

Supplementary File

Variations in the Natural History of High-Risk HPV Types Following HPV-16/18 Bivalent Vaccination in Females Aged 18-45 Years

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Supplementary Method 1. The methods of HPV DNA testing

The HPV DNA enzyme immunoassay method (SPF10-PCR-DEIA, Labo Biomedical Products, Netherlands) was used to qualitatively detect HPV DNA in cervical exfoliated cells and tissue samples. Samples with positive or probably-positive DEIA results were further genotyped for 25 HPV types, including 13 high-risk types (16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, and 68) and 12 intermediate/low-risk types (6, 11, 34, 40, 42, 43, 44, 53, 54, 66, 70, and 74), using a reverse hybridization line probe assay (SPF10-PCR-LiPA25, Labo Biomedical Products, Netherlands) and type-specific DEIA for HPV-16 and HPV-18 (TS16/18, Labo Biomedical Products, Netherlands).

Supplementary Method 2. Multiple testing adjustment

To control for multiple comparisons, we applied a stratified Benjamini-Hochberg false discovery rate (FDR) procedure. Because the analyses included both individual HPV types (HPV-16, -18, -31, -33, -35, -39, -45, -51, -52, -56, -58, -59, and -68) and grouped HPV categories (HPV-16/18, HPV-31/33/45, and HR-HPV), FDR adjustment was performed within each stratum. This approach ensured balanced error control, while avoiding potential dilution of signals from single-type analyses, which may occur because grouped comparisons generally involve larger sample sizes and yield smaller p values.

For each original p value within a stratum, the following steps were performed:

1. **Handling very small p values:** For calculation purposes, any p value reported as <0.0001 was set to 0.0001.
2. **Ranking:** The valid p values were ranked in ascending order. Tied p values were assigned the same average rank. Comparisons without estimable hazard ratios (e.g., when the numerator was zero) were excluded from the ranking and subsequent adjustment.
3. **Adjustment formula:** For a total of m valid comparisons, the FDR-adjusted q value for the i-th ordered p value was calculated as:

$$q_{(i)} = \min_{j \geq i} \left(\frac{p_{(j)} \times m}{j} \right), \quad q_{(i)} \leq 1$$

Where $p_{(j)}$ is the j-th smallest p value and j is its rank. A monotone step-down correction was applied to ensure that the sequence of adjusted q values is non-decreasing.

Supplementary Table 1. Incidences of HR-HPV persistent infections (over 12 months) in the participants who were negative for the corresponding HPV type at baseline

	Vaccine group			Control group			HR (95%CI)	Original p value	FDR-adjusted q value
	n/N*	Person-years at risk	Incidence (95%CI), per 1000 person-years	n/N*	Person-years at risk	Incidence (95%CI), per 1000 person-years			
HPV type									
HPV-16	8/3403	21574.6	0.4 (0.2, 0.7)	48/3392	21269.4	2.3 (1.7, 3.0)	0.17 (0.08, 0.35)	<0.0001	0.0013
HPV-18	4/3447	21867.3	0.2 (0.1, 0.5)	24/3434	21720.0	1.1 (0.7, 1.6)	0.17 (0.06, 0.48)	0.0009	0.0059
HPV-31	12/3453	21897.3	0.5 (0.3, 1.0)	21/3451	21800.6	1.0 (0.6, 1.5)	0.57 (0.28, 1.15)	0.1176	0.3058
HPV-33	12/3449	21854.2	0.5 (0.3, 1.0)	24/3438	21747.2	1.1 (0.7, 1.6)	0.49 (0.25, 0.99)	0.0457	0.1485
HPV-35	18/3459	21907.7	0.8 (0.5, 1.3)	15/3453	21876.4	0.7 (0.4, 1.1)	1.20 (0.60, 2.37)	0.6095	0.7203
HPV-39	41/3438	21652.7	1.9 (1.4, 2.6)	42/3417	21551.6	1.9 (1.4, 2.6)	0.98 (0.64, 1.50)	0.9120	0.9120
HPV-45	1/3465	22011.7	0 (0, 0.3)	2/3456	21950.9	0.1 (0, 0.4)	0.50 (0.05, 5.51)	0.5713	0.7203
HPV-51	54/3413	21419.4	2.5 (1.9, 3.3)	45/3403	21376.0	2.1 (1.6, 2.8)	1.20 (0.81, 1.79)	0.3574	0.7203
HPV-52	129/3293	20389.3	6.3 (5.3, 7.5)	90/3311	20640.0	4.4 (3.5, 5.4)	1.45 (1.11, 1.90)	0.0065	0.0282
HPV-56	32/3448	21734.5	1.5 (1.0, 2.1)	29/3423	21585.1	1.3 (0.9, 1.9)	1.10 (0.67, 1.82)	0.7085	0.7675
HPV-58	45/3435	21645.2	2.1 (1.6, 2.8)	40/3420	21542.0	1.9 (1.4, 2.5)	1.12 (0.73, 1.72)	0.5923	0.7203
HPV-59	11/3460	21932.8	0.5 (0.3, 0.9)	8/3450	21894.0	0.4 (0.2, 0.7)	1.37 (0.55, 3.41)	0.4957	0.7203
HPV-68	27/3442	21720.5	1.2 (0.9, 1.8)	31/3431	21702.1	1.4 (1.0, 2.0)	0.87 (0.52, 1.46)	0.6002	0.7203
HPV group									
HPV-16/18	12/3475	22080.5	0.5 (0.3, 1.0)	72/3463	21983.5	3.3 (2.6, 4.1)	0.17 (0.09, 0.31)	<0.0001	0.0003
HPV-31/33/45	25/3476	22096.2	1.1 (0.8, 1.7)	47/3465	22025.0	2.1 (1.6, 2.8)	0.53 (0.32, 0.86)	0.0105	0.0158
HR-HPV	394/3477	22096.8	17.8 (16.2, 19.7)	419/3465	22025.0	19.0 (17.3, 20.9)	0.94 (0.81, 1.10)	0.4386	0.4386

HR-HPV, high-risk human papillomavirus; HR, hazard ratio; 95%CI, 95% confidence interval; FDR, false discovery rate.

For type-specific analyses, the standard Cox proportional hazards model was used. For HPV-16/18, HPV-31/33/45, and HR-HPV groups, the Wei-Lin-Weissfeld (WLW) Cox model was applied. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

*n, the number of events; N, the number of participants in the analysis set.

Supplementary Table 2. Incidences of HR-HPV-associated CIN2+ among participants who were negative for the corresponding HPV type at baseline and did not have multiple HR-HPV infections during follow-up (sensitivity analysis)

HPV type	Vaccine group			Control group			HR (95%CI)	Original p value	FDR-adjusted q value
	n/N*	Person-years at risk	Incidence (95%CI), per 1000 person-years	n/N*	Person-years at risk	Incidence (95%CI), per 1000 person-years			
HPV-16	1/3467	21472.5	0 (0, 0.3)	9/3404	21090.8	0.4 (0.2, 0.8)	0.11 (0.01, 0.88)	0.0373	0.0933
HPV-18	0/3541	21859.9	0	1/3473	21508.9	0 (0, 0.3)	NE	NE	NE
HPV-31	0/3534	21795.7	0	1/3488	21572.9	0 (0, 0.3)	NE	NE	NE
HPV-33	1/3532	21787.1	0 (0, 0.3)	3/3494	21622.1	0.1 (0, 0.4)	0.38 (0.04, 3.63)	0.3970	0.6617
HPV-35	0/3544	21846.8	0	3/3514	21762.1	0.1 (0, 0.4)	NE	NE	NE
HPV-39	0/3490	21559.8	0	0/3438	21353.5	0	NE	NE	NE
HPV-45	0/3568	22002.6	0	0/3533	21861.1	0	NE	NE	NE
HPV-51	0/3444	21267.3	0	2/3418	21139.7	0.1 (0, 0.4)	NE	NE	NE
HPV-52	9/3285	20361.5	0.4 (0.2, 0.9)	1/3286	20431.2	0 (0, 0.3)	9.17 (1.16, 72.44)	0.0356	0.0933
HPV-56	0/3498	21571.7	0	1/3452	21369.3	0 (0, 0.3)	NE	NE	NE
HPV-58	5/3503	21627.9	0.2 (0.1, 0.6)	5/3459	21439.1	0.2 (0.1, 0.6)	1.08 (0.31, 3.74)	0.9083	0.9950
HPV-59	0/3544	21871.3	0	3/3512	21756.1	0.1 (0, 0.4)	NE	NE	NE
HPV-68	1/3504	21633.9	0 (0, 0.3)	1/3462	21448.7	0 (0, 0.3)	1.01 (0.06, 16.13)	0.9950	0.9950
HPV group									
HPV-16/18	1/3571	22038.2	0 (0, 0.3)	10/3528	21830.1	0.5 (0.2, 0.9)	0.10 (0.01, 0.77)	0.0268	0.0804
HPV-31/33/45	1/3585	22109.7	0 (0, 0.3)	4/3558	22018.3	0.2 (0.1, 0.5)	0.29 (0.03, 2.61)	0.2698	0.2698
HR-HPV	17/3585	22109.7	0.8 (0.5, 1.2)	30/3558	22018.3	1.4 (1.0, 1.9)	0.58 (0.32, 1.06)	0.0757	0.1136

HR-HPV, high-risk human papillomavirus; HR, hazard ratio; 95%CI, 95% confidence interval; NE, not estimated; FDR, false discovery rate.

For type-specific analyses, the standard Cox proportional hazards model was used. For HPV-16/18, HPV-31/33/45, and HR-HPV groups, the Wei-Lin-Weissfeld (WLW) Cox model was applied. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

*n, the number of events; N, the number of participants in the analysis set.

Supplementary Table 3. The persistence of incident HR-HPV infections in the vaccine group and the control group

	Vaccine group			Control group			Original p value	FDR-adjusted q value
	N*	n*	Proportion (95%CI)	N*	n*	Proportion (95%CI)		
HPV type								
HPV-16	92	10	10.9 (5.3, 19.1)	176	75	42.6 (35.2, 50.3)	<0.0001	0.0013
HPV-18	38	4	10.5 (2.9, 24.8)	114	41	36.0 (27.2, 45.5)	0.0029	0.0189
HPV-31	56	17	30.4 (18.8, 44.1)	101	32	31.7 (22.8, 41.7)	0.8636	0.9615
HPV-33	51	21	41.2 (27.6, 55.8)	74	31	41.9 (30.5, 53.9)	0.9364	0.9615
HPV-35	47	26	55.3 (40.1, 69.8)	66	27	40.9 (29.0, 53.7)	0.1303	0.4235
HPV-39	182	73	40.1 (32.9, 47.6)	145	61	42.1 (33.9, 50.5)	0.7204	0.9615
HPV-45	14	6	42.9 (17.7, 71.1)	32	11	34.4 (18.6, 53.2)	0.5834	0.9615
HPV-51	225	86	38.2 (31.8, 44.9)	200	78	39.0 (32.2, 46.1)	0.8694	0.9615
HPV-52	299	160	53.5 (47.7, 59.3)	277	116	41.9 (36.0, 47.9)	0.0052	0.0225
HPV-56	135	61	45.2 (36.6, 54.0)	121	50	41.3 (32.4, 50.6)	0.5335	0.9615
HPV-58	108	57	52.8 (42.9, 62.5)	122	64	52.5 (43.2, 61.6)	0.9615	0.9615
HPV-59	75	25	33.3 (22.9, 45.2)	77	22	28.6 (18.8, 40.0)	0.5254	0.9615
HPV-68	124	50	40.3 (31.6, 49.5)	140	52	37.1 (29.1, 45.7)	0.5964	0.9615
HPV group								
HPV-16/18	130	14	10.8 (6.0, 17.4)	290	116	40.0 (34.3, 45.9)	<0.0001	0.0003
HPV-31/33/45	121	44	36.4 (27.8, 45.6)	207	76	35.7 (29.2, 42.7)	0.9109	0.9109
HR-HPV	1446	601	41.2 (38.7, 43.8)	1645	666	40.1 (37.7, 42.5)	0.5361	0.8042

HR-HPV, high-risk human papillomavirus; 95%CI, 95% confidence interval; FDR, false discovery rate.

p values were determined using the chi-squared test or Fisher's exact test. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

*N, the number of infection events; n, the number of persistent infection events.

