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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	no custom software was used.
Data analysis	FlowJo (Tree Star Inc., Ashland, OR, USA, v10.0.7.r2) ; pLink (v2.3, GitHub https://github.com/pFindStudio/pLink2/tree/master/pSimXL)

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

Data supporting the results and conclusions are available within this paper and the Supplementary Information.

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	Experiments were performed with at least 3 independently prepared samples for statistical tests.
Data exclusions	No data were excluded from analyses.
Replication	The experiments were repeated for at least three times independently.
Randomization	Not relevant to study, 1) no live organisms or human participants or clinical research were involved; 2) no large number of samples to select from that would lead to selection bias.
Blinding	Samples subjected to mass spectrometric analysis, flow cytometry, and DNA sequencing were blinded to the experimentalist.

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	HRP conjugated anti-Hisx6 tag antibody was purchased from Proteintech (Catalog number: HRP-66005, clone name: 1B7G5, Lot number: 21004183). Streptavidin-HRP was purchased from Thermo Fisher Scientific (Catalog number: PI21130, Lot number: VC300763). Alexa Fluor 647 conjugated Hisx6 tag antibody was purchased from Thermo Fisher Scientific (Catalog number: MA1-135-A647, clone name: 4E3D10H2/E3).
Validation	The specificity of the antibodies (HRP conjugated anti-Hisx6 tag antibody and Alexa Fluor 647 conjugated Hisx6 tag antibody) was verified by expressing a model GFP protein with the tag appended at the C-terminus in bacteria and in mammalian cells, followed with western blotting of cell extracts.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	BT-20 (CCLZR058), MCF-7 (CCLZR278), SK-MEL-28 (CCLZR370) were purchased from UCSF Cell and Genome Engineering Core (CGEC). NK-92 (CRL-2407) was purchased from American Type Culture Collection (ATCC).
Authentication	Cell lines were authenticated at UCSF Cell and Genome Engineering Core or ATCC and used immediately following purchase.
Mycoplasma contamination	All cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	Not used in this study.

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 lines were purchased from ATCC. Staining of cells were described in detail in Supplementary Information.
Instrument	BD LSRFortessa cell analyzer, Model No. 649225
Software	FlowJo
Cell population abundance	No cell sorting was carried out. We just used flow cytometry to quantitatively measure the fluorescence intensity of cells.
Gating strategy	Negative control cell samples were used to define the gate for positive signal.

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