

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 <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 <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	The whole slide images used in the STMF dataset were scanned and digitised by Leica Aperio ScanScope CS2. Custom code was used to standardise the data from different sources and generate the final dataset described in the main manuscript.
Data analysis	The custom code for data generation and model implementation is provided on the GitHub repository. <a href="https://github.com/SZY1234567/OMG-Net">https://github.com/SZY1234567/OMG-Net</a>  The original code for the Segment Anything Model can be found here: <a href="https://github.com/facebookresearch/segment-anything">https://github.com/facebookresearch/segment-anything</a>

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 images of the mitotic figures and their contours dilated by the Segment Anything Model are available via the Zenodo repository in accordance with the UKRI Common principles on research data. <https://zenodo.org/records/11521640>

The original images and annotations of the open-source datasets can be found via their own repositories:

ICPR: [http://ludo17.free.fr/mitos\\_2012/index.html](http://ludo17.free.fr/mitos_2012/index.html)

TUPAC: [https://github.com/DeepMicroscopy/TUPAC16\\_AlternativeLabels](https://github.com/DeepMicroscopy/TUPAC16_AlternativeLabels)

CCMCT: [https://github.com/DeepMicroscopy/MITOS\\_WSI\\_CCMCT](https://github.com/DeepMicroscopy/MITOS_WSI_CCMCT)

CMC: [https://github.com/DeepMicroscopy/MITOS\\_WSI\\_CMC](https://github.com/DeepMicroscopy/MITOS_WSI_CMC)

MIDOG++: <https://github.com/DeepMicroscopy/MIDOGpp>

## 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	<input type="text" value="N/A"/>
Reporting on race, ethnicity, or other socially relevant groupings	<input type="text" value="N/A"/>
Population characteristics	<input type="text" value="N/A"/>
Recruitment	<input type="text" value="N/A"/>
Ethics oversight	<input type="text" value="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://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	<input type="text" value="NA"/>
Data exclusions	<input type="text" value="NA"/>
Replication	<input type="text" value="NA"/>
Randomization	<input type="text" value="NA"/>
Blinding	<input type="text" value="NA"/>

## 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 &amp; experimental systems

n/a	Involved in the study
<input type="checkbox"/>	<input checked="" 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

## Methods

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

## Antibodies

Antibodies used	The anti-phosphorylated histone H3 antibody used is a rabbit monoclonal hybridoma Ser10 pHH3 [BC37] (Company: BIO CARE MEDICAL, Catalog Number: ACI 3130 A, C, Dilution 1:100)
Validation	Tacha, D. E. A New Rabbit Monoclonal phospho-histone H3 (pHH3) Hybridoma: An Immunohistochemical Comparison Study with a Rabbit Polyclonal pHH3. <a href="https://api.semanticscholar.org/CorpusID:54518201">https://api.semanticscholar.org/CorpusID:54518201</a> (2015).

## Plants

Seed stocks	NA
Novel plant genotypes	NA
Authentication	NA