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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	No software was used to collect data in this study
Data analysis	R v3.5.0, ggplot2 R package, STAR (v2.5.4b) , Cluster3, Java TreeView, GSEA v3.0, TCGA-assembler , ClueGO via Cytoscape, DESeq2 v 1.18

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

All data generated or analysed during this study are included in this published article (and its supplementary information 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 statistical methods were used to determine sample size .
Data exclusions	No data was excluded . In the cases where partial data was shown for visualization purposes , exclusion criteria is specified in the methods with the original data provided as supplementary data files
Replication	All attempts of data replication were successful
Randomization	No Randomization was performed
Blinding	Investigators were not blinded to group allocations.

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	FDX1 (Proteintech Group, Inc (Catalog Number: 12592-1-AP)) 1:1000, tubulin (ab80779 Abcam) 1:2000
Validation	Validation previously conducted by manufacturer. Antibodies were validated in this study by the size of the bands detected by them.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	T47D- Lindquist lab Lo19S T47D- Modification of the parental T47D K562- Sabatini lab HeLa , 293T-HS , HEK293, HEK293T- Lindquist lab NCIH441, NCIH2030- Jacks lab HDPQ1 and MCF-7 - Golub lab CCLE GFP+/Luc+ MM.1S and KMS11- Ghobrial lab
Authentication	No specific authentication of cell lines was performed in this study
Mycoplasma contamination	All cell lines were mycoplasma negative on routine examinations.
Commonly misidentified lines (See ICLAC register)	Cell lines are not in the list of misidentified cell lines

Animals and other organisms

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

Laboratory animals	25 Female SCID-beige mice at 4-6 weeks of age (Taconic, USA) were utilized for the study.
Wild animals	No wild animals used
Field-collected samples	No field-collected samples used