



Primer	Fwd. Sequence	Rev. Sequence	Product length
E6 HPV16	5' CAG AGC TGC AAA CAA CTA TAC 3'	5' AGT GGC TTT TGA CAG TTA ATA C 3'	280 bp
E6 HPV18	5' GCG ACC CTA CAA GCT ACC TGA T 3'	5' GCA CCG CAG GCA CCT TAT TA 3'	298 bp
E7 HPV16	5' GAC AAG CAG AAC CGG ACA G 3'	5' ATT CCT AGT GTG CCC ATT AAC A 3'	139 bp
E7 HPV18	5' TGT CAC GAG CAA TTA AGC GAC T 3'	5' CAC ACA AAG GAC AGG GTG TTC A 3'	279 bp

Figure S1. Validation of E6/E7 expression on HaCaT-transduced cell models. **a)** The graphs shown the amplification curves and CPs derived from real-time-PCR utilizing specific primers for *E6* and *E7* oncogenes from HPV 16 and 18. Pure plasmid LVX with *E6/E7* of HPV 16 and 18 were included as positive controls, and HaCaT parental cells were also included. **b)** Electrophoresis on 2% agarose gels were addressed to demonstrate the presence of the amplicon; we expected the following lengths: E6 HPV16 = 280 bp, E6 HPV18 = 298 bp, E7 HPV16 = 139 bp, and E7 HPV18 = 279 bp. Positive controls: Pure plasmids LVX with *E6/E7* of HPV 16 or 18; Negative controls: HaCaT and HaCaT pLVX. **c)** Sequences used to amplify *E6* or *E7* from HPV16 or 18.

Supplementary Table S1. Primer sets sequences used in qPCR.

Primer	Fwd. Sequence	Rev. Sequence	Product length	Annealing temp.
CCL2	5' GCA GCA AGT GTC CCA A 3'	5' CCC AAG TCT CTG TAT CTA AAA 3'	337 bp	54°C
CCL28	5' AGC TGT TGC ACG GAG GTT T 3'	5' TTC TTG GCA GCT TGC ACT TTC 3'	191 bp	60°C
CXCL1	5'TCA AGA ATG GGC GGA AAG 3'	5'CTT CTC CTA AGC GAT GCT CAA 3'	231 bp	58°C
CXCL2	5' GCT TGT CTC AAC CCC GCA 3'	5' CAC ATT AGG CGC AAT CCA GGT 3'	192 bp	60°C
CXCL3	5' GGG AGC ACC AAC TGA C 3'	5' GAA CCCTCG TAA GAA ATA GTC 3'	168 bp	56°C
CXCL6	5'GTC TGG ACC CGG AAG C 3'	5'CCC CAC ACT CTT CAA AGT GG3'	219 bp	60°C
CXCL8	5' GTG CAG AGG GTT GTG GA 3'	5' ACC AGG AAT CTT GTC TTG CAT 3'	179 bp	56°C
CXCL10	5' GGC CAT CAA GAA TTT ACT GA 3'	5' CAT TAT AGT GCC AGG GTA GAG 3'	292 bp	54°C
CXCL11	5' AGT GAA AGT GGC AGA TAT TG 3'	5' CTT TTC CAG GAC TTC ATA TGT 3'	200 bp	56°C
RPLP0	5' CCT CAT ATC CGG GGG AAT GTG 3'	5' GCA GCA GCT GGC ACC TTA TTG 3'	95 bp	58°C
RPS18	5' CGA TGG GCG GCG GAA AA 3'	5' CAG TCG CTC CAG GTC TTC ACG G 3'	283 bp	58°C

Supplementary Table S2. Summary of all analyses performed.

Chemokine	¹ Cervical Cancer-derived cell lines (RNAseq)			¹ HaCaT-transduced cell models (RNAseq)		² HaCaT-transduced cell models (2-ΔΔCp)		¹ Expression profile of CESC biopsies from TCGA (RNAseq)	³ Overall Survival Analysis (upregulation / prognosis)
	SiHa	HeLa	C33A	E6/E7 HPV16	E6/E7 HPV18	E6/E7 HPV16	E6/E7 HPV16		
CCL2	▼ -5.13	▼ -3.93	▼ -11.03	▲ 4.62	▲ 3.94	▲ 2.95	▲ 3.03	NS	NS
CCL28	▲ 1.66	▼ -4.99	▼ -5.54	▲ 1.48	▲ 4.28	▲ 2.45	▲ 6.94	▲ 0.69	NS
CXCL1	▼ -5.32	▼ -9.73	▼ -8.24	▲ 3.54	▲ 3.62	▼ -0.18	▲ 1.81	▲ 4.84	Worse
CXCL2	▲ 5.14	▲ 5.30	NS	▲ 2.73	▲ 4.06	▲ 3.82	▲ 3.64	NS	Worse
CXCL3	▲ 3.13	▲ 3.43	NS	NS	▲ 4.75	▲ 4.01	▲ 6.19	▲ 2.41	Worse
CXCL6	▼ -8.09	▼ -7.89	▼ -8.85	▲ 3.02	▲ 2.30	▲ 4.07	▲ 3.26	▲ 2.14	Worse
CXCL8	▼ -3.21	▼ -2.29	▼ -9.66	▲ 1.18	▲ 1.74	▲ 0.85	▲ 3.01	▲ 5.22	Worse
CXCL10	▲ 3.62	▲ 5.05	NS	▲ 4.72	▲ 6.42	▲ 3.99	▲ 5.58	▲ 5.72	Better
CXCL11	▲ 4.36	▲ 3.82	NS	NS	▲ 2.55	▲ 2.42	▲ 2.50	▲ 3.94	Worse

* The table summarizes the results of each analysis executed in the present study. ¹The Differential Expression Analysis was performed on Cervical Cancer-derived cell lines, HaCaT-transduced cell models, and CESC biopsies from the TCGA Database. ²For the Relative Expression Analysis on HaCaT-transduced cell models, to normalize the expression data, the *RPS18* and *RPLP0* were taken as reference genes. The data displayed are the means of the two replicates of each reference gene.

³Overall survival data correlates the upregulation of the chemokine panel with the patient's prognosis. All the resulting outputs from the Differential Expression Analysis (RNAseq) and the Relative Expression (2-ΔΔCp) are shown as Log2 Fold-Change. ▲ Upregulation; ▼ Downregulation; (NS) Non-significant.