

Table SI. Experimental design matrix and parameter levels for the fractional factorial design.

Parameters		Response variable (Y)	
Duration (t)	Volume (v)	Yield	Purity
30	30	Y_{111}^{Yield} , Y_{112}^{Yield}	Y_{111}^{purity} , Y_{112}^{purity}
	50	Y_{121}^{Yield} , Y_{122}^{Yield} , Y_{123}^{Yield} , Y_{124}^{Yield} , Y_{125}^{Yield}	Y_{121}^{purity} , Y_{122}^{purity} , Y_{123}^{purity} , Y_{124}^{purity} , Y_{125}^{purity}
	60		
	75	Y_{141}^{Yield}	Y_{141}^{purity}
40	30	Y_{211}^{Yield} , Y_{212}^{Yield} , Y_{213}^{Yield} , Y_{214}^{Yield}	Y_{211}^{purity} , Y_{212}^{purity} , Y_{213}^{purity} , Y_{214}^{purity}
	50	Y_{221}^{Yield} , Y_{222}^{Yield} , Y_{223}^{Yield} , Y_{224}^{Yield} , Y_{225}^{Yield} , Y_{226}^{Yield} , Y_{227}^{Yield} , Y_{228}^{Yield} , Y_{229}^{Yield} , $Y_{22(10)}^{Yield}$	Y_{221}^{purity} , Y_{222}^{purity} , Y_{223}^{purity} , Y_{224}^{purity} , Y_{225}^{purity} , Y_{226}^{purity} , Y_{227}^{purity} , Y_{228}^{purity} , Y_{229}^{purity} , $Y_{22(10)}^{purity}$
	60	Y_{231}^{Yield}	Y_{231}^{purity}
	75	Y_{241}^{Yield} , Y_{242}^{Yield} , Y_{243}^{Yield} , Y_{244}^{Yield} , Y_{245}^{Yield}	Y_{241}^{purity} , Y_{242}^{purity} , Y_{243}^{purity} , Y_{244}^{purity} , Y_{245}^{purity}

50	30		
	50		
	60	$Y_{331}^{Yield}, Y_{332}^{Yield}$	$Y_{331}^{purity}, Y_{332}^{purity}$
	75		
80	30		
	50	$Y_{421}^{Yield}, Y_{422}^{Yield}, Y_{423}^{Yield},$ $Y_{424}^{Yield}, Y_{425}^{Yield}$	$Y_{421}^{purity}, Y_{422}^{purity}, Y_{423}^{purity},$ $Y_{424}^{purity}, Y_{425}^{purity}$
	60		
	75		
Duration is expressed in minutes (min), and volume is expressed in microliters (μl). The symbols provided in the table correspond to the mathematical models detailed in the Materials and methods section of the main article. The number of technical replicates was varied across conditions to maximize parameter coverage while prioritizing sample conservation.			

Table SII. Jackknife resampling analysis for evaluating the stability of the linear mixed model for DNA yield.

Sample	P-value						AIC	Replications
	e	t	v	t^2	v^2	$t \cdot v$		
HPV 001	0.179	0.475	0.633	0.762	0.257	0.994	507.300	2
HPV 002	0.193	0.274	0.425	0.535	0.188	0.771	507.820	2
HPV 003	0.098	0.297	0.447	0.493	0.116	0.872	505.510	2
HPV 004	0.192	0.298	0.722	0.587	0.226	0.985	508.170	2
HPV 005 A	0.198	0.287	0.583	0.583	0.211	0.914	525.820	1
HPV 005 B	0.160	0.483	0.538	0.769	0.214	0.926	508.060	2
HPV 005 C	0.153	0.456	0.523	0.738	0.229	0.926	508.100	2
HPV 007	0.222	0.240	0.537	0.466	0.142	0.683	508.050	2
HPV 009	0.247	0.409	0.823	0.788	0.231	0.957	455.960	5
HPV 010	0.208	0.349	0.688	0.667	0.203	0.965	473.530	4
HPV 014	0.178	0.185	0.740	0.363	0.131	0.915	489.900	3
HPV 011	0.177	0.244	0.601	0.681	0.180	0.904	524.730	1
HPV 017	0.156	0.264	0.528	0.738	0.144	0.894	524.190	1
HPV 019	0.172	0.282	0.646	0.388	0.174	0.931	522.380	1
HPV 015	0.170	0.222	0.598	0.711	0.176	0.899	523.690	1
HPV 016	0.136	0.343	0.523	0.395	0.114	0.922	521.110	1
HPV 018	0.473	0.137	0.879	0.714	0.375	0.936	476.710	3

The table provides the P-values of parameters in the multivariable evaluation of the linear mixed model when each sample was excluded in turn during jackknife resampling. e indicates the number of elutions, t indicates the duration times, v indicates the elution volume, t^2 indicates the quadratic term of duration times, v^2 indicates the quadratic term of elution volume, and $t \cdot v$ indicates the interaction between duration times and elution volume. The jackknife resampling analysis demonstrated high model stability, with 17 out of 17 resampling iterations yielding results consistent with the full model.

