Supplementary Table 1.

PCR primers for amplification of bisulfite-converted HPV16 DNA

Pair	Forward Primer [a]	Reverse Primer [a]	Product Length [b]
1	7835 - 7859	86 - 115	185
2	99 - 124	435 - 462	364
3	416 - 444	666 - 691	276
4	666 - 692	791 - 816	151
5	822 - 849	1262 - 1288	467
6	1281 - 1310	1568 - 1595	315
7	1774 - 1800	2243 - 2272	499
8	2624 - 2648	3009 - 3026	403
9	3006 - 3035	3372 - 3398	393
10	3386 - 3411	3703 - 3725	340
11	3719 - 3748	3942 - 3966	248
12	3991 - 4015	4278 - 4307	317
13	4326 - 4355	4538 - 4563	238
14	4804 - 4833	5139 - 5168	365
15	5066 - 5095	5420 - 5449	384
16	5556 - 5585	5962 - 5986	431
17	6329 - 6358	6601 - 6627	299
18	6605 - 6632	7048 - 7077	473
19	7061 - 7088	7460 - 7484	424
20	7465 - 7492	7749 - 7778	314
12-1	7893 - 3917	4105 - 4140	248
12-2	4133 - 4162	4289 - 4319	187

[a] Nucleotide number in the HPV16 genome.

[b] Length in base-pairs.

Supplementary Table 2.

HPV16 CpGs with partially missing data

ORF	**CpG** [a]	**No. of samples with missing data**	**DNA methylation in samples with complete data**	
			Frequency [b]	**Level** [c]
E1	1509	1/13	2/12	6.3 ± 4.5
E1	1559	1/13	0/12	N/A
E1	1566	2/13	1/11	4.5 ± 4.5
E5	4016	2/13	0/11	N/A
L2	4247	1/13	3/12	8.2 ± 4.4
L2	4259	1/13	0/12	N/A
L2	4268	5/13	0/8	N/A
L2	4275	6/13	0/7	N/A

[a] Position of the cytosine.
[b] Number of samples with methylation/number of samples with data.
[c] Percent of HPV16 copies with methylated CpG (mean ± S.E.M.).