Supplementary Table 4. The clearance of incident HR-HPV infections in the vaccine group and the control group

HPV type	Vaccine group					Control group					HR (95%CI)	Original p value	FDR-adjusted q value
	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years			
HPV-16	92	91	98.9 (94.1, 100.0)	96.6	94.2 (76.7, 115.7)	176	155	88.1 (82.3, 92.5)	278.4	55.7 (47.6, 65.2)	1.78 (1.36, 2.31)	<0.0001	0.0013
HPV-18	38	38	100 (90.7, 100.0)	45.3	83.9 (61.1, 115.3)	114	101	88.6 (81.3, 93.8)	137.9	73.2 (60.3, 89.0)	1.32 (0.90, 1.93)	0.1496	0.4524
HPV-31	56	53	94.6 (85.1, 98.9)	70.1	75.6 (57.7, 98.9)	101	91	90.1 (82.5, 95.1)	131.7	69.1 (56.2, 84.8)	0.99 (0.70, 1.39)	0.9366	0.9366
HPV-33	51	42	82.4 (69.1, 91.6)	59.3	70.9 (52.4, 95.9)	74	65	87.8 (78.2, 94.3)	103.5	62.8 (49.3, 80.1)	1.25 (0.84, 1.85)	0.2747	0.5822
HPV-35	47	40	85.1 (71.7, 93.8)	70.3	56.9 (41.8, 77.6)	66	60	90.9 (81.3, 96.6)	91.5	65.6 (50.9, 84.5)	0.88 (0.59, 1.32)	0.5427	0.7094
HPV-39	182	170	93.4 (88.8, 96.5)	243.4	69.8 (60.1, 81.2)	145	131	90.3 (84.3, 94.6)	198.6	66.0 (55.6, 78.3)	1.08 (0.86, 1.36)	0.4977	0.7094
HPV-45	14	13	92.9 (66.1, 99.8)	11.1	117.6 (68.3, 202.6)	32	32	100.0 (89.1, 100.0)	35.4	90.3 (63.9, 127.7)	2.39 (1.15, 4.99)	0.0203	0.1320
HPV-51	225	201	89.3 (84.5, 93.0)	284.3	70.7 (61.6, 81.2)	200	183	91.5 (86.7, 95.0)	266.0	68.8 (59.5, 79.5)	1.05 (0.86, 1.28)	0.6463	0.7638
HPV-52	299	239	79.9 (74.9, 84.3)	531.5	45.0 (39.6, 51.0)	277	238	85.9 (81.3, 89.8)	438.4	54.3 (47.8, 61.6)	0.83 (0.70, 1.00)	0.0488	0.2115
HPV-56	135	127	94.1 (88.7, 97.4)	180.7	70.3 (59.1, 83.6)	121	110	90.9 (84.3, 95.4)	167.9	65.5 (54.3, 79.0)	1.08 (0.84, 1.40)	0.5457	0.7094
HPV-58	108	91	84.3 (76.0, 90.6)	176.4	51.6 (42.0, 63.4)	122	101	82.8 (74.9, 89.0)	168.1	60.1 (49.4, 73.0)	0.82 (0.62, 1.09)	0.1740	0.4524
HPV-59	75	72	96.0 (88.8, 99.2)	90.0	80.0 (63.5, 100.7)	77	72	93.5 (85.5, 97.9)	91.7	78.5 (62.3, 98.9)	0.97 (0.70, 1.35)	0.8571	0.9285
HPV-68	124	114	91.9 (85.7, 96.1)	154.7	73.7 (61.3, 88.6)	140	127	90.7 (84.6, 95.0)	187.3	67.8 (57, 80.7)	1.14 (0.88, 1.48)	0.3135	0.5822
HPV group													

	Vaccine group					Control group					HR (95%CI)	Original p value	FDR-adjusted q value
	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years			
HPV-16/18	130	129	99.2 (95.8, 100.0)	141.9	90.9 (76.5, 108.1)	290	256	88.3 (84.0, 91.7)	416.3	61.5 (54.4, 69.5)	1.61 (1.30, 1.99)	<0.0001	0.0003
HPV-31/33/45	121	108	89.3 (82.3, 94.2)	140.5	76.9 (63.7, 92.9)	207	188	90.8 (86.0, 94.4)	270.7	69.5 (60.2, 80.1)	1.17 (0.92, 1.49)	0.1956	0.2209
HR-HPV	1446	1291	89.3 (87.6, 90.8)	2013.7	64.1 (60.7, 67.7)	1645	1466	89.1 (87.5, 90.6)	2296.5	63.8 (60.7, 67.2)	1.05 (0.97, 1.14)	0.2209	0.2209

HR-HPV, high-risk human papillomavirus; HR, hazard ratio; 95%CI, 95% confidence interval; FDR, false discovery rate.

For type-specific analyses, the standard Cox proportional hazards model was used. For HPV-16/18, HPV-31/33/45, and HR-HPV groups, the Wei-Lin-Weissfeld (WLW) Cox model was applied. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

*N, the number of infection events; n, the number of cleared infection events.

Supplementary Table 5. Persistence duration of incident HR-HPV infections in the vaccine group and the control group

	Vaccine group			Control group			Original p value	FDR-adjusted q value
	N*	Mean times (SD), months [#]	Median times (IQR), months	N*	Mean times (SD), months [#]	Median times (IQR), months		
HPV type								
HPV-16	92	2.4 (8.6)	0 (0, 0)	176	7.8 (14.5)	0 (0, 11.1)	<0.0001	0.0013
HPV-18	38	3.7 (15.4)	0 (0, 0)	114	4.9 (10.7)	0 (0, 6.1)	0.0073	0.0316
HPV-31	56	4.3 (9.2)	0 (0, 5.6)	101	6.1 (15.7)	0 (0, 5.5)	0.8601	0.8601
HPV-33	51	4.6 (6.8)	0 (0, 9.3)	74	6.9 (10.6)	0 (0, 12.1)	0.5059	0.7328
HPV-35	47	7.3 (9.4)	5.0 (0, 13.3)	66	5.7 (10.3)	0 (0, 6.9)	0.1393	0.4527
HPV-39	182	4.9 (8.6)	0 (0, 6.3)	145	5.6 (9.1)	0 (0, 9.1)	0.5252	0.7328
HPV-45	14	3.0 (3.9)	0 (0, 5.8)	32	2.5 (4.4)	0 (0, 5.2)	0.6691	0.7908
HPV-51	225	5.2 (9.2)	0 (0, 6.9)	200	4.6 (8.2)	0 (0, 6.8)	0.7744	0.8389
HPV-52	299	11.8 (16.7)	5.2 (0, 17.2)	277	7.7 (12.7)	0 (0, 11.6)	0.0014	0.0091
HPV-56	135	5.5 (8.6)	0 (0, 9.1)	121	5.7 (10.9)	0 (0, 6.8)	0.5604	0.7328
HPV-58	108	9.3 (11.9)	5.4 (0, 16.6)	122	6.9 (10.1)	4.4 (0, 10.9)	0.2353	0.6118
HPV-59	75	3.6 (6.9)	0 (0, 5.7)	77	2.9 (6.3)	0 (0, 4.5)	0.4577	0.7328
HPV-68	124	4.5 (7.7)	0 (0, 6.8)	140	4.4 (8.0)	0 (0, 6.5)	0.5637	0.7328
HPV group								
HPV-16/18	130	2.8 (11.0)	0 (0, 0)	290	6.6 (13.2)	0 (0, 8.5)	<0.0001	0.0003
HPV-31/33/45	121	4.3 (7.7)	0 (0, 5.9)	207	5.8 (12.8)	0 (0, 6.1)	0.8495	0.8495
HR-HPV	1446	6.5 (11.5)	0 (0, 10.5)	1645	5.9 (11.1)	0 (0, 8.0)	0.2290	0.3435

HR-HPV, high-risk human papillomavirus; FDR, false discovery rate; SD, standard deviation; IQR, interquartile range.

p values were determined using the Wilcoxon rank sum test. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

*N, the number of infection events;

[#]The persistence duration of infection exhibited a left-skewed distribution. Due to persistence events occurring in fewer than 50% for certain HPV types, the median times and lower quartile were 0 months. Therefore, we also presented the mean times for each HPV type.

Supplementary Table 6. The clearance time of HR-HPV infections in the vaccine group and the control group

	Vaccine group		Control group		Original p value	FDR-adjusted q value
	N*	Median times (IQR), months	N*	Median times (IQR), months		
HPV type						
HPV-16	92	7.6 (5.7, 13.7)	176	13.1 (6.6, 24.5)	0.0007	0.0091
HPV-18	38	8.3 (5.7, 13.5)	114	11.8 (6.2, 17.0)	0.1148	0.3731
HPV-31	56	13.0 (6.7, 18.2)	101	12.3 (6.2, 17.0)	0.4851	0.7883
HPV-33	51	12.8 (6.1, 17.2)	74	13.2 (6.7, 23.2)	0.2479	0.4604
HPV-35	47	13.1 (7.0, 25.1)	66	13.8 (6.9, 20.8)	0.9281	0.9281
HPV-39	182	12.6 (7.8, 18.4)	145	12.6 (7.1, 18.7)	0.7586	0.8218
HPV-45	14	11.0 (6.1, 11.7)	32	12.7 (6.9, 14.3)	0.0660	0.2860
HPV-51	225	12.1 (6.9, 17.9)	200	12.6 (7.7, 22.6)	0.2355	0.4604
HPV-52	299	14.2 (10.2, 28.5)	277	13.2 (8.7, 26.7)	0.2018	0.4604
HPV-56	135	12.9 (10.5, 19.1)	121	13.2 (10.2, 21.6)	0.5740	0.8218
HPV-58	108	14.7 (10.9, 27.1)	122	12.8 (7.3, 22.5)	0.0518	0.2860
HPV-59	75	12.4 (6.2, 16.6)	77	12.0 (6.7, 15.1)	0.7166	0.8218
HPV-68	124	12.8 (6.9, 18.6)	140	12.6 (10.3, 22.8)	0.6378	0.8218
HPV group						
HPV-16/18	130	7.8 (5.7, 13.5)	290	12.9 (6.2, 22.5)	0.0005	0.0015
HPV-31/33/45	121	12.8 (6.7, 15.7)	207	12.9 (6.4, 18.6)	0.4821	0.6682
HR-HPV	1446	13.0 (6.9, 23.0)	1645	12.9 (6.9, 22.7)	0.6682	0.6682

HR-HPV, high-risk human papillomavirus; FDR, false discovery rate; IQR, interquartile range.

p values were determined using the Wilcoxon rank sum test. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

* N, the number of infection events;

Supplementary Table 7. The persistence of incident single-type HR-HPV infections in the vaccine group and the control group

	Vaccine group			Control group			Original p value	FDR-adjusted q value
	N*	n*	Proportion (95%CI)	N*	n*	Proportion (95%CI)		
HPV type								
HPV-16	52	2	3.9 (0.5, 13.2)	95	38	40.0 (30.1, 50.6)	< 0.0001	0.0013
HPV-18	23	3	13.0 (2.8, 33.6)	60	19	31.7 (20.3, 45.0)	0.0853	0.3696
HPV-31	30	9	30.0 (14.7, 49.4)	45	13	28.9 (16.4, 44.3)	0.9175	0.9411
HPV-33	26	11	42.3 (23.4, 63.1)	37	16	43.2 (27.1, 60.5)	0.9411	0.9411
HPV-35	24	12	50.0 (29.1, 70.9)	35	12	34.3 (19.1, 52.2)	0.2274	0.5912
HPV-39	128	46	35.9 (27.7, 44.9)	78	30	38.5 (27.7, 50.2)	0.7157	0.9411
HPV-45	8	4	50.0 (15.7, 84.3)	16	4	25.0 (7.3, 52.4)	0.2207	0.5912
HPV-51	149	54	36.2 (28.5, 44.5)	125	41	32.8 (24.7, 41.8)	0.5510	0.8954
HPV-52	189	99	52.4 (45.0, 59.7)	166	60	36.1 (28.8, 44.0)	0.0021	0.0137
HPV-56	77	29	37.7 (26.9, 49.4)	59	26	44.1 (31.2, 57.6)	0.4506	0.8368
HPV-58	70	34	48.6 (36.4, 60.8)	69	32	46.4 (34.3, 58.8)	0.7956	0.9411
HPV-59	51	16	31.4 (19.1, 45.9)	49	16	32.7 (20.0, 47.5)	0.8909	0.9411
HPV-68	77	32	41.6 (30.4, 53.4)	81	27	33.3 (23.2, 44.7)	0.2854	0.6184
HPV group								
HPV-16/18	75	5	6.7 (2.2, 14.9)	155	57	36.8 (29.2, 44.9)	< 0.0001	0.0003
HPV-31/33/45	64	24	37.5 (25.7, 50.5)	98	33	33.7 (24.4, 43.9)	0.6181	0.6181
HR-HPV	904	351	38.8 (35.6, 42.1)	915	334	36.5 (33.4, 39.7)	0.3063	0.4595

HR-HPV, high-risk human papillomavirus; 95%CI, 95% confidence interval; FDR, false discovery rate.

p values were determined using the chi-squared test or Fisher's exact test. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

*N, the number of infection events; n, the number of persistent infection events.

