nature portfolio

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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.

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	Structural data collection was done using Blu-Ice. BLI data was collected by Octet HTX.

Data analysis	CCP4i ver 7.0.063
	WinCoot ver 0.8.9
	XSCALE BUILD = 20190806
	XDS BUILD = 20190806
	Phenix ver 1.14-3260
	iMosflm ver 7.2.2
	NIH ImageJ ver 1.53a
	MicobeJ 5.11j
	cellSens Dimension (2019)
	Online 'Guide RNA design for CRISPRi in bacteria' tool in the CRISPR browser @ Pasteur (https://crispr-browser.pasteur.cloud/)
	'PatMatch' search tool in EcoCyc database (https://ecocyc.org/)
	GraphPad Prism ver 9.1.0
	ASTRA ver 6.0.5.3
	Octet Analysis software ver 9.0.0.10
	ATSAS ver 3.2.1
	NSRRC TPS13A SAXS Data Reduction Kit ver 4.79
	UCSF Chimera ver 1.16
	PYMOL ver 1.3

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

All relevant crystallography data are available in a publicly accessible repository. The maps and the coordinates of the refined models have been deposited into the Protein Data Bank with the accession codes for FtsBLQ, FtsBLQ (D59H), FtsBLQ (E56A) are 8HHG, 8HHF, 8HHH, respectively. Previously published PDB codes that referred in this study are also available in the Protein Data Bank, including 5Z2W, 2VH1, 6H9N, 5HLB, 6PL5. All other data generated in this study are present in the paper, the supplementary information and the source data file.

Human research participants

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

Reporting on sex and gender	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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

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	The sample size n>500 should sufficiently represent the population mean given the biological samples are from the same strain with little or no variation.
Data exclusions	The lysed cells were excluded as those cells are damaged and therefore are not qualified for experiment.

Replication	Each statistical datum was obtained from cells collected from 3 independent cultures of a CRISPRi-complementation strain as the biological replicates. Each replicate was tested with three technical repeats in RT-qPCR. All data are included in statistical analysis.
Randomization	Randomization is not applicable if the biological samples are the same strain or the samples are grown in the same flask, etc.
Blinding	Blinding is not applicable if the measurements are objective and easily measurable.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging