

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	N/A
Data analysis	Python open source code was used that required the following packages: numpy, pandas, scipy, nilearn, matplotlib, seaborn, brainspace, and surfplot and can be found https://github.com/jnash22/Stroke_Gradients

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 available on reasonable request by contacting the corresponding author and under an inter-institutional Data Transfer Agreement with Queen’s University.

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

Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.

Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.

Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).

Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)

Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, 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.

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 23 Non human primates were purchased to perform the study and is considerably large in comparison to other non-human primate studies. We were limited by our facilities to animals as well as our staff to follow the animals post-operatively.

Data exclusions N/A

Replication We ensured our results findings were confirmed using both 1) Gradient analysis and 2) network measures as per our reviewers suggestions

Randomization Describe how samples/organisms/participants were allocated into experimental groups. If allocation was not random, describe how covariates were controlled OR if this is not relevant to your study, explain why.

Blinding Describe whether the investigators were blinded to group allocation during data collection and/or analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.

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

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	Cynomolgus Macaques
Wild animals	Data was obtained from 23 male captive-bred cynomolgus macaques (<i>Macaca fascicularis</i>), with an average age of 7.9 ± 1.1 and an average weight of 4.23 ± 1.3 kg (range 3.6 to 5.6 kg).
Reporting on sex	All animals were male, and sex was not considered in our study.
Field-collected samples	N/A
Ethics oversight	All the surgical and experimental procedures were carried out in accordance with the Canadian Council of Animal Care policy on the use of laboratory animal and approved by the Animal Use Subcommittee of Queen's University Council on Animal Care.

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

Plants

Seed stocks	<i>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.</i>
Novel plant genotypes	<i>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.</i>
Authentication	<i>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.</i>

Magnetic resonance imaging

Experimental design

Design type	resting state
Design specifications	Two sessions (pre and post) with 353 volumes per session
Behavioral performance measures	N/A during scanning

Acquisition

Imaging type(s)	functional, structural (eg. BOLD, T2)
Field strength	3T
Sequence & imaging parameters	Baseline, pre-stroke MRI acquisitions were made 48h prior to MCAO. Baseline Scans consisted of a high-resolution, T1-weighted, magnetization-prepared rapid gradient echo (MP-RAGE TR = 1600 ms; TE = 3.92 ms, flip angle = 9°, matrix = 320 × 320, FOV 192 × 192, 120 slices and final voxel size = 0.6 × 0.6 × 0.6 mm. Baseline resting state fMRI data were also acquired using a gradient-echo echo-planar sequence sensitive to BOLD contrast, with volume repetition time (TR) = 2000 ms, T2* echo time

(TE) = 28 ms, flip angle = 80°, slices matrix = 64 × 64, FOV = 768 × 768, 28 slices and a final voxel size = 2 × 2 × 2 mm. In all monkeys, the slices were acquired using contiguous, interleaved acquisition with 353 functional volumes total (11 min. 46 seconds). Immediately following MCAO, animals underwent imaging to confirm vessel occlusion post-stroke using a highresolution MRA sequence; TR = 39 ms; TE = 7.33 ms, flip angle = 15°, matrix = 448 × 448, FOV 112 × 112 mm² and final voxel size = 0.3 × 0.3 × 1 mm³. At thirty days post-stroke, resting state fMRI was again acquired using the same parameters as above. A T2-weighted Fast Spin-Echo was also acquired; TR = 9270 ms; TE = 65 ms, flip angle = 157°, matrix = 256 × 256, FOV 154 × 154 mm², 100 slices and final voxel size = 0.6 × 0.6 × 0.6 mm³.

Area of acquisition

cortical brain scan

Diffusion MRI

☐

Used

☒

Not used

Preprocessing

Preprocessing software

Nipype(1.8.2), using FSL(5.0), ANTs,(2.3.5) AFNI(21.0.06) , and Nilearn (0.9.1)

Normalization

both 12 dof linear and non-linear methods were used to normalize the data

Normalization template

MT v2 Template and CHARM atlas

Noise and artifact removal

CSF, WM, and lesions along with motion parameters from motion correction were used to remove noise from the BOLD signals.

Volume censoring

the first 3 volumes were removed from the series

Statistical modeling & inference

Model type and settings

PCA

Effect(s) tested

pre- to post-stroke

Specify type of analysis:

☐

Whole brain

☐

ROI-based

☒

Both

Anatomical location(s) CHARM atlas, NMT v2

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

FDR

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

LedoitWolf covariance and gradient analysis (eg. PCA)

Graph analysis

Graph metrics were used to calculate: participation coefficient, module degree and network strength and more.

Multivariate modeling and predictive analysis

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