Supplementary Table 8. The clearance of incident single-type HR-HPV infections in the vaccine group and the control group (sensitivity analysis)

HPV type	Vaccine group					Control group					HR (95%CI)	Original p value	FDR-adjusted q value
	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years			
HPV-16	52	52	100.0 (93.2, 100.0)	49.9	104.3 (79.5, 136.9)	95	85	89.5 (81.5, 94.8)	141.4	60.1 (48.6, 74.4)	1.83 (1.28, 2.62)	0.0009	0.0117
HPV-18	23	23	100.0 (85.2, 100.0)	33.6	68.4 (45.4, 102.9)	60	53	88.3 (77.4, 95.2)	64.6	82.1 (62.7, 107.5)	0.96 (0.56, 1.66)	0.8960	0.9998
HPV-31	30	28	93.3 (77.9, 99.2)	36.8	76.2 (52.6, 110.3)	45	40	88.9 (76.0, 96.3)	66.8	59.8 (43.9, 81.6)	1.07 (0.65, 1.76)	0.7928	0.9998
HPV-33	26	19	73.1 (52.2, 88.4)	31.0	61.4 (39.1, 96.2)	37	32	86.5 (71.2, 95.5)	49.6	64.5 (45.6, 91.3)	1.12 (0.62, 2.01)	0.7131	0.9998
HPV-35	24	19	79.2 (57.9, 92.9)	30.8	61.6 (39.3, 96.6)	35	33	94.3 (80.8, 99.3)	46.5	71.0 (50.5, 99.9)	0.89 (0.50, 1.61)	0.7083	0.9998
HPV-39	128	121	94.5 (89.1, 97.8)	172.0	70.3 (58.9, 84.1)	78	71	91.0 (82.4, 96.3)	99.6	71.3 (56.5, 90.0)	0.95 (0.70, 1.27)	0.7090	0.9998
HPV-45	8	7	87.5 (47.4, 99.7)	5.7	122.7 (58.5, 257.3)	16	16	100.0 (79.4, 100.0)	17.3	92.6 (56.8, 151.2)	3.24 (1.06, 9.85)	0.0387	0.1677
HPV-51	149	133	89.3 (83.2, 93.7)	179.7	74.0 (62.4, 87.7)	125	114	91.2 (84.8, 95.5)	156.2	73.0 (60.7, 87.7)	1.00 (0.78, 1.29)	0.9998	0.9998
HPV-52	189	148	78.3 (71.7, 84.0)	348.7	42.4 (36.1, 49.9)	166	145	87.4 (81.3, 92.0)	244.9	59.2 (50.3, 69.7)	0.70 (0.56, 0.89)	0.0030	0.0195
HPV-56	77	72	93.5 (85.5, 97.9)	93.9	76.7 (60.8, 96.6)	59	54	91.5 (81.3, 97.2)	80.1	67.4 (51.6, 88.0)	1.22 (0.84, 1.75)	0.2945	0.7657
HPV-58	70	58	82.9 (72.0, 90.8)	111.2	52.2 (40.3, 67.5)	69	57	82.6 (71.6, 90.7)	90.5	63.0 (48.6, 81.7)	0.77 (0.53, 1.11)	0.1646	0.5350
HPV-59	51	49	96.1 (86.5, 99.5)	64.5	75.9 (57.4, 100.5)	49	46	93.9 (83.1, 98.7)	56.4	81.6 (61.1, 109.0)	0.87 (0.58, 1.31)	0.5123	0.9998
HPV-68	77	70	90.9 (82.2, 96.3)	109.1	64.2 (50.8, 81.1)	81	75	92.6 (84.6, 97.2)	115.3	65.1 (51.9, 81.6)	1.01 (0.72, 1.41)	0.9689	0.9998
HPV group													

	Vaccine group					Control group					HR (95%CI)	Original p value	FDR-adjusted q value
	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years			
HPV-16/18	75	75	100.0 (95.2, 100.0)	83.5	89.8 (71.6, 112.6)	155	138	89.0 (83.0, 93.5)	206.0	67.0 (56.7, 79.2)	1.44 (1.08, 1.92)	0.0125	0.0375
HPV-31/33/45	64	54	84.4 (73.1, 92.2)	73.4	73.5 (56.3, 96.0)	98	88	89.8 (82.0, 95.0)	133.7	65.8 (53.4, 81.1)	1.10 (0.78, 1.55)	0.5826	0.5826
HR-HPV	904	799	88.4 (86.1, 90.4)	1267.0	63.1 (58.8, 67.6)	915	821	89.7 (87.6, 91.6)	1229.0	66.8 (62.4, 71.5)	0.93 (0.85, 1.03)	0.1681	0.2522

HR-HPV, high-risk human papillomavirus; HR, hazard ratio; 95%CI, 95% confidence interval; FDR, false discovery rate.

For type-specific analyses, the standard Cox proportional hazards model was used. For HPV-16/18, HPV-31/33/45, and HR-HPV groups, the Wei-Lin-Weissfeld (WLW) Cox model was applied. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

*N, the number of infection events; n, the number of cleared infection events.

Supplementary Table 9. Persistence duration of incident single-type HR-HPV infections in the vaccine group and the control group (sensitivity analysis)

	Vaccine group			Control group			Original p value	FDR-adjusted q value
	N*	Mean times (SD), months [#]	Median times (IQR), months	N*	Mean times (SD), months [#]	Median times (IQR), months		
HPV type								
HPV-16	52	0.6 (3.4)	0 (0, 0)	95	6.7 (14.2)	0 (0, 9.1)	<0.0001	0.0013
HPV-18	23	5.7 (19.5)	0 (0, 0)	60	3.8 (6.8)	0 (0, 5.7)	0.1571	0.5408
HPV-31	30	4.2 (9.4)	0 (0, 5.9)	45	7.5 (19.9)	0 (0, 5.0)	0.9786	0.9786
HPV-33	26	4.9 (7.2)	0 (0, 11.0)	37	6.1 (9.0)	0 (0, 12.1)	0.7276	0.8599
HPV-35	24	6.9 (10.3)	2.5 (0, 11.7)	35	3.9 (6.6)	0 (0, 5.8)	0.2348	0.5408
HPV-39	128	4.2 (7.8)	0 (0, 5.8)	78	5.0 (9.3)	0 (0, 6.7)	0.6619	0.8599
HPV-45	8	3.4 (4.2)	2.3 (0, 5.4)	16	1.2 (2.5)	0 (0, 0.4)	0.2285	0.5408
HPV-51	149	4.5 (8.0)	0 (0, 6.6)	125	4.0 (8.2)	0 (0, 5.3)	0.5270	0.7612
HPV-52	189	11.8 (16.8)	5.1 (0, 17.2)	166	6.4 (12.2)	0 (0, 7.6)	0.0004	0.0026
HPV-56	77	4.1 (6.1)	0 (0, 6.8)	59	5.5 (9.3)	0 (0, 10.6)	0.5172	0.7612
HPV-58	70	8.6 (10.8)	0 (0, 17.5)	69	5.9 (8.6)	0 (0, 8.5)	0.2500	0.5408
HPV-59	51	3.3 (6.9)	0 (0, 5.4)	49	3.2 (5.7)	0 (0, 5.1)	0.8448	0.9152
HPV-68	77	5.3 (9.0)	0 (0, 10.7)	81	4.5 (8.8)	0 (0, 6.7)	0.2912	0.5408
HPV group								
HPV-16/18	75	2.1 (11.3)	0 (0, 0)	155	5.6 (11.9)	0 (0, 8.0)	<0.0001	0.0003
HPV-31/33/45	64	4.4 (8.0)	0 (0, 5.9)	98	6.0 (14.7)	0 (0, 5.6)	0.7925	0.7925
HR-HPV	904	6.1 (11.3)	0 (0, 9.4)	915	5.2 (10.6)	0 (0, 6.7)	0.1229	0.1844

HR-HPV, high-risk human papillomavirus; FDR, false discovery rate; SD, standard deviation; IQR, interquartile range.

p values were determined using the Wilcoxon rank sum test. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

*N, the number of infection events;

[#]The persistence duration of infection exhibited a left-skewed distribution. Due to persistence events occurring in fewer than 50% for certain HPV types, the median times and lower quartile were 0 months. Therefore, we also presented the mean times for each HPV type.

Supplementary Table 10. The clearance time of single-type HR-HPV infections in the vaccine group and the control group (sensitivity analysis)

	Vaccine group		Control group		Original p value	FDR-adjusted q value
	N*	Median times (IQR), months	N*	Median times (IQR), months		
HPV type						
HPV-16	52	7.2 (5.7, 13.2)	95	13.0 (5.9, 24.5)	0.0196	0.2158
HPV-18	23	9.7 (5.6, 18.2)	60	11.7 (6.0, 13.8)	0.5619	0.8175
HPV-31	30	13.0 (6.8, 18.0)	45	12.3 (6.2, 22.1)	0.9139	0.9384
HPV-33	26	12.9 (6.9, 17.9)	37	13.1 (6.9, 22.7)	0.6804	0.8175
HPV-35	24	13.0 (7.7, 19.7)	35	14.3 (7.0, 24.4)	0.6545	0.8175
HPV-39	128	13.2 (8.2, 17.9)	78	12.2 (7.0, 17.0)	0.4802	0.8175
HPV-45	8	9.1 (5.4, 11.3)	16	13.4 (6.0, 14.3)	0.0498	0.2158
HPV-51	149	12.0 (7.1, 17.0)	125	12.1 (6.9, 19.3)	0.9384	0.9384
HPV-52	189	16.0 (10.6, 28.7)	166	13.1 (8.0, 25.4)	0.0428	0.2158
HPV-56	77	12.5 (10.5, 18.2)	59	13.1 (6.9, 23.5)	0.3704	0.8175
HPV-58	70	14.8 (11.3, 25.7)	69	12.9 (7.0, 22.5)	0.0779	0.2532
HPV-59	51	12.6 (7.3, 18.0)	49	12.3 (6.7, 17.2)	0.6147	0.8175
HPV-68	77	14.0 (11.4, 22.8)	81	12.9 (10.0, 23.9)	0.6917	0.8175
HPV group						
HPV-16/18	75	7.9 (5.6, 13.9)	155	12.2 (5.9, 18.6)	0.0382	0.1146
HPV-31/33/45	64	12.5 (6.7, 16.5)	98	12.9 (6.2, 20.1)	0.4448	0.4448
HR-HPV	904	13.0 (7.3, 23.4)	915	12.7 (6.9, 22.5)	0.3424	0.4448

HR-HPV, high-risk human papillomavirus; FDR, false discovery rate; IQR, interquartile range.

p values were determined using the Wilcoxon rank sum test. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

* N, the number of infection events;

Supplementary Table 11. The clearance of incident HR-HPV infections in the vaccine group and the control group, defined by two consecutive negative results (sensitivity analysis)

