

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                                                                                                                                                                                                                                                                                      |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> The exact sample size ( <i>n</i> ) for each experimental group/condition, given as a discrete number and unit of measurement                                                                                                                               |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly                                                                                                                                    |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>                                                               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested                                                                                                                                                                                                                                |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons                                                                                                                                                   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> 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) |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> 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<br><i>Give P values as exact values whenever suitable.</i>                     |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings                                                                                                                                                                      |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes                                                                                                                                                |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> 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 | n.a. |
|-----------------|------|

## Data analysis

1) Image reconstruction was performed with the gold-standard filtered-back projection algorithm incorporating single distance phase retrieval<sup>72</sup> using in-house developed software, Tomwar v1.0.0 (<https://gitlab.esrf.fr/tomotools/tomwar>). The 3D topographies for each acquisition time point were reconstructed taking into account parameters such as centre-of-rotation alignment, single material complex refraction index ratio [ $\Delta/\beta = 1000$  (frying), 6000 (post-frying)] and ring artefact removal to obtain cross-section image stacks of 3D distribution of material phases. Subsequently, images were imported in Avizo 3D 2021.2 (FEI Thermo Fisher Scientific, Waltham, MA, USA) for further image processing. The reconstructed 32-bit volumes were cast as 16-bit considering 1%–99 % intensity values in the volume histogram to subsequently characterize the phases of interest. Following this, a 3D non-local means filter was applied to denoise the image while preserving thin structures.

2) Image segmentation of imaging data from post-frying process was performed with the help of machine learning assisted pixel classification in Ilastik v1.4.058. Sparse manual annotations were marked based on spatial context and greyscale intensities across 10 % of the reconstructed images (150 cross-sectional slices) for each timestep and for each sample group from the different deep-frying temperatures (180, 150 and 120 °C) as training data for the random forest classifier to label pixels into four classes: oil, gas, solid and TSC. The models were trained iteratively to reduce the uncertainty between classes and reduce out-of-bag (OOB) error for the annotated pixels. Corresponding probability maps were segmented using a global threshold set to 0.5 in MATLAB (version 2019b, MathWorks, Natick, MA, USA). The segmented images stacks were then reimported in Avizo to perform several morphological operations (filter by measure, ambient occlusion etc.) to isolate the sample and the oil inside the sample. The local structure thickness distribution (expressed in  $\mu\text{m}$ ) of the starch-gluten matrix was evaluated for the sample and the separated crust and core regions using CTAn (Version 1.18.8.0, Bruker SkyScan, Kontich, Belgium). The sphere-fitting algorithm in the 3D analysis module provided the local thickness of the structure as represented by the diameter of the largest enclosed sphere

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 that support the findings of this study are available from the ESRF data portal (<https://doi.esrf.fr/10.15151/ESRF-ES-930328408>), Zenodo (<https://www.doi.org/10.5281/zenodo.14507722>), and from the corresponding authors upon request.

## 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](https://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

We analyzed a minimum of n=3 SEPARATE samples undergoing deep-frying process at each temperature during imaging. Furthermore, the imaging observations during deep-frying at 180 °C was performed at 10 s and 3 s time interval with n=3 SEPARATE samples. So, each "rep" within one of the three temperatures studied was a unique sample undergoing the deep-frying process. In our minds, this represented the

most stringent way to determine if the effects were real. Having only n=3 replicates also put a tall requirement to detect statistical significance. Even under these conditions, our differences were highly statistically significant.

Data exclusions No data were excluded from the analysis.

Replication All imaging and analytical measurements were performed at least in triplicate and all attempts at replication were successful. In the specific case of post-frying samples at 150 °C analysis, due to reconstruction issues in one replicate, only 2 replicates were used as notified in the reported data.

Randomization Allocation of samples into experimental groups was random.

Blinding The investigators and technicians were blinded to group allocation during data collection and 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

### Methods

- | n/a                                 | Involved in the study                                  |
|-------------------------------------|--------------------------------------------------------|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies                    |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data                 |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Plants                        |

- | n/a                                 | Involved in the study                           |
|-------------------------------------|-------------------------------------------------|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |

### Plants

Seed stocks n.a.

Novel plant genotypes n.a.

Authentication n.a.