

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	The data was collected from Inverted microscopy (NIS-Elements AR 5.30.01), Scanning electron microscopy (TESCAN VEGA-II LSU, FEI Magellan)
Data analysis	The graphing and stat's software we use was Prism 9. No external custom code or algorithms was used.

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 data supporting the findings of this study are available in the supporting primary research paper.

Human research participants

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

Reporting on sex and gender	<input type="text"/>
Population characteristics	<input type="text"/>
Recruitment	<input type="text"/>
Ethics oversight	<input type="text"/>

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	1. Figure 2d-e: SEM images of the templates (n=3 independent experiments)
Data exclusions	No data was excluded.
Replication	1. Microgel preparation efficiency and diameter measurement were based on 3 independent experiments;
Randomization	1. Microgel preparation efficiency and diameter measurement were based on 9 pictures from 3 independent experiments. These images were
Blinding	1. The microgel preparation preparation was performed 3 times. he first two rounds were completed by first author Lei Tian, and the third round

Behavioural & social sciences study design

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

Study description	<input type="text"/>
Research sample	<input type="text"/>
Sampling strategy	<input type="text"/>
Data collection	<input type="text"/>
Timing	<input type="text"/>
Data exclusions	<input type="text"/>
Non-participation	<input type="text"/>
Randomization	<input type="text"/>

Ecological, evolutionary & environmental sciences study design

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

Study description	<input type="text"/>
Research sample	<input type="text"/>
Sampling strategy	<input type="text"/>
Data collection	<input type="text"/>
Timing and spatial scale	<input type="text"/>
Data exclusions	<input type="text"/>
Reproducibility	<input type="text"/>
Randomization	<input type="text"/>

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
<input type="radio"/>	<input type="radio"/> Antibodies
<input type="radio"/>	<input type="radio"/> Eukaryotic cell lines
<input type="radio"/>	<input type="radio"/> Palaeontology and archaeology
<input type="radio"/>	<input type="radio"/> Animals and other organisms
<input type="radio"/>	<input type="radio"/> Clinical data
<input type="radio"/>	<input type="radio"/> Dual use research of concern

Methods

n/a	Involved in the study
<input type="radio"/>	<input type="radio"/> ChIP-seq
<input type="radio"/>	<input type="radio"/> Flow cytometry
<input type="radio"/>	<input type="radio"/> 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	
Wild animals	
Reporting on sex	
Field-collected samples	
Ethics oversight	

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"/>
<input type="radio"/>	<input type="radio"/>
<input type="radio"/>	<input type="radio"/>
<input type="radio"/>	<input type="radio"/>
<input type="radio"/>	<input type="radio"/>
<input type="radio"/>	<input type="radio"/>

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
<input type="radio"/>	<input type="radio"/>
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<input type="radio"/>	<input type="radio"/>
<input type="radio"/>	<input type="radio"/>
<input type="radio"/>	<input type="radio"/>
<input type="radio"/>	<input type="radio"/>

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

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>	
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"/>
Design specifications	<input type="text"/>
Behavioral performance measures	<input type="text"/>

Acquisition

Imaging type(s)	<input type="text"/>
Field strength	<input type="text"/>
Sequence & imaging parameters	<input type="text"/>
Area of acquisition	<input type="text"/>
Diffusion MRI	<input type="radio"/> Used <input 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	<input type="text"/>
Graph analysis	<input type="text"/>
Multivariate modeling and predictive analysis	<input type="text"/>

