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Corresponding author(s): Tom Barker

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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 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	Volocity 6.3.1 software for acquiring fluorescence images. Asylum Research Scanning Probe Microscope Software version 14 for AFM force data collection. Xcalibur 4.1 for MS data acquisition.
Data analysis	GraphPad Prism 8.2.0 for statistics analysis. "Customized Matlab code" available at https://github.com/Barker-MBEL/ratiometric Proteome Discoverer 2.1 for peptide analysis. PyMOL(TM) 2.3.4 for figure 2C

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 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 Figs 1e, 1f, 2a, 3c-e, 3g, 4c, 4d, 4f, 4g and Supplementary Figs 1c, 2, 3, 4, 5a, 5b, 7b, 8b have been provided in Supplementary Table 2 —Statistic Source Data. All other data supporting the findings of this study are available from the corresponding author on 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	Fig. 1e, 1f, Supp 1c: In order to account for global tissue heterogeneity and spacial variability within the specified lung disease, we imaged at least 20 random fields of interest per condition from the stained sections. Those were then quantified with the provided Matlab code and the medians of the pixel-by-pixel ratio intensity were reported as visible data points in the figures. Fig. 2a, 3g, 4c: In order to account for the heterogeneity within the dECM substrates, we quantified at least 20 random regions of interest. Those were then quantified with the provided Matlab code and the medians of the pixel-by-pixel ratio intensity were reported as visible data points in the figures. The assays were replicated 3 times, leading to the same conclusions, in agreement. Fig. 4f, 4g: In order to account for not only the dECM substrates heterogeneity, but also the heterogeneity of fibroblasts, for which multiple subpopulations have been reported, we randomly selected and imaged at least 50 cells of interest per condition. Each cell readout was reported as one visible data point in the figures.
Data exclusions	no data was excluded, no outliers analysis was performed
Replication	Our result are replicated three times
Randomization	Each data point (fibers, cells, field within a tissue section) is randomly picked
Blinding	There is no blinding happened in this paper. Given that in each study, we first check if samples look normal, then we randomly pick data points.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used	Anti-glutathione antibody (Virogen, 101-A, mAb100,) anti-fibronectin antibody (Abcam, ab2413) active αvβ3 (WOW-1, gift of Sanford Shattil, University of California, San Diego) active β1 (BD Pharmingen, 553715, 9EG7), α-SMA PE conjugated (R&D Systems, MAB1420, 1A4), anti-MKL1 (Sigma-Aldrich, HPA030782), anti-paxillin (Abcam, ab32084, Y113).
Validation	Anti-glutathione antibody (Virogen, 101-A, mAb100,), validated in paper "S-glutathionylation of cryptic cysteines enhances titin elasticity by blocking protein folding" anti-fibronectin antibody (Abcam, ab2413), validated in manufacturer's website: https://www.abcam.com/fibronectin-antibody-ab2413.html active αvβ3 (WOW-1, gift of Sanford Shattil, University of California, San Diego)

active β1 (BD Pharmingen, 553715, 9EG7), validated in paper "A fundamental difference in the capacity to induce proliferation of naive T cells between CD28 and other co-stimulatory molecules"
α-SMA PE conjugated (R&D Systems, MAB1420, 1A4), validated in manufacturer's website: https://www.rndsystems.com/products/human-mouse-rat-alpha-smooth-muscle-actin-antibody-1a4_mab1420
anti-MKL1 (Sigma-Aldrich, HPA030782), validated in manufacturer's website: https://www.sigmaaldrich.com/catalog/product/sigma/hpa030782?lang=en&region=US
anti-paxillin (Abcam, ab32084, Y113), validated in manufacturer's website: https://www.abcam.com/paxillin-antibody-y113-ab32084.html

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Human Foreskin Fibroblasts (HFF) cells from ATCC. (HFF-1 (ATCC® SCRC-1041™); HEK-293 also from ATCC (293 [HEK-293] (ATCC® CRL-1573™))
Authentication	Bought from provider
Mycoplasma contamination	Cell lines tested negative
Commonly misidentified lines (See ICLAC register)	N/A