HPV type	Vaccine group					Control group					HR (95%CI)	Original p value	FDR-adjusted q value
	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years			
HPV-16	80	76	95.0 (87.7, 98.6)	85.0	89.4 (71.4, 112)	144	112	77.8 (70.1, 84.3)	212.9	52.6 (43.7, 63.3)	1.60 (1.20, 2.12)	0.0013	0.0169
HPV-18	35	33	94.3 (80.8, 99.3)	35.5	92.9 (66.1, 130.7)	94	77	81.9 (72.6, 89.1)	117.1	65.8 (52.6, 82.2)	1.41 (0.95, 2.09)	0.0927	0.4017
HPV-31	50	41	82.0 (68.6, 91.4)	66.6	61.5 (45.3, 83.6)	86	73	84.9 (75.5, 91.7)	124.0	58.9 (46.8, 74.0)	1.03 (0.72, 1.49)	0.8583	0.9241
HPV-33	40	34	85.0 (70.2, 94.3)	47.2	72.1 (51.5, 100.9)	61	50	82.0 (70.0, 90.6)	80.1	62.4 (47.3, 82.3)	1.27 (0.83, 1.93)	0.2758	0.7171
HPV-35	40	30	75.0 (58.8, 87.3)	59.3	50.6 (35.4, 72.4)	53	48	90.6 (79.3, 96.9)	68.4	70.2 (52.9, 93.2)	0.92 (0.60, 1.42)	0.7067	0.9241
HPV-39	142	116	81.7 (74.3, 87.7)	210.1	55.2 (46.0, 66.3)	120	102	85.0 (77.3, 90.9)	186.7	54.6 (45.0, 66.3)	1.08 (0.84, 1.38)	0.5457	0.9241
HPV-45	12	12	100.0 (73.5, 100.0)	12.5	96.0 (54.5, 169)	29	27	93.1 (77.2, 99.2)	31.0	87.1 (59.8, 127.0)	0.97 (0.47, 1.97)	0.9241	0.9241
HPV-51	183	160	87.4 (81.7, 91.9)	241.8	66.2 (56.7, 77.3)	158	135	85.4 (79.0, 90.5)	209.7	64.4 (54.4, 76.2)	0.99 (0.79, 1.23)	0.9230	0.9241
HPV-52	246	171	69.5 (63.4, 75.2)	466.0	36.7 (31.6, 42.6)	214	168	78.5 (72.4, 83.8)	349.1	48.1 (41.4, 56.0)	0.82 (0.67, 1.00)	0.0446	0.2899
HPV-56	111	96	86.5 (78.7, 92.2)	136.1	70.5 (57.7, 86.1)	98	86	87.8 (79.6, 93.5)	131.8	65.2 (52.8, 80.6)	1.21 (0.92, 1.61)	0.1765	0.5736
HPV-58	86	66	76.7 (66.4, 85.2)	155.3	42.5 (33.4, 54.1)	100	73	73.0 (63.2, 81.4)	160.8	45.4 (36.1, 57.1)	0.94 (0.69, 1.29)	0.7172	0.9241
HPV-59	66	61	92.4 (83.2, 97.5)	78.1	78.1 (60.8, 100.4)	62	57	91.9 (82.2, 97.3)	71.7	79.5 (61.3, 103.0)	0.95 (0.66, 1.35)	0.7620	0.9241
HPV-68	97	88	90.7 (83.1, 95.7)	122.8	71.7 (58.1, 88.3)	109	92	84.4 (76.2, 90.6)	142.6	64.5 (52.6, 79.1)	1.09 (0.82, 1.45)	0.5606	0.9241
HPV group													

	Vaccine group					Control group					HR (95%CI)	Original p value	FDR-adjusted q value
	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years	N*	n*	Proportion (95%CI)	Person -years at risk	Clearance (95%CI), per 100 person-years			
HPV-16/18	115	109	94.8 (89.0, 98.1)	120.5	90.5 (75.0, 109.1)	238	189	79.4 (73.7, 84.4)	330.0	57.3 (49.7, 66.1)	1.62 (1.27, 2.07)	0.0001	0.0003
HPV-31/33/45	102	87	85.3 (76.9, 91.5)	126.3	68.9 (55.8, 85.0)	176	150	85.2 (79.1, 90.1)	235.1	63.8 (54.4, 74.9)	1.03 (0.79, 1.34)	0.8434	0.8434
HR-HPV	118 8	981	82.6 (80.3, 84.7)	1716.3	57.2 (53.7, 60.9)	1328	1103	83.1 (80.9, 85.0)	1886.0	58.5 (55.1, 62.0)	1.01 (0.92, 1.11)	0.8389	0.8434

HR-HPV, high-risk human papillomavirus; HR, hazard ratio; 95%CI, 95% confidence interval; FDR, false discovery rate.

For type-specific analyses, the standard Cox proportional hazards model was used. For HPV-16/18, HPV-31/33/45, and HR-HPV groups, the Wei-Lin-Weissfeld (WLW) Cox model was applied. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

*N, the number of infection events; n, the number of cleared infection events.

Supplementary Table 12. The clearance time of HR-HPV infections in the vaccine group and the control group, defined by two consecutive negative results (sensitivity analysis)

	Vaccine group		Control group		Original p value	FDR-adjusted q value
	N*	Median times (IQR), months	N*	Median times (IQR), months		
HPV type						
HPV-16	80	6.9 (5.6, 13.0)	144	12.9 (5.9, 24.3)	0.0196	0.2158
HPV-18	35	7.7 (5.6, 13.2)	94	11.4 (6.0, 18.6)	0.5619	0.8175
HPV-31	50	13.0 (6.7, 18.9)	86	11.1 (6.1, 22.3)	0.9139	0.9384
HPV-33	40	12.4 (6.1, 17.6)	61	13.1 (6.8, 18.8)	0.6804	0.8175
HPV-35	40	12.9 (6.7, 22.2)	53	12.3 (6.0, 17.8)	0.6545	0.8175
HPV-39	142	12.9 (9.1, 22.8)	120	13.3 (10.4, 23.7)	0.4802	0.8175
HPV-45	12	11.0 (5.8, 13.1)	29	12.3 (6.0, 14.1)	0.0498	0.2158
HPV-51	183	12.1 (6.8, 19.0)	158	12.3 (7.1, 22.6)	0.9384	0.9384
HPV-52	246	16.5 (9.8, 30.8)	214	13.1 (8.9, 28.5)	0.0428	0.2158
HPV-56	111	12.5 (6.8, 17.7)	98	13.0 (9.7, 17.9)	0.3704	0.8175
HPV-58	86	18.1 (11.3, 28.9)	100	13.8 (10.4, 23.8)	0.0779	0.2532
HPV-59	66	12.6 (7.0, 16.8)	62	12.1 (6.1, 17.2)	0.6147	0.8175
HPV-68	97	12.7 (6.8, 18.6)	109	12.6 (7.0, 18.6)	0.6917	0.8175
HPV group						
HPV-16/18	115	7.1 (5.6, 13.0)	238	12.1 (5.9, 23.1)	0.0382	0.1146
HPV-31/33/45	102	12.5 (6.1, 17.5)	176	12.4 (6.2, 18.5)	0.4448	0.4448
HR-HPV	1188	12.9 (6.8, 23.1)	1328	12.8 (6.8, 23.1)	0.3424	0.4448

HR-HPV, high-risk human papillomavirus; FDR, false discovery rate; IQR, interquartile range.

p values were determined using the Wilcoxon rank sum test. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

* N, the number of infection events;

Supplementary Table 13. The persistence and clearance of HPV-52 single infection and multiple infection in the control group

	n*	N*	Proportion (95%CI)	P value	Person- years at risk	Incidence (95%CI), per 100 person-years	HR (95%CI)	P value^	Mean times (SD), months#	Median times (IQR), months	P value&
Persistence											
HPV 52 single infection	60	166	36.1 (28.8, 44.0)	-	-	-	-	-	6.4 (12.2)	0 (0, 7.6)	-
HPV 52 multiple infection~	18	49	36.7 (23.4, 51.7)	0.9398	-	-	-	-	5.4 (9.2)	0 (0, 6.2)	0.9915
HPV-16/18/31/33/45	6	20	30.0 (11.9, 54.3)	0.5874	-	-	-	-	4.0 (7.7)	0 (0, 4.4)	0.5205
HPV-35/39/51/56/58/59/68	12	29	41.4 (23.5, 61.1)	0.5899	-	-	-	-	6.4 (10.1)	0 (0, 11.2)	0.5965
Clearance											
HPV 52 single infection	145	166	87.4 (81.3, 92.0)	-	244.9	49.3 (41.9, 58.1)	-	-	-	13.1 (8.0, 25.4)	-
HPV 52 multiple infection~	42	49	85.7 (72.8, 94.1)	0.7651	68.2	51.3 (37.9, 69.5)	1.02 (0.72, 1.44)	0.9110	-	13.1 (6.9, 25.3)	0.9385
HPV-16/18/31/33/45	17	20	85.0 (62.1, 96.8)	0.7672	24.3	58.3 (36.2, 93.8)	1.24 (0.75, 2.07)	0.3999	-	13.0 (6.3, 22.3)	0.4135
HPV-35/39/51/56/58/59/68	25	29	86.2 (68.3, 96.1)	0.8652	43.9	47.5 (32.1, 70.3)	0.90 (0.59, 1.38)	0.6432	-	13.8 (11.1, 27.2)	0.5768

HPV, human papillomavirus; HR, hazard ratio; 95%CI, 95% confidence interval; SD, standard deviation; IQR, interquartile range.

All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

*N, the number of infection events; n, the number of persistent or cleared infection events.

#The persistence duration of infection exhibited a left-skewed distribution. Due to persistence events occurring in fewer than 50% for certain groups, the median times and lower quartile were 0 months. Therefore, we also presented the mean times for each HPV type.

&P values were determined using the Wilcoxon rank sum test.

^P values were determined using the Cox regression model.

~Recognizing that prolonged HPV-52 infection duration inherently increases multiple infection risk due to expanded temporal exposure (key source of collinearity), we operationally defined HPV-52 multiple infections as only those episodes with strictly simultaneous onset of both HPV-52 and another HR-HPV type.

Supplementary Table 14. The persistence and clearance of HPV-52 infection in the non-surgical and postoperatively censored participants in the vaccine group and the control group

	n*	N*	Proportion (95%CI)	P value	Person- years at risk	Incidence (95%CI), per 100 person-years	HR (95%CI)	P value^	Mean times (SD), months [#]	Median times (IQR), months	P value ^{&}
Persistence											
Vaccine group	160	297	53.9 (48.0, 59.7)	0.0039	-	-	-	-	11.8 (16.7)	5.2 (0, 17.2)	0.0009
Control group	115	275	41.8 (35.9, 47.9)	-	-	-	-	-	7.5 (12.4)	0 (0, 11.6)	-
Clearance											
Vaccine group	232	297	78.1 (73.0, 82.7)	0.0427	522.0	44.4 (39.1, 50.6)	0.82 (0.69, 0.99)	0.0382	-	14.2 (10.2, 27.9)	0.1569
Control group	233	275	84.7 (79.9, 88.8)	-	427.0	54.6 (48.0, 62.0)	-	-	-	13.1 (8.0, 26.5)	-

HPV, human papillomavirus; HR, hazard ratio; 95%CI, 95% confidence interval; SD, standard deviation; IQR, interquartile range.

