nature portfolio

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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	All instruments were controlled with commercial software provided by the manufacturer.
Data analysis	Excel(Microsoft365), pymol v3.1.6.1, Image Studio Light v5.2, Empiria Studio v3.0, GraphPad Prism v11, CytoFLEX S, FlowJo 10.6.2, Zen blue v2.3, Duolink ImageTool 1.0.1.2, Bio-Rad CFX Manager v 2.3, pyteomics, SnapGene v7.1.1, package in python, HADDOCK2.4. FragPipe pipeline (v18.0) , R (v4.1.0) RStudio, mixOmics package (v6.26.0), limma, dagLogo, pyteomics package in python

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 mass spectrometry proteomics data have been deposited to: https://massive.ucsd.edu/ProteoSAFe/dataset.jsp?task=8df29c17a96a4822989f039120df504c

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	not applicable
Reporting on race, ethnicity, or other socially relevant groupings	not applicable
Population characteristics	not applicable
Recruitment	not applicable
Ethics oversight	not applicable

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	No sample size calculations were performed. Experiments were performed with replicates, as described in detail below.
Data exclusions	*Describe any 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.*
Replication	All experiments were confirmed with multiple biological replicates as indicated in the materials and methods, figure legends, and shown as individual replicates. - Fig. 1 b,c: The initial screen was performed on 4 independent biological replicates. - Fig. 1f,h: Representative of 5 and 4 independent biological replicates respectively (as quantified in g and i). - Fig. 2b: 3 PLA summary of all points from three independent biological replicates, each replicate is indicated with a different symbol. - Fig. 2d,e: Peptide cleavage assays were performed from two independent experiments, each in triplicates. - Fig. 2e,f: peptide competition assays, at least 3 independent experiment, each in triplicates. - Fig.3b-e, representative images of at least three independent biological replicates. Summarized in graph shown in Fig. 3f. - Fig. 3g: representative images of two independent biological replicates. Summarized in graph shown in Fig. 3i. - Fig. 4a-c: Peptide cleavage assays were performed from two independent experiments, each in triplicates. - Fig. 4d,e: representative experiment of three independent biological replicates. - Fig. 4g-n: representative images of at least three independent biological replicates. - Fig. 5a: three independent biological replicates, each in technical triplicates. - Fig. 5b: three independent biological replicates. - Fig. 5c: three independent biological replicates, each in technical triplicates. - Fig. 5d: three independent biological replicates, each with 6 replicates. - Fig. 5g,h: five independent biological replicates, each in technical triplicates. - Fig. 5i: four independent biological replicates, each in technical triplicates.
Randomization	no randomization was performed as it does not apply to the in vitro and cellular systems used in this study.
Blinding	Researches were not blinded to PLA images, however Duolink ImageTool (Sigma) was used for automated quantification.

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
[ ]	[x] Antibodies
[ ]	[x] 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
[ ]	[x] Flow cytometry
[ ]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used

anti-CTSZ, rabbit, monoclonal IgG, Abcam, Cat No#Ab180580, Clone: EPR14357, Lot: 1069895-5)

anti-CTSV, rabbit, monoclonal IgG, Abcam, Cat No#Ab166894, Clone: EPR10723(B), Lot: 1043268-12)

anti-StfB, mouse, monoclonal IgG, Proteintech, Cat No#66812-1-Ig, Clone: 2G9B8, Lot: 0007252

anti-CTSB, rabbit, monoclonal IgG, CellSignaling, Cat No#31718, Clone: D1C7Y, Lot: 4

anti-DPP9, rabbit, polyclonal IgG, Abcam, Cat No# ab42080, Lot: 1013941-1

anti-DPP9, rabbit, monoclonal IgG, Abcam, Cat No# ab302903, Clone: EPR26469-62, Lot: 1006634-26

anti-DPP9, goat, polyclonal, self-made, RRID:AB_2889071, previously published in Justa Schuch etal. (2016) https:// doi.org/10.7554/eLife.16370 and Bolgi et al. (2022) https://doi.org/10.15252/embr.202154136)

anti-StrepII, mouse, monoclonal IgG, ThermoFisher Scientific, Cat No#MA5-37747, Clone: 1810CT579.47.56.10, Lot: AB4622222)

anti-LAMP1, mouse, monoclonal IgG, Cell Signaling, Cat No#15665, Clone: D4O1S, Lot: 5)

anti-Vinculin, mouse, monoclonal IgG, SigmaAldrich, Cat No#V9131, Clone: V9131, Lot: 0000324943

anti-ß-Actin, mouse, monoclonal IgG, SigmaAldrich, Cat No# A1978, Clone: AC-15, Lot: 0000137631

anti-GFP, mouse, mix of two monoclonal IgGs, Roche, Cat No#11814460001, Clone: 7.1 and 13.1

