

S2 Table. Primer sequences used for APOT assay, ChIP-qPCR and generation of FISH probe

Primer	Sequence (5'→3')	Purpose	Product length (bp)
Amplicon 1F	TAAACGAGGGCAGAGAGAGC	Probe against 20861 amplified cellular flanking sequence	2,184
Amplicon 1R	CAGGCCCTGTCTAAGCACT		
Amplicon 2F	CCCAGAATCTGAGCCAAGCA	Probe against 20861 amplified cellular flanking sequence	2,191
Amplicon 2R	TCATCCCCGGGAATCTGACT		
Amplicon 3F	AAAACAGGCTGGTGGGAACA	Probe against 20861 amplified cellular flanking sequence	2,473
Amplicon 3R	TTTTGCCCCCACTGACAACCT		
Amplicon 4F	TGTTTCCCTATCCACGGTGC	Probe against 20861 amplified cellular flanking sequence	2,442
Amplicon 4R	GTGGGGTCATGACTTGGAGG		
Amplicon 5F	CCGATGCTGTTGATTAGAGGC	Probe against 20861 amplified cellular flanking sequence	2,377
Amplicon 5R	ATTGGGCACACACATTTGC		
Amplicon 6F	ACCTGTCTCTCCCCATCC	Probe against 20861 amplified cellular flanking sequence	2,396
Amplicon 6R	CCTCTCTGCCCAACAGAG		
Amplicon 7F	GATCATTGAACGAGGCACGC	Probe against 20861 amplified cellular flanking sequence	2,497
Amplicon 7R	TGCCTTGAATCAGGGGCAG		
Amplicon 8F	CTGCGAGCTCTGAGAGAGAC	Probe against 20861 amplified cellular flanking sequence	2,035
Amplicon 8R	TGGTGGCTCTGTTATCTGCG		
Amplicon 9F	CTGTGTGCTTTAGGGGCGT	Probe against 20861 amplified cellular flanking sequence	2,181
Amplicon 9R	TTGATGGGATTGCCCTGGGAC		
APOT 20861_P1	CGGACAGAGCCATTACAAT	To determine viral-cellular junction transcript in 20861 cells by amplification of papillomavirus oncogene transcripts, APOT (see (30))	-
Linker sequence (P3)	GACTCGAGTCGACATCG		
APOT 20861_P2	CCTTTTGTGCAAGTGTGACTCTACG		
Oligo(dT)17-P3	GACTCGAGTCGACATCGATTTTTTTTTTTTTTTTTT		
F flank seq F	TCGCCACCAGCCTTAGCA	To determine copy number of cellular flanking sequence at chr2 20861 integration site	114
F flank seq R	AATGCCAGCTGATAAATGTAGAGTGAGTG		
ACTB F	TCGTCCACGCAAATGC	Normalization gene; copy number analysis of cellular flanking sequence at chr2 20861 integration site	76
ACTB R	CGCAAGTTAGGTTTTGTCAAGAAA		
URR F	TTCGGTTGCATGCTTTTTGGCACA	ChIP-qPCR	97
URR R	CACGCATGGCAAGCAGGAAACGTAC		
L1 F	GGCTGCCTAGTGAGGCCACTG	ChIP-qPCR	79
L1 R	GCGTGCAACATATTCATCCGTGC		
E2 F	CGCCGCGACCATAACCAAG	ChIP-qPCR	93
E2 R	GGGGTTTCCGGTGTCTGGCT		
IGLL5 F	CTTGAGGATTGCAGATGGGC	ChIP-qPCR; negative control for super-enhancer	77
IGLL5 R	TGACCCTGATCCTGACCCTA		
CCND2 F	CCTTCTGCTCCACCTTCTCT	ChIP-qPCR; positive control for super-enhancer	76
CCND2 R	CTGACCTCCTCTTTGGCT		
FOSL1 F	AACGTCCTGTTCCATTCT	ChIP-qPCR; positive control for super-enhancer	92
FOSL1 R	GGCAGAGCTAGAACCCACTT		
PPIA F	AGAATTCATCCTAAAGCATAACGG	RT-qPCR; normalization gene	121
PPIA R	TGCTTGCCATCCAACCACTC		
E6*1 F	ACAGTTACTGCGACGTGAGGTG	RT-qPCR	56
E6*1 R	TTCTTCAGGACACAGTGG		
20861 fusion F	TCTACCATGGCTGATCCTGCAGGTATGT	RT-qPCR; viral-host fusion mRNA at chr2 integration site in 20861 cells	105
20861 fusion R	GAGTCATCAAACGATGCTAAGGCTGGTG		
20831/62 fusion F	GCTTTGTAATCAGATGGGATATTATG	RT-qPCR; viral-host fusion mRNA at chr3 integration site in 20831 and 20862 cells	84
20831/62 fusion R	TTGTACATTGTATACTGCAGTGTCTG		