All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

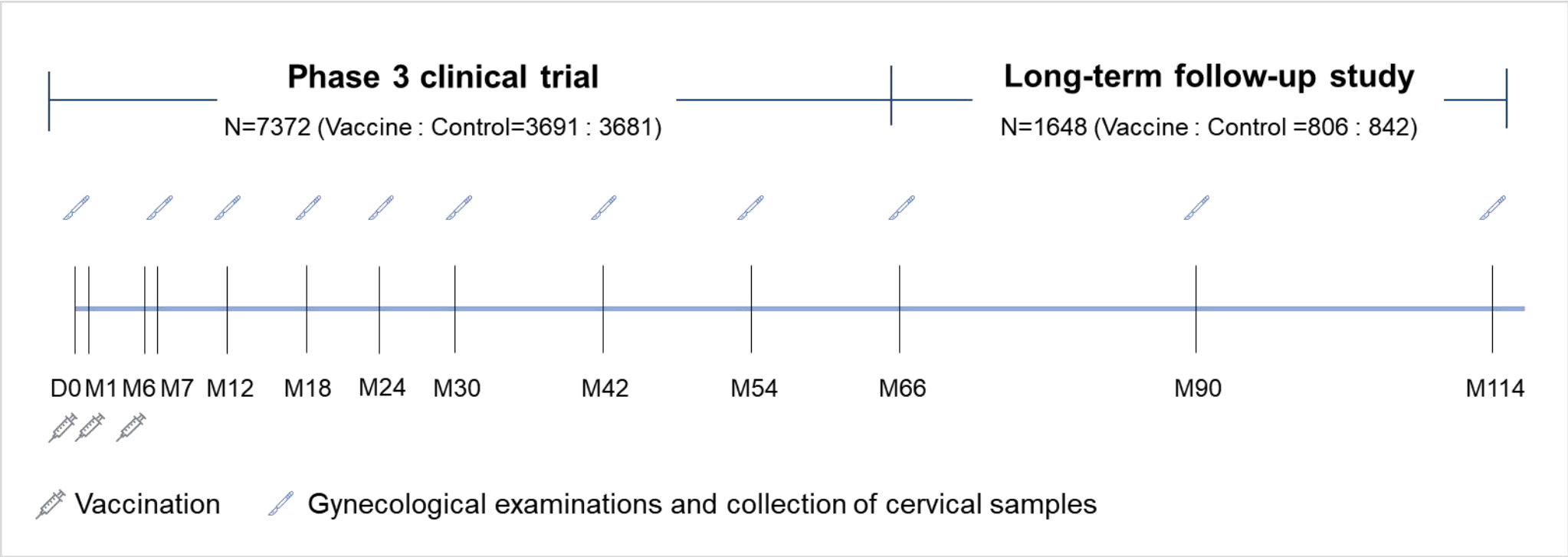
*N, the number of infection events; n, the number of persistent or cleared infection events.

[#]The persistence duration of infection exhibited a left-skewed distribution. Due to persistence events occurring in fewer than 50% for certain groups, the median times and lower quartile were 0 months. Therefore, we also presented the mean times for each HPV type.

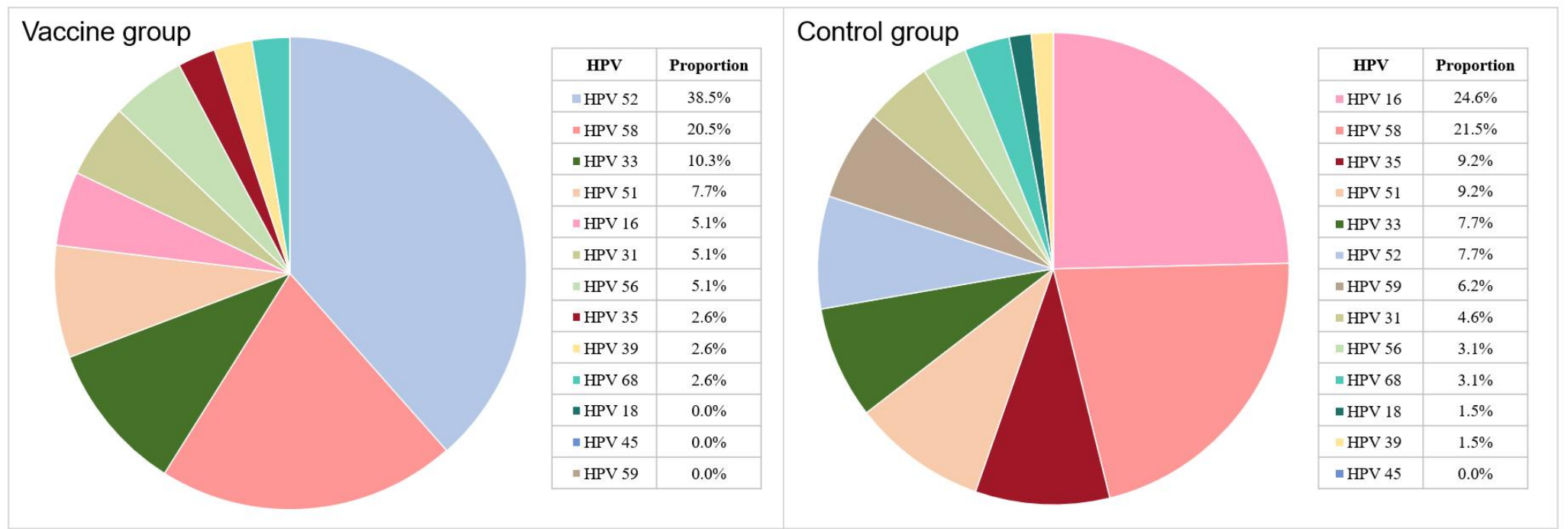
[&]P values were determined using the Wilcoxon rank sum test.

[^]P values were determined using the Cox regression model.

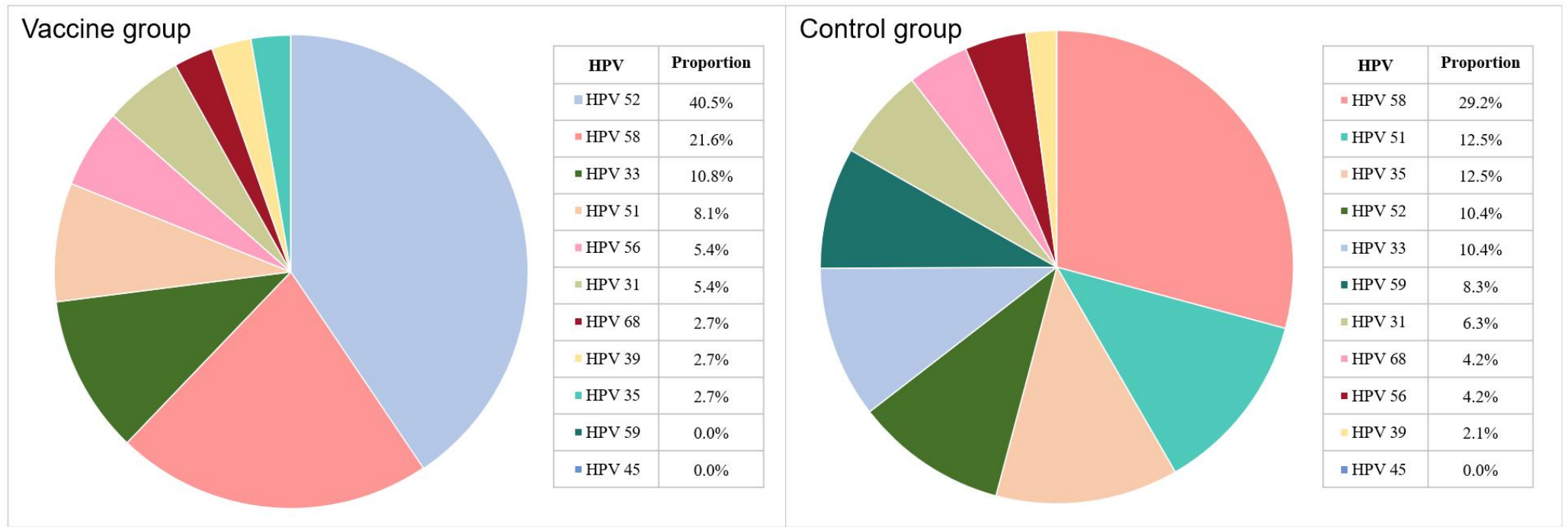
Supplementary Figure 1. The study design



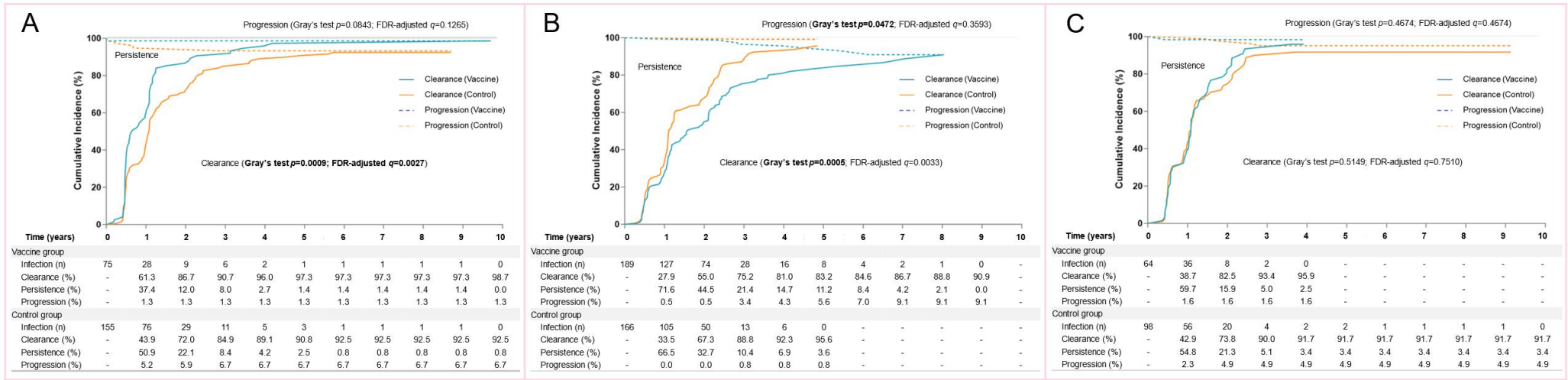
Supplementary Figure 2. Constituent ratio of HR-HPV associated cervical intraepithelial neoplasia grade 2 or greater in the vaccine group and the control group



Supplementary Figure 3. Constituent ratio of HR-HPV associated cervical intraepithelial neoplasia grade 2 or greater in the vaccine group and the control group (excluding HPV-16/18 related cases)



Supplementary Figure 4. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-16/18, HPV-52 and HPV-31/33/45 single infections in the vaccine group and the control group

