDQYDSQFQVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 414
 HPV21_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----EYSKIDQYDSQFQVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 416
 HPV25_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----DYSKIDQYDSQFQVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 416
 HPV63_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----ETYSADQYDSQFQVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 415
 HPV17_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----GAVTEYNSQIREYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 403
 HPV19_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----DVAKTADYNSANFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 409
 HPV09_L1 : NKPYWLQRAQGHNGICWGNQLFVTVVDTTRTNNTLCAVTT-----AQTEYNSANFKVYLRHGEV'DLQFI'FOLCKITLTDVMTYIHSNMPAI : 444

HPV16 and -18 L1 Loop HI-continued

NRPFWLORAQCHNNGIILWANOQMFVTVDNTRNTNFTSIVYTGNG	ELKNITDYKSTQFREYLRAHVEE	EISLILOJCKPIPKADVLQAQINAMNSSL	411
NRPFWLORAQCHNNGIILWNGNQMTFTVDNTRNTNFTSIVSDG	NAINENYSEINFRELRHVEE	QLSILIOJCKPIPKAEVLTQINAMNSGI	409
NRSVFLORACOGNGNICWRNLQFTIVGDNTRGTSLSISMKNNAS	TTVYSNANENDFRELFDEFLDSFTLOJCKVKYLPENLAYITHMDPNI		404
NRPYLARAQGTNGNICWNLQFVLVDNTHNTNFTSIVKTI	EADDSYKYKAGDFQFYLRHIEE	WEFEFFJOJCTVPLTADVAHLNVWNPNI	409
NRPFWLORAQCHNNGIICWNLQFTIVADNTRNTNFTSIVSDG	QPTPEYVNSTLREYLRAHVEE	EISIILOJCKVPLEPVLQAQINAMNSGI	409
NRPFWLARAQCHNNGIILWNGNQMTFTVDNTRNTNFTSIVSDTN	GETEYVNSTOTLREYLRAHVEE	QLSIILOJCKVPLEPVLQAQINAMNSGI	409
NRPYLARAQGTNGNICWNLQFVLVDNTHNTNFTSIVSKS	DGANDNYQYKASDFQFYLRHIEE	WEFEFFJOJCKVPLTADVAHLNVWNPNI	409
NRPFWLORAQCHNNGIICWNLQFTIVVDNTRNTNFTSIVTENG	KVTIDNEYDANKFREYQRHVEE	EISIILOJCKPIPKADVLQAQINAMPSL	416
NRPFWLORAQCHNNGIILWANOQMFVTVDNTRNTNFTSIVSDNQ	NVDNI.PNYDSQKFREYLRAHVEE	EISLILOJCKVPLPKAEVLTQINAMNSL	414
NRPFWLKRAQCHNNGIILWNNQMFVTADNTRNTNFTSIVTND	SSLEKYDATKIREFTTHVEE	QLSFILOJCKLCRIPKAEVLTQINAMNSDI	404
NRPFWLORAQCHNNGIILWANOQMTFTVDNTRNTNFTSIVYNQAG	ALKVDYADNADFREYQRHVEE	EISIILOJCKVPLPKAEVLTQINAMNSSL	412
NRPFWLORAQCHNNGIILWANOQMTFTVDNTRNTNFTSIVSYQAG	DIKIDQDYNADNDFREYQRHVEE	EISVFILOJCKVPLPKAEVLTQINAMNSSL	402
NRPFWLKRAQCHNNGIILWNNQMFVTADNTRNTNFTSIVASD	GTTVNDYDARKIREYFRHVEE	QLSVFILOJCKLCRIPLEAEVLTQINAMNHGI	404
NRPFWLORAQCHNNGIILWANOQMTFTVDNTRNTNFTSIVYNNNG	ALKINDYADNADFREYQRHVEE	EISIILOJCKVPLPKAEVLTQINAMNSHGI	414
NRPFWLORAQCHNNGIILWANOQMTFTVDNTRNTNFTSIVYNOAG	PLKVDYADNADFREYQRHVEE	EISIILOJCKVPLPKAEVLTQINAMNSSL	423
NRPYLHRAQGANNGICWNGLOFTIIVDNTNTRNTNLSISVYK	QQAIDNRYKYQBEDFQFYLRHTEE	VEELILRUCKYPLPNPDVAHLNVMDKNI	409
NRPYLARAQGTNGNICWNGELFTFVDNTRHNVTNFTSIVKNDKTALTENY	IDNGCYKNADDFQFYLRHTEE	EIEIFYOLCKYNLTADVAHLNVMPRI	412
NRPYWIRAQGTNGNICWNGEAVFTVDNTRNTNFTNFTSIVKVDNPLDPLV	ASSYNNKSEEFLEATHTEE	QOAFLOJCKVGLDADLAHLNVMDPRI	415
NRPFWLORAQCHNNGIILWNEAFVTVDDTRTGNTFTSIVPEGD	ASSYNNKSEEFLEATHTEE	QOAFLOJCKVGLDADLAHLNVMDPSI	429

