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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 neuroimaging data was acquired on a Siemens 3T Skyra scanner running standard software. All histology images were acquired on Zeiss LSM 780 confocal microscope and Hitachi 7500 electron microscope systems running standard software.
Data analysis	MATLAB(R2023a), AFNI(21.0.08), FMRIB Software Library (FSL 6.0.4), Advanced Normalization Tools (ANTs v2.4.1), ITK-SNAP(3.6.0), MRtrix3 (3.0.3), and FIJI software (1.54)

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

Data availability
The functional MRI data generated in this study have been deposited in the DANDI database (https://doi.org/10.48324/dandi.001773/0.260412.1743). Openly

available resources used in this study such as the NMT atlas is accessible through the Primate Data and Resource Exchange (PRIME-DRE; https://prime-re.github.io/). Source data are provided with this paper.

Code availability
The custom MATLAB scripts used to analyze the functional MRI data are available in the DANDI database (https://doi.org/10.48324/dandi.001773/0.260412.1743).

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	This study did not involve human subjects.
Reporting on race, ethnicity, or other socially relevant groupings	This study did not involve human subjects.
Population characteristics	This study did not involve human subjects.
Recruitment	This study did not involve human subjects.
Ethics oversight	This study did not involve human subjects.

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	The number of animals was determined using standard practices in the field for working with macaques that balance the ethical and practical constraints of conducting research in non-human primates. We referred to previous studies with similar methodologies (Turchi et al. Neuron 2018, Hirabayashi et al. Neuron 2021, Froesel et al. Nature Communications 2022, Liu et al. Nature Communications 2022, Noritake et al. Nature Communications 2023). Given the limited number of animals inherent to non-human primate studies, statistical analyses incorporated multiple within-subject measurements (e.g., voxel-wise or field-level observations) to improve the precision of estimates. These measurements are technical replicates derived from the same experimental units and were not treated as independent biological replicates. Biological variability was accounted for by including monkey as a factor in the statistical model. Importantly, consistent effects were confirmed across animals to evaluate the robustness of the findings despite the limited number of biological replicates.
Data exclusions	Diffusion weighted imaging data in the voxels where deep brain stimulation lead tracts overlapped were excluded. For g-ratio measurement in electron microscopy imaging, myelin regions that exhibited fixation artifacts or noncompaction were excluded from the analysis. Some axons were sectioned obliquely and demonstrated that the ratio of the longest axon diameter to the shortest axon diameter was over two. These axons were excluded in order to focus on the CB fibers running in the anterior-posterior direction and connecting subcallosal anterior cingulate cortex and posterior cingulate cortex. Otherwise no selection criteria were applied to the data.
Replication	Our analyses were conducted within subject meaning that each animal served as their own control. We conducted approximately six repeats of the resting-functional MRI runs and three repeats of the diffusion weighted imaging runs for each session to achieve robust signals and reducing the physiological noises. Similarly for the analysis of numbers of oligodendrocytes or g-ratio we analyzed data taken from multiple levels. Consistent effects were observed across animals for all measures.
Randomization	Monkeys were randomly assigned to the study. Images for histology were randomly captured within the regions. Axons were randomly counted.
Blinding	Cell count of oligodendrocytes in immunofluorescence studies was conducted by blinded counters. The g-ratio measurement in electron microscopy images was confirmed by a blinded counter separately. MRI data collection and analysis were not performed blind due to the limitations of staff cleared to work with non-human primates. Analyses performed in MATLAB, AFNI, FSL, ANTs, MRtrix3, and ITK-SNAP were conducted using standard scripts applied uniformly to all data, reducing the need for blinding. Behavioral analysis comparing before deep brain stimulation implantation (DBS) and after chronic stimulation was not performed blind because it could be discriminated by DBS implantation. Behavioral analysis was focused on objective movements in order to reduce the need of blinding.

