# natureresearch

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## Reporting Summary

**X** Life sciences

Nature Research 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 Research policies, seeAuthors & Referees and theEditorial 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				
	$\mathbf{x}$ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement				
	🗶 A statement o	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. <i>F</i> , <i>t</i> , <i>r</i> ) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.				
×	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings				
×	For hierarchic	al and complex designs, identification of the appropriate level for tests and full reporting of outcomes			
×	Estimates of e	effect sizes (e.g. Cohen's $d$ , Pearson's $r$ ), indicating how they were calculated			
	•	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.			
So	ftware and c	ode			
Poli	cy information abou	ut <u>availability of computer code</u>			
Data collection Fig		Fig. 2a-c, f-i, Fig. 3c,d, Fig. 4a-f, Fig. 5a,b,g-i used CHI software, version 17.01, from CH instruments, Inc.			
Data analysis		Microsoft Excel and OriginPro 8.0 were used for data analysis and plotting.			
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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.					
Da	ta				
All	manuscripts must i - Accession codes, uni - A list of figures that	ut <u>availability of data</u> include a <u>data availability statement</u> . This statement should provide the following information, where applicable: ique identifiers, or web links for publicly available datasets have associated raw data restrictions on data availability			
The authors declare that the main data supporting the results in this study are available within the paper and its Supplementary Information. The raw and analysed datasets generated during the study are available for research purposes from the corresponding author on reasonable request.					
Fi	eld-speci	fic 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.

Ecological, evolutionary & environmental sciences

Behavioural & social sciences

### Life sciences study design

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

Sample size

The work was explorative; therefore, we did not estimate the sample size needed.

We used 3 independent sensors for characterizing performance of NO detection (Fig. 2a-i).

We used 3 biologically independent human aortic vascular smooth muscle cells for biocompatibility test of the NO sensor (Fig. 3a.b) We used 3 biologically independent mice's cells and organs for characterizing the NO detection ability of the sensor in vitro (Fig. 3c,d, Fig.

4a,b).

We used 3 biologically independent rabbits's organs for characterizing the NO detection ability of the sensor in vitro (Fig. 4c-f, Fig. 5a,b).

We used 3 biologically independent rabbits for characterizing the NO detection in vivo (Fig. 5g-j).

Data exclusions

No data were excluded from the analyses.

Replication

The in vitro and in vivo NO detection measurements, and the biodegradable property studies of the sensor were carried out more than 3 times to ensure replicability. The results were consistent and replicable.

Randomization

All devices and animals tested were selected randomly.

Blinding

No blinding was necessary as there were no significant variations in the animals tested

#### Behavioural & social sciences study design

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

Study description

Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).

Research sample

State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.

Sampling strategy

Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.

Data collection

Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.

Timing

Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.

Data exclusions

If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.

Non-participation

State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.

Randomization

If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.

### Ecological, evolutionary & environmental sciences study design

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

Study description

Briefly describe the study. For quantitative data include treatment factors and interactions, design structure (e.g. factorial, nested, hierarchical), nature and number of experimental units and replicates.

Research sample

Describe the research sample (e.g. a group of tagged Passer domesticus, all Stenocereus thurberi within Organ Pipe Cactus National Monument), and provide a rationale for the sample choice. When relevant, describe the organism taxa, source, sex, age range and any manipulations. State what population the sample is meant to represent when applicable. For studies involving existing datasets, describe the data and its source.

