nature research

Corresponding author(s): Kun-Liang Guan

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.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Igor 6.34A software for AFM data collection. NIS elements imaging software for immunofluorescence data collection.
Data analysis	The Statistical analyses were performed with Microsoft Excel for t test and Graphpad Prism 6 for two-way ANOVA test. NIS elements imaging software and Image J for immunofluorescence analyses. Igor 6.34A software for AFM data analyses.

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 upon request. 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

Data availability. The source data for the graph representations can be found in the online version of the paper. For uncropped images of Western blot data, see

Supplementary Figure 1. The RNA sequencing data is available in GEO DataSets with the accession number GSE98547. All other data that support the findings of this study are available upon request from the corresponding author.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	We did not use statistical method to pre-determine sample size. The sample size was based on the literature that tested the same cell lines or performed the similar assays.
Data exclusions	We did not exclude any data.
Replication	All the experiments have been at least replicated once. All the results have been validated in the repeat experiments.
Randomization	For the xenograft studies, the mice were randomly divided into different groups according to ID number.
Blinding	The investigators were blinded to group allocations during the data collection and analyses.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

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

Antibodies

Antibodies used

Antibodies
Gene Usage Vendor Catalog Dilution
Actin WB Sigma A5441 1:3000
ARHGAP29 WB Santa Cruz Biotechnology sc-365554 1:400
beta-catenin IF BD Biosciences 610154 1:250
DYKDDDDK (Flag) Tag IF Cell Signaling Technology 8146 1:500
pERK1/2 WB Cell Signaling Technology 4370 1:2000
Flag WB Sigma F1804 1:2000
GAPDH WB Cell Signaling Technology 5174 1:2500
GFP IF Cell Signaling Technology 2956 1:100
GM130 IHC BD Biosciences 610823 1:500
GST WB Sigma SAB4200237 1:5000
HA IF Cell Signaling Technology 3724 1:500
HA WB Biolegend 901513 1:2000
HLA class 1 IHC Abcam ab70328 1:100
Laminin V IHC EMD Millipore MAB19562X 1:1000
LATS1 WB Cell Signaling Technology 3477 1:2000
pLATS-HM (pLATS1-T1079) Cell Signaling Technology 8654 1:2000
MST1 WB Cell Signaling Technology 3682 1:2000
MST2 WB Abcam ab52641 1:2000
PDZGEF2 WB Santa Cruz Biotechnology sc-398642 1:400
RhoA WB Cell Signaling Technology 2117 1:1000

Ras WB Cell Signaling Technology 3339 1:2000
Ras (G12V) WB Cell Signaling Technology 14412 1:2000
PLCγ1 WB Cell Signaling Technology 5690 1:1000
PLD1 WB R&D systems F5615-SP 1:1000
PLD2 WB Cell Signaling Technology 13904 1:1000
RAP2 WB BD Biosciences 610215 1:1000
TWIST IF Santa Cruz Biotechnology sc-81417 1:100
vinculin WB Sigma V9131 1:3000
YAP/TAZ IHC Cell Signaling Technology 8418 1:100
YAP/TAZ IF/WB Santa Cruz Biotechnology sc-101199 1:200 (IF) or 1:1000 (WB)
pYAP-S127 Cell Signaling Technology 4911 1:2000

Validation

Most of the antibodies are validated by Western blot or immunofluorescence with CRISPR KO cells or the cells without the expression of the antigens.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

HEK293A cells were provided by Ryan Russel (Univ. of Ottawa). MCF10A, MCF7, and MDA-MB-468 cells are from ATCC.

Authentication

No authentication has been used.

Mycoplasma contamination

The cells were tested for mycoplasma and they are free of mycoplasma contamination.

Commonly misidentified lines
(See ICLAC register)

None of the cells is listed in ICLAC.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals

NOD/SCID mice from JAX. 8-9 weeks old. Female.
Nude mice from UCSD. 8-9 weeks old. Female.

Wild animals

The study did not involve in wild animals.

Field-collected samples

The study did not involve in field-collected samples.