Reporting Summary

Nature Research 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 Research 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

☐ 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 specific computer code was used for data collection

Data analysis

Custom codes (EM algorithm and clustering algorithm) have been uploaded to the following github repository: https://github.com/birthw/code. We further used GCTA (v.1.91.1 beta), GATK (v.3.4.07), BOLT-LMM (v.2.1), LDpred (v.1.0.8) and R 3.5 to analyse data and produce plots for this manuscript.

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 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

GWAS summary statistics from this study are deposited at https://www.decode.com/summarydata/. Publicly available datasets used in this study were: Early Growth Genetics (EGG) Consortium datasets: [http://mccarthy.well.ox.ac.uk/publications/2019/EggBirthWeight_NatureGenetics/Fetal_BW_European_meta.NG2019.txt.gz](http://mccarthy.well.ox.ac.uk/publications/2019/EggBirthWeight_NatureGenetics/Fetal_BW_European_meta.NG2019.txt.gz), [http://mccarthy.well.ox.ac.uk/publications/2019/EggBirthWeight_NatureGenetics/Maternal_BW_European_meta.NG2019.txt.gz](http://mccarthy.well.ox.ac.uk/publications/2019/EggBirthWeight_NatureGenetics/Maternal_BW_European_meta.NG2019.txt.gz). Other data generated or analysed during this study are included in this published article and Supplementary Tables 1-12.
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 sample size was determined by the data in the Icelandic Birth Registry combined with publicly available data on fetal growth phenotypes.

Data exclusions
The study included births recorded in the Icelandic Birth Registry from 1982 to 2016 with the exclusion of multiple births, infant deaths and out of term births, defined as gestational age less than 258 days or 294 days or more.

Replication
Our study was a meta-analysis of available GWAS studies with no direct replication. We checked for evidence of heterogeneity between previously published data and the new Icelandic data and reported variants that had previously been associated with fetal growth but were not significant in our study.

Randomization
No randomizations were used in this study as this is a GWAS study.

Blinding
This is an observational study and no blinding was required.

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
☒ ☐ Human research participants
☒ ☐ Clinical data
☒ ☐ Dual use research of concern

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 study included all live singleton term births recorded in the Icelandic Birth Register from 1982 to 2016 after excluding out of term births (gestational age < 258 days and gestational age ≥ 294 days). The mean birth year was 1997 (s.d. 11.1) and 49% of the newborns were females. Mean birth year of mothers was 1969 (s.d. 11.4) and fathers 1967 (s.d. 11.7), mean age of mothers at the birth of first child was 26.6 (s.d. 5.9) and fathers mean age was 29.1 (s.d. 6.6).

Recruitment
In Iceland, a large fraction of the population of 360 thousand inhabitants has participated in a nationwide research program at deCODE Genetics. Participants in this current study were identified in the Icelandic Birth Register, which covers the entire population for the recorded period, and recruited into the study based on available data in the nationwide research program. Using this approach, any selection bias is unlikely and thus it is unlikely that the recruitment method has any impact on the results.

Ethics oversight
The study was approved by the National Bioethics Committee, Iceland (approval no. VSN-15-169) following evaluation of the Icelandic Data Protection Authority. We have obtained informed consent for all participants in this study who donated samples. All data processing complies with the instructions of the Data Protection Authority, Iceland (PV_201708095056).

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