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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	N/A
Data analysis	R (v4.3.0), edgeR (v3.43.8), ComplexHeatmap (v2.17.0), WGCNA (v1.72-1), clusterProfiler (v4.9.3), Python (v3.12), REVIGO (http://revigo.irb.hr/)

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 authors declare that the data supporting the findings of this study are available within the paper and its supplementary materials.

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	For the Brainspan dataset, transcriptomic data from 19 biologically female and 23 male donors were used in this study. For the Allen Human Brain Atlas (AHBA) dataset, transcriptomic data from 1 biologically female and 5 male donors were used in this study. No other sex or gender information was available in this study.
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	For the Brainspan dataset, the donors ages span from 8 post-conception weeks (PCW) to middle adulthood (approximately 40 years old) and represented diverse ethnic backgrounds. Detailed information regarding sample collection, sequencing protocols, and quality control procedures is available in the BrainSpan technical white paper (https://help.brain-map.org/display/devhumanbrain/Documentation). The Allen Human Brain Atlas (AHBA) datasets encompass samples from six neurotypical adult donors, ranging in age from 24 to 57 years. The developmental single-cell transcriptome data were derived from both fetal (5 to 20 PCW) and adult neocortical brain tissues.
Recruitment	N/A
Ethics oversight	N/A

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

Ecological, evolutionary & environmental sciences study design

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

Study description	Investigating the expression enrichment patterns of the neuropsychiatric risk gene sets derived from unbiased genome-wide studies in different spatiotemporal and single cell transcriptomic data.
Research sample	The up-to-date published GWAS of IQ, ASD, ADHD, TS, OCD, ANO, Neuroticism, Panic disorder, MDD, BIP, Schizophrenia, AD, PD and Epilepsy, as well as exome sequencing studies of ASD and Schizophrenia were carefully investigated to curate unbiased genome-wide risk gene sets for each trait (Supplementary Table 1).
Sampling strategy	To reduce bias in the gene-sets spatiotemporal expression enrichment analysis in this study, only risk genes derived from data-driven, hypothesis-free genome-wide association/sequencing studies or alike databases were included. For some of those studies, multiple risk gene sets with different gene mapping strategies or criteria were selected for intra-trait comparison of their spatiotemporal expression patterns.
Data collection	Risk gene data were collected from the qualified published papers, supplemental materials and additionally from SFARI for ASD by Dr. Weiqing Liu. Transcriptome datasets were downloaded from the corresponding websites (https://www.brainspan.org/static/download.html, https://human.brain-map.org/static/download/, http://resource.psychencode.org/#) respectively for the BrainSpan, the Allen Human Brain Atlas, and the PsychENCODE single cell transcriptome data by Dr. Weiqing Liu.
Timing and spatial scale	Risk gene datasets were collected between Dec 2021 to Nov 2025; BrainSpan datasets were downloaded on Dec 13 2023; AHBA datasets were downloaded on Jun 11 2024; the PsychENCODE single cell transcriptome datasets were downloaded on Jun 26 2024.
Data exclusions	No data were excluded in the risk gene spatiotemporal expression enrichment analysis. Three samples in the BrainSpan were excluded in the WGCNA analysis using a cut height of 100,000 on the sample dendrogram to achieve a higher sample homogeneity.
Reproducibility	The risk gene sets of different mapping strategies for the same trait were merged to form a pan risk gene set for the 15 traits, and the 15 merged gene sets yielded clustering patterns comparable to those observed using individual gene sets, indicating the robustness of their spatiotemporal enrichment patterns. The enrichment of different co-expression modules in the developmental single cell transcriptomes were partly replicated in the adult single cell datasets.
Randomization	As negative controls, we used randomly generated gene sets from the genome with varying sample sizes. The random gene sets were generated by "sample" function in R to randomly select genes from the genome with no replacement.

Blinding | Blinding was not relevant to this study because its' data driven design.

Did the study involve field work? ☐ Yes ☒ No

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 | NA

Novel plant genotypes | NA

Authentication | NA