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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 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	Quantitative analysis of the images detecting TUNEL+ nuclei; colonogenic assay using crystal violet for colony formation and protein band intensity was performed using ImageJ software; Quantitative analysis of the IHC images was performed using image analyzing software by Visiopharm; FLOWJO was used to quantify cell-death using flowcytometry;
Data analysis	Graphpad Prism, FLOWJO and ImageJ software

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

DAS statement included. Raw data provided as source data files.

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	No sample-size calculations were performed. Sample size was determined to be adequate based on the magnitude and consistency of measurable differences between groups.
Data exclusions	no data was exlcuded
Replication	The experiments were reliably reproduced by the coauthors listed. Replicated experiments were successful.
Randomization	For xenograft experiments, female athymic nu/nu mice injected with tumor cells were randomized before being allocated to respective cages
Blinding	All other in vitro experiments conducted were not randomized, and investigators were not blinded to either allocation during experiments or to outcome assessments.

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	The following antibodies were used: PBEF/NAMPT (Cell Signalling Technologies (CST), D1K6D #61122), NAPRT1 (ThermoFischer Scientific, #PA5-31880), NAD Synthetase (Abcam, ab171942), NMRK1 Antibody (Santa cruz, F-8 #sc-398852), NMRK1 (Abcam, Anti-C9orf95 antibody EPR11190 #ab169548), NMRK2 or ITGB1BP3 (ThermoFischer, #PA5-24607). All were used at a dilution of 1:1000. All description about antibodies including manufacturer, species are noted in the method section of the manuscript.
Validation	Validation of each primary antibody for the species and application, were based on manufacturer's statement available on their respective company website

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	The NCI-60 cell-line panel was a gift from A. Shiau (Ludwig Institute of Cancer Research). LNCaP, PC9, CAPAN1, U-87, HEK293, IMR90, HeLa, RPE-1 and MCF10A used in this study were obtained from ATCC. Normal human astrocytes (NHA) were obtained from Lonza. KYSE-510, KYSE-140, BHY were obtained from Leibniz-Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Germany. OE21 was obtained from Sigma. Please refer to Methods.
Authentication	Cell lines were obtained from NCI, ATCC, DSMZ and Sigma and therefore were not authenticated.
Mycoplasma contamination	All cell lines used were tested for mycoplasma contamination. All tested negative.

Commonly misidentified lines (See ICLAC register)	Yes--MDA-MB-435, NCI-ADR-RES, and SNB-19. Included as they are part of NCI60.

Animals and other organisms

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

Laboratory animals	Five-six-week-old female athymic nu/nu mice were purchased from Harlan Sprague Dawley
Wild animals	Did not involve wild animals
Field-collected samples	Did not involve samples collected from the field.

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	*For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.*
Files in database submission	*Provide a list of all files available in the database submission.*
Genome browser session (e.g. UCSC)	*Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.*

Methodology

Replicates	*Describe the experimental replicates, specifying number, type and replicate agreement.*
Sequencing depth	*Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.*
Antibodies	*Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.*
Peak calling parameters	*Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.*
Data quality	*Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.*
Software	*Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.*

Flow Cytometry

Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Cell pellets were fixed in 80% EtOH overnight. PBS was added to cell pellets in equal volume to EtOH & stained with Propidium iodide & RNase A. (Check methods sections for details).
Instrument	BD LSRII flow cytometer (BD Biosciences)
Software	FLOWJO
Cell population abundance	Not applicable.

Gating strategy

FSC/SSC gates were marked & that whole population was sub-gated as FSC (area) by FSC (width). 100% of the cells in this gate were used to obtain histograms for PI positivity.

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.