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.

☑️ 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

☐ 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

☐ 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

Software and code

Policy information about availability of computer code

Data collection

- Zetasizer Software v7.12
- IMAGE jv1.52a
- TheoCompassTM software
- Chrinscan Spectrometer Control Panel software v4.4

Data analysis

- Data Analysis software v4.1 (Bruker Daltonics, Bremen, Germany)
- IMAGE jv1.52a
- Zetasizer Software v7.12
- TheoCompassTM software
- Chrinscan Spectrometer Control Panel software v4.4
- GraphPad software Prism v6
- Origin software 2019b

Code used to analyse enzymatic mass spectrometric fingerprinting data is publicly available along with the data at Zenodo.

For manuscripts utilizing custom algorithms or software that are not already publicly available, algorithm code, software, or executables must be made available to editors/reviewers upon request.

Our web collection on statistics for biologists contains articles on many of the points above.

Biology

Dear [Author(s)],

This manuscript has been reviewed by the Editors of Nature Portfolio and has been accepted for publication. The following changes are required:

1. Please ensure that all references are up-to-date and that all authors listed are in alphabetical order.

2. Please provide a detailed description of any methods or procedures that are new or not commonly used in this field.

3. Please ensure that all tables and figures are clearly labeled and that all data is presented in a consistent and reproducible manner.

4. Please ensure that all permissions are obtained for any copyrighted material.

Please submit your revised manuscript and all necessary files to the Editorial Office within 4 weeks of the date of this letter.

Best regards,

[Editors Name]

[Editors Email]
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 underlying the Figures are publicly available at Zenodo.

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

All studies must disclose these points even when the disclosure is negative.

- **Sample size**: not relevant, as no experiments on individual organisms were performed
- **Data exclusions**: no data were excluded
- **Replication**: Measurements were repeated at least twice independently with similar results, except for large-scale enzymatic preparation of N-acetylated chitosan which was performed only once.
- **Randomization**: randomization was not relevant for our study
- **Blinding**: not relevant as data are based on objective measurements

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 |
|-----|------------------------|
| x   | Antibodies             |
|     | Eukaryotic cell lines  |
| x   | Palaeontology and archaeology |
| x   | Animals and other organisms |
| x   | Human research participants |
| x   | Clinical data           |
| x   | Dual use research of concern |

**Methods**

| n/a | Involved in the study |
|-----|------------------------|
| x   | ChIP-seq               |
| x   | Flow cytometry         |
| x   | MRI-based neuroimaging |

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf
# Eukaryotic cell lines

**Policy Information about cell lines**

**Cell line source(s)**

| Cell line | Source                                    |
|-----------|-------------------------------------------|
| HaCaT     | Dermatology Clinic, University Hospital Münster |
| MCF-7     | Holzel Diagnostika GmbH, Germany           |
| HUVEC     | Institute for Physiological Chemistry and Pathobiology, University Hospital Münster |
| HEK293    | Clinic for Dermatology and Venerology, University Hospital Hamburg, Eppendorf |

**Authentication**

The cell lines used were not authenticated.

**Mycoplasma contamination**

All cell lines tested negative for mycoplasma contamination.

**Commonly misidentified lines**

| Commonly misidentified lines |
|-----------------------------|
| n/a                         |

(See ECAC register)