Supplementary Materials

Human Papillomavirus Genotype Distribution and Co-Infection Patterns in Clinically Selected Iraqi Women: A Cross-Sectional Study

Table S1. Complete genotype classification, including manufacturer-assigned risk category, study-applied classification, and detection frequency among the 65 HPV-positive participants. HPV-67 was assigned to the study-applied HR/PHR category based on its IARC Group 2B classification. HPV-62 and HPV-81 share a single probe and are reported as HPV-62/81. Percentages use HPV-positive participants (n = 65) as the denominator, whereas Figure 2 uses total genotype detections (n = 88). Manufacturer-assigned categories followed the assay classification; study-applied categories followed the predefined framework described in the Methods.

Genotype	Manufacturer Category	Study-Applied Category	n (of 65 positive)	% of Positive
HPV-16	HR/PHR	HR/PHR	6	9.2%
HPV-18	HR/PHR	HR/PHR	1	1.5%
HPV-26	HR/PHR	HR/PHR	0	0.0%
HPV-31	HR/PHR	HR/PHR	1	1.5%
HPV-33	HR/PHR	HR/PHR	0	0.0%
HPV-35	HR/PHR	HR/PHR	0	0.0%
HPV-39	HR/PHR	HR/PHR	1	1.5%
HPV-45	HR/PHR	HR/PHR	0	0.0%
HPV-51	HR/PHR	HR/PHR	0	0.0%
HPV-52	HR/PHR	HR/PHR	3	4.6%
HPV-53	HR/PHR	HR/PHR	0	0.0%
HPV-56	HR/PHR	HR/PHR	1	1.5%
HPV-58	HR/PHR	HR/PHR	1	1.5%
HPV-59	HR/PHR	HR/PHR	1	1.5%
HPV-66	HR/PHR	HR/PHR	1	1.5%
HPV-67	LR (manufacturer default)	HR/PHR (reclassified)	3	4.6%
HPV-68	HR/PHR	HR/PHR	0	0.0%
HPV-73	HR/PHR	HR/PHR	0	0.0%
HPV-82	HR/PHR	HR/PHR	0	0.0%
HPV-6	LR	LR	36	55.4%
HPV-11	LR	LR	27	41.5%
HPV-40	LR	LR	1	1.5%
HPV-42	LR	LR	0	0.0%
HPV-43	LR	LR	3	4.6%
HPV-44	LR	LR	0	0.0%
HPV-54	LR	LR	1	1.5%

Genotype	Manufacturer Category	Study-Applied Category	n (of 65 positive)	% of Positive
HPV-55	LR	LR	0	0.0%
HPV-61	LR	LR	0	0.0%
HPV-69	LR	LR	0	0.0%
HPV-70	LR	LR	0	0.0%
HPV-71	LR	LR	0	0.0%
HPV-72	LR	LR	0	0.0%
HPV-84	LR	LR	0	0.0%
HPV-62/81 (combined)	LR / LR	LR / LR (probe-shared)	1	1.5%

LR, low-risk; HR/PHR, high-risk/probably or potentially high-risk; IARC, International Agency for Research on Cancer.

Table S2. Age distribution by HPV risk category, expressed as median, interquartile range (IQR), and range.

Risk Category	n	Median Age (years)	IQR (Q1–Q3)	Range (Min–Max)
Negative	35	32.0	28.5–36.0	20–48
LR	48	30.0	26.8–33.0	20–50
HR/PHR	9	33.0	29.0–35.0	25–40
Mixed	8	31.5	26.8–33.5	23–40

LR, low-risk; HR/PHR, high-risk/probably or potentially high-risk; IQR, interquartile range.

Table S3. Aggregated frequency distribution of individual HPV genotypes detected among the 65 HPV-positive participants (n = 88 genotype detections total). This table reports summary counts only; no individual-level participant data are included, consistent with the Data Availability Statement. .

HPV Genotype	Risk Category	n (detections)	% of Detections (n = 88)
6	LR	36	40.9%
11	LR	27	30.7%
16	HR/PHR	6	6.8%
67	HR/PHR	3	3.4%
43	LR	3	3.4%
52	HR/PHR	3	3.4%
18	HR/PHR	1	1.1%
31	HR/PHR	1	1.1%
39	HR/PHR	1	1.1%
56	HR/PHR	1	1.1%
58	HR/PHR	1	1.1%
59	HR/PHR	1	1.1%
66	HR/PHR	1	1.1%
40	LR	1	1.1%
54	LR	1	1.1%
62/81	LR	1	1.1%

LR, low-risk; HR/PHR, high-risk/probably or potentially high-risk.

Table S4. STROBE checklist for the cross-sectional study, showing reporting items and corresponding manuscript sections.

This checklist confirms that the manuscript reports the required items for cross-sectional studies per the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) guideline.