Table SIII. Jackknife resampling analysis for evaluating the stability of the generalized linear mixed model for purity.

Sample	P-value						AIC	Replications
	e	t	v	t^2	v^2	$t \cdot v$		
HPV 001	0.001	0.001	0.001	0.001	0.001	0.001	46.420	2
HPV 002	0.243	0.037	0.589	0.562	0.172	0.011	47.460	2
HPV 003	0.270	0.738	0.898	0.276	0.261	0.217	46.820	2
HPV 004	0.174	0.542	0.741	0.288	0.353	0.097	48.830	2
HPV 005 A	0.099	0.517	0.989	0.255	0.204	0.067	48.540	1
HPV 005 B	0.118	0.471	0.993	0.292	0.206	0.067	48.440	2
HPV 005 C	0.582	0.699	0.052	0.127	0.954	0.058	46.260	2
HPV 007	0.244	0.052	0.072	0.473	0.589	0.010	48.590	2
HPV 009	0.086	0.880	0.395	0.154	0.760	0.085	42.600	5
HPV 010	0.182	0.786	0.534	0.152	0.569	0.086	47.990	4
HPV 014	0.001	0.001	0.001	0.001	0.001	0.001	45.690	3
HPV 011	0.148	0.555	0.596	0.206	0.341	0.053	49.550	1
HPV 017	0.148	0.269	0.630	0.279	0.293	0.038	48.180	1
HPV 019	0.148	0.269	0.630	0.279	0.293	0.038	48.180	1
HPV 015	0.148	0.555	0.596	0.206	0.341	0.053	49.550	1
HPV 016	0.999	0.999	0.999	0.999	0.999	0.999	38.530	1
HPV 018	0.179	0.250	0.185	0.349	0.883	0.026	46.660	3

The table provides the P-values of parameters in the multivariable evaluation of the generalized linear mixed model in the event that a particular sample was excluded in each jackknife resampling. e indicates the number of elutions, t indicates the duration times, v indicates the elution volume, t^2 indicates the quadratic term of duration times, v^2 indicates the quadratic term of elution volume, and $t \cdot v$ indicates the interaction between duration times and elution volume. The jackknife resampling analysis demonstrated high model stability, with 10 out of 17 resampling iterations yielding results consistent with the full model.

Table SIV. DNA integrity number from TapeStation, and quality assessment, storage temperature and DNA yield of HPV cervicovaginal ThinPrep samples.

Sample ID	Storage temperature (°C)	DNA integrity number	Yield (ng)
HPV 001	-80	4.5	1,275
HPV 001	-80	4.5	258
HPV 002	-80	7.6	3,225
HPV 002	-80	7.6	570
HPV 003	-80	8.4	1,350
HPV 003	-80	8.4	850
HPV 004	-80	7.1	825
HPV 004	-80	7.1	4,020
HPV 005 A	-20	7.5	85
HPV 005 B	-20	7.5	383.5
HPV 005 B	-20	7.5	148
HPV 005 C	-20	6	500
HPV 005 C	-20	6	360
HPV 007	-20	5.7	97.2
HPV 007	-20	6.6	2,150
HPV 009	-20	2.9	2,500
HPV 009	-20	2.9	3,800
HPV 009	-20	2.9	189
HPV 009	-20	2.9	390
HPV 009	-20	2.9	371.25
HPV 010	-20	5.1	3,500
HPV 010	-20	5.1	1,300
HPV 010	-20	5.1	480
HPV 010	-20	5.1	487.5
HPV 014	-20	7.9	845
HPV 014	-20	7.9	1,665
HPV 014	-20	7.9	1,020
HPV 011	-20	6.4	1,550
HPV 017	-80	7.9	2,850

HPV 019	-80	6	8,150
HPV 015	-20	6.1	874
HPV 016	-20	6.2	7,075
HPV 018	-80	7	8,400
HPV 018	-80	7	600
HPV 018	-80	7	7,300

The table summarizes the DNA integrity number, storage temperature and DNA yield of all HPV samples evaluated by TapeStation analysis. These data are presented as part of the post-extraction quality assessment to characterize DNA integrity and sample-to-sample variability following the extraction procedure. As DNA integrity was not included as an optimization endpoint, the results are provided for descriptive quality-control purposes.
