

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](#).

Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study.

For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

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	Open Ephys and SpikeGLX were used as our software for data collection
Data analysis	MATLAB 2020a, DREdge, SpikeInterface, and Kilosort (V1.0 + V2.5) software packages were used in the data post-processing pipelines for data

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](#)

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	Both males and females were approached by the research team to inquire about enrolling in this research. To date, the data
Population characteristics	To date with the use of the procedures described in this manuscript, the mean age of study participants was 60 (range from 34
Recruitment	Prospective participants between 18-80 years of age were recruited through their primary physician and were approached in
Ethics oversight	Mass General Brigham IRB

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

Life sciences study design

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

Sample size	At the time of writing this protocol, the procedure had been performed with 28 participants
Data exclusions	No data was excluded from analyses as no conclusions were made in this paper from data analyses
Replication	The protocol describes what is still a cutting-edge procedure, but consistency in our execution for acquiring data and maintaining a good signal to
Randomization	This was a pilot study aimed at testing novel neurophysiological devices with no control condition
Blinding	This was a pilot study and thus there was no control group

Behavioural & social sciences study design

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

Study description	
Research sample	
Sampling strategy	
Data collection	
Timing	
Data exclusions	
Non-participation	
Randomization	

Ecological, evolutionary & environmental sciences study design

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

Study description	
Research sample	
Sampling strategy	
Data collection	
Timing and spatial scale	
Data exclusions	
Reproducibility	
Randomization	

Blinding

Did the study involve field work? Yes No

Field work, collection and transport

Field conditions

Location

Access & import/export

Disturbance

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

Methods

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

Antibodies

Antibodies used

Validation

Eukaryotic cell lines

Policy information about [cell lines](#) and [Sex and Gender in Research](#)

Cell line source(s)

Authentication

Mycoplasma contamination

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

Palaeontology and Archaeology

Specimen provenance

Specimen deposition

Dating methods

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

Ethics oversight

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	No laboratory animals were used in the study
Wild animals	The study did not involve wild animals
Reporting on sex	No sex-based analyses were performed. Sex characteristics for participants was collected verbally from each subject. The study was
Field-collected samples	No field-collected samples were used in this study.
Ethics oversight	Mass General Brigham IRB

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	
Study protocol	
Data collection	
Outcomes	

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 | |
| <input type="radio"/> | <input type="radio"/> | Public health |
| <input type="radio"/> | <input type="radio"/> | National security |
| <input type="radio"/> | <input type="radio"/> | Crops and/or livestock |
| <input type="radio"/> | <input type="radio"/> | Ecosystems |
| <input type="radio"/> | <input type="radio"/> | Any other significant area |

Experiments of concern

Does the work involve any of these experiments of concern:

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

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

Files in database submission

Genome browser session

(e.g. [UCSC](#))

Methodology

Replicates	<input type="text"/>
Sequencing depth	<input type="text"/>
Antibodies	<input type="text"/>
Peak calling parameters	<input type="text"/>
Data quality	<input type="text"/>
Software	<input type="text"/>

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	<input type="text"/>
Instrument	<input type="text"/>
Software	<input type="text"/>
Cell population abundance	<input type="text"/>
Gating strategy	<input type="text"/>

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	<input type="text" value="N/A, clinically-indicated MRI use only"/>
Design specifications	<input type="text" value="No trials - structural MRI data only"/>
Behavioral performance measures	<input type="text" value="No behavioral measures taken"/>

Acquisition

Imaging type(s)	<input type="text" value="Structural"/>
Field strength	<input type="text" value="??"/>
Sequence & imaging parameters	<input type="text" value="??"/>
Area of acquisition	<input type="text" value="Whole brain scan"/>
Diffusion MRI	<input type="radio"/> Used <input checked="" type="radio"/> Not used

Preprocessing

Preprocessing software	<input type="text"/>
Normalization	<input type="text"/>
Normalization template	<input type="text"/>
Noise and artifact removal	<input type="text"/>
Volume censoring	<input type="text"/>

Statistical modeling & inference

Model type and settings	<input type="text"/>
Effect(s) tested	<input type="text"/>
Specify type of analysis:	<input type="radio"/> Whole brain <input type="radio"/> ROI-based <input type="radio"/> Both
Statistic type for inference (See Eklund et al. 2016)	<input type="text"/>
Correction	<input type="text"/>

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

Graph analysis

Multivariate modeling and predictive analysis



