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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 Authors & Referees 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	Both online and local NCBI BLAST (v2.2.30+) were used to search the NCBI database. The license of NCBI BLAST: Public domain For the assembly of phage genome sequencing, programs canu v1.7.11, pilon v1.22 and circlator v1.5.5 were used. The license of canu/pilon/circlator: Public domain
Data analysis	Multiple alignments and phylogenetic tree constructions were performed using MEGA (v5.22). ImageLab 3.0 software was used for imaging analysis. The licenses for the above software were described as follow: MEGA: protected under the copyright law, but FREE for use in research and education. It is not allowed to redistribute the MEGA software and associated materials partially or fully in any form.

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.

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 atomic coordinates and structure factors of SspB and the magnesium ion-bound SspB from S. clavuligerus ATCC 27064 have been deposited in the Protein Data Bank with the accession numbers 6JUF and 6LB9, respectively. The atomic coordinates and structure factors of SspE from S. yokosukanensis DSM 40224 has the accession number as 6JIV.

List of the figures that have associated raw data: Figure 1-4, Extended Data Figure 2-4 and 6-7, Supplementary Figure 1-9 and 11-13.
The annotated genome data of phage JXY1 has been submitted to NCBI with accession number MN994275 and will be released at Feb 17, 2020.

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	No sample-size calculation was performed. For gel imaging studies we perform at least 2 independent experiments and for assays with statistical analysis, at least three independent experiments were performed in order to get enough data for P value calculation.
Data exclusions	No data exclusions.
Replication	Values represent the mean ± SD of at least three analyses.
Randomization	This is not relevant to our study. This study focuses on the discovery of novel bacterial defense systems
Blinding	This is not relevant to our study. This study focuses on the discovery of novel bacterial defense systems

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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies

Antibodies used	Anti-RNA polymerase beta antibody (ab191598) (Catalog number:ab191598, CloneNo: EPR18704, Lot: GR224168-11, dilution: 1/2000, Abcam, Cambridge, UK) 6*His, His-Tag Antibody (Catalog number: 66005-1-Ig, CloneNo.: 1B7G5, Lot: 10004365, dilution: 1/10000, Proteintech, Wuhan, China) GST Monoclonal Antibody (Mix) (Catalog number: YM3144, Lot: 411005100205, dilution: 1/5000, Immunoway, Plano, USA)
Validation	Anti-RNA polymerase beta antibody has been validated by abcam as it is capable of detecting a approximately 150 kDa band in western-blot of E. coli RNA polymerase beta subunit with 10 µg E. coli whole cell lysate. 6*His, His-Tag Antibody is species-independent and has been validated by Proteintech in western-blot to detect a 50 kDa 6xHis-tagged fusion protein (20 µg/lane) at dilution folds from 1/5000 to 1/160000. GST Monoclonal Antibody (Mix) is species-independent and has been validated in western blot to detect GST fusion protein, diluted at 1/10000.