

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection Rokotiitus closed data collection system SPSS (version 31.0.1.0) and Microsoft Excel

Data analysis R studio (version, v.2024.04.1), using the following packages: tidyverse (v. 2.0.0), dplyr (v. 1.1.4), stats (v. 4.4.0), plyr (v. 1.8.9) and rlist (v. 0.4.6.2), for data management and descriptive statistics and ggplot2 (v. 3.5.1), grid (v. 4.4.0) and gridExtra (v. 2.3) Microsoft Excel version 2603 (v19822.20180)

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Anonymous study data from the 2 previously completed trials (of the Finnish HPV-vaccination trial and screening trial (F-VAC)) is available upon reasonable request

to Matti Lehtinen (matti.lehtinen@tuni.fi) after assessment of the F-VAC data access committee. R code for this study has been made available publicly on GitHub upon publication (https://github.com/Monicaortegallobet/naturalHPVhistory_ageofvaccination_finnishvacandscreeningdata). The study protocols for the two trials used in this post-hoc analysis can be found at www.clinicaltrials.gov with ID: NCT00534638 and ID: NCT02149030 respectively.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	Only females were included in this study.
Reporting on race, ethnicity, or other socially relevant groupings	Race and ethnicity were not part of the ethical permission and therefore not included.
Population characteristics	Participants were aged 13 to 25 years old. The mean age at vaccination was 14.3 years old for the HPV-vaccinated at ages 12 to 15 and 18.7 years old for the HPV-vaccinated at the age of 18. The self-reported age of sexual debut was 16.5 years old for the first group and 16.6 years for the later. The reported number of lifetime partners is reported as well for all stratified groups in Table 1. Further characteristics of the population are reported in the respective original trials' previously published papers (Lehtinen M, Int J Cancer 2018; 142: 949–958 and Ortega Llobet M, Int J Cancer 2026; 158(7):1941–1951)
Recruitment	HPV 16/18 vaccinated females born 1992–1995. Previous participants of a community randomized trial of HPV-vaccination strategy in Finland from 33 different Finnish communities
Ethics oversight	Both trials utilized in this study have pertinent ethical permits and are registered at clinicaltrials.gov (HPV-vaccination trial NCT00534638 and screening trial NCT02149030) (PI ML) which were approved by the ethical review board of the Pirkanmaa Hospital District, Tampere, Finland (HPV004 R13149, 19.2.2014) and they have ethical review board clearance (Tampere University Hospital/PIRHA Ethical Review Board), registry-linkage permissions (THL, Valvira) and data protection (FinData) approvals. All participants have provided informed consent covering health registry, data linkage and retrieval of samples from pathology laboratories and biobanked. In the case of minors, informed consent was provided by the parents or legal guardians and informed assent was obtained from the participant.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	All 16,969 women who were HPV16/18-vaccinated at either at 12-to-15 years of age, or at 18 years of age (born between 1992 and 1995) participating in the Finnish HPV-vaccination randomized trial, were invited.
Data exclusions	Women with immunocompromising disease or with HPV 6/11/16/18 vaccination were excluded from the data.
Replication	The results of this trials have been confirmed by more than one co-author. Original analysis done by MO and checked by PG. Underlying data has been verified by TE.
Randomization	In this post-hoc analysis there was no randomization. There was randomization in the previously completed vaccination trial.
Blinding	All study participants in the original vaccination trial were blinded until the age of 18.5 years old when they were offered cross-vaccination.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	NCT00534638 and NCT02149030
Study protocol	Full study protocols for the previously completed vaccination and screening trials are available at clinicaltrials.gov .
Data collection	Data for this study was obtained in 2025 from the archival database of the two previously completed trials.
Outcomes	The outcomes of this study are type-specific and age-specific prevalence, incidence, clearance and proportion of persistence of screen detected HPV infection as well as vaccine effectiveness.

Plants

Seed stocks	<i>Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.</i>
Novel plant genotypes	<i>Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.</i>
Authentication	<i>Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.</i>