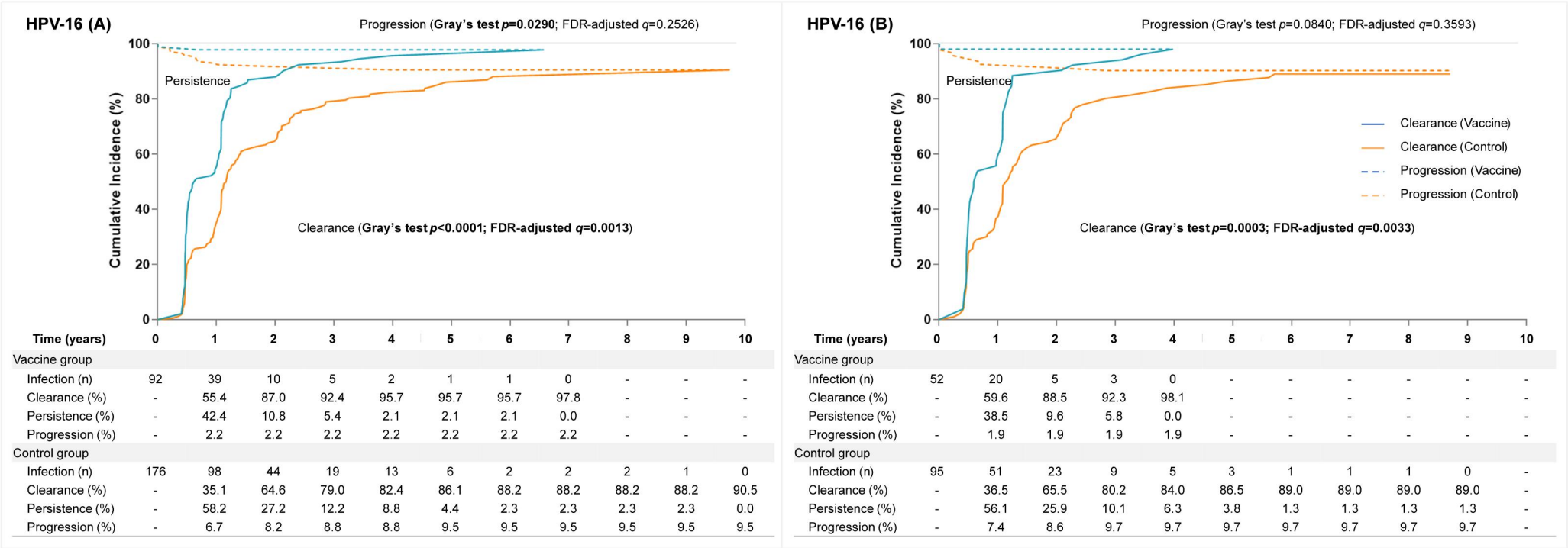


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

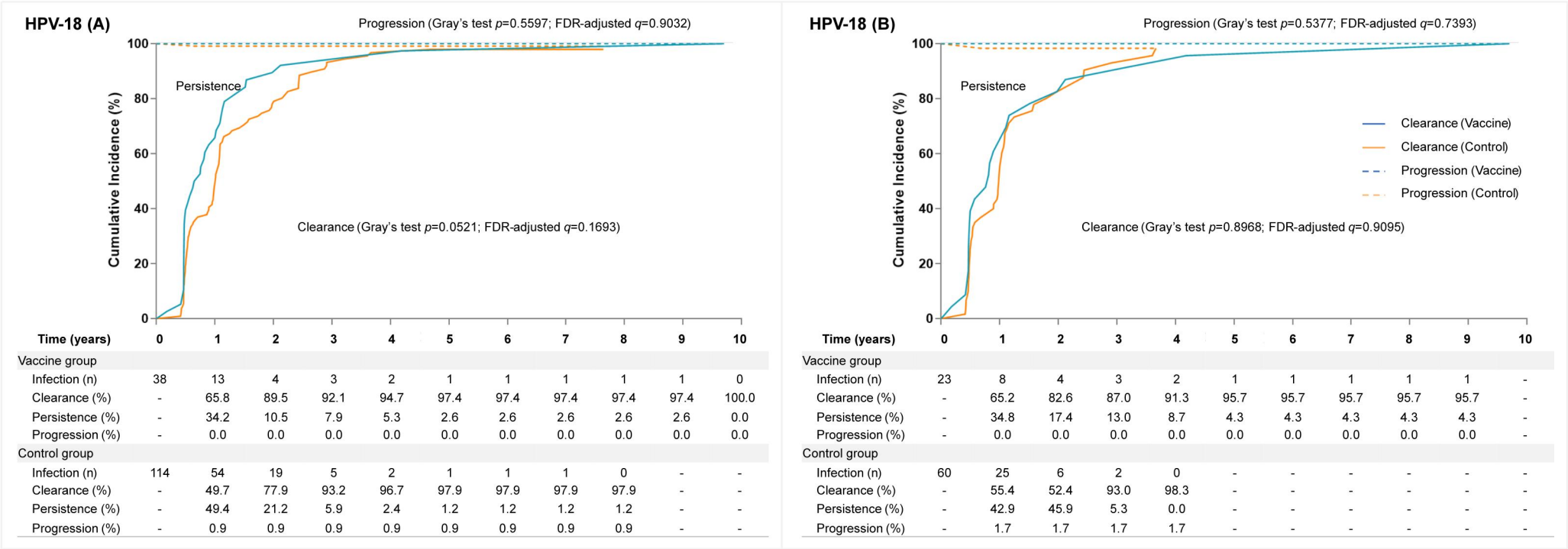
A HPV-16/18; **B** HPV-52; **C** HPV-31/33/45;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 5. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-16 infections in the vaccine group and the control group



Supplementary Figure 6. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-18 infections in the vaccine group and the control group

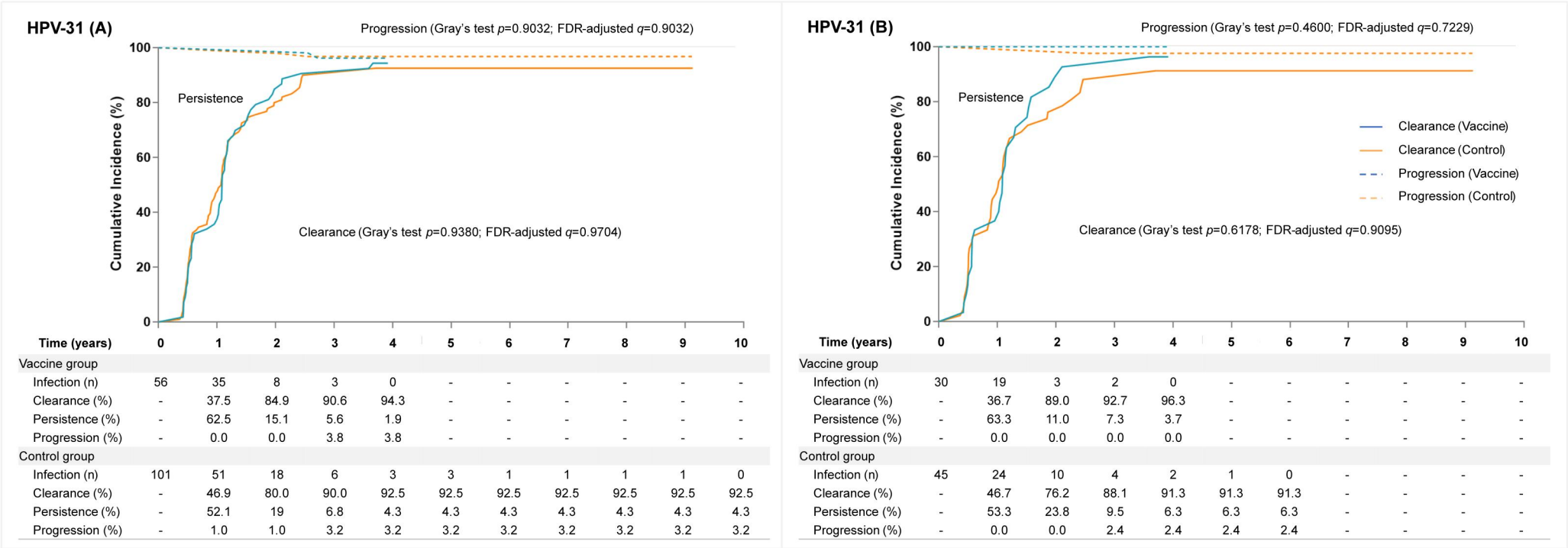


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

A Overall population; **B** Participants without multiple HR-HPV infections;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 7. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-31 infections in the vaccine group and the control group

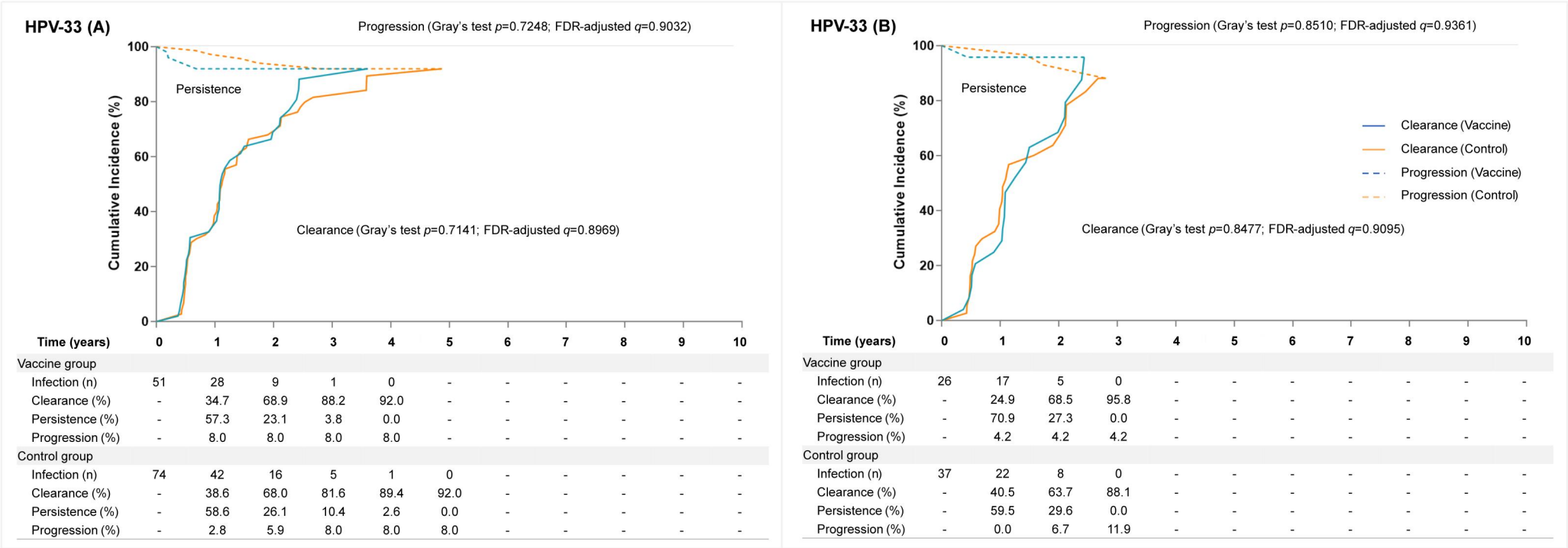


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

A Overall population; **B** Participants without multiple HR-HPV infections;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 8. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-33 infections in the vaccine group and the control group

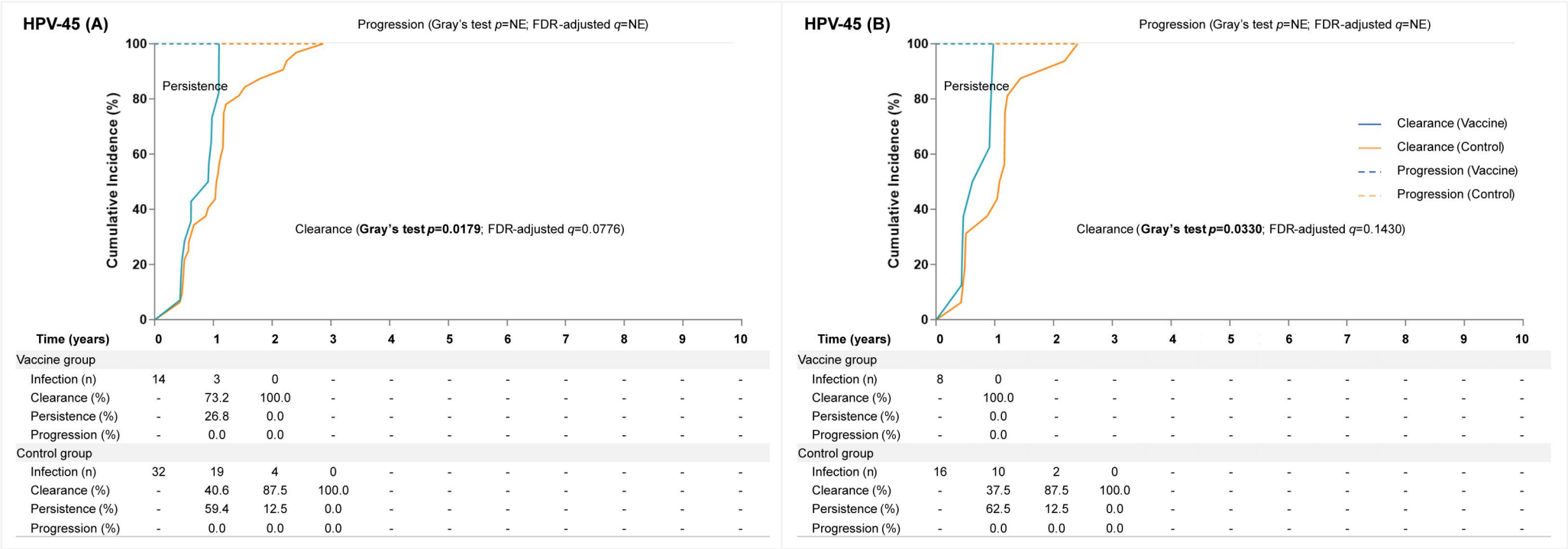


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

A Overall population; **B** Participants without multiple HR-HPV infections;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 9. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-45 infections in the vaccine group and the control group

