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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	Following software was used for data collection: MARS®, Version V4.20, BMG Labtech, Germany CytExpert®, Version 2.4, Beckman-Coulter, California, USA QuantStudio 3 RealTime-PCR software, Thermo Fisher Scientific, Massachusetts, USA
Data analysis	All data were analyzed using the following software or webtools: JMP®, Version 16 Pro., SAS Institute Inc., Cary, NC, 1989–2021 MARS®, Version V4.20, BMG Labtech, Germany CytExpert®, Version 2.4, Beckman-Coulter, California, USA Benchling [Biology Software]. (2023). Retrieved from https://benchling.com. QuantStudio 3 RealTime-PCR software, Thermo Fisher Scientific, Massachusetts, USA Porechop – Wick, R.R.; Judd, L.M.; Gorrie, C.L.; Holt, K.E. Completing bacterial genome assemblies with multiplex MinION sequencing. Microb Genom. 2017, 3(10):e000132. doi:10.1099/mgen.0.000132. Retrieved from https://usegalaxy.org.au/. Unicycler - Wick, R.R.; Judd, L.M.; Gorrie, C.L.; Holt, K.E. Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. PLOS Computational Biology. 2017, 13(6): e1005595. doi.org/10.1371/journal.pcbi.1005595. Retrieved from https://usegalaxy.org.au/.

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 underlying this article are available in the article and in its online supplementary material. Genome data of P. putida P15 and P. putida P15-L is available at NCBI (49) under accession numbers CP135115 and CP135114, respectively.

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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	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	For all experiments where variation is expected, a sample size of three or more was taken to capture potential variation and enable statistical analysis
Data exclusions	No data was excluded from the manuscript
Replication	Data was reproducible in multiple biological replicates. During the different strain iterations in this study, we always compared with new datapoints from strains of the previous iterations and had no issues with reproducibility.
Randomization	There was no intentional randomisation in data collection. However, in plate assays replicate groups were assigned an arbitrary location in the plate. Apart from edge effects in the plates (more aeration/evaporation on the sides of plate), we do not expect this to influence results. These effects are also accounted for by having replicates and checking consistency of results across assays. The effects are also expected to be minimal due to the more limited timeframe of measurements.
Blinding	There was no blinding during sample collection/analysis.

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
☒	☐ Plants

Methods

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

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	First, overnight cultures were prepared in duplo in M9 medium with the appropriate antibiotics. Each overnight culture was diluted 20-fold in fresh M9 medium in a clear 96-well plate with a flat bottom and incubated for 2h in shaking conditions. At this point, the required inducer(s) was added: 0, 0.01 or 1 mM 3mBz (and 10 mM Rha for strains carrying the growth-decoupling module). For a total of six hours, hourly samples were taken from each cell culture, diluted tenfold in 200 µL PBS medium (pH 7.4, filter-sterilized (0.22 µm)) and analyzed on a CytoFLEXS® Flow Cytometry device
Instrument	CytoFLEXS® Flow Cytometry
Software	CytExpert®, Version 2.4
Cell population abundance	Bacterial populations, when present as single cells, all cluster together on FSC-A vs FSC-H plots with FSC-H values above 50,000, which was used as a quality check. A large majority of 5,000 recorded events fell within the FSC-A threshold of >50,000. The few remaining outliers were filtered out by gating.
Gating strategy	Cells were gated to have a FSC-H value above 50,000. Cells with FITC-msfGFP values above 10^4 are considered induced or positive for msfGFP fluorescence, values below this are considered negative.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.