

Additional files

Table S1. Performance of methylated gene combinations in scrapings of cervical lesions.

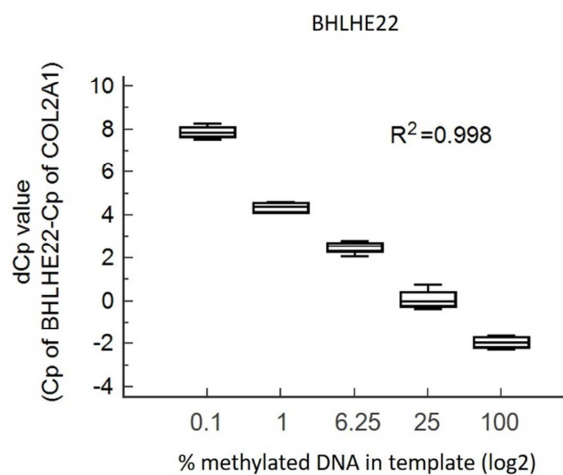
Variables	CIN 2/CIN 3	CIS/SCC
Number of cases	10	9
DNA Methylation		
<i>BHLHE22+CDO1</i>		
High	0	1 (11.1%)
Low	10 (100%)	8 (88.9%)
<i>BHLHE22+CDO1+HAND2</i>		
High	0	0
Low	10 (100%)	9 (100%)
<i>BHLHE22+CDO1+TBX5</i>		
High	0	1 (11.1%)
Low	10 (100%)	8 (88.9%)

The cut-off values were listed in Table 2.

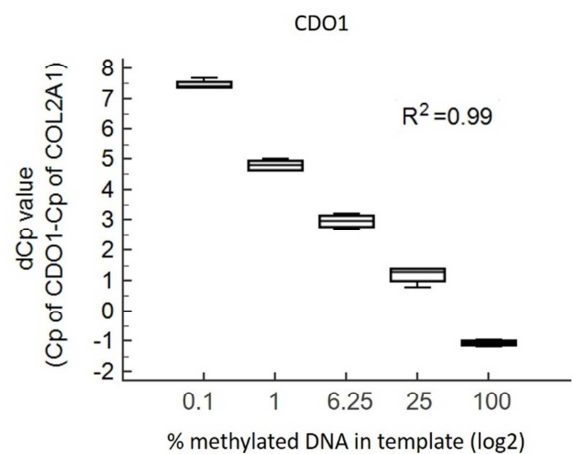
CIN, Cervical intraepithelial neoplasia; CIS, cervical carcinoma in situ; SCC, Squamous Cell Carcinoma.

Figure S1. The analytical sensitivity of target genes and limit of *COL2A1* detection. Linear regression analysis was performed to assess assay linearity. **(A and B)** The ΔC_p values and serial percentages of methylated DNA showed a high correlation ($R^2 = 0.998$ and 0.99 for *BHLHEE22* and *CDO1*, respectively). The mean ΔC_p values of 0.1% methylated DNA were 7.87 and 7.45 for *BHLHEE22* and *CDO1*, respectively. Additionally, when the DNA template was 118 copies, the mean C_p value of *COL2A1* was 35.8 **(C)**. Therefore, we defined clinical samples with C_p values of *COL2A1* >36 as not detectable.

A.



B.



C.

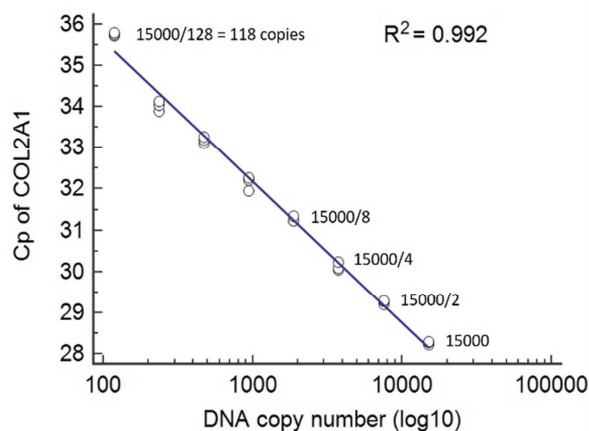


Figure S2. *PTEN* and *TP53* mutations in cervical squamous cell carcinoma. We visualized these two genetic mutations from cBioPortal (<https://www.cbioportal.org/>). Copy number alteration data including 278 samples from The Cancer Genome Atlas and the PanCancer Atlas studies were chosen for mutation analysis.

