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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 (*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 software was used
Data analysis	Statistical analysis was conducted using SPSS 27 (SPSS Inc., Chicago, Illinois, USA), with exception of relative risk and rate ratios, which were calculated using Medcalc online (Medcalc software, Ostend, Belgium) and Multivariate Poisson Regression which was modelled using Stata 16 (StatCorp, College Station, Texas, USA). Microsoft Excel was used to tabulate data including incident appointment scheduling and attendance.

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 three administrative datasets that support the findings are available from the participating Clinical Genetic Health Services but strict restrictions apply to the availability of these data. As these data relate to patient clinical records they are not publicly available. Australian Census Datasets used in the current study are available from the Australian Bureau of Statistics repository, [https://www.abs.gov.au/statistics/people/aboriginal-and-torres-strait-islander-peoples/estimates-aboriginal-and-torres-strait-islander-australians/latest-release#data-download].

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 is a cross sectional study, involving quantitative data
Research sample	In Australia, there are eight states and territories, each with its own model of clinical genetic health service provision. Our sample includes all people scheduled an appointment at a Clinical Genetic Health Service from three of these: Queensland (2015-17), Western Australia (2015-18), and the Northern Territory (2014-18). Theses three services serve a resident population of 7.65 million people, roughly a third of the total Australian population, and are likely generalizable to the wider Australian population. These three jurisdictions were chosen as they had complete administrative datasets and agreed to partake in the study. This study involved analysis of data from an existing administrative patient database of the state-funded clinical genetic health service in each state: the Northern Territory Genetics Service (Microsoft Excel, for years 2014-2018), Genetic Services of Western Australia (KinTrak, for years 2015-2018), and Genetic Health Queensland (KinTrak, for years 2015-2017).
Sampling strategy	NA
Data collection	NA, administrative data from Clinical Genetic Health Services
Timing	NA
Data exclusions	Some data for the state of Western Australia has been excluded in these analyses as 19.7% of patients (2,247 people) did not have Aboriginal and/or Torres Strait Islander status recorded. As we were examining equity of appointment scheduling and attendance for Aboriginal and/or Torres Strait Islander people reporting of this varaible was paramount to inclusion.
Non-participation	NA
Randomization	NA

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	see above
Recruitment	Not applicable. This study involved the analysis of pre-existing administrative data from clinical genetic health services relating to appointment scheduling and appointment attendance.
Ethics oversight	Ethics approval was obtained from the following Human Research Ethics Committees: The University of Melbourne (HREC-1648489.4), Northern Territory Department of Health and Menzies School of Health Research (HREC-2018-3075) and

the Central Australian Health Service (HREC-18 3112), The Queensland Department of Health (HREC/18/QTHS/51), the Aboriginal Health Council of Western Australia (HREC-810) and the King Edward Memorial Hospital (RGS0000000513). The Aboriginal Medical Services Alliance Northern Territory, Machado-Joseph Disease Foundation, Bega Garnbirringu Health Service (Kalgoorlie), and the Aboriginal Health Council of Western Australia (via Ethics support), all provided formal support for the project. Additional support for the project was received from 14 Aboriginal Health Organisations that were involved in extensive stakeholder consultation and engagement activities.

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