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

Antibodies

Antibodies used: Anti-CC1 primary antibody (anti-APC[CC-1] mouse monoclonal antibody, clone CC-1, 1:5000, Cat# ab16794, RRID:AB_443473, Abcam, Cambridge, UK), goat polyclonal secondary antibody (IgG (H+L) Highly Cross-Adsorbed Goat anti-Mouse, Alexa Fluor™ Plus 555, 1:500, Cat# A32727, RRID:AB_2633276, Thermo Fisher Scientific, Waltham, MA, USA)

Validation: All antibodies were validated by the manufacturers and validation data are publicly available. See manufacturer's website (https://www.abcam.com/en-us/products/primary-antibodies/apc-antibody-cc-1-ab16794) or Research Resource Identification Portal for citations to published works using these resources.

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: Three male rhesus macaques (Macaca mulatta, 7–9 years old; monkeys N, T, and D) were implanted with deep brain stimulation electrodes. Resting-state functional MRI data from an additional three monkeys (B, W, and H, no DBS surgery) were also included.

Wild animals: This study did not involve wild caught animals. Both animals were acquired from breeding facilities within the USA.

Reporting on sex: Due to the practical and ethical limitations of working with non-human primates we only studied macaques. To the best of our knowledge, findings in this study reflect general neural mechanisms that should apply to both male and female animals. Sex was therefore not considered as a variable in the experimental design.

Field-collected samples: This study did not involve samples collected from the field.

Ethics oversight: Icahn School of Medicine Animal Care and Use Commitee (IACUC-2014-0224)

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

Plants

Seed stocks: NA

Novel plant genotypes: NA

Authentication: NA

Magnetic resonance imaging

Experimental design

Design type: Resting-state functional imaging and diffusion weighted imaging

Design specifications: Each resting-state functional imaging session consisted of six approximately 10-minute/300 volume runs. Each diffusion

Design specifications: weighted imaging session consisted of three runs of dataset, reversed the phase encode direction, and collected additional three runs.

Behavioral performance measures: This study did not involve behavioral tasks.

Acquisition

Imaging type(s): Functional, Diffusion-weighted, and Structual

Field strength: 3 Tesla

Sequence & imaging parameters: Structural: Tl-weighted, 0.5 mm isotropic, FOV 288 x 288, Matrix size 288 x 288, TR/TE 2500/2.81 ms, flip angle 8°, coronal orientation
Functional: Echo planar image, 1.6 mm isotropic, FOV 602 x 602, Matrix size 86 x 86, TR/TE 2120/16ms, flip angle 45°, coronal orientation

Area of acquisition: Whole brain

Diffusion MRI ☒ Used ☐ Not used

Parameters: Diffusion weighted imaging: b=1000 s/mm2, TR 6900ms, TE 96.0ms, 72 direction, resolution 1.5mm isotropic voxel, 8 unweighted volumes per scan, multi-band acceleration =3, two opposite phase encoding = AP/PA

Preprocessing

Preprocessing software: AFNI(ver 21.0.9), FSL(ver 6.0.4), ANTs(ver 2.4.1), MRtrix3(ver 3.0.3), and ITK-SNAP(ver 3.6.0)

Normalization: The Tl-weighted images were spatially normalized, then skull-stripped using the U-Net model built from Primate Data-Exchange open datasets

Normalization template: NMT version 2.0 atlas

Noise and artifact removal: Functional imaging: Blur: FWHM of 3 mm
Diffusion weighted imaging: Removed DBS lead tract from diffusion weighted analysis. Principal component analysis denoising using dwinoise. Distortion correction using dwifslpreproc. Bias correction using dwibiascorrect.

Volume censoring: The first two TRs of each functional scan were removed to avoid magnetization effects on the data. The regress_censor_motion (limit 0.10) and regress_censor_outliers (limit 0.02) settings in AFNI's afni_proc.py function were used to censor volumes with excess motion.

Statistical modeling & inference

Model type and settings: Where appropriate we used parametric, non-parametric and count based statistics to analyze our data.

Effect(s) tested: We tested for effects between before DBS versus after chronic DBS stimulation across our functional MRI and diffusion weighted imaging. In addition, we examined the DBS effects on functional connectivity between DBS group and non-surgical control group.

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☒ Both

Anatomical location(s): All ROIs for functional MRI analysis were taken from standard macaque templates (for example, D99 atlas). White matter tract ROIs were made based on the previous study (Folloni et al., 2019).

Statistic type for inference (See Eklund et al. 2016): Voxel-wise false discovery rate

Correction: Cluster correction using AFNI's 3DClusterize function

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: Pearson correlation