

**Supplemental Table 1. Primers used in analysis of HPV transcription and genome copies**

Primer	Sequence (5' to 3') <sup>a</sup>	Strand	Nucleotide position(s) <sup>a</sup>	ORF(s) <sup>b</sup>	Product length (bp) <sup>c</sup>	Amplification Efficiency <sup>d</sup>
16QE6A	GAACAGCAATACAACAACCG	Sense	368-388	E6	132	1.96
16QE6B	CCACCGACCCCTTATATTATG	Antisense	479-499	E6		
16QE6.2A	GCAACAGTTACTGCGACGTG	Sense	205-224	E6*	176	1.95
16QE6.2B	CAACAAGACATACATCGACCG	Antisense	502-522	E6*		
16QE7A	CAGCTCAGAGGAGGAGGATG	Sense	651-670	E7	114	1.93
16QE7B	CACAACCGAAGCGTAGAGTC	Antisense	745-764	E7		
16QE1E4A	CCATCTGTTCTCAGAAACCAT	Sense	836-856	E1^E4	90	1.94
16QE1E4B	GGCCAAGTGCTGCCTAAT	Antisense	3385-3402	E1^E4		
31QE6A	GCTCGGCATTGGAAATACCC	Sense	154-173	E6	137	2.02
31QE6B	CTCCGTGTGGTGTGTCGTCC	Antisense	272-291	E6		
31QE6.2B	TGCTATGCAACGTCCTGTCC	Antisense	502-521	E6*	164 <sup>e</sup>	2 <sup>e</sup>
31QE7A	ATGAGCAATTACCCGACAGC	Sense	633-652	E7	182	2.02
31QE7B	AGCCATTAACAGCTCTTGC	Antisense	796-815	E7		
31QE1E4A	GGCTCATTTGGAATCGTGTGC	Sense	812-832	E1^E4	167	1.99
31QE1E4B	CTTCACTGGTGCCCAAGG	Antisense	3395-3378	E1^E4		
QTBPA	CACGGCACTGATTTTCAGTTCT	Sense	868-889	TBP	80	2.1
QTBPB	TTCTTGCTGCCAGTCTGGACT	Antisense	968-947	TBP		
16QLCRA	TTCCTGACCTGCACTGCTTG	Sense	7567-7586	LCR	129	1.96
16QLCRB	CAGCGGTATGTAAGGCGTTG	Antisense	7676-7695	LCR		
31QLCRA	GGTGTACGCCATAGTAAAAG	Sense	7384-7404	LCR	168	2.01
31QLCRB	GGAAACCAAAAACCGCAGAAC	Antisense	7531-7551	LCR		
QGAPDHA	GAGAGACCCCTCACTGCTG	Sense	1052-1070	GADPH	136	1.98
QGAPDHB	GATGGTACATGACAAGGTGC	Antisense	1268-1287	GADPH		

<sup>a</sup> Corresponding to the sequence and numbering of HPV16 (GenBank accession number: K02718), HPV31 (GenBank accession number: J04353), TBP (GenBank accession number: M55654), or GAPDH (GenBank accession number: NM\_002046).

<sup>b</sup> Open read frame (ORF) or region of specified gene.

<sup>c</sup> Amplicon length in base pairs.

<sup>d</sup> Actual amplification efficiency of PCR by calculation according to Q-Gen software (32).

<sup>e</sup> Sense primer used in this PCR is 31QE6A

## Supplemental Figure Legend

**Supplemental Figure 1. Genomic organization of HPV16 and HPV31 including general structures of the polycistronic early transcripts.** The circular genome of  $\approx 7900$  base pairs is linearized at the late polyadenylation (polyA) signal to illustrate the long control regulatory region (LCR), open reading frames (ORFs), and main early mRNAs (A-E). Nucleotide numbering is below the thin horizontal rule (based on HPV16 [GenBank accession number: K02718], HPV31 [GenBank accession number: J04353]). Bent arrows mark the major early and late promoters. Early and late polyA sites are indicated. Shaded boxes illustrate ORFs located in all three reading frames for each viral genome aligned with the polycistronic early transcripts (A-E). Each of the primer pairs for qPCR is represented by a node and the products as lines connecting each primer node. Long vertical lines demark the boundaries of the ORFs and the E6\* and E1<sup>E4</sup> introns are shaded the length of the figure. Note that when the amplification products span introns, only spliced RNAs are amplified as the PCR cycle profile does not amplify >200 bp (verified by gel electrophoresis). The specificity of the products and their sizes is given for each (LCR, E6, E6\*, E7, E1<sup>E4</sup>). (A-E) Thick black lines represent noncoding sequences and thin lines represent introns.