Donkey IRDye 680RD anti-mouse IgG, purchased from LiCor, Cat No#926-68072, Lot: D30912-05

Donkey IRDye 800CW anti-mouse IgG, purchased from LiCor, Cat No#926-32212, Lot: D50402-03

Donkey IRDye 800CW anti-rabbit IgG, purchased from LiCor, Cat No#926-32213, Lot: D40625-25

Donkey Alexa Fluor 488 anti-mouse, Thermo Fisher Scientific, Cat No# A-21202, Lot: 2266877

Validation

The anti-DPP9 (goat) Ab was validated via IF on DPP9 silenced and also on DPP9KO cells (Justa Schuch et al. (2016) https://doi.org/10.7554/eLife.16370 and Bolgi et al. (2022) https://doi.org/10.15252/embr.202154136)

The rabbit anti-DPP9 Abs (Abcam ab42080 & ab302903) were validated via WB on DPP9KO cells in this study (Fig.1f,h). Further publications are mentioned on the manufacturer's website (Abcam ab42080: 39 publications): https://www.abcam.com/en-us/products/primary-antibodies/dpp9-antibody-catalytic-domain-ab42080

All other antibodies have been validated extensively in peer reviewed publications as detailed on the manufacturers website:

anti-CTSZ Ab was verified by several publications mentioned on the manufacturers website (2): https://www.abcam.com/en-us/products/primary-antibodies/cathepsin-z-antibody-epr14357-ab180580. E.g Ulrich et al. (2024) doi: 10.1038/s41467-023-44683-0.

anti-CTSV Ab was validated via WB and IF on CTSV silenced cells by Wen-Juan et al. (2018) doi:10.1080/15384101.2018.1456601. Ab is suitable for WB and IF. Further publications are mentioned on the manufacturer's website (3): https://www.abcam.com/en-us/products/primary-antibodies/cathepsin-v-antibody-epr10723b-ab166894

anti-StfB, was validated via WB on StfB silenced MCF-7 cells by the manufacturer and is suitable for IF. Manufacturers website: https://www.ptglab.com/products/Cystatin-B-Antibody-66812-1-Ig.htm?srsltid=AfmBOoph9aFaxkW-Zg6tuOyVEuA9Cz1fRmn6Nu1bIkc-FM-S9hdHsp9u

anti-CTSB is suitable for WB, IF and IHC and is cited 206 times. Manufacturers website: https://www.cellsignal.com/products/primary-antibodies/cathepsin-b-d1c7y-rabbit-monoclonal-antibody/31718)

anti-StrepII Ab is suitable for WB, was Cited 3 times. Manufacturer website: https://www.thermofisher.com/antibody/product/Strep-Tag-II-Antibody-clone-1810CT579-47-56-10-Monoclonal/MA5-37747,

anti-LAMP1 Ab is suitable for WB and IF and is cited 123 times. Manufacturers website: https://www.cellsignal.com/products/primary-antibodies/lamp1-d4o1s-mouse-monoclonal-antibody/15665)

anti-Vinculin Ab is suitable for WB and IF and is cited 2013 times. Manufacturers website: https://www.sigmaaldrich.com/DE/de/product/sigma/v9131)

anti-ß-Actin Ab is suitable for WB and IF and is cited over 4100 times. Manufacturers website: https://www.sigmaaldrich.com/DE/de/product/sigma/a1978)

anti-GFP Ab is cited 1127 times. Manufacturers website: https://www.sigmaaldrich.com/DE/de/product/roche/11814460001?srsltid=AfmBOoqA3nsPCXJwuwMmYawvRPbZABx4QrxcOyjIlAELRZBaH_dyRoa4)

Donkey IRDye 680RD anti-mouse IgG. Manufacturers website: https://shop.licorbio.com/irdye-secondary-antibodies/irdye-680rd-donkey-anti-mouse-igg-secondary-antibody/

Donkey IRDye 800CW anti-mouse IgG. Manufacturers website: https://shop.licorbio.com/irdye-secondary-antibodies/irdye-800cw-donkey-anti-mouse-igg-secondary-antibody/

Donkey IRDye 800CW anti-rabbit IgG. Manufacturers website: https://shop.licorbio.com/irdye-secondary-antibodies/irdye-800cw-donkey-anti-rabbit-igg-secondary-antibody/

