

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 data was collected in this study.
Data analysis	We used our implementation of the proposed method, Relate, which can be downloaded from https://myersgroup.github.io/relate under an Academic Use Licence. External software used in the current study were downloaded from the following URLs: ARGweaver, https://github.com/mdrasmus/argweaver (24 Jan 2017); RENT+, https://github.com/SajadMirzaei/RentPlus (2 Oct 2017); msprime, https://github.com/tskit-dev/msprime (22 Jul 2017); msmc, https://github.com/stschiff/msmc2 (14 Oct 2017); SMC++, https://github.com/popgenmethods/smcpp (14 Oct 2017); simuPOP, http://simupop.sourceforge.net/ (27 Jun 2018); mbs, http://www.sendou.soken.ac.jp/esb/innan/InnanLab/ (27 Jun 2018); SDS, https://github.com/yairf/SDS (27 Jun 2018); selscan, https://github.com/szpiech/selscan (31 Jul 2018); hapbin, https://github.com/evotools/hapbin (11 Dec 2018)

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

Datasets used in the current study were obtained from the following URLs:

1000 Genomes Project phased dataset, https://mathgen.stats.ox.ac.uk/impute/1000GP_Phase3.html (13 Jan 2017); Genomic mask, ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/supporting/accessible_genome_masks/ (20 Jul 2017); Human ancestral genome, ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/phase1/analysis_results/supporting/ancestral_alignments/ (20 Jul 2017); GWAS catalogue, <https://www.ebi.ac.uk/gwas/api/search/downloads/full> (9 Nov 2017); PGC GWAS study, <https://www.med.unc.edu/pgc/results-and-downloads> (23 Nov 2018); HaploReg, http://archive.broadinstitute.org/mammals/haploreg/data/haploreg_v4.0_20151021.vcf.gz (21 Oct 2017); GTEx eQTL https://storage.googleapis.com/gtex_analysis_v7/single_tissue_eqtl_data/GTEX_Analysis_v7_eQTL.tar.gz (13 Jan 2019); UK Biobank GWAS summary statistics, <http://www.nealelab.is/uk-biobank> (4 Oct 2018); PopHumanScan, <https://pophumanscan.uab.cat> (13 Jan 2019)

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	The sample size was predetermined by the data set used (1000 Genomes Project Phase 3). This data set comprises 2504 samples. We confirmed using simulations that this sample size is sufficient for the applications considered in this study.
Data exclusions	We excluded one individual (two haplotypes) from each of the 26 populations for future applications, where this individual was chosen uniformly at random.
Replication	For each application, we confirmed that our findings are consistent known results in the literature. We did not replicate our analysis on an independent data set, because such a data set was not available.
Randomization	Randomisation was performed when necessary using standard techniques that account for ascertainment effects or structure in the data such as linkage-disequilibrium (LD).
Blinding	We were not blinded to group allocation, but randomly permuted samples where necessary.

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