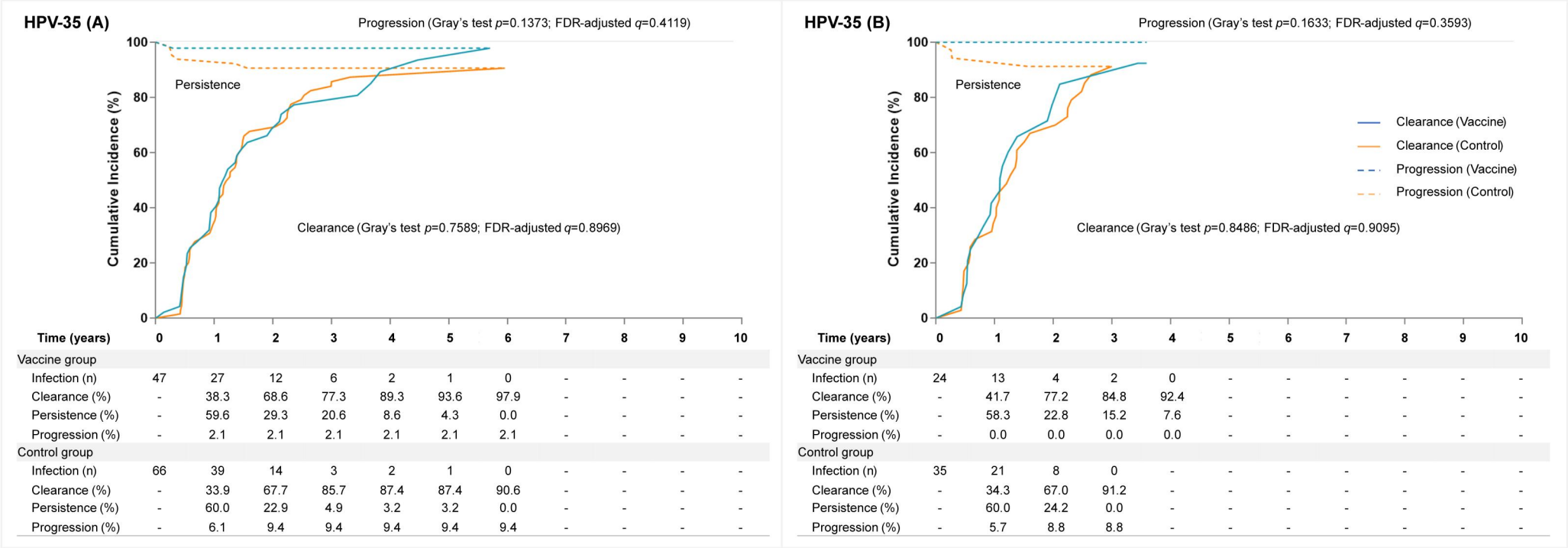


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

A Overall population; **B** Participants without multiple HR-HPV infections;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 10. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-35 infections in the vaccine group and the control group

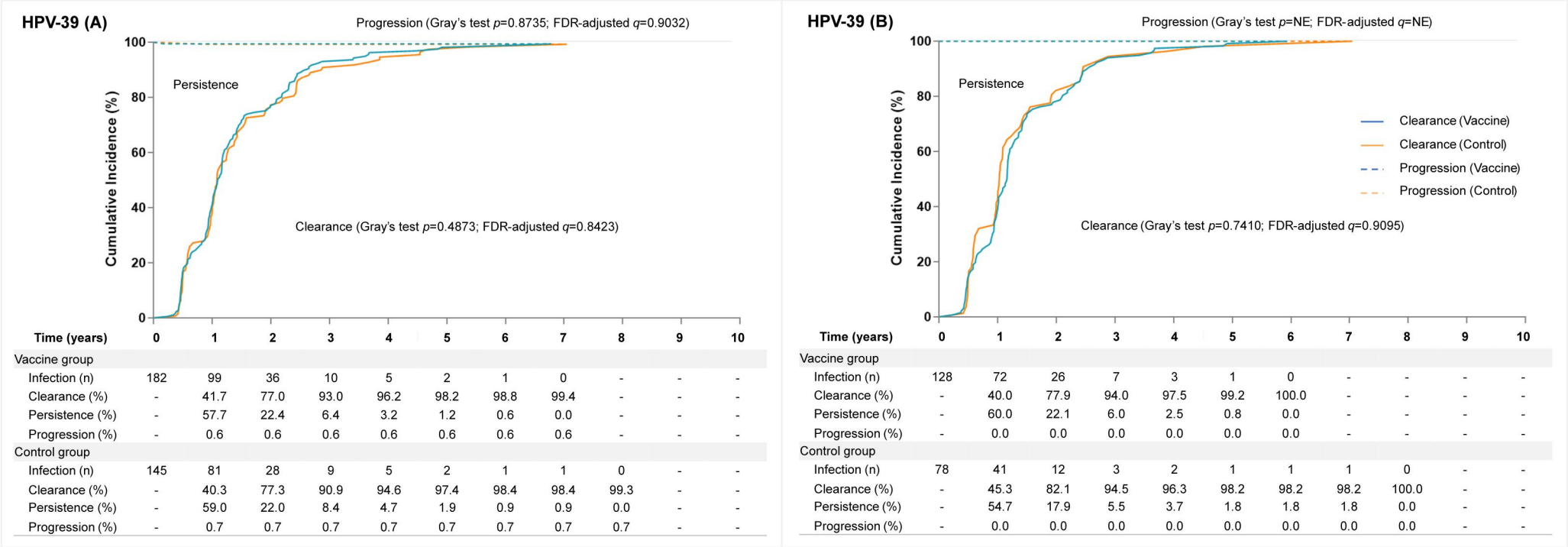


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

A Overall population; **B** Participants without multiple HR-HPV infections;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 11. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-39 infections in the vaccine group and the control group

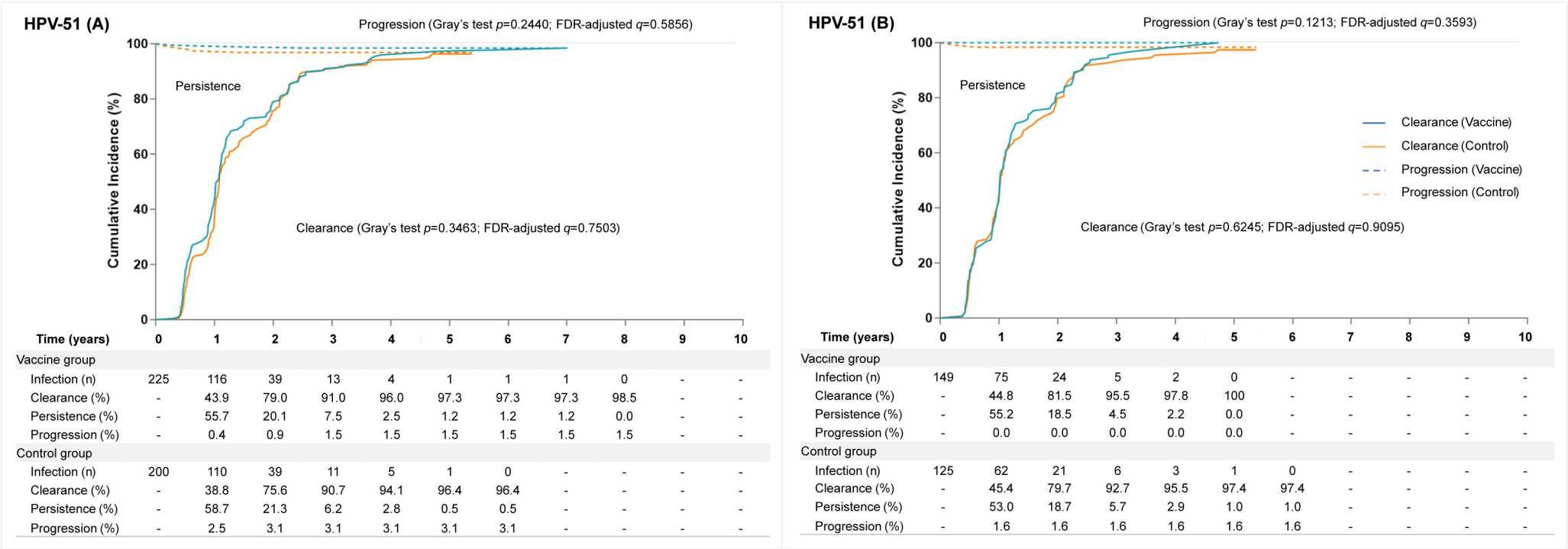


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

A Overall population; **B** Participants without multiple HR-HPV infections;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 12. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-51 infections in the vaccine group and the control group

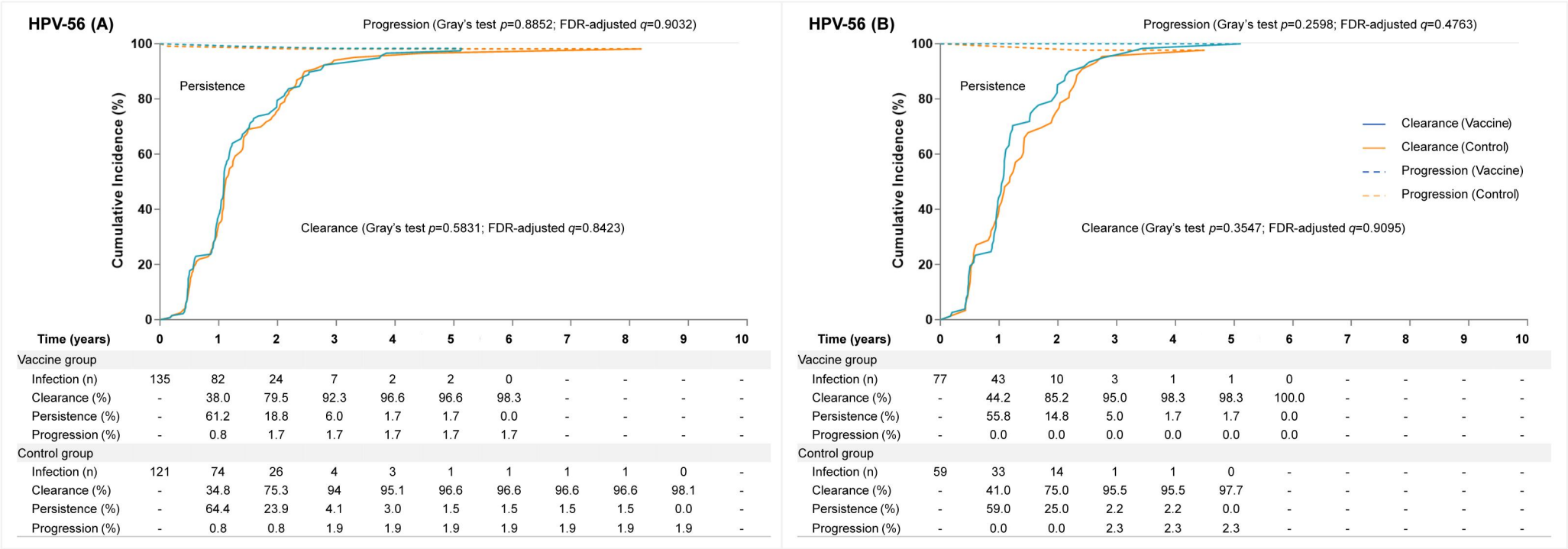


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

A Overall population; **B** Participants without multiple HR-HPV infections;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 13. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-56 infections in the vaccine group and the control group

