

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	We use pre-existing data. Data access methods are specified in Supplementary Table 1 of the submitted Supplementary Document. For datasets from The National Institute of Mental Health Data Archive (NDA), we used NDA download manager to download data. For other open datasets, we downloaded directly from the websites. For datasets provided by collaborators, data were shared via dropbox.
Data analysis	For surface-based morphometry(SBM), FreeSurfer version 7.1.0 was used for preprocessing data and statistical analysis. MRIQC 0.15.2 (https://mriqc.readthedocs.io/en/latest/about.html) was used for quality control of images. Eigenstrapping (https://github.com/SNG-Newy/eigenstrapping) was used to generate null maps. For voxel-based morphometry(VBM), CAT12 (version 8.1, http://dbm.neuro.uni-jena.de/cat/), which is included in the Statistical Parametric Mapping software (SPM12, http://www.fil.ion.ucl.ac.uk/spm/software/spm12) in MATLAB r2021a was used for preprocessing data and statistical analysis. BrainSMASH(https://brainsmash.readthedocs.io/en/latest/) was used to generate null maps. NeuroCombat package in Python (https://github.com/Jfortin1/neuroCombat) was used to adjust for side-effects. For other analysis and generating figures, MATLAB r2023b was used.

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.

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 access methods are specified in Supplementary Table 1, which we re-produce here

Dataset - Accessibility

Autism Brain Imaging Data Exchange I (ABIDE I)

Available in the ABIDE I repository, http://fcon_1000.projects.nitrc.org/indi/abide/abide_I.html

Autism Brain Imaging Data Exchange (ABIDE II)

Available in the ABIDE II repository, http://fcon_1000.projects.nitrc.org/indi/abide/abide_II.html

Australian Imaging, Biomarker & Lifestyle (AIBL)

Available in the AIBL repository, subject to the approval of the AIBL Management Committee <https://aibl.org.au/>
<https://ida.loni.usc.edu/>

Advancing innovative brain imaging to detect altered glutamate modulation and network dynamics in schizophrenia (AIS*)

Available on NDA, subject to the approval of Data Access Committee
https://nda.nih.gov/edit_collection.html?id=2488

Bipolar & Schizophrenia Consortium for Parsing Intermediate Phenotypes (B-SNIP 1)

Available on NDA, subject to the approval of Data Access Committee
https://nda.nih.gov/edit_collection.html?id=2274

Bipolar & Schizophrenia Consortium for Parsing Intermediate Phenotypes (B-SNIP 2) Available on NDA, subject to the approval of Data Access Committee

https://nda.nih.gov/edit_collection.html?id=2165

The Autistic Brain Over 45: The Anatomic, Functional, and Cognitive Phenotype(ASD45*)

Available on NDA, subject to the approval of Data Access Committee
https://nda.nih.gov/edit_collection.html?id=2291

Glutamatergic and Neuronal Dysfunction in Gray and White Matter (BrainGluSchi)

Available in the BrainGluSchi repository,
<http://schizconnect.org/>

The Center for Biomedical Research Excellence (COBRE)

Available in the COBRE repository,
http://fcon_1000.projects.nitrc.org/indi/retro/cobre.html

The Determinants of Social Disconnectedness: A Spectrum from the General Community to Severe Mental Illness(DSD*)

Available on NDA, subject to the approval of Data Access Committee
https://nda.nih.gov/edit_collection.html?id=2481

Human Connectome Project for Early Psychosis (HCP-EP)

Available on NDA, subject to the approval of Data Access Committee
<https://www.humanconnectome.org/study/human-connectome-project-for-early-psychosis>
https://nda.nih.gov/edit_collection.html?id=2914

Singapore Memory Ageing and Cognition Centre (MACC) Harmonization Project (Harmonization)

Available from the principal investigator of the study, subject to local ethics committee requirements

Inhibitory dysfunction in autism (IDAUT*)

Available on NDA, subject to the approval of Data Access Committee
https://nda.nih.gov/edit_collection.html?id=2266

Monash Brain and Behaviour Project (MBBP) Available from the principal investigator of the study, subject to local ethics committee requirements

MIND Clinical Imaging Consortium (MCIC)

Available in the MCIC repository,
<http://schizconnect.org/>

Modulation of ventrolateral prefrontal cortical activity during reward processing by transcranial direct current stimulation (MRITDCS*)

Available on NDA, subject to the approval of Data Access Committee
https://nda.nih.gov/edit_collection.html?id=2432

A Multidimensional Investigation of Cognitive Control Deficits in Psychopathology (MICCD*)

Available on NDA, subject to the approval of Data Access Committee
https://nda.nih.gov/edit_collection.html?id=2102

