

Reporting Summary

Nature Research 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 Research policies, see [Authors & Referees](#) 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

LC-MS data were collected by Masslynx 4.0; Locomotor activity data were collected by EthoVision version 7.0 software; Self-administration data were collected by Anilab 6.40. Dendritic structure and immunohistochemistry data were collected by Fiji ImageJ 1.51p and Sholl analysis plugin; Immunoblotting data were analyzed by Chemi analysis software (2.5.10.2); Gating parameters and data analysis of flow cytometry assay were performed using FlowJo 10.0.7 software (Tree Star, USA).

Data analysis

Untargeted lipidomic analysis was conducted with Progenesis Q1 software (v2.0); The other data were analyzed with Graphpad Prism version 7.

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

The data that support the findings of this study are available from the corresponding author upon reasonable request. The lipids were identified from Lipid Maps Database (www.lipidmaps.org) and the Human Metabolome Database (<http://www.hmdb.ca/>).

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	No statistical methods were used to pre-determine sample sizes but our sample sizes are similar to those reported in previous publications [1-3]. 1. Hebert-Chatelain, E., et al., A cannabinoid link between mitochondria and memory. <i>Nature</i> , 2016. 539(7630): p. 555-559. 2. Anderson, E.M., et al., Overexpression of the Histone Dimethyltransferase G9a in Nucleus Accumbens Shell Increases Cocaine Self-Administration, Stress-Induced Reinstatement, and Anxiety. <i>J Neurosci</i> , 2018. 38(4): p. 803-813. 3. Strong, C.E., et al., Locomotor sensitization to intermittent ketamine administration is associated with nucleus accumbens plasticity in male and female rats. <i>Neuropharmacology</i> , 2017. 121: p. 195-203.
Data exclusions	No samples were excluded from the study.
Replication	qPCR and immunoblotting were replicated three times. Immunohistochemistry, ChIP-qPCR and target LC-MS were replicated twice. All attempts were successful.
Randomization	Animal/samples (mice) were assigned randomly to the various experimental groups.
Blinding	In data collection and analysis (e.g., lipidomics, qPCR, as well as imaging and data analysis of IHC and Golgi-Cox staining), the performer(s) was blinded with experimental design.

Behavioural & social sciences study design

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

Study description	Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).
Research sample	State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.
Sampling strategy	Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.
Data collection	Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.
Timing	Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.
Data exclusions	If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.
Non-participation	State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.
Randomization	If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.

Ecological, evolutionary & environmental sciences study design

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

Study description	Briefly describe the study. For quantitative data include treatment factors and interactions, design structure (e.g. factorial, nested, hierarchical), nature and number of experimental units and replicates.
Research sample	Describe the research sample (e.g. a group of tagged <i>Passer domesticus</i> , all <i>Stenocereus thurberi</i> within Organ Pipe Cactus National Monument), and provide a rationale for the sample choice. When relevant, describe the organism taxa, source, sex, age range and any manipulations. State what population the sample is meant to represent when applicable. For studies involving existing datasets, describe the data and its source.
Sampling strategy	Note the sampling procedure. Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.
Data collection	Describe the data collection procedure, including who recorded the data and how.
Timing and spatial scale	Indicate the start and stop dates of data collection, noting the frequency and periodicity of sampling and providing a rationale for these choices. If there is a gap between collection periods, state the dates for each sample cohort. Specify the spatial scale from which the data are taken
Data exclusions	If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.
Reproducibility	Describe the measures taken to verify the reproducibility of experimental findings. For each experiment, note whether any attempts to repeat the experiment failed OR state that all attempts to repeat the experiment were successful.
Randomization	Describe how samples/organisms/participants were allocated into groups. If allocation was not random, describe how covariates were controlled. If this is not relevant to your study, explain why.
Blinding	Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.
Did the study involve field work?	☐ Yes ☐ No

Field work, collection and transport

Field conditions	Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).
Location	State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).
Access and import/export	Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible manner and in compliance with local, national and international laws, noting any permits that were obtained (give the name of the issuing authority, the date of issue, and any identifying information).
Disturbance	Describe any disturbance caused by the study and how it was minimized.

