nature portfolio

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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	n/a
Data analysis	n/a

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 data is presented in the manuscript or the supplementary files

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	n/a
Reporting on race, ethnicity, or other socially relevant groupings	n/a
Population characteristics	n/a
Recruitment	n/a
Ethics oversight	n/a

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 sizes (n = 3–7 biologicallyindependent replicates per condition, or n = 100 individual cells for correlation) were chosen based on standard practices in cell viability assays and pilot experiments to detect biologically meaningful differences.
Data exclusions	No data were excluded from the analyses.
Replication	All key findings are supported by at least three independent experiments with multiple technical/biological replicates per condition (n = 3–7); correlation was performed on 100 individual cells in a single experiment. Results were highly reproducible.
Randomization	Cells/wells were randomly allocated to treatment groups for viability experiments. Fields of view for imaging and subsequent Pearson's correlation analysis (n=100 cells) were selected randomly across the sample to ensure unbiased representation.
Blinding	No. Blinding was not performed because treatments were applied and measured by the same experimenter and some conditions were visually distinguishable; however, all quantifications were automated.

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	IL13Rα2 polyclonal antibody (PA5-106798) and GAPDH ((14C10) Rabbit Monoclonal Antibody, #3683
Validation	IL13Rα2 polyclonal antibody (PA5-106798) was purchased from Thermo Scientific. Specificity validated by manufacturer via peptide competition assay (preincubation with immunizing peptide prevented binding in Western Blot. GAPDH ((14C10) Rabbit Monoclonal Antibody, #3683) was purchased from Cell Signaling Technology which employs an Orthogonal Strategy for Antibody Validation. I do not the specifics for this antibody and did not do additional validation.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	(U-87 MG) cells were obtained from American Type Culture Collection (ATCC HTB-14) SJ-GBM2 was obtained from the Children's Oncology Group (COG, Texas Tech University, Health Science Center, TX, USA). The NP53 cell line were kindly provided by Dr. Oren Becher, Northwestern Medicine, Feinberg School of Medicine, Ann and Robert H. Lurie Children's Hospital of Chicago. H35, was generously provided by Dr. Dennis A. Steindler (Tufts University, Boston MA, USA). Human derived vascular smooth muscle cells (VSMC) were obtained from Sciencell (Carlsbad, CA, USA).
Authentication	Cell lines were authenticated according to the standards of their respective suppliers or providing laboratories. U87 authenticated by short tandem repeat (STR) profiling, Y-chromosome painting, Q-band assay, and karyotyping, confirming male origin, reference STR profile match, and hypodiploid karyotype. SJ-GBM2 was authenticated by STR profiling against the original patient sample, with validation of identity . The murine NP53 cell line was verified genetically through sequencing or PCR for defining mutations (PDGF-B overexpression, p53 loss, H3.3K27M) in the RCAS transgenic mouse model, with phenotypic consistency confirmed in publications. H35 was characterized as human adult hippocampal neural progenitors via marker expression (e.g., nestin) and differentiation potential assays. VSMC is a primary cell line authenticated by immunofluorescence showing >90–95% purity with positive staining for α-smooth muscle actin, calponin, and smooth muscle myosin heavy chain, and negative for endothelial and fibroblast markers. No additional authentification was done in my lab. All primary cell lines were expanded and frozen to maintain stock of relatively low passage numbers.
Mycoplasma contamination	All cell lines were routinely tested for mycoplasma using LookOut mycoplasma PCR detection kit
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines (per ICLAC register) were used.

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a