Figure 3K

HPV16 and -18 L1 C-term invading arm

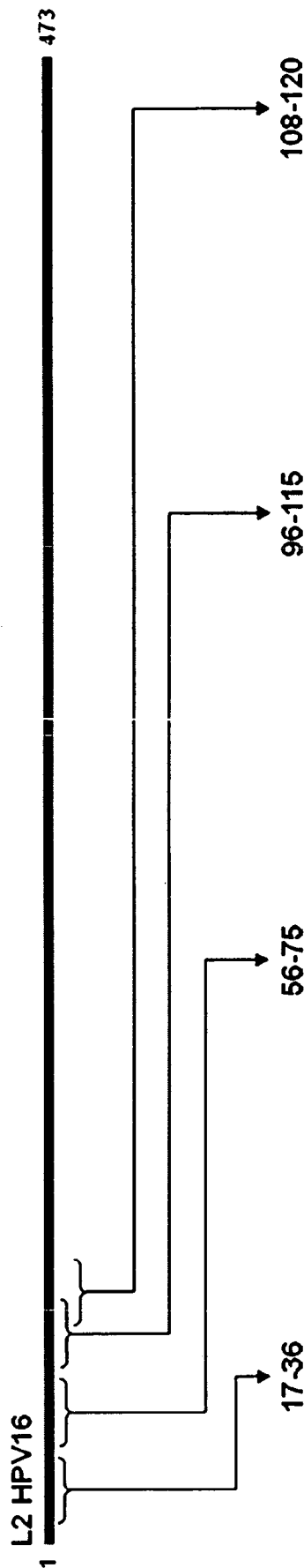
HPV16_L1	: 399	: LEDWNGFLGPPGGTLEDTRYFVTS-QAIIACQKH-TTPAPKEDPLKKYTFWEVNLKEKFSADLDQFPILGR-----KFLIQ-----	: 471
HPV18_L1	: 400	: LEDWNGVPPPTTSIVDTYRFVQS-VAITCOKDAPAEK-KDPYDKLFKFWVDLKEKFSLDLDQYPLGR-----KFLVQ-----	: 472
HPV31_L1		: LEDWNGFLTPPSSGSLDTRYFVTS-QAITCOKT-APQKEDDPKDYFWEVNLKEKFSADLDQFPILGR-----KFLQAG-----YRARPKEKAG	: 484
HPV35_L1		: LEDWNGFLTPPSSGSLDTRYFVTS-QAITCOKP-SAPKEDDPKDYFWEVNLKEKFSADLDQFPILGR-----KFLQAG-----LKARNPFRLG	: 481
HPV52_L1		: LEDWQFGLTPPSSASLEDTRYFVTS-TAITCOKN-TTPKGEDPLKDYFWEVDLKEKFSADLDQFPILGR-----KFLQAG-----LQARPKLKR-	: 512
HPV33_L1		: LEDWQFGLTPPSSASLEDTRYFVTS-QAITCOKT-VPPKEDDPKDYFWEVDLKEKFSADLDQFPILGR-----KFLQAG-----LQARPKLKR-	: 481
HPV58_L1		: LEDWQFGLTPPSSASLEDTRYFVTS-QAITCOKT-APKEDDPKDYFWEVNLKEKFSADLDQFPILGR-----KFLQSG-----LKAKPRLR-	: 507
HPV67_L1		: LEDWQFGLTPPSSGSLDTRYFVTS-QAITCOKT-SPPTAKEDPLKKYSFWINLKEKFSADLDQFPILGR-----KFLQAG-----FTAKPRLKR-	: 511
HPV34_L1		: LEDWNGFLTPPSSGSLDTRYFVTS-QAITCOKP-OPPKETEDPGKMTFWEVDLKEKFSADLDQFPILGR-----KFLQAG-----MRARPRLQAS	: 508
HPV32_L1		: LEDWNGVAPPPSGTLEDTRYFVQS-QAITCOKP-VTAPEKDPFSDYSFWVDLKEKFSADLDQFPILGR-----KFLQAG-----LRARPRLTAV	: 482
HPV54_L1		: LEDWNGFLTPPSSGSLDTRYFVQS-QAIIACQKNAPEKEDPYSKNEFWVDLKEKFSADLDQFPILGR-----KFLQAG-----LRARPRLRPV	: 477
HPV11_L1		: LEDWNGFLSPPPNGTLEDTRYVQS-QAITCOKP-TPEKEKQDPYKMSFWVDLKEKFSADLDQFPILGR-----KFLQSG-----YRGTSARTG	: 479
HPV13_L1		: LEDWNGFLSPPPNGTLEDTRYVQS-QAITCOKP-TPEKEKQDPYKMSFWVDLKEKFSADLDQFPILGR-----KFLQSG-----YGRSSPIRVG	: 478
HPV68_L1		: LEDWNGFLSPPPNGTLEDTRYVQS-QAITCOKP-TPEKEKQDPYKMSFWVDLKEKFSADLDQFPILGR-----KFLQSG-----YGRSSIRTG	: 478
HPV6A_L1		: LEDWNGFLSPPPNGTLEDTRYVQS-QAITCOKP-TPEKEKQDPYKMSFWVDLKEKFSADLDQFPILGR-----KFLQSG-----YGRSSIRTG	: 478
HPV42_L1		: LEDWNGVAPPPSGTLEDTRYVQS-EAIRCQAK-VTTPEKEDPYKMSFWVDLKEKFSADLDQFPILGR-----KFLQAG-----LRARPRLSVG	: 482
HPV10_L1		: LEDWNGFLTPPSTLEDTRYFLSS-SAITCOKDTPTEK-ODPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----RSRSASVSR	: 511
HPV55_L1		: LEDWNGFLSPPPNGTLEDTRYVQS-QAITCOKP-PPEKAKQDPYAKLSFWVDLKEKFSADLDQFPILGR-----KFLQSG-----VOARSSVRVG	: 480
HPV28_L1		: LEDWNGFLTPPSTLEDTRYFESS-SAITCOKDASPTTK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----GARSVSVR	: 482
HPV03_L1		: LEDWNGFLTPPSTLEDTRYFELTS-SAITCOKDAPTEK-ODPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----GTSSISVR	: 512
