

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	Cellaca MX High-throughput Automated Cell Counter integrated software, BioProfile® FLEX2 Automated Cell Culture Analyzer integrated software, SCADA data acquisition, XCell ATF2 system (Repligen) integrated software, PuraLev® Fluid Handling 37 Console LCO-i100, NIS Elements F software, ISIsScan Nova software, SimpliAmp™ Thermal Cycler (Applied Biosystems™) integrated software, CFX384™ Real-Time PCR Detection System (Bio-Rad) integrated software, NanoDrop™ One Microvolume UV-Vis 20 spectrophotometer (Thermo Fisher Scientific) integrated software, Waters Acquity UPLC integrated software
Data analysis	MS Office 2016

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 data generated or analyzed during this study are included in this published article (and its supplementary information files).

Human research participants

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

Reporting on sex and gender

Population characteristics

Recruitment

Ethics oversight

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	Initial sample size per experiment was determined based on preliminary studies, and were different for different types of assays, as necessary to achieve statistical significance of data. Experiments were performed multiple times, unless indicated otherwise. Images were analyzed from multiple fields (>2).
Data exclusions	No data exclusion was done on bulk quantifications and limited n quantification (qPCR, etc.).
Replication	Experiments were repeated multiple times, unless indicated otherwise. qPCR were successfully performed in triplicate technical repeats. Growth kinetics in various cell culture media were successfully performed in biological triplicates. Bioreactor culture data were performed with similar aims and comparable results independently, metabolites were analyzed as biological and technical singlet samples.
Randomization	Treatments were allocated randomly within the same well plate the experiment was conducted in.
Blinding	Investigators providing specific analytical assessments and mass analysis were blinded to experimental group allocation.

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)

The derivation and characterization of the cell line used in this research was described in our previously peer-reviewed and published article, "Spontaneous immortalization of chicken fibroblasts generates stable, high-yield cell lines for serum-free production of cultured meat" (Pasitka and Cohen et al., 2022, <https://doi.org/10.1038/s43016-022-00658-w>).

Authentication

The cell line used within were authenticated routinely by morphology, species identification by PCR and qPCR.

Mycoplasma contamination

Cultures were routinely checked for infection using a PCR-based assay (HY-MYCOPLASMA PCR KIT) and tested negative.

Commonly misidentified lines
(See [ICLAC](#) register)

No commonly misidentified lines were used in this study.