Cortical myelin measured by the T1w/T2w ratio in individuals with depressive disorders and healthy controls (Myelin*)

Available in the repository

<https://openneuro.org/datasets/ds003653/versions/1.0.0>

Open Access Series of Imaging Studies (OASIS-3)

Available on OASIS repository, subject to the approval of Knight ADRC

<https://www.oasis-brains.org>

Open Access Series of Imaging Studies (OASIS-4)

Available on OASIS repository, subject to the approval of Knight ADRC

<https://www.oasis-brains.org>

Psychosis and Affective Research Domains and Intermediate Phenotypes (PARDIP)

Available on NDA, subject to the approval of Data Access Committee

https://nda.nih.gov/edit_collection.html?id=2126

Resting state with closed eyes for patients with depression and healthy participants (RD*)

Available in the repository

<https://openneuro.org/datasets/ds002748/versions/1.0.5>

Japanese Strategic Research Program for the Promotion of Brain Science (SRPBS)

Available in the SRPBS repository, subject to the approval of the DecNef Consortium

<https://bicr.atr.jp/decnefro/data/>

Specificity of Hippocampal Subregion Cerebral Blood Volume Abnormalities in Psychiatric Disorders (SHSCBV*)

Available on NDA, subject to the approval of Data Access Committee

https://nda.nih.gov/edit_collection.html?id=3199

A Study of the neural and psychological correlates of emotion and motivation processing deficits in individuals with schizophrenia vs. controls (EMOSZ*)

Available on NDA, subject to the approval of Data Access Committee

https://nda.nih.gov/edit_collection.html?id=2703

The Transdiagnostic Connectome Project (TCP)

Available in the repository

<https://openneuro.org/datasets/ds005237>

UCLA Consortium for Neuropsychiatric Phenomics (UCLA-CNP)

Available in the UCLA repository

<https://openneuro.org/datasets/ds000030/versions/00016>

Youth Depression Alleviation-Combined Treatment (YoDA)

Available from the principal investigator of the study, subject to local ethics committee requirements

Minimal Interval Resonance Imaging in Alzheimer's Disease (MIRIAD)

Available in the MIRIAD repository,

<https://www.ucl.ac.uk/drc/research-clinical-trials/minimal-interval-resonance-imaging-alzheimers-disease-miriad>

Brain correlates of speech perception in schizophrenia patients with and without auditory hallucinations (Speech*)

Available in the repository

<https://openneuro.org/datasets/ds004302/versions/1.0.0>

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 information was provided by self-reporting.
Reporting on race, ethnicity, or other socially relevant groupings	We did not use information on race, ethnicity or other socially relevant groupings.
Population characteristics	We used current diagnosis and medication information provided by the datasets (where they are available).
Recruitment	We did not recruit participants for this study. Hence, compensation information from the data that we used are not available to us.
Ethics oversight	Monash University Ethics Committee

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](https://www.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	We did not predetermine the sample size. With used all the data that we could access and which passed quality control, excluding sites with less than 20 participants per group. This yielded a final data pool of 3091 cases (AD and psychiatric disorders) and 3002 controls from 66 sites for the SBM analysis and a total of 2427 cases and 2353 controls from 42 sites for the VBM analysis.
Data exclusions	We only retained data from participants from 18 to 60 years of age in each site (except for sites for Alzheimer's disease) and where T1-weighted MRI and sufficient clinical or demographic data (e.g., indication of diagnosis, age, sex, or scanner site) were available. We further excluded sites with fewer than 20 participants per diagnostic group. We chose the cut-off of 20 participants as it is a common sample size in the field and smaller samples are likely to yield very unreliable findings. After preprocessing, we performed additional quality control checks and excluded participants with images that did not successfully complete our preprocessing pipeline or with low-quality image outputs according to the specific criteria outlined in the manuscript. Sites with fewer than 20 participants per group remaining after these procedures were also excluded.
Replication	The results of study can be reproduced by the provided code, given access to the data.
Randomization	Randomization was not performed because participants were not placed into experimental groups - case and control groups are defined based on diagnosis. Participants without a diagnosis of a psychiatric disorder were in the control group. Participants diagnosed with a psychiatric disorder were placed in the clinical groups with specific diagnosis (schizophrenia, schizoaffective disorder, autism spectrum disorder, major depressive disorder, and bipolar disorder, and Alzheimer's disease)
Blinding	Blinding is not relevant to this study because participants were not placed into experimental groups.

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, mosaicism, off-target gene editing) were examined.

