

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 (<i>n</i>) 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ 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. <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> |
| ☒ | ☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	Pictures of plaque assays and gels were taken using Image Lab (TM) Version 6.0.1 (C) 2017, Bio-Rad Laboratories, Inc. Growth curve assays were collected using BioTek Synergy H1 software Gen5 3.05.11.
Data analysis	Data were analyzed in Microsoft Excel Version 14.6.7 and plotted using GraphPad Prism 6.0 software. Clustal Omega was used to generate a multiple sequence alignment for AmrZ homologs through the EMBL-EBI webform on April 25, 2019. Sequence alignments were visualized using Jalview 2, version 2.10.2. PBD structures were visualized using PyMol, version 2.0.7.

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

Source data and statistics used to generate Figures 1-4 and Extended Data Figures 2-4 are provided with the paper. Additional data supporting the findings of this paper will be made available from the corresponding author by 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](https://www.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 to determine sample size. The majority of experiments use a sample size of three, as is standard in the field. This study uses isogenic, clonal bacterial strains that show a high degree of reproducibility.
Data exclusions	No data were excluded.
Replication	Phage quantification (efficiency of plaquing, efficiency of immunity, total PFU counts, etc) and growth curves were all performed at least twice, showing replication each time. Here we show representative examples. Pictures of plaque assays shown are representative examples of phenotypes observed throughout the sample(s), with consistent results seen between replicates. lacZ activity profiling of csy3:lacZ and sfCherry measurements were replicated for each mutant two times or more, with consistent results seen. Pyocyanin repression was visually assessed in three independent replicates with consistent results seen. Pyocyanin levels were quantified for representative samples.
Randomization	Samples were organized into experimental groups depending on genotype, including genes and crRNAs encoded by the bacterial strain. Randomization was not performed in this study.
Blinding	Blinding was not performed in this study, all results are quantitative. No group allocation occurred.

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

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	This study did not involve laboratory animals
Wild animals	This study did not involve wild animals
Field-collected samples	This study did not involve field collected samples
Ethics oversight	No ethical approval was required as this study uses only phages and bacteria which do not require ethical oversight in their study.

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