# 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 | Software used for data collection includes the commercially available Nikon NIS Elements imaging software (Version 4) |
| Data analysis | Software used for data analysis includes the open source image analysis software ImageJ; statistics were also calculated using the default settings of Prism 8 (Version 8.4.3) custom code was also used for data analysis and has been deposited in GitHub: https://doi.org/10.5281/zenodo.7072658 |

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

Source data are provided with this paper. Where indicated in methods, we searched the UP000000430 Acinetobacter baylyi database downloaded from Uniprot.org.

## Field-specific reporting
Life sciences

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

- **Sample size**: Sample sizes were chosen based on historical data and no statistical methods were used to predetermine sample size (see Ellison et al. Nature Communications 2021).
- **Data exclusions**: No data were excluded from the analysis.
- **Replication**: All data are from a minimum of three independent experiments. All replication attempts were successful.
- **Randomization**: There was no randomization in these experiments. Strains used were grown under similar conditions and were therefore equivalent at the start of.
- **Blinding**: No blinding was used in these experiments. Strains used were grown under similar conditions and were therefore equivalent at the start of.

**Behavioural & social sciences study design**

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

- **Study description**
- **Research sample**
- **Sampling strategy**
- **Data collection**
- **Timing**
- **Data exclusions**
- **Non-participation**
- **Randomization**

**Ecological, evolutionary & environmental sciences study design**

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

- **Study description**
- **Research sample**
- **Sampling strategy**
- **Data collection**
- **Timing and spatial scale**
- **Data exclusions**
- **Reproducibility**
- **Randomization**
- **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

| 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

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

### Antibodies

| Antibodies used |
|----------------|

| Validation |
|-----------|

### Eukaryotic cell lines

| Policy information about cell lines |
|-------------------------------------|
| 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 organisms

| Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research |
|----------------------------------------------------------------------------------------------------------------|
| Laboratory animals                                           |
| Wild animals                                                 |
| Field-collected samples                                     |

### Human research participants

| Policy information about studies involving human research participants |
|-------------------------------------------------------------------------|
| Population characteristics                                             |
| Recruitment                                                             |

### 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 |
|----------------------------|

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](on) | ![Public health](off) |
| ![National security](on) | ![National security](off) |
| ![Crops and/or livestock](on) | ![Crops and/or livestock](off) |
| ![Ecosystems](on) | ![Ecosystems](off) |
| ![Any other significant area](on) | ![Any other significant area](off) |

Experiments of concern
Does the work involve any of these experiments of concern:

| No | Yes |
|----|-----|
| ![Demonstrate how to render a vaccine ineffective](on) | ![Demonstrate how to render a vaccine ineffective](off) |
| ![Confer resistance to therapeutically useful antibiotics or antiviral agents](on) | ![Confer resistance to therapeutically useful antibiotics or antiviral agents](off) |
| ![Enhance the virulence of a pathogen or render a nonpathogen virulent](on) | ![Enhance the virulence of a pathogen or render a nonpathogen virulent](off) |
| ![Increase transmissibility of a pathogen](on) | ![Increase transmissibility of a pathogen](off) |
| ![Alter the host range of a pathogen](on) | ![Alter the host range of a pathogen](off) |
| ![Enable evasion of diagnostic/detection modalities](on) | ![Enable evasion of diagnostic/detection modalities](off) |
| ![Enable the weaponization of a biological agent or toxin](on) | ![Enable the weaponization of a biological agent or toxin](off) |
| ![Any other potentially harmful combination of experiments and agents](on) | ![Any other potentially harmful combination of experiments and agents](off) |

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.

Files in database submission

Genome browser session
(e.g. UCSC)

Methodology

Replicates
Sequencing depth
Antibodies
Peak calling parameters
Data quality
Software

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**

**Instrument**

**Software**

**Cell population abundance**

**Gating strategy**

- 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**

- **Design specifications**

- **Behavioral performance measures**

**Acquisition**

- **Imaging type(s)**

- **Field strength**

- **Sequence & imaging parameters**

- **Area of acquisition**

- **Diffusion MRI**

- Used

- Not used

**Preprocessing**

- **Preprocessing software**

- **Normalization**

- **Normalization template**

- **Noise and artifact removal**

- **Volume censoring**

**Statistical modeling & inference**

- **Model type and settings**

- **Effect(s) tested**

- **Specify type of analysis:**

  - Whole brain

  - ROI-based

  - Both

- **Statistic type for inference**

  (See Eklund et al. 2016)

- **Correction**

**Models & analysis**

- **n/a**

  - Involved in the study

  - Functional and/or effective connectivity

  - Graph analysis

  - Multivariate modeling and predictive analysis

  - Functional and/or effective connectivity

  - Graph analysis

  - Multivariate modeling and predictive analysis

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