HPV07_L1		: LEDWNGFLTPPSTLEDTRYFELTN-KAIIACQKD-APPKEDDPKDYFWEVNLKEKFSADLDQFPILGR-----KFLQAG-----LRTGPKFKSR	: 482
HPV40_L1		: LEDWNGFLTPPSTLEDTRYFELTN-KAIIACQKD-APPKEDDPKDYFWEVNLKEKFSADLDQFPILGR-----KFLQAG-----VRAGPRFKSR	: 482
HPV29_L1		: LEDWNGFLTPPSTLEDTRYFVTS-SAITCOKDAPTEK-ODPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----RRSSVPSR	: 484
HPV44_L1		: LEDWNGFLSPPPNGTLEDTRYVQS-QAITCOKP-PPEKAKQDPYAKLSFWVDLKEKFSADLDQFPILGR-----KFLQSG-----VOARSSVRVG	: 480
HPV27_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKPPTPKTP-TDPVANMTFWDVLDKRFSLDLDQFPILGR-----KFLQSG-----AMPTVSR	: 490
HPV57_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKPPTPKTP-TDPVANMTFWDVLDKRFSLDLDQFPILGR-----KFLQSG-----AMPTVSR	: 491
HPV2A_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKPPTPKTP-TDPVANMTFWDVLDKRFSLDLDQFPILGR-----KFLQSG-----AMPTVSR	: 490
HPV26_L1		: LEDWNGFLTPPSTLEDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV43_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV30_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV53_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV45_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV51_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV36_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV61_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV82_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV36_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV62_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV39_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV70_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV69_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV68_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV38_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV20_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV14_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV21_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV25_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV63_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV17_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV19_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484
HPV09_L1		: LEDWNGVPPPPSLDTRYVQS-QAITCOKDAPTEK-EDPYAKLNFWDVLDKRFSLDLDQFPILGR-----KFLQAG-----IQRAPKLGTK	: 484