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies used

anti-FAAH (rabbit, abcam, CAT#ab128917, 1:1000), anti-NAPE-PLD (rabbit, abcam, CAT#ab95397, 1:200), anti-CB1R (mouse, abcam, CAT#ab172970, 1:1000), anti-MAGL (goat, abcam, CAT#ab77398, 1:1000), anti-DAGLα (rabbit, abcam, CAT#ab106979, 1:1000), anti-DAGLβ (rabbit, abcam, CAT#ab84733, 1:1000), anti-phospho-CREB-Ser133 (rabbit, cell signaling, CAT#9198, 1:1000), anti-CREB (rabbit, cell signaling, CAT#9197, 1:1000), and anti-p44/42 MAPK (Erk1/2) (rabbit, cell signaling, CAT#4370, 1:1000), anti-Phospho-p44/42 MAPK (Erk1/2) (rabbit, cell signaling, CAT#4695, 1:2000), anti-PKA (rabbit, abcam, CAT#ab75911, 1:2000), anti-PRDM5 (mouse, Santa Cruz, sc-376277, 1:1000), anti-Histone 3 (rabbit, abcam, CAT#ab1791, 1:1000), anti-cofilin (rabbit, abcam, CAT#ab134963, 1:1000), anti-phospho-cofilin (rabbit, cell signaling, CAT#3313, 1:1000), anti-NMDAR1 (rabbit, abcam, CAT#ab109182, 1:1000), anti-AMPA (rabbit, abcam, CAT#ab109450, 1:1000), anti-phospho AMPA(S845) (rabbit, abcam, CAT#ab76321, 1:1000), anti-phospho AMPA(S831) (rabbit, abcam, CAT#ab109464, 1:1000), anti-GAPDH (rabbit, cell signaling, CAT#2118, 1:2000), anti-β-Actin (rabbit, cell signaling, CAT#4967, 1:2000), anti-β-Tubulin (rabbit, cell signaling, CAT#2146s, 1:2000), anti-MAGL (rabbit, Cayman, CAT#100035, 1:100), anti-PRDM5 (rabbit, Novus, CAT#NBP2-13810, 1:200), anti-GFAP (chicken, abcam, CAT#ab4674, 1:1000), anti-NEUN (mouse, abcam, CAT#ab104224, 1:1000), anti-DARPP32 (rabbit, Cell Signaling, CAT#2306, 1:200).

anti-rabbit HRP (cell signaling, CAT#7074s, 1:2000) or anti-mouse HRP (cell signaling, CAT#7076s, 1:2000), anti-goat HRP (abcam, CAT#ab6741, 1:2000). Donkey anti-mouse 488 nm (Alfa Fluor 488, Invitrogen, CAT#A21202, 1:400), Donkey anti-Rabbit 568 nm (Alfa Fluor 568, Invitrogen, CAT#A10042, 1:400), Donkey anti-chicken 640 nm (Alfa Fluor 647, Jackson Immuno, CAT#703-035-155, 1:400).

Validation

Antibodies specific for the required antigens/epitopes were purchased from commercial sources. The validation tests could be found on the websites of manufacturers.

