nature research

Corresponding author(s): Ethan Garner

Last updated by author(s): Mar 18, 2019

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	All microscopic data was collected using Nikon Elements or GE SoftWorks.
Data analysis	All statistical analysis was conducted in Graphpad Prism. All particle tracking was done with the Trackmate plugin within FIJI, then analyzed using custom Matlab (version R2016b) code available at https://bitbucket.org/garnerlab/hussain-2017-elife. Filament density calculations and filament simulations were done with custom code available at https://bitbucket.org/garnerlab/dion-2018/src/.

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

All datasets and raw data or all figures (Figure 1-5, Figure S1-S5 generated and/or analyzed during this study are available from the corresponding author on reasonable request. All proteomic data can be downloaded at https://garnerlab.fas.harvard.edu/Dion2019/Raw-MS-data-Dion2019.zip

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	No sample size calculation was conducted, as we ensured that all measurements of width, growth, and filament density were conducted upon a large number of cells. As shown in our tables, the majority of our data points are drawn from samples with over 100 cells. Even with the more difficult samples, we ensured measures were at least above 40 points. For bulk growth measures and simulations, we measured 5 independent samples. Our reported mean values of width and growth rates are very similar to the medians 0.98 +/- 0.8 % on average.
Data exclusions	No data was excluded from this study.
Replication	Given the extremely large number of data points used study, not all experiments were replicated. However, we ensured that all key results (all measures of width and growth, filament density) could not only be replicated, but also replicated with similar means and SDs. All data sets were combined in the final analysis, without excluding any data.. How experiments were conducted, and which ones were replicated is detailed in the Materials and methods.
Randomization	We did not randomize any of our data, as after data collection, all measurements and analysis was fully automated to prevent bias. Furthermore, after measurement and analysis no data was excluded in the reporting.
Blinding	We did not blind any of our data, as after data collection, all measurements and analysis was fully automated to prevent bias. Furthermore, after measurement and analysis no data was excluded in the reporting.

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	The only antibodies used in this study were to quantitate MreB across the MreBCD induction range. This consisted of 1) rat anti-MreB polyclonal antibody - Primary - 1:10,000 - Gift of R. Carballido. 2) rabbit anti-SigA polyclonal antibody - Primary - 1:20,000 - Gift of R. Losick. 3) anti-rabbit IgG-HRP conjugate from GenScript - Secondary - 1:20,000 - Cat # L00241, lot # C20021701 4) anti-rat IgG-HRP from MilliporeSigma - Secondary - 1:200 - cat# A9037, lot# SLBX9373
Validation	- The anti-MreB and anti-SigA antibiotics have been validated in previous work in the Carballido and Losick labs, and have been used in multiple publications. - WB-1 Solution (containing anti-rabbit IgG-HRP conjugate) are validated on the manufacturers website, https://www.genscript.com/antibody/A10253-Goat_Anti_Human_IgG_H_L_HRP_pAb.html - anti-rat IgG-HRP (MilliporeSigma, MA) is also validated on the manufacturers website at http://www.emdmillipore.com/US/en/product/Goat-Anti-Rat-IgG-Antibody-HRP-conjugate,MM_NF-AP136P#documentation