

Supplementary Table S5 Predictive margins for abnormal (LSIL/HSIL) cytology based on HPV or HPV + *ZNF582*

Outcome	MER	Predictors		Predicted Probability Statistics						
	at	HPV ^a	ZNF ^b	Margin ^c	SE	z	P>z	95% CI		
Univariable logit model										
NILM (0), LSIL/HSIL (1)	1	0	-	0.16	0.06	2.52	0.01	0.04	to	0.28
	2	1	-	0.53^d	0.08	6.81	0.00	0.38	to	0.68
	3	2	-	0.87	0.04	21.93	0.00	0.79	to	0.94
	4	3	-	0.97	0.01	73.23	0.00	0.95	to	1.00
Multivariable logit model										
NILM (0), LSIL/HSIL (1)	1	0	0	0.08	0.05	1.64	0.10	-0.01	to	0.17
	2	0	1	0.55	0.21	2.57	0.01	0.13	to	0.96
	3	1	0	0.33^d	0.10	3.41	0.00	0.14	to	0.52
	4	1	1	0.88	0.08	10.55	0.00	0.72	to	1.04
	5	2	0	0.75	0.07	10.72	0.00	0.61	to	0.89
	6	2	1	0.98	0.02	54.45	0.00	0.94	to	1.01
	7	3	0	0.95	0.03	36.30	0.00	0.90	to	1.00
	8	3	1	1.00	0.00	275.01	0.00	0.99	to	1.00

at, number of possible combinations of representative values from each predictor variable; HPV, human papillomavirus; HSIL, high-grade squamous intraepithelial lesion; LSIL, low-grade squamous intraepithelial lesion; MER, marginal effect at representative values (a statistical method to calculate margins); NILM, negative for intraepithelial lesion/malignancy; ZNF, *ZNF582* gene; SE, standard error; z, z-score.

^aThe HPV genotype identified in each sample was coded accordingly: HPV undetected (0), not classifiable (1), possibly carcinogenic (2), and carcinogenic (3).

^bThe quantified promoter methylation value (%) of *ZNF582* gene at CpG-position 3 of each sample was binarized accordingly: <1.1 (0), ≥1.1 (1).

^cThe margin is the predicted probability for the outcome of interest based on representative values from each predictor variable.

^dThe margins (in bold) are the positive outcome or “classification threshold” probabilities used for classification of outcomes and the evaluation of diagnostic test performance. The classification threshold is estimated by using the maximum sum of sensitivity and specificity (Youden’s index).