Antibody Manufacturer validation

FAAH	https://www.abcam.cn/faah1-antibody-epr7549-ab128917.html
NAPE-PLD	https://www.abcam.cn/nape-pld-antibody-ab95397.html
CB1R	https://www.abcam.cn/cannabinoid-receptor-i-antibody-epr2224nb-ab172970.html
DAGLα	https://www.abcam.cn/dagla-antibody-ab106979.html
DAGLβ	https://www.abcam.cn/daglb-antibody-ab84733.html
phospho -CREB-Ser133	https://www.cellsignal.com/products/primary-antibodies/phospho-creb-ser133-87g3-rabbit-mab/9198
CREB	https://www.cellsignal.com/products/primary-antibodies/creb-48h2-rabbit-mab/9197
MAGL	https://www.abcam.cn/monoacylglycerol-lipase-mgl-antibody-ab77398.html
p44/42 MAPK (Erk1/2)	https://www.cst-c.com.cn/products/primary-antibodies/phospho-p44-42-mapk-erk1-2-thr202-tyr204-d13-14-4e-xp-rabbit-mab/4370
Phospho-p44/42 MAPK	https://www.cst-c.com.cn/products/primary-antibodies/p44-42-mapk-erk1-2-137f5-rabbit-mab/4695
PKA	https://www.abcam.cn/pka-alphabeta-gamma-catalytic-subunit-phospho-t197-antibody-ep2606y-ab75991.html
PRDM5	https://www.scbt.com/zh/p/prdm5-antibody-a-12
PRDM5(ChIP grade)	https://www.scbt.com/zh/p/prdm5-antibody-a-12
Histone 3	https://www.abcam.cn/histone-h3-antibody-nuclear-loading-control-and-chip-grade-ab1791.html
cofilin	https://www.abcam.com/cofilin-antibody-ep6376-ab134963.html
phospho-cofilin	https://www.cst-c.com.cn/products/primary-antibodies/phospho-cofilin-ser3-77g2-rabbit-mab/3313
NMDAR1	https://www.abcam.cn/nmdar1-antibody-epr24812-ab109182.html
AMPA	https://www.abcam.cn/glutamate-receptor-1-ampa-subtype-antibody-epr5479-ab109450.html
phospho AMPA(S845)	https://www.abcam.cn/glutamate-receptor-1-ampa-subtype-phospho-s845-antibody-epr2148-ab76321.html
phospho AMPA(S831)	https://www.abcam.cn/glutamate-receptor-1-ampa-subtype-phospho-s831-antibody-epr1887-ab109464.html
anti-DARPP32	https://www.cellsignal.cn/products/primary-antibodies/darpp-32-19a3-rabbit-mab/2306?N=4294956287&Ntt=2306&fromPage=plp
GAPDH	https://www.cst-c.com.cn/products/primary-antibodies/gapdh-14c10-rabbit-mab/2118
β-Actin	https://www.cst-c.com.cn/products/primary-antibodies/b-actin-antibody/4967
β-Tubulin	https://www.cst-c.com.cn/products/primary-antibodies/b-tubulin-antibody/2146?site-search-type=Products&N=4294956287&Ntt=2146s&fromPage=plp&_requestid=1819237
anti-rabbit HRP	https://www.cst-c.com.cn/products/secondary-antibodies/anti-rabbit-igg-hrp-linked-antibody/7074?site-search-type=Products&N=4294956287&Ntt=7074s&fromPage=plp&_requestid=1819493
anti-mouse HRP	https://www.cst-c.com.cn/products/secondary-antibodies/anti-mouse-igg-hrp-linked-antibody/7076?site-search-type=Products&N=4294956287&Ntt=7076s&fromPage=plp&_requestid=1820095
Anti-goat HRP	https://www.abcam.cn/rabbit-goat-igg-hl-hrp-ab6741.html
MAGL (immunostaining)	https://www.caymanchem.com/product/100035
PRDM5(immunostaining)	https://www.novusbio.com/products/prdm5-antibody_nbp2-13810
GFAP (immunostaining)	https://www.abcam.com/gfap-antibody-ab4674.html
NeuN (immunostaining)	https://www.abcam.com/neun-antibody-1b7-neuronal-marker-ab104224.html
Alfa Fluor 488 (mouse)	https://www.thermofisher.com/cn/zh/antibody/product/Donkey-anti-Mouse-IgG-H-L-Highly-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A-21202
Alfa Fluor 568(rabbit)	https://www.thermofisher.com/cn/zh/antibody/product/Donkey-anti-Rabbit-IgG-H-L-Highly-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A10042

Alxa Fluor 647(chicken)

<https://www.jacksonimmuno.com/catalog/products/703-605-155>

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)

primary cultured SPNs of rat; 293T cell line.

