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	HPLC: Shimadzu Corporation LabSolutions version 5.86; LC-MS/MS: Mascot version 2.3.02 (Matrix Science, London, UK); Western blotting imaging: Tanon MP version 1.0 (Tanon, Shanghai, China); Integrated density of the Western blotting bands: ImageJ software (1.53K); Glucose: SBA-40D biosensor analyzer (Institute of Biology, Shandong Academy of Sciences, Jinan, China); OD600: MAPADA V-1100D spectrophotometer (MAPADA Instruments, Shanghai, China); Molecular weight: on-line tool (https://web.expasy.org/compute_pi/);
Data analysis	Excel 2019 (Microsoft): mean, SE, P value, plotting; ProteoWizard (3.0.10577): MS/MS data processing; Mascot version 2.3.02 (Matrix Science, London, UK): protein identification; ChemDraw 2014: chemical structure; Office 2021 v2409 (Microsoft): plotting; Origin 8.5 (OriginLab): plotting; SPSS Statistics 19.0 (IBMA): one-way ANOVA; R language version 4.3.3, R Studio 2023.12.1 Build 402: plotting, curve fitting;

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

Data supporting the findings of this study are available within the paper and its Supplementary Information file. The GenBank (https://www.ncbi.nlm.nih.gov/genbank/) accession numbers and codon-optimized nucleotide sequences of the genes referenced in this study are provided in this paper. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD056539 (https://www.ebi.ac.uk/pride/archive/projects/PXD056539). Source data are provided with this paper.

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	No human participants involved.
Reporting on race, ethnicity, or other socially relevant groupings	No human participants involved.
Population characteristics	No human participants involved.
Recruitment	No human participants involved.
Ethics oversight	No human participants involved.

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	No specific calculations were used to determine sample size for each experiment. This experiment was performed on bacteria fermentation and transformation for the production of chemicals, involving a large population of individual cells. All presented data represent measurements from at least 3 biological replicates, grown and performed independently. To ensure the reproducibility, some experiments were performed for several times with relevant independent replicates. For each experiment, the detailed sample sizes were stated in legend. For kinetic analysis, 3 biological replicates per substrate concentration group were performed.
Data exclusions	No data were excluded from our analyses.
Replication	All the fermentations, biotransformations and enzymatic assays were performed at least three times. The exact number of independent experiments were described in the legend.
Randomization	At least three single colonies of each recombinant strain were randomly selected from plates, each of which was subjected to independent flask cultures, batch fermentations and chemical analyses.
Blinding	Blinding was not relevant to this study. We designed and carried out the experiments to achieve our goal. All samples were extracted and assayed in the same way, without any differences.

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

Antibodies

Antibodies used: For Western blotting analysis, anti-Flag tag mouse monoclonal antibody (Cat. No. D191041), anti-6×His tag mouse monoclonal antibody (Cat. No. D191001), and horseradish peroxidase-conjugated goat anti-mouse IgG (Cat. No. D110087) from Sangon Biotech (Shanghai, China) were used at 1:4000, 1:4000, and 1:5000, respectively.

Validation: All three antibodies used in this study are commercially available and validation statements are given on manufacturer's websites. The website of Cat. No. D191041, Cat. No. D191001, and Cat. No. D110087 is https://store.sangon.com/productDetail?productInfo.code=D191041, https://store.sangon.com/productDetail?productInfo.code=D191001 and https://store.sangon.com/productDetail?productInfo.code=D110087, respectively.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	No eukaryotic cell lines involved.
Authentication	No eukaryotic cell lines involved.
Mycoplasma contamination	No eukaryotic cell lines involved.
Commonly misidentified lines (See ICLAC register)	No eukaryotic cell lines involved.

Palaeontology and Archaeology

Specimen provenance	This study did not involve specimens.
Specimen deposition	This study did not involve specimens.
Dating methods	This study did not involve specimens.

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight	This study did not involve specimens.

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	This study did not involve animals.
Wild animals	This study did not involve animals.
Reporting on sex	This study did not involve animals.
Field-collected samples	This study did not involve animals.
Ethics oversight	This study did not involve animals.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	This study did not involve clinical trial.
Study protocol	This study did not involve clinical trial.
Data collection	This study did not involve clinical trial.
Outcomes	This study did not involve clinical trial.

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☒	☐	Public health
☒	☐	National security
☒	☐	Crops and/or livestock
☒	☐	Ecosystems
☒	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☒	☐	Demonstrate how to render a vaccine ineffective
☒	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐	Increase transmissibility of a pathogen
☒	☐	Alter the host range of a pathogen
☒	☐	Enable evasion of diagnostic/detection modalities
☒	☐	Enable the weaponization of a biological agent or toxin
☒	☐	Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	This study did not involve plants.
Novel plant genotypes	This study did not involve plants.
Authentication	This study did not involve plants.

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	This study did not involve ChIP-seq experiment.
Files in database submission	This study did not involve ChIP-seq experiment.
Genome browser session (e.g. UCSC)	This study did not involve ChIP-seq experiment.

Methodology

Replicates	This study did not involve ChIP-seq experiment.
Sequencing depth	This study did not involve ChIP-seq experiment.
Antibodies	This study did not involve ChIP-seq experiment.
Peak calling parameters	This study did not involve ChIP-seq experiment.
Data quality	This study did not involve ChIP-seq experiment.
Software	This study did not involve ChIP-seq experiment.

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	This study did not involve flow cytometry.
Instrument	This study did not involve flow cytometry.
Software	This study did not involve flow cytometry.
Cell population abundance	This study did not involve flow cytometry.
Gating strategy	This study did not involve flow cytometry.

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

Magnetic resonance imaging

Experimental design

Design type	This study did not involve magnetic resonance imaging.
Design specifications	This study did not involve magnetic resonance imaging.
Behavioral performance measures	This study did not involve magnetic resonance imaging.

Acquisition

Imaging type(s)	This study did not involve magnetic resonance imaging.
Field strength	This study did not involve magnetic resonance imaging.
Sequence & imaging parameters	This study did not involve magnetic resonance imaging.
Area of acquisition	This study did not involve magnetic resonance imaging.

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software	This study did not involve magnetic resonance imaging.
Normalization	This study did not involve magnetic resonance imaging.
Normalization template	This study did not involve magnetic resonance imaging.
Noise and artifact removal	This study did not involve magnetic resonance imaging.
Volume censoring	This study did not involve magnetic resonance imaging.

Statistical modeling & inference

Model type and settings	This study did not involve magnetic resonance imaging.
Effect(s) tested	This study did not involve magnetic resonance imaging.

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference (See Eklund et al. 2016)	This study did not involve magnetic resonance imaging.
Correction	This study did not involve magnetic resonance imaging.

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity	This study did not involve magnetic resonance imaging.
Graph analysis	This study did not involve magnetic resonance imaging.
Multivariate modeling and predictive analysis	This study did not involve magnetic resonance imaging.