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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	Neuroimaging and behavioral data were derived from publicly available open-access datasets, including HCP-YA, HCP-D, MSC and the UK Biobank. Detailed information regarding data acquisition can be found in the following references: HCP-YA (1200 release) - Van Essen et al., 2013; HCP-D - Somerville et al., 2018; MSC - Gardon el al. 2017; and UK Biobank - Sudlow et al., 2015.
Data analysis	We used the hctsa toolbox (version 1.06) in MATLAB R2020a to extract rsfMRI BOLD time-series features.Subsequent data analysis and visualization were conducted in Python 3.6.13 with the following packages: pandas (1.1.5), numpy (1.19.5), scipy (1.5.4), pingouin (0.3.12), sklearn (0.24.2), matplotlib (3.3.4), seaborn (0.9.0), nilearn (0.7.1), altair (4.1.0) and statsmodels (0.12.2). Heritability analyses were conducted using the Sequential Oligogenic Linkage Analysis Routines (SOLAR, version 9.0.0; http://www.nitrc.org/projects/se_linux). Code for analyses is available on GitHub (https://github.com/linktianx/RSRD_BWAS) and on Zenodo (https://zenodo.org/records/17115208).

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

This study utilized four publicly available human neuroimaging datasets. The Human Connectome Project Young Adult (HCP-YA) dataset is accessible at https://db.humanconnectome.org/ to users who agree to the open-access data use terms. Data from the Midnight Scan Club (MSC) are available via the OpenNeuro repository at https://openneuro.org/datasets/ds000224/versions/1.0.4. The Lifespan Human Connectome Project Development (HCP-D) dataset is available through the NIMH Data Archive (https://nda.nih.gov/ccf) and requires eligibility and institutional sponsorship for access. The UK Biobank resource (https://biobank.ndph.ox.ac.uk/showcase/label.cgi?id=100) is available to approved researchers through a formal application and project approval process by the UK Biobank Access Management team.

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	Recognizing the influence of sex differences on human behavior, we did not treat sex as a confounder in the multivariate modeling of the relationship between RSRD and various human behaviors. Instead, after identifying the two brain-behavior modes, we independently examined the effect of sex on the brain-behavior patterns within each mode for males and females.
Reporting on race, ethnicity, or other socially relevant groupings	We did not consider socially relevant groupings in our study.
Population characteristics	This study included 998 healthy young adults (22–37 years, mean: 28.7 ± 3.7 years; 531 females) from the HCP-YA study, 10 healthy young adults (five females; mean age = 29.1 ± 3.3 years) from the MSC study; 623 typically developing participants (mean: 173.4 ± 48.7 months; 351 females) from the HCP-D study, and 28,517 middle-aged to elderly participants (45–82 years, mean: 64 ± 7.6 years; 14,769 females) from the UK Biobank study.
Recruitment	Full recruitment procedures are available for the Human Connectome Project (Van Essen et al., 2013), the Human Connectome Project Development Dataset (Harms et al., 2018; Somerville et al., 2018), the Midnight Scan Club (Gardon el al. 2017), and the UK Biobank study (Miller et al., 2016).
Ethics oversight	The datasets in this study were approved by their respective ethical review boards: the Human Connectome Project by the Institutional Review Board at Washington University in St. Louis, the MSC study was approved by the Washington University School of Medicine Human Studies Committee and the Institutional Review Board, and the UK Biobank by the NHS North West Centre for Research Ethics (reference: 11/NW/0382).

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	The sample size was determined by the availability of rs-fMRI and behavioral data, no statistical methods were applied to pre-determine it. The sample size for each analysis is explicitly reported alongside the corresponding results.
Data exclusions	For HCP-YA and HCP-D, participants who did not provide complete data for all four rs-fMRI sessions were excluded from the analysis. For the UK Biobank, participants without resting-state fMRI data were initially excluded. Among the remaining participants, as many as possible who had completed the extraction of regional time-series features were included. Additionally, participants lacking relevant behavioral phenotypes were excluded. These exclusions were made due to the absence of essential data required for the analysis.
Replication	We conducted external (cross-cohort) replication and validation using data from MSC, HCP-D and the UK Biobank.
Randomization	There was no group allocation.

Blinding | There was no group allocation.

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

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, mosiacism, off-target gene editing) were examined.*

Magnetic resonance imaging

Experimental design

Design type | We used resting-state fMRI and behavioral phenotypic data to investigate the associations between common inter-individual variability in spontaneous brain regional dynamics and human behaviors. Additionally, we leveraged large-scale, independent datasets spanning the lifespan to assess the external generalizability of BWAS findings across cohorts

Design specifications | Details are published in the relevant papers for the Human Connectome Project Development Dataset (Harms et al., 2018; Somerville et al., 2018), the Midnight Scan Club (Gardon el al. 2017), the Human Connectome Project (Van Essen et al., 2013), and the UK Biobank study (Miller et al. 2016).

