

Reporting Summary

Nature Research 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 Research 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

- | | | |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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 Not applicable. The study involves analysis of existing data.

Data analysis Data analysis was completed using R 4.0. Code used for data analysis is available at <https://github.com/eswk-im/PCRSanalysis-git>.

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 Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

UK Biobank data are available through application to the UK Biobank Access Management System (AMS), <https://www.ukbiobank.ac.uk/enable-your-research/register>. GWAS summary statistics of the single-nucleotide polymorphisms (SNPs) used for polygenic risk score (PRS) construction for each trait is available in the supplementary information section with relevant source literatures.

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	We studied 160,586 UKBB unrelated female participants of White British ancestry aged 40-71 with 6,886 incident cancer cases over the course of follow-up. No statistical method was used to predetermine sample size. Maximal dataset was retained for analysis after data exclusions.
Data exclusions	Prior to data analysis, we removed related female UK Biobank participants of White British ancestry from the phenotype data. We excluded individuals who were lost to follow-up, with genetic sex and self-reported sex mismatch, or individuals with cancer diagnosis prior to baseline assessment (prevalent cancers). Participants without imputed genotype data were excluded from the analysis.
Replication	Our UK Biobank dataset was split into training and test set. We trained and validated a Cox proportional hazards model that allows estimation of absolute risk of developing at least one of the eight common cancers among women. Results can be replicated by using the code provided above. Codes were reviewed thoroughly. Results were replicated successfully.
Randomization	Not an experimental study. Randomization was not relevant.
Blinding	Blinding was not relevant.

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

Methods

n/a	Involved in the study	n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies	<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines	<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology	<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms		
<input type="checkbox"/>	<input checked="" type="checkbox"/> Human research participants		
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data		
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern		

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	The study involves analysis of existing data and does not involve new human research participants. Descriptive statistics of the UK Biobank participants included in our analysis are available in the supplementary information section.
Recruitment	UK Biobank is a prospective epidemiological cohort study with over 500,000 participants. Individuals aged 40-69 at baseline were recruited across the United Kingdom from 2006-2010. More information on participant recruitment available at Bycroft, C., Freeman, C., Petkova, D. et al. The UK Biobank resource with deep phenotyping and genomic data. Nature 562, 203–209 (2018). https://doi.org/10.1038/s41586-018-0579-z .
Ethics oversight	Please refer to https://www.ukbiobank.ac.uk/learn-more-about-uk-biobank/about-us/ethics for detailed information on UK Biobank research ethics approval.

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