Figure 3L

HPV16 and -18 L1 C-term invading arm-continued

HPV08_L1 : LEEWQLGFEVPTPDPIHDTYRVIDS-LATRCDDK-SPPKEKDPDYAKFNFWNDLTERLSLDLDQYSLGR-----KELFQAGLQ-----Q-TTV : 494
HPV15_L1 : LEDWQLGFEVPTPDNAVQDIYRYIDS-KATKCPDA-VQPKDEDPFQKTFWNVDLTERLSLDLDQYPLGR-----KELFQAGLQ-----R-RPR : 490
HPV1A_L1 : LEDWQLSVSQPTNPLEDQYRFLGSSLAACKPEQ-APPEPQTDPIYSQKFEVDLTERMSQLOQFPLGR-----KFLYQSG-----WTQR : 484
HPV65_L1 : LDNMQLNFVPPPPSGIEDQYRIQS-RATRCPTQ-SPSTEKEDPYKDLSEFWGVDLTERFSSLSQFSLSGR-----RFLYQSGLI-----NGTLK : 491
HPV49_L1 : LENWQLGFEVPTPDPIHDTYRVIDS-LATRCDDK-QPAPERKDPYEQNFMTVDLTERLSLDLDQYSLGR-----KELFQAGLQ-----R-ASR : 490
HPV37_L1 : LEEWQLGFEVPTPDNSVHDLYRYINS-KATKCPDA-VVEKEKEDPKAKTFWNVDLTERLSLDLDQYPLGR-----KFLYQSGLQ-----S-RPR : 490
HPV04_L1 : LDNMQLNFVPPPPSGIEDQYRIQS-RATRCPTQ-TPATEKEDPYKDLSEFWVVDLTERFSSLSQFSLSGR-----RFLYQSGLI-----NGSLK : 491
HPV24_L1 : LEEWQLGFEVPPAPDNPLQSTYRYIES-LATPCDDK-VAPKEREDPYAPTFWNVDLTERLSLDLDQYSLGR-----KELFQAGLV-----O-KTS : 497
HPV12_L1 : LEDWQLGFEVPTPDPIHDTYRYIES-LATRCDDK-NPPKEKDPDYDGLSFMTVDLTERLSLDLDQYSLGR-----KELFQAGLQ-----Q-TTV : 495
HPV23_L1 : LDNMQLNFVPTPDNAVHDTYRYIAS-LATRCDDK-VQPKDEDPFQKTFWNVDMTERLSLDLDQYPLGR-----KELFQAGLQ-----R-VRS : 485
HPV05_L1 : LEDWQLGFEVPTPDPIQDTYRYIDS-LATRCDDK-NPPKEKEDPYKGLHFWVDLTERLSLDLDQYSLGR-----KELFQAGLQ-----Q-TTV : 495
HPV47_L1 : LEEWQLGFEVPTPDPIQDTYRYLES-LATRCDDK-SPPKEKVDYKGLHFWVDLTERLSLDLDQYSLGR-----KELFQAGLQ-----Q-TTV : 493
HPV22_L1 : LENWQLGFEVPTPDNSVHDYRYLQS-KATKCPDA-VQPKDEDPFQKTFWNVDMSEKLSLDLDQYPLGR-----KELFQAGLQ-----R-ARA : 485
HPV36_L1 : LEDWQLGFEVPTPDPIQDTYRYIDS-LATRCDDK-TPPKEKEDPYKGLHFWVDLTERLSLDLDQYSLGR-----KELFQAGLQ-----Q-TTV : 495
HPV5B_L1 : LEDWQLGFEVPTPDPIQDTYRYIDS-LATRCDDK-NPPKEKEDPYKGLHFWVDLTERLSLDLDQYSLGR-----KELFQAGLQ-----H-TTV : 504
HPV60_L1 : LEDWQLSFVPPPPQGGIEDAYRYIMS-QATMCPTD-VPNTEREDPYKQTFMTIDLQERFSSLSQFSLSGK-----RYLYQYGLL-----N----- : 485
HPV48_L1 : LEEWQLAFVPPAPTGGIEDYRYIKS-MATKCPA-EP-EEDTDPYKAYFWTLDLTERFSSLSQFSLSGR-----KFLYQYGLL-----NG----- : 490
HPV50_L1 : LENWQLAYVPPAPSGGGIEDYRYILKS-DATKCPAK-DSSAEVVDYKAYTFWNVNTERFSSLSQFSLSGR-----KFLYQYGLL-----K----- : 493
HPV41_L1 : IEDWHLAVTSPNSVLEHDYRYILS-IATKCFESK-DADDTSTDPYKDLKFEWVDLDRMTEQLDQDTPLGR-----KELFQAGLQ-----QSSN : 511

