

**Supplementary Table S3** Logistic regression analysis of HPV and HPV + *ZNF582* for predicting abnormal (LSIL/HSIL) cytology

Variable	Coefficient ( $\beta$ )	SE	z	P>z	OR	95% CI		
Univariable model								
HPV <sup>a</sup>	1.77	0.27	6.50	0.00	5.86	3.44	to	9.99
constant	-1.66	0.47	-3.52	0.00	0.19	0.08	to	0.48
Multivariable model								
HPV <sup>a</sup>	1.80	0.31	5.84	0.00	6.04	3.30	to	11.04
<i>ZNF582</i> <sup>b</sup>	2.69	0.88	3.05	0.00	14.72	2.61	to	83.06
constant	-2.51	0.66	-3.80	0.00	0.08	0.02	to	0.30

HPV, human papillomavirus; HSIL, high-grade squamous intraepithelial lesion; LSIL, low-grade squamous intraepithelial lesion; ZNF, *ZNF582* gene; SE, standard error; z, z-score.

<sup>a</sup>The HPV genotype identified in each sample was coded accordingly: HPV undetected (0), not classifiable (1), possibly carcinogenic (2), and carcinogenic (3).

<sup>b</sup>The quantified promoter methylation value (%) of *ZNF582* gene at CpG-position 3 of each sample was binarized accordingly: <1.1 (0),  $\geq$ 1.1 (1).