

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 (<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	Details of all data collection are provided in the methods section. Proteomics was conducted at Proteomics and Mass Spectrometry Core Facility at University of Delaware. All liquid chromatography mass spectrometry for metabolomics were conducted on in-house instruments at Northwestern University as described in the method section.
Data analysis	Details of data analysis and related software are provided in the methods section. All isotopologue analyses were performed using MAVEN Version 2011.6.17 and corrected for the natural abundance of 13C using IsoCor v2. Quantification of intracellular metabolite pools were conducted on ThermoScientific XcaliburTM 3.0 Quan Browser. INCA software on Matlab platform was used for kinetic 13C-fluxomics analysis. Flux balance analysis was performed using COBRApy library. The mass spectra collected for proteomics were processed using the Spectronaut software (version 19.1) and a library-free DIA analysis workflow with directDIA+ and the P. putida KT2440 protein sequence as reference. Bioinformatics analyses for proteomics data were performed using the Perseus software (version 1.6.2.3).

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](#)

The data supporting the findings in this study are available within the paper, supplementary information and supplementary datasets. Additionally, proteomic mass spectral data are available via the MassIVE repository (massive.ucsd.edu) under accession number MSV000095008. Stable isotope assisted metabolomics LC-MS data are available in Metabolights repository (www.ebi.ac.uk/metabolights/) under the accession MTBLS11484.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	Not applicable in this study.
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable in this study.
Population characteristics	Not applicable in this study.
Recruitment	Not applicable in this study.
Ethics oversight	Not applicable in this study.

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](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	Sample sizes were chosen for each experiment to be a minimum of three biological replicates to be sufficient to support the conclusions. We did not use statistical methods to determine the sample size. Sample sizes are reported in figure captions.
Data exclusions	There was no data exclusions in this study.
Replication	Each experiment had a minimum of 3 replicates and maximum of 4 replicates.
Randomization	Randomization was not utilized in this study, and was not relevant to these bacterial experiments.
Blinding	Not relevant because neither animals nor human subjects were used in this study.

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

Involvement in the study
- ☒

☐ Antibodies
- ☒

☐ Eukaryotic cell lines
- ☒

☐ Palaeontology and archaeology
- ☒

☐ Animals and other organisms
- ☒

☐ Clinical data
- ☒

☐ Dual use research of concern
- ☒

☐ Plants

Methods

- n/a

Involvement in the study
- ☒

☐ ChIP-seq
- ☒

☐ Flow cytometry
- ☒

☐ MRI-based neuroimaging

Plants

Seed stocks

Not applicable in this study.

Novel plant genotypes

Not applicable in this study.

Authentication

Not applicable in this study.