Figure 4



L2 HPV16	17-QLYKTKCKQAGTCPPDIIPKV-36	L2 HPV16	56-GGLGIGTGSGGRTGYVPL-75	L2 HPV16	96-DPVGSPDSIVSLVEETSFI-115	L2 HPV16	108-LVEETSFIIDAGAP-120
L2 HPV18	16-DLYKTKCKQAGTCPPDVVPKV-35	L2 HPV6	55-GGLGIGTGSGGRTGYVPL-74	L2 HPV18	94-EPVGTDPISIVTLIEDSSV-113	L2 HPV18	106-LIEDSSVITGAP-118
L2 HPV6	16-QLYQTKCKLGTCPDVIPKV-36	L2 HPV11	54-GGLGIGTGAGSGRAGYVPL-73	L2 HPV6	95-EPVAPSPDSIVSLIEESAI-114	L2 HPV6	107-LIEESAIINAGAP-119
L2 HPV11	15-QLYQTKCKATGTCPPDVIPKV-35	L2 HPV31	56-GGLGIGTGSGGRTGYVPL-75	L2 HPV31	96-DPVGPLDPSIVSLVEESGIV-115	L2 HPV31	108-LVEESGIVDVGAP-120
L2 HPV31	17-QLYQTKCKAAGTCPSDVIPKI-36	L2 HPV33	55-GGLGIGTGSGGRTGYVPL-74	L2 HPV33	95-DTVGPLDSSIVSLIEETSFI-114	L2 HPV33	107-LIEETSFIIEAGAP-119
L2 HPV35	17-QLYRTCKAAGTCPPDVIPKV-36	L2 HPV35	56-GGLGIGTGSGGRTGYVPL-75	L2 HPV35	100-DTIGPLDSSIVSLVEETSFI-119	L2 HPV35	112-LVEETSFIIEAGAP-124
L2 HPV39	16-DLYRTCKQSGTCPPDVVDKV-35	L2 HPV39	55-GGLGIGTGSGGRTGYVPL-74	L2 HPV39	94-EPVGPSEPSIVQLVEDSSVI-113	L2 HPV39	106-LVEDSSVITSGTP-118
L2 HPV45	16-DLYRTCKQSGTCPPDVINKV-35	L2 HPV45	55-GGLGIGTGSGGRTGYVPL-74	L2 HPV45	94-EPVGTDPISIVTLVEDSSV-113	L2 HPV45	106-LVEDSSVWASGAP-118
L2 HPV51	16-QLYSTCKAAGTCPPDVVNVK-35	L2 HPV51	55-GGLGIGTGSGGRTGYVPL-74	L2 HPV51	95-DLWHHTEPSIVNLVEDSSII-114	L2 HPV51	107-LVEDSSIIQSGSP-119
L2 HPV52	16-QLYQTKCKASGTCPPDVIPKV-36	L2 HPV52	55-GGLGIGTGAGSGRAGYVPL-74	L2 HPV52	95-EPVGTDPISIVSLIEETSFI-114	L2 HPV52	107-MIEETTFIESGAP-119
L2 HPV56	16-QLYKTKCKLSGTCPEDEVNKI-35	L2 HPV56	55-GGLGIGTGSGGRTGYVPL-74	L2 HPV56	94-ESVGTDPISIVTLVEESSVI-113	L2 HPV56	106-LVEESSVIESGAG-118
L2 HPV59	16-DLYKTKCKQAGTCPSDVINKV-35	L2 HPV66	55-GGLGIGTGSGGRTGYVPL-74	L2 HPV58	95-DTVGPLDSSIVSLIEETSFI-114	L2 HPV58	107-LIEESSFIIDAGAP-119
L2 HPV66	16-QLYKTKCKLSGTCPEDEVINKV-35	L2 HPV68A	55-GGLGIGTGSGGRTGYVPL-74	L2 HPV59	94-EPVGTDPISIVTLVEDSSVI-113	L2 HPV59	106-LVEDSSVITGAP-118
L2 HPV68A	16-DLYKTKCKQAGTCPSDVINKV-35	L2 HPV73	57-GGLGIGTGSGGRTGYVPL-76	L2 HPV68A	94-EPVGTPEPSIVQLVEDSSVI-113	L2 HPV66	106-LVEESSVINSGAG-118
L2 HPV73	18-QLYKTKCKQAGTCPPDVIPKV-37	L2 HPV73	98-TSVGSPDSSIVSLVEESSFI-117	L2 HPV73	98-TSVGSPDSSIVSLVEESSFI-117	L2 HPV68A	106-LVEDSSVITSGTP-118
						L2 HPV73	110-LVEESSFIIEGIP-122

