Software and code

Policy information about software

Software

Policy information about code

Availability

Data analysis

Ancestry was determined with SNPweights v2.1 (https://www.hsph.harvard.edu/alkes-price/software/). Quality control, imputation, and data analysis were performed using software described in the Supplementary Information. Genetic association analyses were performed with linear mixed models in GEMMA v0.96. The UKBB data (UKBB) were analyzed with BGenie v1.2. All analyses were performed under the assumption that the distribution of allelic effects was normal. For null hypothesis testing, the test statistic (e.g. t) with confidence intervals, effect sizes, degrees of freedom and P values were calculated. Give P values as exact values whenever suitable.

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. Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency.

Materials & experimental systems

Materials

Methods

Details of the study

Data analysis

Recruitment

Ethics oversight

Corresponding author(s)

Last updated by author:

October 2018

Field-specific reporting

Pathogen and other organisms

Antibodies

Human research participants

Policy information about human research participants

Population characteristics

Recruitment

Ethics oversight

Note that full disclosure of the approval process must also be presented in the manuscript.