

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

DNA samples were genotyped by using either Affymetrix (Mountain View, CA) Axiom LAT-1 arrays or by using Illumina (San Diego, CA) Multi-Ethnic Genotyping Array (MEGA) arrays. Genotype calling was performed following default parameters using Affymetrix's Genotyping Console software and Illumina's GenomeStudio 2.0 application, respectively. The average call rate was 98.5% for all newly genotyped samples. Before filtering and merging, the total number of SNPs called on the Axiom LAT-1 and Illumina MEGA platforms were 813,036 and 1,738,289 respectively. To remove genotyping errors, all samples genotyped on the same array were filtered together using Plink 1.9, eliminating the following: individuals missing more than 1% of genotypes sites (mind .01), SNPs missing in more than 1% of individuals (geno .01), and SNPs out of Hardy-Weinberg equilibrium with a p-value below $10e-110$.

Data analysis

PLINK 1.9, EIGENSOFT 7.2.1, ADMIXTURE 1.3.0, R 3.5.2, ggplot2 3.1.0, Pophelper 2.2.9, Compositions 1.4.0, SHAPEITv2.837, RFMixv1.5.4, GERMLINE 1.5.3, qgraph, Tracts 1.0, ALDER 1.0, MALDER 1.0, badmixture 1.0, Affymetrix's Genotyping Console 4.0, GenomeStudio 2.0, UCSC liftover 1.0, fourpop from TreeMix 1.1, fastsimcoal 2.6, custom matrix completion code is available at <https://github.com/AlexIoannidis/completion>

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

Individual-level genotypes for new data presented in this study are available through a data access agreement to respect the privacy of the participants for the

transfer of genetic data from the European Genome Archive (EGA).

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	No statistical methods were used to predetermine sample size. The sample size was selected before analysis was begun based on available samples and budgetary constraints for genotyping. We sought to include sufficient sample to power statistical comparisons.
Data exclusions	Standard pre-established genotype quality controls were applied to remove all individuals missing more than 1% of genotypes sites (mind .01), SNPs missing in more than 1% of individuals (geno .01), and SNPs out of Hardy-Weinberg equilibrium with a p-value below 10e-110.
Replication	No experiments were conducted, so replication of experimental results is not relevant.
Randomization	This is not relevant as our study does not consider variable assignments or categories.
Blinding	Blinding was not relevant to this study, which is standard in the population genetics field.

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	No covariate-relevant population characteristics were used as recruitment criteria for any of the samplings, other than the geographic location of participants throughout the various sampling sites.
Recruitment	The samples used for this analysis were collected by the University of Chile, the University of Oxford, and Stanford University during various expeditions across Latin America and the Pacific. No self-selection bias was introduced as recruitment procedures were inclusive and addressed to the general population at each sampling site.
Ethics oversight	Written informed consent was obtained from all participants and research/ethics approval and permits were obtained from the following institutions: Stanford University Institutional Review Board (IRB approval No. 20839), Oxford University Tropical Research Ethics Committee (reference No. 537-14), and the Scientific Ethics Committee of the Catholic University of Chile (reference No. 1971092).

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