Donkey Alexa Fluor 488 anti-mouse, cited 7272 times. Manufacturers website: https://www.thermofisher.com/antibody/product/Donkey-anti-Mouse-IgG-H-L-Highly-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A-21202

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	HEK293 FLP-InTM T-RexTM cells, Thermo Fisher Scientific (Cat #R78007, RRID:CVCL_U427). Corresponding CRISPR-Cas9 mediated DPP9KO cells and Flp-In T-REx-293 DPP9KO cells with stable inducible expression of different DPP9 isoforms (DPP9-S, DPP9-SS730A, DPP9-L, DPP9-LS758G) were previously published by us in Bolgi et al. (2022) https://doi.org/10.15252/embr.202154136. FLP-InTM T-RexTM 293 WT and DPP9KO cells with stable inducible expression of the Ubiquitin-CTSZ(1-22)-eGFP-StrepII reporter were generated in this study. HeLa Flp-In T-REx WT were a kind gift from Prof. Matthias Hentze. The HeLa Flp-In T-REx DPP9KO cell line was generated and published in Sewald et al. (2025) https://doi.org/10.1038/s41467-025-58493-z. Corresponding HeLa Flp-In T-REx DPP9KO cells with stable inducible DPP9 isoforms (DPP9-S, DPP9-SS730A, DPP9-L) were generated in this study as described in Bolgi et al. (2022) https://doi.org/10.15252/embr.202154136. MCF7 shDPP9 cells were generated and published in Bettecken et al. (2023) doi:10.3390/cells12162031. MCF7 cells were obtained from ATCC (Identifier: HTB22, website: https://www.atcc.org/products/htb-22). The MCF7 DPP9KO cell line was generated in this study as described in Bolgi et al. (2022) https://doi.org/10.15252/embr.202154136. HEPG2 cells were obtained from ATCC (Identifier: HB-8065, website: https://www.atcc.org/products/hb-8065).
Authentication	HEPG2 and HEK293 FLP-InTM T-RexTM cells were verified by the manufacturer's website. The identity of all cells were frequently checked by their morphological features. Inducible expression or silencing was verified by Immuno-blots.
Mycoplasma contamination	The cell lines used were tested negative for mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used in the study

Palaeontology and Archaeology

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). Permits should encompass collection and, where applicable, export.*
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.

Ethics oversight	*Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.*

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	*For laboratory animals, report species, strain and age OR state that the study did not involve laboratory animals.*
Wild animals	*Provide details on animals observed in or captured in the field; report species and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.*
Reporting on sex	*Indicate if findings apply to only one sex; describe whether sex was considered in study design, methods used for assigning sex. Provide data disaggregated for sex where this information has been collected in the source data as appropriate; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex-based analyses where performed, justify reasons for lack of sex-based analysis.*
Field-collected samples	*For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.*
Ethics oversight	*Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.*

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 should 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.*

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☐	☐	Public health
☐	☐	National security
☐	☐	Crops and/or livestock
☐	☐	Ecosystems
☐	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☐	☐	Demonstrate how to render a vaccine ineffective
☐	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☐	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☐	☐	Increase transmissibility of a pathogen
☐	☐	Alter the host range of a pathogen
☐	☐	Enable evasion of diagnostic/detection modalities
☐	☐	Enable the weaponization of a biological agent or toxin
☐	☐	Any other potentially harmful combination of experiments and agents

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.*

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 *May remain private before publication.*	*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	Cells were seeded into 24-well plates and incubated for 24 h. DPP9 expression was induced by Dox (50 ng / mL, 24 h). Cells were harvested, centrifuged (300 rcf, 5 min), and washed with DPBS before resuspension in FACS buffer (4 % FCS and 5 mM EDTA in DPBS) with LysoTracker™ Green DND-26 (Thermo Fisher Scientific; 1:10,000).
Instrument	CytoFLEX S (Beckman Coulter, Singapore) Serial number AD28076
Software	CytExpert v2.4.0.28, FlowJo 10.6.2 software (BD)
Cell population abundance	This study did not involve low abundant subpopulations of cell. Flow cytometry was used as a tool to measure lysotracker staining
Gating strategy	Cell debris and doublets were excluded using forward and side scatter. For the assessment of acidic compartments in live cells, LysoTrackerTM Green intensity was measured (FITC). Histograms of different DPP9 expressing cells were stacked. MFI was normalized to WT cells and plotted.

☐ 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

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

(See Eklund et al. 2016)

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	Involved 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.