

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

Data analysis

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](#)

All the plasmids and strains containing the refactored xylose pathway, the shikimate pathway, xylose transporters, shikimate transporters, and the noroclaurine pathway and any additional data that support the findings of this study are available from the corresponding author upon reasonable request.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	No information on sex and gender because there was no human research conducted.
Population characteristics	No information on population characteristics because there was no human research conducted.
Recruitment	No recruitment method was used because there was no human research conducted.
Ethics oversight	No ethics oversight was implemented because there was no human research conducted.

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	Sample sizes were selected to best adhere with standard practices in yeast engineering whilst being consistent with throughput of the methods. Either three or four biological replicates were performed in each experiment and clearly marked along with the corresponding texts.
Data exclusions	No data was excluded from the analysis.
Replication	All biochemical experiments were performed using at least three independent biological replicates. A biological replicate in the context of our experimentation was one distinct yeast colony (as opposed to one individual culture from the same inoculum, which in our interpretation represents as a technical replicate).
Randomization	Randomization was not performed as the nature of the biochemical experiments and the associated data does not potentiate human bias influencing the final conclusions.
Blinding	Blinding was not performed as the nature of the biochemical experiments and the associated data generated does not potentiate human bias influencing the final conclusions.

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

Methods

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

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	S. cerevisiae YSG50 strain (requested from Dr. Huimin Zhao at UIUC) S. cerevisiae BY4741 strain (requested from Dr. Huimin Zhao at UIUC)
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S. cerevisiae CEN.PK2-1C strain (requested from Dr. Huimin Zhao at UIUC)
 S. stipitis FPL-UC7 strain (requested from Dr. Thomas W. Jeffries, professor emeritus at University of Wisconsin)
 S. stipitis FPL-UC7 leu2Δ strain (derived from S. stipitis FPL-UC7 via the deletion of the gene encoding Leu2)

Authentication Cell lines were used without any further authentication.

Mycoplasma contamination Cells lines were not tested for mycoplasma contamination.

Commonly misidentified lines
 (See [ICLAC](#) register) N/A

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 No animals were used.

Wild animals No wild animals were used.

Reporting on sex No information on animal sex because no animals were used.

Field-collected samples No field collected samples were used.

Ethics oversight No ethics oversight was implemented because no animals were used.

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