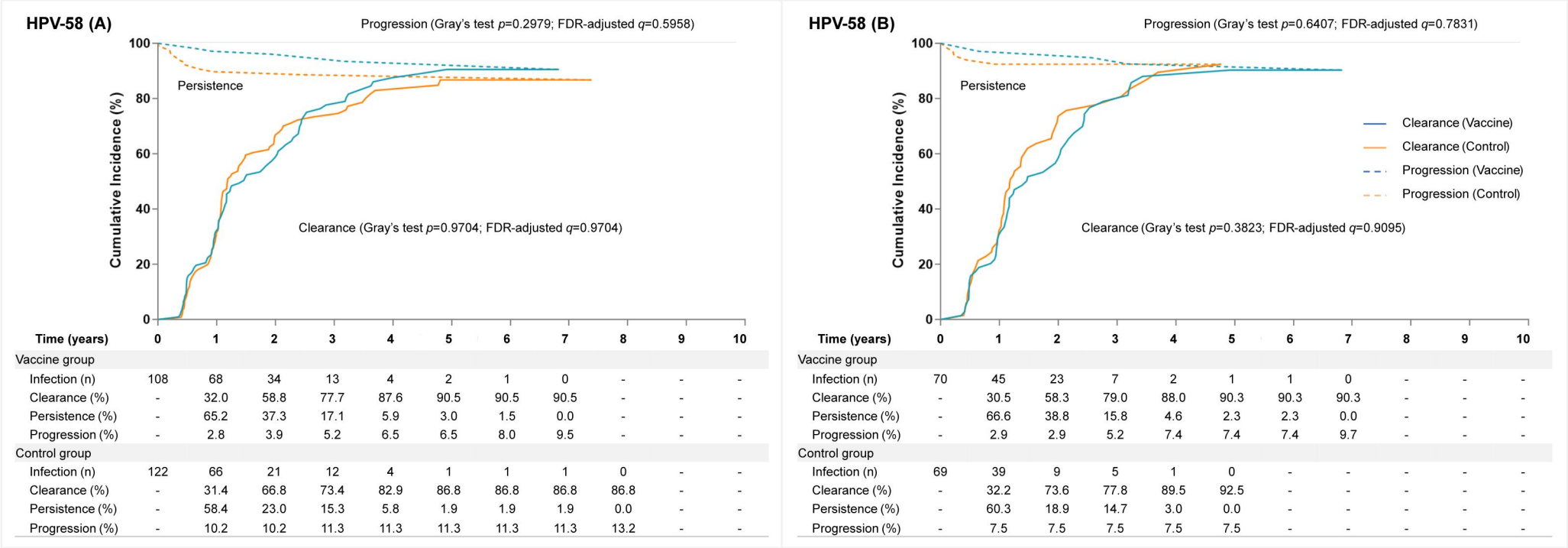


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

A Overall population; **B** Participants without multiple HR-HPV infections;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 14. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-58 infections in the vaccine group and the control group

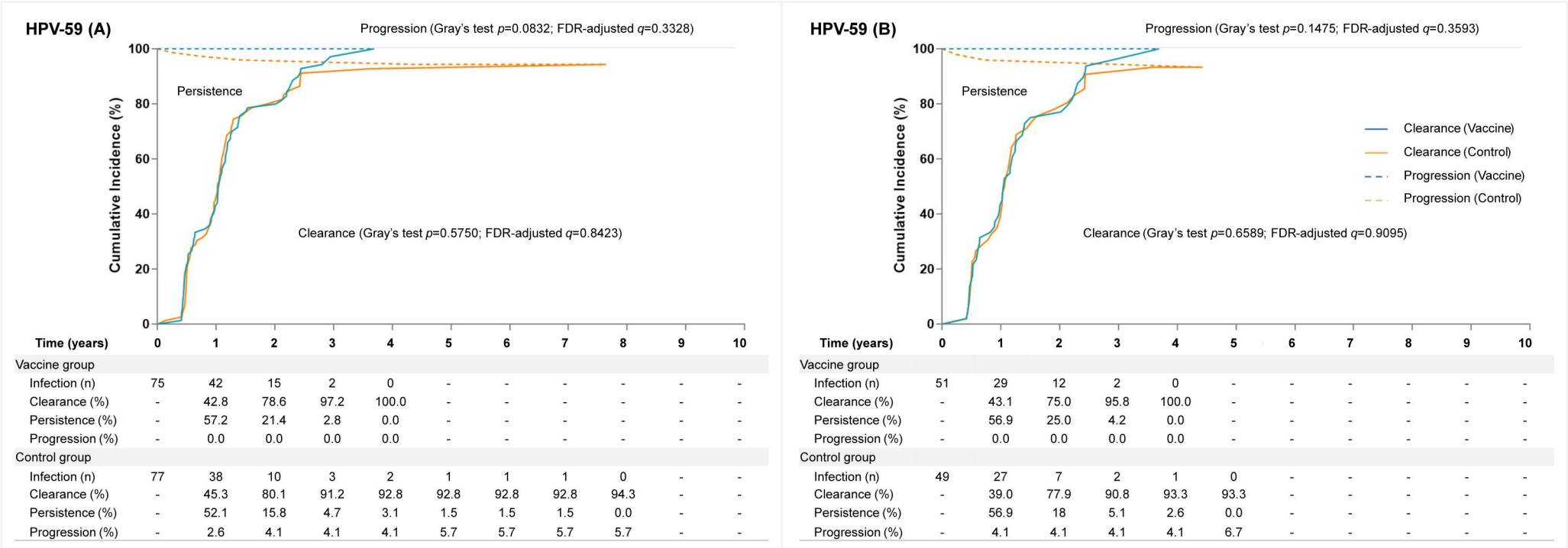


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

A Overall population; **B** Participants without multiple HR-HPV infections;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 15. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-59 infections in the vaccine group and the control group

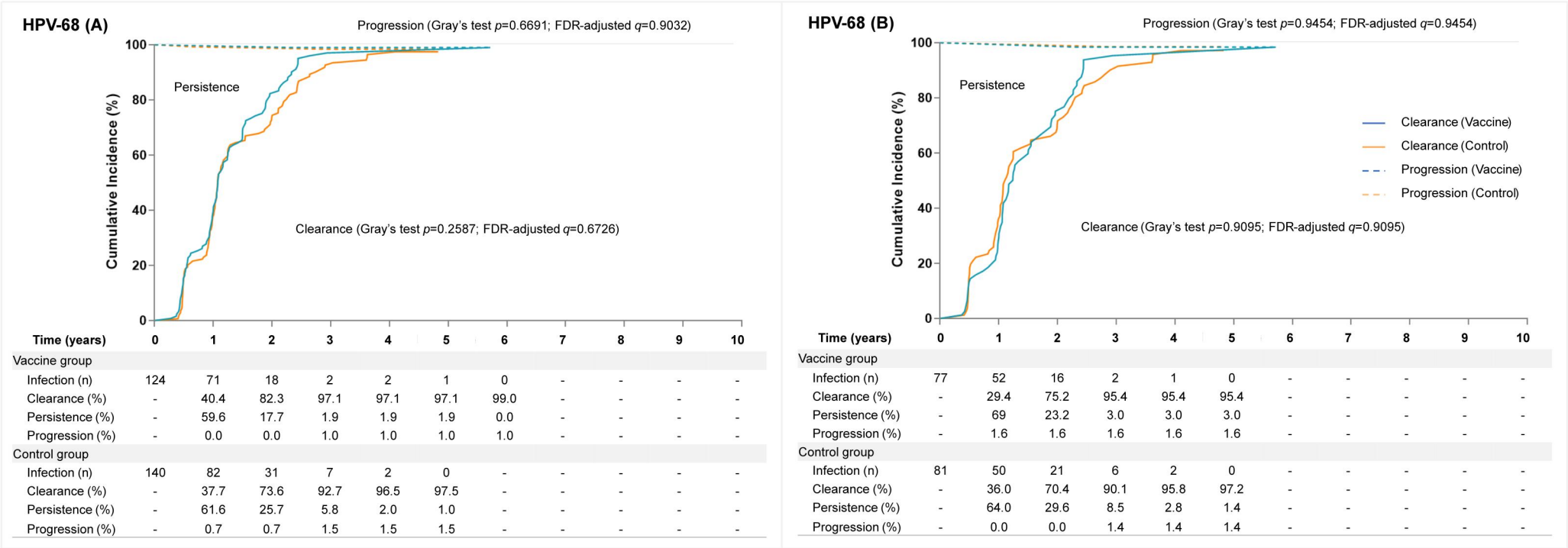


CIN2+, cervical intraepithelial neoplasia grade 2 or greater; HR-HPV, high-risk human papillomavirus; FDR, false discovery rate.

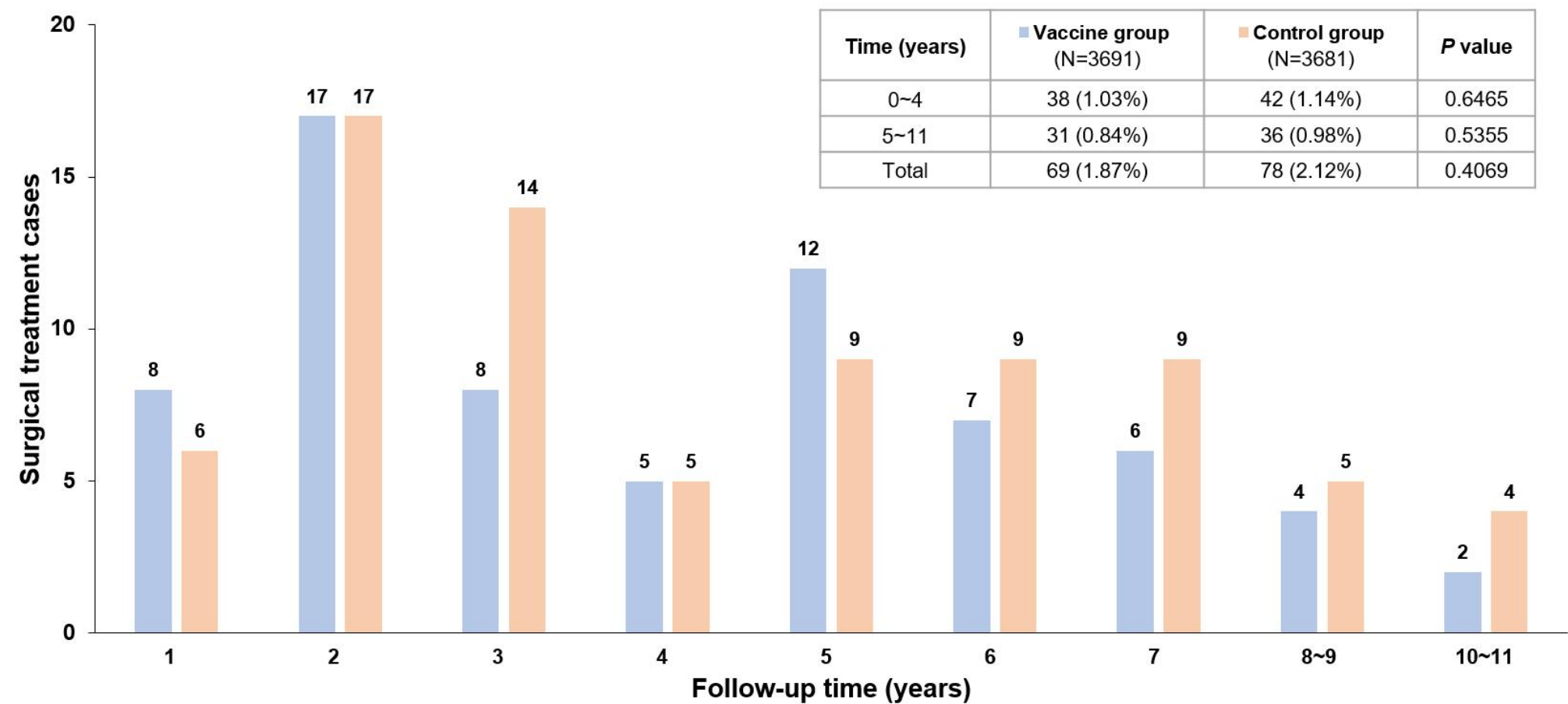
A Overall population; **B** Participants without multiple HR-HPV infections;

In competing risk analyses, the estimates for progression (to CIN2+), clearance, and persistence add up to 100% at each time point. A stratified Benjamini-Hochberg FDR procedure was used to adjust for multiple comparisons. All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.

Supplementary Figure 16. Competing cumulative risks of clearance, progression (to CIN2+), and persistence of HPV-68 infections in the vaccine group and the control group



Supplementary Figure 17. Temporal distributions of surgical treatment in the vaccine group and the control group



p values were determined using the chi-squared test or Fisher’s exact test.
All statistical tests were two-sided, with a significance level of $\alpha = 0.05$.