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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 <u>Authors & Referees</u> and the <u>Editorial Policy Checklist</u>.

Statistical parameters

		atistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main Methods section).
n/a	Cor	nfirmed
	\square	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
	\square	An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	\boxtimes	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.
	\square	A description of all covariates tested
	\square	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	\boxtimes	A full description of the statistics including <u>central tendency</u> (e.g. means) or other basic estimates (e.g. regression coefficient) AND <u>variation</u> (e.g. standard deviation) or associated <u>estimates of uncertainty</u> (e.g. confidence intervals)
	\boxtimes	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> .
\boxtimes		For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
\boxtimes		For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
\boxtimes		Estimates of effect sizes (e.g. Cohen's d, Pearson's r), indicating how they were calculated
	\boxtimes	Clearly defined error bars State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	No software was used.
Data analysis	ImageJ was used to analyze images, Graphpad Prism 7.03.

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 upon request. 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

The authors declare that all data supporting the findings of this study are available within the paper and its supplementary information. The data in the figures are available from the corresponding author upon request.

Field-specific reporting

Life sciences

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see <u>nature.com/authors/policies/ReportingSummary-flat.pdf</u>

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.				
Sample size	Sample sizes were selected on the basis of statistical-power calculations and of previous experience with these metrics.			
Data exclusions	No data were excluded.			
Replication	Findings were reliably reproduced.			
Randomization	Samples/animals were randomly allocated into experimental groups.			
Blinding	Blinding was not done. Phage can easily contaminate the samples and hence it is essential for the user to know what groups contain phage.			

Reporting for specific materials, systems and methods

Materials & experimental systems		Methods	
n/a	Involved in the study	n/a	Involved in the study
	Unique biological materials	\boxtimes	ChIP-seq
	X Antibodies	\boxtimes	Flow cytometry
	Eukaryotic cell lines	\boxtimes	MRI-based neuroimaging
\ge	Palaeontology		
	Animals and other organisms		
\boxtimes	Human research participants		

Unique biological materials

Policy information about availability of materials

Obtaining unique materials Phages were isolated and catalogued by the Biofilm Laboratory at CDC or obtained from banks available to scientific community. All are available to the scientific community.

Antibodies

Antibodies used	Primary Antibody: Anti-Pseudomonas antibody from Abcam. Catalog number: ab68538. Clonality: Polyclonal Abcam website states that it is tested for Immonofluorescence and Immunohistochemistry. It also provides 4 references on the website. No validation was done in our lab. Secondary Antibody: Alkaline phosphatase (ALP)-conjugated anti-mouse antibody. Jackson Immunoresearch. Catalog Number: 715-055-151. Clonality: Polyclonal
Validation	Primary Antibody: Anti-Pseudomonas antibody from Abcam. Catalog number: ab68538. Clonality: Polyclonal Abcam website states that it is tested for Immonofluorescence and Immunohistochemistry. It also provides 4 references on the website. No validation was done in our lab. Secondary Antibody: Alkaline phosphatase (ALP)-conjugated anti-mouse antibody. Jackson Immunoresearch. Catalog Number: 715-055-151. Clonality: Polyclonal

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Eukaryotic cell lines

Policy information about <u>cell lines</u>					
Cell line source(s)	RAW264.7 (ATCC)				
Authentication	Cell lines were visually examined for described morphology and growth conditions. No other authentication was used.				
Mycoplasma contamination	Our lab regularly (once a year) tests all cell lines for Mycoplasma contamination. No mycoplasma contamination was found.				
Commonly misidentified lines (See <u>ICLAC</u> register)	No commonly misidentified lines were used.				
Commonly misidentified lines	Our lab regularly (once a year) tests all cell lines for Mycoplasma contamination. No mycoplasma contamination was found. No commonly misidentified lines were used.				

Animals and other organisms

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

Laboratory animals	Information on the animals used is clearly described in the relevant figure captions.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.