nature portfolio

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Last updated by author(s): 11-04-2025

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	
☐	☒	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	Data were collected using Microsoft Excel (16.77), Graph Pad Prism 9, IGOR Pro7, ShapeIn (Zellmechanik Dresden), custom-made micropipette aspiration setup equipped with a 50x objective (NA 0.8) and a Thorlabs camera, Leica TCS SP5 laser scan confocal microscope using a 20x/1.0 W-Plan-Apochromat objective (NA 0.75), a Leica M205 FA stereomicroscope, an inverted Olympus spinning disk using a 30x Plan-Apochromat objective (NA 0.8), a NextSeq200 sequencer (illumina Inc), NanoWizard 5 AFM (Brucker), IVIS Lumina II (PerkinElmer)
Data analysis	Data were analyzed using Microsoft Excel (16.77), Graph Pad Prism 9, Matlab 2016, IMARIS 9.5.1, ImageJ 1.53f51 (FIJI), R, Brucker software, Live Imaging software (PerkinElmer)

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 raw numerical data supporting the findings of this study, including the source data used to generate graphs and perform statistical analyses, are provided with the paper. Due to their large size, the original microscopy and imaging files are available from the corresponding author upon reasonable 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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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

Life sciences study design

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

Sample size	Sample size was determined by pilot studies that have given statistically significant results and literature search. In the case of mouse experimentation the 3R ethical guidelines were applied.
Data exclusions	Micropipette aspiration recordings were excluded from the analysis when it clearly appeared that the membrane of the cell had ruptured, as the measurement would then not be relevant to whole-cell mechanics. Zebrafish embryos containing more than 20 arrested cells within the first 5 minutes of circulation upon injections were excluded from early circulation / arrest analyses as we experimentally determined that circulation was biased past this threshold. In the in vivo bioluminescence-based pan-organ metastasis assay, mice that were not properly injected in the left ventricle were excluded from the analysis.
Replication	A different number of replicates were done depending on the type of experiment. Biological replicate data (N) and sample size (n) are presented for each figure panel in the figure legends.
Randomization	Animals were randomly allocated into all the experimental groups.

Blinding | Investigators were not blinded during data collection and/or 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

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used

Anti-non-muscle myosin IIA, rabbit, polyclonal, Sigma-Aldrich (M8064), dilution 1/500
Anti-vimentin, rabbit, recombinant monoclonal, Cell Signaling (D21H3), dilution 1/1000
Anti-lamin A/C, rabbit, polyclonal, Santa Cruz (sc-20681), dilution 1/1000
Anti-caveolin-1, rabbit, recombinant monoclonal, Cell Signaling (D46G3), dilution 1/1000
Anti-transgelin, rabbit, polyclonal, Abcam (ab14106), dilution 1/1000
Anti-GAPDH, mouse, monoclonal (Clone 6C5), Millipore (MAB374), dilution 1/2000

Validation

Anti-non-muscle myosin IIA, rabbit, Sigma-Aldrich (M8064) was successfully used for WB in Chen et al., 2013, Journal of Thrombosis and Haemostasis.
Anti-vimentin, rabbit, Cell Signaling (D21H3) was validated for WB by the manufacturer (https://www.cellsignal.com/products/primary-antibodies/vimentin-d21h3-xp-rabbit-mab/5741)
Anti-caveolin-1, rabbit, Cell Signaling (D46G3) was successfully used for WB in Hitvoka et al., 2013, PLoS Pathog.
Anti-transgelin, rabbit, Abcam (ab14106) was validated for WB by the manufacturer (https://www.abcam.com/en-us/products/primary-antibodies/tagln-transgelin-antibody-ab14106?srsltid=AfmBOoqjrBkuWiUv9zd3xnDxYVjfR23Sk-N2q7EjXe3-h6utuy0_XG_Z#tab=datasheet)
Anti-GAPDH, mouse, Millipore (MAB374) was validated for WB by the manufacturer (https://www.merckmillipore.com/FR/fr/product/Anti-Glyceraldehyde-3-Phosphate-Dehydrogenase-Antibody-clone-6C5,MM_NF-MAB374)

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)

D2A1 were kindly gifted by R. Weinberg. ZMEL-1 were gifted by R. White. A431 and 1675 were gifted by F. Saltel. 4T1 were gifted by M. Thery. CTC-45 and CPP-45 were gifted by Julie Pannequin. M229 R and M229 S were gifted by Marcel and Sophie Deckert. MCF-7 and MDA-MB-231 were gifted by Fabien Alpy.

Authentication

Consistency in cell line phenotypes was ensured in all cases by the application of the seed-loot system for cell banking, where master and working stocks were generated from an initial (commercial, or not) vial. Experiments were performed with low-passage working stock vials. All cell lines were validated by assessing doubling time and mycoplasma negativity.

Mycoplasma contamination

All cell lines used were mycoplasma negative. Tested with the Venor GeMOneStep Mycoplasma detection kit, Thermo Fisher.

Commonly misidentified lines
(See ICLAC register)

No commonly misidentified cell lines were used in this study.

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals

Mouse (mus musculus), BALB/c from 8 to 12 weeks old from Charles Rivers laboratories were breeded in-house. Tg(fli1a:eGFP) and Tg(kdrl:Hsa.HRAS-mCherry) Zebrafish (Danio rerio) embryos from a Tubingen background were kindly provided by the zebrafish facility of EMBL (Heidelberg, Germany) and further grown and bred in our in-house Zebrafish facility. Embryos were maintained as previously described (Goetz et al., 2014 Cell Reports)

Wild animals	*Provide details on animals observed in or captured in the field; report species and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.*
Reporting on sex	*Indicate if findings apply to only one sex; describe whether sex was considered in study design, methods used for assigning sex. Provide data disaggregated for sex where this information has been collected in the source data as appropriate; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex-based analyses where performed, justify reasons for lack of sex-based analysis.*
Field-collected samples	*For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.*
Ethics oversight	Mice used in this study were housed under pathogen-free conditions and all procedures were performed in accordance with the European Union Guideline 2010/63/EU. The study was approved by the Regional Ethical Committee for Animal Experimentation of Strasbourg, CREMEAS (CEEA 35) and registered under the APAFIS authorization 13945-2018030710396087.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*