

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	☒ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☐	☒ 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 <i>d</i> , Pearson's <i>r</i>), 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	European GWAS summary statistics were obtained from https://www.ebi.ac.uk/gwas/studies/GCST90102470 .
Data analysis	For GWAS, we applied the generalized mixed model implemented in SAIGE version 1.0.5The Manhattan and quantile- quantile plots were generated using FUMA v1.6.0., and regional association plots were generated using LocusZoom

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](#)

The summary statistics of Japanese GWAS for POP will be available from Database Center for Life Science (DBCLS) website (<https://humandbs.dbcls.jp/en/>). Accession code will be provided once the registration procedure is completed.

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	We obtained sex information from the results of X chromosome genotype data, and we analyzed female only in this study.
Reporting on race, ethnicity, or other socially relevant groupings	We analyzed Japanese subpopulations, Hondo and Ryuktu, determined by a result of principal component analysis using genome-wide single nucleotide polymorphisms genotype information.
Population characteristics	We analyzed female patients with pelvic organ prolapse and female controls aged ≥ 40 years.
Recruitment	All participants provided written informed consent before enrollment of this study.
Ethics oversight	The protocol was approved by the ethics committees of University of the Ryukyus (Nishihara, Japan) for Medical and Health Research Involving Human Subjects (Approval No 21-1826-08-02-00, 17-171-03-01-00), and the RIKEN Center for Integrative Medical Sciences (Yokohama, Japan) (Approval No. RIKEN-Y-2022-068)

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	771 cases and 76,625 controls in the Japanese GWAS, and 28,857 cases and 622,916 controls in the cross-ancestry GWAS meta-analysis.
Data exclusions	We excluded individuals with (1) sample call rates < 0.98 , (2) individuals having a shared identity-by-descent ($\pi^2 \geq 0.95$), (3) sex mismatch between genotypic and phenotypic information, and (4) outliers from the East Asians identified by a principal component analysis. We excluded SNPs with (1) call rate < 0.98 , (2) genotype distributions were not in accordance with Hardy–Weinberg equilibrium ($p < 1 \times 10^{-6}$), and (3) minor allele frequency (MAF) < 0.01 .
Replication	none
Randomization	Age, and PC1-3 were included as covariates
Blinding	The analyses were performed in a case-control study design; therefore blinding could not be applicable.

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

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	not applicable
Study protocol	not applicable
Data collection	Clinical data was obtained from the electrical record.
Outcomes	not applicable

Plants

Seed stocks	not applicable
Novel plant genotypes	not applicable
Authentication	not applicable