

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	Data management were performed using SAS, version 9.4 (SAS Institute Inc).
Data analysis	Data analyses were performed using the R packages Survival (version 3.5.5), drgee (version 1.1.10), and OpenMx (version 2.21.8) in RStudio (version 2025.9.0.387).

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](#)

Data from the Swedish registers used in this study cannot be shared due to data protection regulations. Researchers who are interested in replicating this study can apply for individual level data through Statistics Sweden (<https://www.scb.se/en/>) and the National Board of Health and Welfare (<https://www.socialstyrelsen.se/en/>).

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	Sex for the total cohort is reported on page 5 and in Table 1. Sex for individuals specifically exposed to victimization and transport accidents is also reported on page 5. All analyses were adjusted for sex.
Reporting on race, ethnicity, or other socially relevant groupings	Ethnicity is not reported because Swedish national health and population registers do not collect this information for legal and ethical reasons.
Population characteristics	See below.
Recruitment	This study was population-based and included all individuals born in Sweden between 1975-2008 with complete information on both biological parents.
Ethics oversight	This study involved human participants and was approved by the Swedish Ethical Review Authority (reference number 2020-06540). Because the study was register-based and individuals were not identifiable at any time, the requirement for informed consent was waived.

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

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	This was a population-based longitudinal study. The methods were quantitative.
Research sample	The study cohort was population-based and representative, including all individuals born in Sweden between 1975 and 2008 with complete information on both biological parents. The total cohort comprised 3,340,945 individuals, of whom 1,624,248 (48.6%) were female and 1,716,697 (51.4%) were male. Participants were followed longitudinally from birth until the date of OCD diagnosis, emigration, death, or the end of follow-up (31 December 2020), whichever occurred first, contributing data at different ages.
Sampling strategy	Not applicable. The study did not involve a sampling procedure. The study population consisted of all individuals born in Sweden between 1975 and 2008 with complete information on both biological parents, identified through nationwide registers. As the study used the entire eligible population, no a priori sample size calculation was performed.
Data collection	The researchers had no role in data collection. The data used in this study were obtained from several nationwide Swedish health and administrative registers. The Total Population Register, which contains information on all Swedish inhabitants since 1968, was used to ascertain the study cohort and demographic data for the cohort members. The migration register, which contains records on every immigration into and emigration out of Sweden, was used to obtain migration data. Data on deaths were retrieved from the Cause of Death Register, which records the dates and causes of all deaths since 1961. Data on clinical diagnoses were obtained from the National Patient Register (NPR), which covers inpatient hospital admissions since 1969 and outpatient specialist care since 2001. Biological kinships were identified using the Multi-Generation Register, which contains information on individuals registered as residents in Sweden after 1960, and those born from 1932. The registers were linked using the unique Swedish personal identification number. Because the study relied exclusively on routinely collected register data, no researchers were present during data collection and blinding to experimental conditions was not applicable.
Timing	Not applicable. Data collection was not conducted by the researchers, as the study used routinely collected nationwide register data. In the defined cohort, individuals were followed from birth until the end of follow-up (31 December 2020).
Data exclusions	We excluded 137,415 individuals who had missing information on their biological parents or who died or emigrated before age 6. Information on biological parents was required for the planned familial analyses. Individuals who died or emigrated before age 6 could not contribute to the analysis because the minimum age for an OCD diagnosis was set at 6 years to avoid case misclassification, following recommended register-based practices. These exclusion criteria were defined a priori.
Non-participation	Not applicable. This was a population-based register study including all eligible individuals in the defined cohort. As the study relied on routinely collected administrative data, no participants were recruited and therefore no individuals declined participation or dropped out.

Randomization

Not applicable. This was a population-based register study with an observational design. Participants were not allocated to experimental groups; exposure status was determined based on information recorded in the registers.

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

Methods

- 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

- n/a Involved in the study
- ☒ ☐ ChIP-seq
 - ☒ ☐ Flow cytometry
 - ☒ ☐ MRI-based neuroimaging

Plants

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.