Item No.	Item	Reported in
1	Title and abstract: Indicate the study's design and provide an informative summary	Title; Abstract
2	Background/rationale: Explain the scientific background and rationale	Section 1 (Introduction)
3	Objectives: State specific objectives, including any prespecified hypotheses	Section 1 (Introduction, final paragraph: study aim)
4	Study design: Present key elements of study design early in the paper	Section 2.1
5	Setting: Describe setting, locations, and relevant dates	Section 2.1
6	Participants: Give eligibility criteria and methods of selection	Section 2.1
7	Variables: Define all outcomes, exposures, predictors, and confounders	Sections 2.4–2.6
8	Data sources/measurement: Give sources of data and details of methods of assessment	Sections 2.1–2.5
9	Bias: Describe efforts to address potential sources of bias	Sections 2.1 and 2.5; Section 4 (limitations)
10	Study size: Explain how the study size was arrived at	Section 2.1 (no formal sample-size calculation)
11	Quantitative variables: Explain how quantitative variables were handled	Section 2.6
12	Statistical methods: Describe all statistical methods	Sections 2.5–2.6
13	Participants: Report numbers at each stage of the study	Sections 2.5 and 3.1
14	Descriptive data: Give characteristics of study participants	Section 3.1; Tables 1 and 2
15	Outcome data: Report numbers of outcome events or summary measures	Sections 3.1–3.4
16	Main results: Give unadjusted estimates and precision (e.g., 95% CI)	Sections 3.1–3.2; Tables 1 and 2
17	Other analyses: Report other analyses done	Sections 3.3–3.4
18	Key results: Summarize key results with reference to study objectives	Section 4 (first paragraph)
19	Limitations: Discuss limitations, sources of bias and imprecision	Section 4 (limitations)
20	Interpretation: Give cautious overall interpretation of results	Sections 4 and 5
21	Generalizability: Discuss the generalizability of the study results	Section 4 (limitations)
22	Funding: Give source of funding and role of funders	Funding statement

STROBE, Strengthening the Reporting of Observational Studies in Epidemiology; CI, confidence interval.

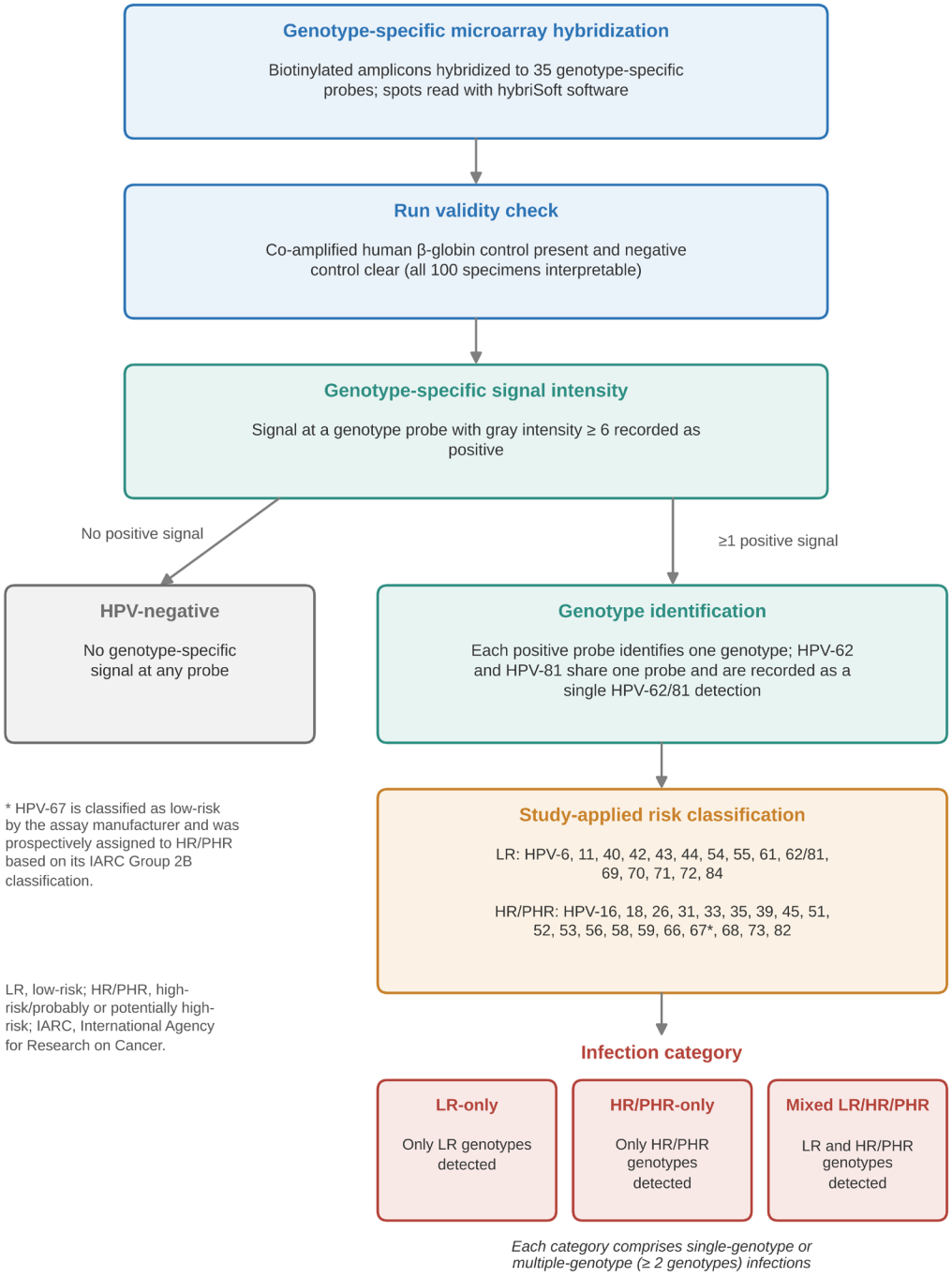


Figure S1. Schematic representation of microarray-based HPV genotype detection and result interpretation. The schematic illustrates the interpretation pathway from genotype-specific microarray hybridiza-tion signals to HPV genotype identification, risk classification, and categorization of single- versus multiple-genotype infections. Detected genotypes were classified as low-risk (LR) or high-risk/potentially high-risk (HR/PHR) according to the predefined study classification. HPV-62/81 represents a combined assay signal recorded as a single genotype detection because the assay did not distinguish between the two genotypes.