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Corresponding author(s): NCOMMS-21-15472

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Reporting Summary

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, 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: Circular dichroism spectroscopy (JASCO Corporation, JC-1500); Attenuated total ref
Data analysis: Bar graph, curves and the relevant statistics were analyzed by Microsoft office 2015

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 Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

All the primary data that support the findings of this study are available from the corresponding author on request.

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: Sample sizes were based on our previous experience and other publications. The sample
Data exclusions: No data were excluded from the analyses.
Replication: All experiments were replicated at least twice. The biological replicates were n=3, 5
Randomization: All samples were allocated to groups randomly.
Blinding: For the in vivo end-point evaluations, the investigators were blinded to group allocation

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, qualita

Research sample State the research sample (e.g. Harvard university undergraduates, villagers in ru
Sampling strategy Describe the sampling procedure (e.g. random, snowball, stratified, convenience)
Data collection Provide details about the data collection procedure, including the instruments or
Timing Indicate the start and stop dates of data collection. If there is a gap between collection
Data exclusions If no data were excluded from the analyses, state so OR if data were excluded, pro
Non-participation State how many participants dropped out/declined participation and the reason(s)
Randomization If participants were not allocated into experimental groups, state so OR describe ho

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
Research sample Describe the research sample (e.g. a group of tagged Passer domesticus, all Stenoc
Sampling strategy Note the sampling procedure. Describe the statistical methods that were used to
Data collection Describe the data collection procedure, including who recorded the data and
Timing and spatial scale Indicate the start and stop dates of data collection, noting the frequenc
Data exclusions If no data were excluded from the analyses, state so OR if data were excluded, des
Reproducibility Describe the measures taken to verify the reproducibility of experimental findings
Randomization Describe how samples/organisms/participants were allocated into groups. If allocatio
Blinding Describe the extent of blinding used during data acquisition and analysis. If blinding wa

Did the study involve field work? ☐ Yes ☐ No

Field work, collection and transport

Field conditions Describe the study conditions for field work, providing relevant parameters (e.g.
Location State the location of the sampling or experiment, providing relevant parameters (e.g. lat
Access & import/export Describe the efforts you have made to access habitats and to collect and im
Disturbance Describe any disturbance caused by the study and how it was

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
●	☐ Human research participants
●	☐ Clinical data
●	☐ Dual use research of concern

Methods n/a

Involved in the study
● ☐ ChIP-seq
● ☐ Flow cytometry
● ☐ MRI-based neuroimaging

Antibodies

Antibodies used Describe all antibodies used in the study; as applicable, provide supplier name, c
Validation Describe the validation of each primary antibody for the species and application, notin

Eukaryotic cell lines Policy information about cell lines

Cell line source(s) State the source of each cell line
Authentication Describe the authentication procedures for each cell line used OR declare that none
Mycoplasma contamination Confirm that all cell lines tested negative for mycoplasma contamination

Commonly misidentified lines (See ICLAC register) *Name any commonly misidentified cell lines used in the study and provide a rationale for their use.*

Palaeontology and Archaeology

Specimen provenance Provide provenance information for specimens and describe permits that were ob
Specimen deposition Indicate where the specimens have been deposited to permit free access by othe
Dating methods If new dates are provided, describe how they were obtained (e.g. collection, storag

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

Ethics oversight Identify the organization(s) that approved or provided guidance on the study prot

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

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting a

Laboratory animals For laboratory animals, report species, strain, sex and age OR state that the s
Wild animals This study did not involve wild animals.

Field-collected samples This study did not involve samples collected from fields.
Ethics oversight All the animal experiments were performed in accordance with the Guide for the C

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	Describe the covariate-relevant population characteristics of the human
Recruitment	Describe how participants were recruited. Outline any potential self-selection bias or
Ethics oversight	Identify the organization(s) that approved the study

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	Provide the trial registration number from ClinicalTrials.gov or an eq
Study protocol	Note where the full trial protocol can be accessed OR if not available, explain
Data collection	Describe the settings and locales of data collection, noting the time periods of r
Outcomes	Describe how you pre-defined primary and secondary outcome measures and how you assessed

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	
☐	☐	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	
☐	☐	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 *May remain private before publication.*	For "Initial submission" or "Revised version" documents, provide revie data.
Files in database submission	Provide a list of all files available in the database
Genome browser session (e.g. UCSC)	*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
Sequencing depth	Describe the sequencing depth for each experiment, providing the total number of
Antibodies	Describe the antibodies used for the ChIP-seq experiments; as applicable, provide suppl
Peak calling parameters	Specify the command line program and parameters used for read mapping and
Data quality	Describe the methods used to ensure data quality in full detail, including how many p
Software	Describe the software used to collect and analyze the ChIP-seq data. For custom code that

Flow Cytometry

Plots

Confirm that:

The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

Methodology

Sample preparation Describe the sample preparation, detailing the biological source of the cells a

Instrument Identify the instrument used for data collection, specifying make and model

Software Describe the software used to collect and analyze the flow cytometry data. For custom cod

Cell population abundance Describe the abundance of the relevant cell populations within post-sort

Gating strategy Describe the gating strategy used for all relevant experiments, specifying the pre

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 Indicate task or resting state; event-related or block

Design specifications Specify the number of blocks, trials or experimental units per session and/o

Behavioral performance measures State number and/or type of variables recorded (e.g. correct butto

Acquisition

Imaging type(s) Specify: functional, structural, diffusion,

Field strength Specify in

Sequence & imaging parameters Specify the pulse sequence type (gradient echo, spin echo, etc.), im

Area of acquisition State whether a whole brain scan was used OR define the area of acquisition, d

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software Provide detail on software version and revision number and on specific para

Normalization If data were normalized/standardized, describe the approach(es): specify linear or n

Normalization template Describe the template used for normalization/transformation, specifying sub

Noise and artifact removal Describe your procedure(s) for artifact and structured noise removal, s

Volume censoring Define your software and/or method and criteria for volume censoring, and state t

Statistical modeling & inference

Model type and settings Specify type (mass univariate, multivariate, RSA, predictive, etc.) and de

Effect(s) tested Define precise effect in terms of the task or stimulus conditions instead of psyc

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

Statistic type for inference (See Eklund et al. 2016)

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

Correction Describe the type of correction and how it is obtained for multiple comparisons (e.g. F

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 deta

Graph analysis Report the dependent variable and connectivity measure, specifying weighted graph c

Multivariate modeling and predictive analysis Specify independent variables, features extraction a