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Reporting Summary

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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	No software was used
Data analysis	R version 3.6.1. (https://cran.r-project.org) R package TwoSampleMR version 0.4.23 (https://github.com/MRCIEU/TwoSampleMR) R package RadialMR version 0.3 (https://github.com/WSpiller/RadialMR) R package phenoscanner version 1.0. (https://github.com/phenoscanner/phenoscanner) R package circlize version 0.4.7: https://github.com/jokergoo/circlize PLINK version 1.9 and 2.0 (https://www.cog-genomics.org/plink/1.9/ and https://www.cog-genomics.org/plink/2.0/) KING version 2.0 (http://people.virginia.edu/~wc9c/KING/) LDSC version 1.0.0 (https://github.com/bulik/ldsc/)

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/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

The datasets analyzed during the current study are publicly available from the UK Biobank at: https://www.ukbiobank.ac.uk and summary statistics from the previously published genome-wide association study (GWAS) from the OncoArray Lung Cancer collaboration (McKay & Hung et al. 2017, PMID: 28604730). Data

from this study are available from the database of Genotypes and Phenotypes (dbGaP) under accession phs001273.v2.p2. Original OncoArray data can be obtained by completing a proposal request form at http://oncoarray.dartmouth.edu/.

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

Life sciences study design

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

Sample size	The UK Biobank is a population-based prospective cohort of 502,611 individuals in the United Kingdom. Study participants were aged 40 to 69 at recruitment between 2006 and 2010, at which time all participants provided detailed information about lifestyle and health-related factors, provided biological samples, and completed a range of physical measures. After relevant exclusions (described below) the final sample size available for analysis was as follows: n=372,750 for FEV1, n=370,638 for FVC, and n=368,817 for FEV1/FVC. The discovery stage of the genome-wide association analysis used 70% of the study population, with 30% reserved for replication. The OncoArray Lung Cancer Collaboration was a pooled genome-wide association study and meta-analysis which included 29,266 cases and 56,450 controls. Details of the lung cancer study population have been previously described (PMID: 28604730).
Data exclusions	Analyses in the UK Biobank were limited to individuals with self-reported European ancestry with concordant self-reported and genetic sex. To further minimize potential population stratification, we excluded individuals for whom either of the first two genetic ancestry principal components (PC's) were >5 standard deviations away from the mean of the population. Based on a subset of genotyped autosomal variants with minor allele frequency (MAF) ≥0.01 and genotype call rate ≥97%, we excluded samples with call rates <97% and/or heterozygosity more than five standard deviations from the mean of the population. With the same subset of SNPs, we used KING to estimate relatedness among the samples. We excluded one individual from each pair of first-degree relatives. We further restricted analyses to individuals who completed a pulmonary function (spirometry) assessment and had at least two valid, reproducible blows. If the difference in forced volume vital capacity (FVC) and Forced Expiratory Volume in 1 second (FEV1) was less than 5%, a third blow was not required. Genome-wide summary statistics from the OncoArray lung cancer study are based on analyses of individuals of predominantly European ancestry (≥80%).
Replication	Replication of the genome-wide association analyses was undertaken in the UK Biobank cohort (n=111,825 for FEV1, n=111,192 FVC, n=110,645 for FEV1/FVC).
Randomization	Genome-wide association analyses of pulmonary function phenotypes in the UK Biobank cohort were conducted linear regression models with adjustment for age at cohort enrollment, age squared, sex, height, height squared, cigarette pack-years, first 15 genetic ancestry PCs, and genotyping array.
Blinding	Genotyping for Lung Cancer OncoArray was done blinded by their cancer status. The UK Biobank study is a prospective population-based observational cohort, with no treatment or specific control groups. The spirometery and the genotyping in UK Biobank was performed independently from each other. The researchers who carried out the analysis for this manuscript had no influence on how genotyping or lung function measurement was performed in UK Biobank.

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	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Human research participants

Policy information about studies involving human research participants

Population characteristics	The UK Biobank is a population-based prospective cohort of 502,611 individuals in the United Kingdom. Study participants were aged 40 to 69 at recruitment between 2006 and 2010, at which time all participants provided detailed information about lifestyle and health-related factors, provided biological samples, and completed a range of physical measures. Analyses were based on data from individuals of predominantly European ancestry, based on self-report and genetic ancestry principal components (PC's), and those with concordant self-reported and genetic sex. The OncoArray Lung Cancer Collaboration was a pooled genome-wide association study and meta-analysis which included 29,266 cases and 56,450 controls of predominantly European ancestry (≥80%). Details of the lung cancer study population have been previously described (PMID: 28604730).
Recruitment	The UK Biobank is a population-based cohort of 500,000 participants recruited in the United Kingdom between 2006-2010. Approximately 9.2 million individuals aged 40-69 years who lived within 25 miles of one of 22 assessment centers in England, Wales, and Scotland were invited to enter to cohort, and 5.5% completed the baseline assessment. The UK Biobank is not representative of the general population across several sociodemographic, physical, lifestyle and health-related characteristics, with evidence of a "healthy volunteer" selection bias, details of which are published elsewhere (Fry et al, Am J Epidemiol 2017;186:1026-34. PMID 28641372).
Ethics oversight	The study was approved by the UK Biobank data access committee under applications 14105 and 23261.

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