Fig 5: purification schemes chimeras L1/L2

Chimera # 1	Chimera # 2	Chimera # 3	Chimera # 4	Chimera # 7	Chimera # 9	Chimera # 10
Extraction Bme 4%/pH 8.5	Extraction Bme 4%/pH 8.5	Extraction Bme 4%/ 2% emipen/ pH 8.7	Extraction Bme 4%/ 2% emipen/ pH 8.7	Extraction Bme 4%/pH 8.5	Extraction Bme 4%/pH 8.5	Extraction Bme 4%/pH 8.5
↓	↓	↓	↓	↓	↓	↓
Centrifugation	Centrifugation Clarification	Centrifugation	Centrifugation Clarification	Centrifugation Clarification	Centrifugation Clarification	Centrifugation
↓	↓	↓	↓	↓	↓	↓
TMAE	TMAE	TMAE	TMAE	DMAE	DMAE	DMAE
↓	↓	↓	↓	↓	↓	↓
HA Type I	HA Type I	HA Type I	HA Type I	HA Type I	HA Type I	HA Type I
↓	↓	↓	↓	↓	↓	↓
2-20x dilution Sephadex G25	Sephadex G25	Sephadex G25	Sephadex G25	Sephadex G25	Sephadex G25	Sephadex G25
↓	↓	↓	↓	↓	↓	↓
Maturation	Maturation	Maturation	Maturation	Maturation	Maturation	Maturation
↓	↓	↓	↓	↓	↓	↓
0.45 μm sterilizing filtration	0.05% tween addition 0.22 μm sterilizing filtration	0.05% tween addition 0.22 μm sterilizing filtration	0.05% tween addition 0.22 μm sterilizing filtration	0.22 μm sterilizing filtration	0.05% tween addition 0.22 μm sterilizing filtration	0.05% tween addition 0.22 μm sterilizing filtration
↓	↓	↓	↓	↓	↓	↓
Purified bulk Storage -70°C	Purified bulk Storage -70°C	Purified bulk Storage -70°C	Purified bulk Storage -70°C	Purified bulk Storage -70°C	Purified bulk Storage -70°C	Purified bulk Storage -70°C