

CERVICAL CANCER SCREENING

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Table S1 Number of true-positive, false-positive, false-negative, and true-negative results in 1000 women with a positive hrHPV test result at screening and triaged with one of six selected scenarios; PPV, NNR (= 1/PPV), NPV, and cNPV estimated for three situations of underlying background risk of CIN3+: low risk, 5%; intermediate risk, 8%; high risk, 17%

Scenario	Triage test	Pre-test							Post-test positive		Post-test negative	Referral	
		Sen	Spec	Risk	TP	FN	FP	TN	PPV ^a	NPV	cNPV ^a	Test-positive	NNR
<i>Low risk</i>													
1a	Cytology at a threshold of ASC-US+	0.78	0.75	0.05	39	11	240	710	0.140	0.98	0.015	0.28	7
1b	Cytology at a threshold of ASC-US+ with knowledge of HPV status	0.82	0.69	0.05	41	9	294	656	0.122	0.99	0.014	0.34	8
2	HPV16/18 genotyping	0.61	0.75	0.05	31	19	238	712	0.115	0.97	0.026	0.27	9
3	p16/Ki-67 dual staining	0.85	0.64	0.05	43	7	344	606	0.111	0.99	0.011	0.39	9
4	VIA	0.69	0.79	0.05	34	16	203	747	0.143	0.98	0.021	0.24	7
5	HPV16/18 genotyping > cytology at a threshold of ASC-US+	0.86	0.68	0.05	43	7	309	641	0.122	0.99	0.011	0.35	8
6	HPV16/18 genotyping > VIA ^b	0.92	0.58	0.05	46	4	404	546	0.102	0.99	0.007	0.45	10
<i>Intermediate risk</i>													
1a	Cytology at a threshold of ASC-US+	0.78	0.75	0.08	62	18	233	687	0.210	0.97	0.026	0.30	5
1b	Cytology at a threshold of ASC-US+ with knowledge of HPV status	0.82	0.69	0.08	66	14	284	636	0.189	0.98	0.022	0.35	5
2	HPV16/18 genotyping	0.61	0.75	0.08	49	31	231	689	0.175	0.96	0.043	0.28	6
3	p16/Ki-67 dual staining	0.85	0.64	0.08	68	12	333	587	0.170	0.98	0.020	0.40	6
4	VIA	0.69	0.79	0.08	55	25	197	723	0.218	0.97	0.033	0.25	5
5	HPV16/18 genotyping > cytology at a threshold of ASC-US+	0.86	0.68	0.08	69	11	299	621	0.188	0.98	0.017	0.37	5
6	HPV16/18 genotyping > VIA ^b	0.92	0.58	0.08	73	7	391	529	0.157	0.99	0.013	0.46	6

Table S1 (continued)

Scenario	Triage test	Pre-test							Post-test positive		Post-test negative	Referral	
		Sen	Spec	Risk	TP	FN	FP	TN	PPV ^a	NPV	cNPV ^a	Test-positive	NNR
<i>High risk</i>													
1a	Cytology at a threshold of ASC-US+	0.78	0.75	0.17	132	38	210	621	0.386	0.94	0.058	0.34	3
1b	Cytology at a threshold of ASC-US+ with knowledge of HPV status	0.82	0.69	0.17	139	31	256	574	0.352	0.95	0.051	0.40	3
2	HPV16/18 genotyping	0.61	0.75	0.17	104	66	208	622	0.333	0.90	0.096	0.31	3
3	p16/Ki-67 dual staining	0.85	0.64	0.17	145	25	300	530	0.326	0.95	0.045	0.45	3
4	VIA	0.69	0.79	0.17	117	53	178	652	0.397	0.92	0.075	0.30	3
5	HPV16/18 genotyping > cytology at a threshold of ASC-US+	0.86	0.68	0.17	146	24	270	560	0.351	0.96	0.041	0.42	3
6	HPV16/18 genotyping > VIA ^b	0.92	0.58	0.17	156	14	353	477	0.306	0.97	0.029	0.51	3

ASC-US+, atypical squamous cells of undetermined significance or worse; CIN3+, cervical intraepithelial neoplasia grade 3 or worse; cNPV, complement of NPV ($= 1 - NPV =$ post-test risk of CIN3+ if triage-negative); FN, number of false negatives; FP, number of false positives; HPV, human papillomavirus; hrHPV, high-risk human papillomavirus; NNR, number needed to refer = number of women who must be referred for colposcopy to detect 1 case of CIN3+ ($= 1/PPV$); NPV, negative predictive value; PPV, positive predictive value ($=$ post-test risk of CIN3+ if triage-positive); Sen, sensitivity of the triage strategy; Spec, specificity of the triage strategy; TN, number of true negatives; TP, number of true positives; VIA, visual inspection with acetic acid.

^a The shading indicates a risk of CIN3+ > 10% if triage-positive (PPV) and < 1% if triage-negative (cNPV).

^b Based on only 2 studies [unstable estimates].

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