nature portfolio

Corresponding author(s): DBPR; COMMSBIO-23-5092A

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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	*Provide a description of all commercial, open source and custom code used to collect the data in this study, specifying the version used OR state that no software was used.*
Data analysis	*Provide a description of all commercial, open source and custom code used to analyse the data in this study, specifying the version used OR state that no software was used.*

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

Provide your data availability statement here.

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

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 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.*
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	For cell experiments, three samples at least are chosen for each trial. This sample size is based on our previous experience and literature reports, where using three or more replicates in cell experiments is common practice. This number is sufficient to yield reliable results while maintaining experiment efficiency and economy.In animal experiments, five animal samples are selected for each trial. The choice of this sample size is based on standard operating procedures for animal experiments and principles of statistics.
Data exclusions	no data were excluded from the analyses
Replication	We have taken multiple measures to verify the reproducibility of the experimental results. This includes using the same experimental conditions, repeating experimental procedures, conducting repeated tests at different time points, and independent replicates by different experimenters.
Randomization	The allocation of cells or animals was not applicable or critical to our research objectives; therefore, we did not perform random allocation or control for covariates in grouping.
Blinding	N/A

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

Methods

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

Antibodies

Antibodies used: anti-FGFR1 antibody (CST#9740S), anti-CD71 antibody (Abcam#ab214039), anti-CD71 antibody (Santa#sc-32272), anti-CD71 antibody (Proteintech#10084-2-AP), anti-DMT1 antibody (Proteintech#20507-1-AP), anti-β-actin antibody (Santa#sc-47778), anti-p-ERK antibody (CST#4370S), anti-ERK antibody (CST#4695S), anti-IRP2 antibody (Proteintech#29976-1-AP), anti-IRP2 antibody (Santa#sc-33682), anti-Bcl-2 antibody (CST#15071S), anti-BAX antibody (CST#2772S), anti-c-MYC antibody (Santa#sc-40), anti-IL-6 antibody (Santa#sc-57315), anti-GPX-4 antibody (Santa#sc-166570), anti-SOD-2 antibody (Santa#sc-137254), anti-P65 antibody (CST#8242S), anti-Nrf2 antibody (CST#12721), anti-IRP1 antibody (Santa#sc-166022), anti-P53 antibody (CST#30313), anti-FBXL5 antibody (Abcam#ab140175), anti-FBXL5 antibody (Santa#sc-390102), anti-Ubiquitin antibody (CST#3936T), anti-PCNA antibody (CST#2586S), Goat Anti-Mouse IgG (Jackson#115-005-003), Goat Anti-Rabbit IgG (Jackson#111-035-003), Mouse monoclonal Anti-Rabbit IgG light chain (HRP) (Abcam#ab99697), Cy™5 AffiniPure™ Goat Anti-Mouse IgG (Jackson#115-175-146), Fluorescein (FITC) AffiniPure™ Goat Anti-Rabbit IgG (Jackson#111-095-144).

Validation: All validation were obtained by the manufacturer's website or manufacturer's technical support.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s): ATCC

Authentication: STR profiling by Genetic Testing Biotechnology Corporation

Mycoplasma contamination: all cell lines tested negative for mycoplasma contamination

Commonly misidentified lines (See ICLAC register): *Name any commonly misidentified cell lines used in the study and provide a rationale for their use.*

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: TRAMP mice, C57BL6J, nude mice

Wild animals: the study did not involve wild animals

Reporting on sex: only male animals were selected for this Prostate cancer study

Field-collected samples: The samples of Prostate tumor and Xenograft tumor were collected in a biosafety cabinet

Ethics oversight: All animal experiments were performed according to the animal guidelines, and with prior approval from the Animal Experimentations Ethics Committee, Wenzhou Medical University.

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

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	The cells, originating from cell lines, are enzymatically dissociated into single-cell suspensions using trypsin digestion.
Instrument	BECKMAN CytoFLEX S
Software	flow jo
Cell population abundance	cancer cell lines
Gating strategy	The gating strategy primarily relies on the forward scatter (FSC) and side scatter (SSC) parameters to capture the tumor cell population, without involving immune cell subpopulations.

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