Authentication

Authentication for 293T cells was performed by ATCC

Mycoplasma contamination

All cell line tested negative for mycoplasma contamination

Commonly misidentified lines
(See [ICLAC](#) register)

No commonly misidentified lines were used

Palaeontology

Specimen provenance

Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information).

Specimen deposition

Indicate where the specimens have been deposited to permit free access by other researchers.

Dating methods

If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals

Male C57BL/6J mice (6~8 weeks old) Sprague-Dawley rat at embryonic day 19. All of the mice were housed in the animal facility under a standard 12-h light/12-h dark cycle and a constant room temperature.

Wild animals

No wild animals were used in the study.

Field-collected samples

No field collected samples were used in the study.

Ethics oversight

All experimental procedures and use of the animals were in accordance with the guidelines established by the Association for Assessment and Accreditation of Laboratory Animal Care and the Institutional Animal Care and Use Committee of Sichuan University.

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

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, gender, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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

Clinical data

Policy information about [clinical studies](#)

All manuscripts must comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.
Study protocol	Note where the full trial protocol can be accessed OR if not available, explain why.
Data collection	Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.
Outcomes	Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.

ChIP-seq

Data deposition

- ☐ Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- ☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links <i>May remain private before publication.</i>	For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.
Files in database submission	Provide a list of all files available in the database submission.
Genome browser session (e.g. UCSC)	Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.

Methodology

Replicates	Describe the experimental replicates, specifying number, type and replicate agreement.
Sequencing depth	Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.
Antibodies	Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.
Peak calling parameters	Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.
Data quality	Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.
Software	Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.

Flow Cytometry

Plots

Confirm that:

- ☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☒ All plots are contour plots with outliers or pseudocolor plots.
- ☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Brain tissue was dissected on ice and enzymatically digested using Adult Brain Dissociation kit (#130-107-677, Miltenyi) according to the manufacturer's procedure. Briefly, brain tissues were cut into small pieces and digested with enzymes (included in the kit). After digestion, tissues were passed through a 70 um cell strainer to make single cell suspensions. Single-cell suspensions from CPu were centrifuged and the pellet was resuspended with a viability dye Fixable Viability Stain 780 (1:1000; BD) for live or dead cell discrimination, followed by incubation with blocking buffer containing CD16/CD32 (1:100; BD) for 10 min.
Instrument	FACSAria SORP (BD, USA)

Software	FlowJo V10.0.7
Cell population abundance	For flow sorting, post-sort cells were analyzed by flow cytometry and the purity was at least 90%.
Gating strategy	A sample gating strategy is provided in supplementary figure.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type	Indicate task or resting state; event-related or block design.
Design specifications	Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.
Behavioral performance measures	State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).

Acquisition

Imaging type(s)	Specify: functional, structural, diffusion, perfusion.
Field strength	Specify in Tesla
Sequence & imaging parameters	Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.
Area of acquisition	State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.
Diffusion MRI	☐ Used ☐ Not used

Preprocessing

Preprocessing software	Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).
Normalization	If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.
Normalization template	Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.
Noise and artifact removal	Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).
Volume censoring	Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.

Statistical modeling & inference

Model type and settings	Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).
Effect(s) tested	Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.
Specify type of analysis:	☐ Whole brain ☐ ROI-based ☐ Both
Statistic type for inference (See Eklund et al. 2016)	Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.
Correction	Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).

Models & analysis

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

Functional and/or effective connectivity

Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).

Graph analysis

Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).

Multivariate modeling and predictive analysis

Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.