Behavioral performance measures | We included 159 behavioral phenotypes in the HCP-YA dataset, covering domains such as cognitive performance, sensory-motor functions, personality traits, and substance use, as detailed in Supplementary Table S4. For the HCP-D cohort, we selected phenotypes that closely matched those in the HCP-YA study, identifying 9 phenotypes for the Substance Use Mode and 11 for the Cognition Mode to support generalization analyses. In the UK Biobank cohort, informed by prior research, we performed two separate principal component analyses (PCAs) to derive composite scores for substance use and externalizing problems. Additionally, we included performance metrics from five widely used cognitive tasks. Details regarding the behavioral phenotypes and their preprocessing are provided in the Methods section and Supplementary Methods.

Acquisition

Imaging type(s): resting-state fMRI

Field strength: 3T

Sequence & imaging parameters: Details are published in the relevant papers for the Human Connectome Project Development Dataset (Harms et al., 2018; Somerville et al., 2018), the Human Connectome Project (Smith el al,.2013; Van Essen et al., 2013), the Midnight Scan Club (Gardon el al. 2017), and the UK Biobank study (Miller et al. 2016)

Area of acquisition: Whole brain scans

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software: We used the officially preprocessed data for the HCP-YA, HCP-D, and UK Biobank cohorts. Specifically, the HCP-YA data were processed using the ICA-FIX pipeline (Glasser et al., 2013), the HCP-D data using the MSMAll pipeline—an extension of ICA-FIX incorporating surface-based alignment (Robinson et al., 2014)—and the UK Biobank data following the procedures described by Alfaro-Almagro et al. (2018). For the MSC dataset, preprocessing was conducted using fMRIPrep (version 20.2.1; Esteban et al., 2019).

Normalization: nonlinear

Normalization template: MNI152 template

Noise and artifact removal: The HCP-YA data were preprocessed using the Human Connectome Project (HCP) ICA-FIX pipeline, as described in Glasser et al. (2013), with minimally preprocessed volumetric rs-fMRI data obtained from the official HCP repository. This pipeline included corrections for head motion and spatially structured physiological noise using the ICA+FIX method. The HCP-D rs-fMRI data were preprocessed using the HCP MSMAll pipeline, an extension of the ICA-FIX pipeline that incorporates surface-based functional alignment through the multimodal surface matching (MSM) algorithm (Robinson et al., 2014). For the UK Biobank, the officially released preprocessed volumetric rs-fMRI data underwent motion correction, grand-mean intensity normalization, EPI and GDC unwarping, and structured artifact removal using the ICA+FIX method. For more details, see Alfaro-Almagro et al. (2018). For the MSC dataset, preprocessing was performed using fMRIPrep (version 20.2.1; Esteban et al., 2019), which included standard corrections for head motion and susceptibility distortions, spatial normalization, and denoising using component-based noise correction (CompCor).

Volume censoring: N/A

Statistical modeling & inference

Model type and settings: Univariate Analysis: The analysis includes methods from the hctsa toolbox for time-series analysis, intraclass correlation coefficient (ICC), Pearson correlation, Spearman's rank correlation, and two-sample t-tests.
Multivariate Analysis: Principal component analysis (PCA), least squares decomposition, partial least squares correlation (PLSC), and canonical correlation analysis (CCA).

Effect(s) tested: Pearson's correlation and Spearman's correlation

Specify type of analysis: ☐ Whole brain ☒ ROI-based ☐ Both

Anatomical location(s): We analyzed 271 ROIs spanning the whole brain using three parcellations: 200 cortical regions from the Schaefer200 parcellation, covering seven functional networks (Schaefer et al., 2018); 54 subcortical regions from the Melbourne Subcortex Atlas (3T version, scale IV; Tian et al., 2020); and 17 cerebellar regions from the Buckner Atlas, each corresponding to specific functional networks (Buckner et al., 2011).

Statistic type for inference: cluster-wise

(See Eklund et al. 2016)

Correction: FWE and permutation-based correction methods were applied according to the specific conditions. Detailed descriptions were provided in the Methods section.

Models & analysis

n/a	Involved in the study
☐	☒ Functional and/or effective connectivity
☒	☐ Graph analysis
☐	☒ Multivariate modeling or predictive analysis

Functional and/or effective connectivity	Pearson correlation
Multivariate modeling and predictive analysis	Principal component analysis (PCA), least squares decomposition, partial least squares correlation (PLSC), and canonical correlation analysis (CCA).