Supplementary Table S1: HPV type-specific primer sequences and product size.

HPV TYPES	PRIMER SET (5'-3') FORWARD (3'-5') REVERSE	PRODUCT SIZE
HPV6	TCCATTAGCCTCCACGGGTG TAGTGGGCCTATGGCTCGTC	75
HPV7	AGTGTATTTACCACCGCCCA CGGGCAAGCGTACTCTAAAC	206
HPV11	CGAGCAGACGTCCGTCCTCG GGAATACATGCGCCATGTGG	360
HPV16	TCAAAGCCACTGTGTCCTGA CGTGTTCTTGATGATCTGCAA	119
HPV18	CCGAGCACGACAGGAACGACT TCGTTTTCTTCCTCTGAGTCGCTT	173
HPV14	GGATGATGACGAACAGTGGC TGAGTCTGCTTGTCCTCCTG	220
HPV19	AGGAGGGCGAAAATGGAGAA TAACACCCTTTCGCCTAGCA	166
HPV20	GTTGTTGTTGCCAGCTACCA CCTTCATCAGCGCTGTCTTC	209
HPV21	AAAGTCCAAGCGGTGTCAAC TGAGTCTGCTTGTCCTCCTG	197
HPV25	TGTTAGGTCAGCATTCGGGT GTTTCAACACGAGGCACAGT	223
HPV31	CTACAGTAAGCATTGTGCTATGC ACGTAATGGAGAGGTTGCAATAACCC	155
HPV32	GGACATTTCTCCTCCCACCA CATAGTAGGGCGAGGTCCAG	244
HPV33	GCACACTCCATGCGTATCAG ATGATAGATGATGTAACGCC	456
HPV34	GGAGACACTGTGCAAACGTT TTGCAGTCCCATTTCACGTG	154
HPV39	CACAGAGTCACAACGCCAAA AAAGCGGGACATTGCAACAT	199
HPV43	CTAAGTCCCAGGTTGCATGC CCCCTCCCACACCCTTTATT	188

HPV45	ACCAGATTTGTGCACAGAAT TTTTTTCCAGTGTCTCTCCA	236
HPV52	TTCAGAGTGTTGGAGACCCC TGTGGCTTGTTCTGCTTGTC	197
HPV53	GGTGGTGCCCTGTTTACAAG TGTCCTTGCTGCCATCAAAC	209
HPV56	CAGGATTTGGCGCTATGGAC CCCCAACTTTACCAGCCCTA	198
HPV58	TGCTGTAGAGGACTGTGTGG CATTTAAGTCTGCGTCGCCA	188
HPV59	ATGTGCAGTACCAGTGACGA GTAGACTGAGGGTGCTGTGT	173
HPV61	CACGACAAGCAGGACTAACG ATCGTTGTGGCTGCGTATTC	189
HPV66	GGGTTTGGTGCAATGGACTT CCCCAACATTACCTGCCCTA	196
HPV68	TTTTGTATGGCCGGGTTGTG AGGAGATACGTTGGTTGCCA	212
HPV70	TGTAACCCGCCCTTCATCTT TGAACCTGTGCCCCAATTTG	213
HPV71	CCCGTCTGGCTGATGTAGAT TTCGCCAATCCCCTTCTTCT	183
HPV73	AGACACACATCCTGGTCCAG CTTTGCATCAGTAGGTCGCC	203
HPV82	TTGCAGGTGTTCGAGTGTTG GCCTCCACATAAAACCACCC	191
HPV84	GGGAGGTGTATATGGGAGGC CCGGTGTCCTTGTGTAGAGT	245
HPV85	TACGAGATCTCCAGCAGCTG GTCCTCGTCCTCATCCTCTG	194
HPV86	ATTCACCATGCATGCGACTC GAATGCTCGCTTGTCTCCTG	213
HPV87	GAGTACTCCAGCTACGGACC CAGTTGCTGCACTTTCCTGT	179
HPV90	CATCGCTCTAAACGTCGCAA AGAAGACACCCAAGCTACCC	151
HPV91	GTTGTGGGCTCAAACGTCAT GGCTCTCCTCCAACAGTTCT	230

HPV92	GAAGAAACGAAAACGGGCCT GCAGGCGATCACTATTTGCA	168
HPV97	GCAAAACAACCTTGGAACGC TTCAACGGTTTCTGGCACTG	235
HPV114	TGGCACGTGTTACCATACCT GCAGCAACACACTACACCAA	204
HPV118	TGCGAGCCAGGAGAGTTAAA CACACGTACTCCAGGACCTT	236
HPV152	AACAGGAGAGTGAGGACAGC AGGCGGAGGAGTATTGTCAG	242
HPV195	TATGGGAGTGCTGGTGTGTT ATGTCTGCAGGCCCAATAGT	170
HPV196	TTAGCTCCACTGGACACTGG TTGTTGCTTCTCGGTGGTTG	182
HPV220	CCTTTACCTGCCTCCTCCAA CCTTATCACCCGCCACATTG	152
HPV224	TGGTACAGGGAGCAGTCTTG GCCCCTGGACGAACAATTTT	201