Sampling strategy	Note the sampling procedure. Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.		
Data collection	Describe the data collection procedure, including who recorded the data and how.		
Timing and spatial scale	Indicate the start and stop dates of data collection, noting the frequency and periodicity of sampling and providing a rationale for these choices. If there is a gap between collection periods, state the dates for each sample cohort. Specify the spatial scale from which the data are taken		
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.		
Reproducibility	Describe the measures taken to verify the reproducibility of experimental findings. For each experiment, note whether any attempts to repeat the experiment failed OR state that all attempts to repeat the experiment were successful.		
Randomization	Describe how samples/organisms/participants were allocated into groups. If allocation was not random, describe how covariates were controlled. If this is not relevant to your study, explain why.		
Blinding	Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.		
Did the study involve field work? Yes No			
Field work, collec	tion and transport		
Field conditions	Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).		
Location	State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).		
Access and import/export  Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible in compliance with local, national and international laws, noting any permits that were obtained (give the national authority, the date of issue, and any identifying information).			
Disturbance	Describe any disturbance caused by the study and how it was minimized.		
	er specific materials, systems and methods authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material,		
	evant 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 & experime	ental systems Methods		
n/a Involved in the study	<u> </u>		
X Antibodies	<b>x</b> ☐ ChIP-seq		
Eukaryotic cell lines			
Palaeontology	MRI-based neuroimaging		
Animals and other of	prganisms		

## Antibodies

Antibodies used

Clinical data

Describe all antibodies used in the study; as applicable, provide supplier name, catalog number, clone name, and lot number.

Validation

Describe the validation of each primary antibody for the species and application, noting any validation statements on the manufacturer's website, relevant citations, antibody profiles in online databases, or data provided in the manuscript.

#### Eukaryotic cell lines

Policy information about **cell lines** 

Human research participants

Cell line source(s)

HA-VSMCs were purchased from ATCC(Cat No., CRL-1999)

Authentication

HA-VSMCs were stained with smooth muscle cell markers (SMA and SM22). Both of the two markers were positive

Mycoplasma contamination	HA-VSMCs were not tested for mycoplasma contamination		
Commonly misidentified lines (See ICLAC register)	None		
alaeontology			
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).		
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 th	at the raw and calibrated dates are available in the paper or in Supplementary Information.		
nimals and other o	rganisms		
licy information about studie	s involving animals; ARRIVE guidelines recommended for reporting animal research		
Laboratory animals	New Zealand white rabbits, male, 3 months old		
Wild animals	The study did not involve wild animals.		
Field-collected samples	The study did not involve samples collected from the field.		
All animal procedures were completed in agreement with the institutional guidelines of the Beijing Institute of Traumato Orthopaedics. The experimental protocol was reviewed and approved by the Institutional Animal Care and Use Committee (IACUC) at Beijing Institute of Traumatology and Orthopaedics.			
	s involving human research participants		
Population characteristics	Describe the covariate-relevant population characteristics of the human research participants (e.g. age, gender, 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.		
te that full information on the ap	proval of the study protocol must also be provided in the manuscript.		
linical data			
licy information about <u>clinica</u> manuscripts should comply with	I studies the ICMJEguidelines 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.		
Outcomes	Describe now you pre-defined primary and secondary outcome measures and now you assessed these measures.		
hIP-seq	Describe now you pre-defined primary and secondary outcome measures and now you assessed these measures.		

#### Data deposition

Confirm that both raw and final processed data have been deposited in a public database such as <u>GEO</u>. 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. <u>UCSC</u> )	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	escribe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a ommunity repository, provide accession details.			
Flow Cytometry				
Plots				

PIOLS						
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	Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.					
Instrument	Identify the instrument used for data collection, specifying make and model number.					
Software	Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.					
Cell population abundance	Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.					
Gating strategy	Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.					
Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.						

#### Magnetic resonance imaging

#### Experimental design

Design specifications

Indicate task or resting state; event-related or block design. Design type

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: fund	ctional, structural, diffusion, perfusion.		
Field strength Spec		rsla		
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 wheth	er 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		il on software version and revision number and on specific parameters (model/functions, brain extraction, on, smoothing kernel size, etc.).		
		normalized/standardized, describe the approach(es): specify linear or non-linear and define image types insformation OR indicate that data were not normalized and explain rationale for lack of normalization.		
Normalization template		template used for normalization/transformation, specifying subject space or group standardized space (e.g. iirach, MNI305, ICBM152) OR indicate that the data were not normalized.		
Noise and artifact removal		or procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and all 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	e			
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: Who	le brain	ROI-based		
Statistic type for inference (See <u>Eklund et al. 2016</u> )	Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.			
Correction	Describe the Carlo).	type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte		
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.		