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Reporting Summary

Nature Research 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 Research policies, see Authors & Referees 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	Microscopy data were collected using Nikon NIS Elements 5.0.2.
Data analysis	Data were analyzed using FIJI 2.0.0, Matlab 2016 and Fiesta 1.05.

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

Source data for Figures 1D (histogram), 1E (coverage), 1F (density after adding tau), 1H-(density after removing tau), 2B (decay times), 3C (Tau density change) and Supplementary Figures 1A (nucleations), 1B (growth velocity), 1C (island lengths), 1D (coverage), 1E (coverage after long time), 1F (density change after 30s), 1G (example fits at 0 nM), 1H (disassembly velocity), 1I (fission rate), 2A (binding and unbinding), 2B (20 nM replacement), 2C (100 nM replacement), 2D (decay times), 2E (histogram), 2F (diffusion coefficient), 3A (fast framerate flush out), 3B (saturation), 3C (density vs. density), 4A (velocity), 4B (dwell time), 4C (landing rate), 4D (katanin cutting surrounding), 4E (katanin cutting islands), 4E (island shrink velocity), 4G (Kip3 velocity), 4H (Kip3 landing), 4I (island displacement rate), 5B (intensity after flushout), 5C (line scan, high curvature, SD-Katanin cutting probability), 5G (bend assembly), 5H (density at 20 nM) and quantifications given in main text (island density) have been provided as Supplementary Table 1 (Statistics Source Data). Exemplary raw movies are available at BioStudies (https://www.ebi.ac.uk/biostudies/), accession number S-BSST266. All other data supporting the findings of this study is available from the corresponding authors on reasonable request.

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	During each independent experiment (in each individual flow chamber) microscopy fields of view were chosen randomly within the flow chambers. In each field of view, a certain number of molecules, islands or microtubules were present, thus determining the sample size per measurement. If experimentally possible (for image acquisition times of ten minutes or shorter), several fields of view per flow channel were imaged.
Data exclusions	No data was excluded.
Replication	Experiments were performed over several months by three independent experimentalists, all replication attempts (that were not impeded by unrelated events, like an image-acquisition software malfunction) were successful. For each quantified experiment and each exemplary image or kymograph 'N' describes the number of either biologically independent samples (individual tau molecules, islands of tau molecules or microtubules, respectively) or the number of independent events (island nucleation, island merging or island fission, respectively). In all cases the number of independent experiments, during which the data was gathered in the course of several days, refers to the number of independent flow chambers, which were assembled, filled with assay components and imaged individually.
Randomization	The allocation of samples into different groups was not required, since one advantage of in vitro experiments is that during one set of experiments all variants but one (for example the concentration of the protein of interest) are kept constant, hence the control of covariants is not relevant to this study.
Blinding	The study did not involve animals and/or human research participants; therefore, investigators were not blinded to the variance in the tested parameters during data collection and analysis. Blinding to group allocation was not relevant to this study (please see above).

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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies

Antibodies used	Biotin antibodies - Sigma B3640, diluted 20 µg/ml in PBS, binding unspecifically to DDS-treated microscopy coverslips, were used to immobilize biotinylated microtubules, in our flow chambers, on these microscopy coverslips.
Validation	In absence of biotin antibodies, the biotinylated microtubules did not bind to the micrososcope surface. Immobilizing the microtubules was the sole purpose of the antibodies, hence, no further tests were performed.