nature portfolio

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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	No software was used for data collection
Data analysis	LOCUSZOOM (v. 0.14.0): http://locuszoom.sph.umich.edu/; LD score regression software: https://github.com/bulik/ldsc; METAL software (5th May 2020 release): http://csg.sph.umich.edu/abecasis/Metal/; PLINK software (v.1.9): www.cog-genomics.org/plink/1.9/; R: https://cran.r-project.org/; REGENIE software (v 2.2.4): https://rgcgithub.github.io/regenie/overview/; GCTA-COJO (v. 1.94.4): https://yanglab.westlake.edu.cn/software/gcta/#COJO; GCTA-mtCOJO (v. 1.94.4): https://yanglab.westlake.edu.cn/software/gcta/#mtCOJO; TwoSampleMR: https://github.com/MRCIEU/TwoSampleMR; CMplot: https://github.com/YinLiLin/CMplot.

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

Individual-level data from the UK Biobank were accessed under application number 25331. UK Biobank data are available through the UK Biobank Access Management System at https://www.ukbiobank.ac.uk/. FinnGen Data are available via https://www.finngen.fi/en.

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	Genetic-based sex is included in our analysis as a covariate. All GWAS data used in this study adjusted for sex.We didn't conduct sex-specific analysis here.
Reporting on race, ethnicity, or other socially relevant groupings	We only involved samples whose genetic background is similar to European ancestral groups. Details are described in the method section. Briefly, we extracted the genetic information and self-reported ethnicity of individuals, and only selected samples with consistent genetic feature and self-reported ethnicity.
Population characteristics	Samples used in this are all adults with European ancestries.
Recruitment	Recruitment of the different cohorts upon the each study's own criteria.
Ethics oversight	The study protocols from different study were approved by different organizations. The detailed information was mentioned in Methods and Acknowledgments sections.

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

Life sciences study design

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

Sample size	Sample size was determined by strabismus cases and non-strabismus controls. In this meta-analvsis, the definitions of cases and controls are different across cohorts. We listed the sample size (summary of cases and summary of controls) in the manuscript. We assembled the largest possible sample size to maximize the power of novel loci discovery.
Data exclusions	We excluded data which lack genotype of phenotype information and some samples were excluded based on genetic ancestry.
Replication	We replicated the previously reported strabismus loci. Since the replication of our GWAS loci requires the cohort with similar sample size, unfortunately, we don't have access to the data at this scale and cannot perform the replication at this stage.
Randomization	Samples were from collected study cohorts and were not randomized.
Blinding	Genotyping and quality control for the genetic data was conducted without knowledge of the phenotypes.

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 and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Plants

Seed stocks

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.

Novel plant genotypes

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.

Authentication

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, mosiacism, off-target gene editing) were examined.