Magnetic resonance imaging

Experimental design

Design type	We used pre-existing T1 weighted MRI.
Design specifications	Specific data acquisition procedures are described in the original studies listed in Supplementary Table 1.
Behavioral performance measures	Behavioral data was not used in this study.

Acquisition

Imaging type(s)	T1 weighted MRI.
Field strength	Specific data acquisition procedures are described in the original studies listed in Supplementary Table 1 and summarised in Supplementary Table 5. Some used 3T, some used 1.5T.
Sequence & imaging parameters	Specific data acquisition procedures are described in the original studies listed in Supplementary Table 1 and summarised in Supplementary Table 5.
Area of acquisition	Whole brain scans were used.
Diffusion MRI	☐ Used ☒ Not used

Preprocessing

Preprocessing software	<p>For surface-based morphometry(SBM), FreeSurfer version 7.1.0 was used for preprocessing data. The FreeSurfer SBM pipeline includes: volumetric registration to MNI305 atlas; bias field estimation and removal; removal of non-brain tissue using a deformable template model; tissue and broad brain region segmentation using a combination of intensity and atlas-based approaches; generation and refinement of a triangular surface mesh model of the white matter surface by following the intensity gradients between the white and grey matter; generation of a pial surface model by expanding the white matter surface to follow intensity gradients between the grey matter and cerebrospinal fluid (CSF); and then estimation of cortical thickness at each surface vertex as the average distance between the closest points on the white and the pial surfaces. The pial surface was inflated and aligned via spherical registration to the fsaverage atlas, which comprises 163,842 vertices per hemisphere. The cortical thickness measures were then smoothed using a surface-based Gaussian kernel with a full-width at half maximum (FWHM) of 10 (results reported in the main text), 15, and 20 mm.</p> <p>For voxel-based morphometry(VBM), CAT12 (version 8.1, http://dbm.neuro.uni-jena.de/cat/), which is included in the Statistical Parametric Mapping software (SPM12, http://www.fil.ion.ucl.ac.uk/spm/software/spm12) in MATLAB r2021a . The CAT12 pipeline includes the following steps: spatial adaptive non-local means (SANLM) denoising filter, resampling, bias correction, affine registration, initial unified segmentation, refined segmentation and skull-stripping, local intensity correction, adaptive maximum a posteriori (AMAP) segmentation, partial volume estimation, and spatial normalization to MNI space using the MNI152Nlin2009cAsym template by Geodesic Shooting. We applied volumetric Gaussian smoothing with kernels sizes (FWHM) of 6, 8, and 12 mm to the preprocessed maps to improve signal-to-noise ratio. To constrain our analyses to grey matter voxels, a common mask was generated from all the normalized, modulated, warped grey matter maps retaining voxels with a tissue probability ≥ 0.2.</p> <p>NeuroCombat package in Python (https://github.com/Jfortin1/neuroCombat) was used to adjust for side-effects.</p>
Normalization	See above.
Normalization template	See above.
Noise and artifact removal	See above.
Volume censoring	See above.

Statistical modeling & inference

Model type and settings	Mass univariate models were used.
Effect(s) tested	To test the statistical significance of the consistency estimates, we compared the observed values to null models obtained by correlating randomized maps with similar autocorrelation to the empirical data as generated using eigenstrapping and BrainSMASH. We also considered a permutation-based null model that involved shuffling patient and control labels before re-estimating group difference maps.
Specify type of analysis:	☐ Whole brain ☐ ROI-based ☒ Both

Anatomical location(s)

For SBM, we used Desikan-Killiany⁵² and Schaefer-100, Schaefer-500, and Schaefer-1000 atlases⁵³, resulting in 34, 50, 250, and 500 regions per hemisphere.

For VBM, we used Schaefer-100, Schaefer-500, and Schaefer-1000 region parcellations (7-network version), combined with the Melbourne subcortical parcellation (32 regions) and Buckner cerebellar parcellation (7 regions).

Statistic type for inference

(See [Eklund et al. 2016](#))

For SBM, we analysed the vertex-wised, cluster-wised, and ROI maps.

For VBM, we analysed the voxel-wised, cluster-wised, and ROI maps.

Correction

For SBM, the corrected threshold map was estimated using a commonly-used cluster-wise correction procedure in which clusters of contiguous vertices showing statistically significant effects are identified and their significance evaluated using permutation testing.

For VBM, we used family-wise error rate (FWER) correction at $p < 0.05$ at the cluster level, with an initial height threshold of 0.05 and extent threshold of 0 voxels.

Models & analysis

n/a | Involved in the study

- ☒ ☐ Functional and/or effective connectivity
- ☒ ☐ Graph analysis
- ☒ ☐ Multivariate modeling or predictive analysis