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	All images were collected using Andor's Fusion 2.4 software. Flow sort data were collected using Cell Sorter Software 3.2.0.
Data analysis	Images were stitched using commercial software Fusion (version 2.4) Stitcher (https://fusion.help.andor.com/display/fusionum/Andor+Stitcher). To segment the cells, membrane masks were segmented using Cellpose 0.6.1 (https://www.cellpose.org/). All the other analysis was performed using customized code (https://github.com/GaublommeLab/CRISPRmap-Pipeline). R (4.3.2), pyhton (3.7.10), Numpy (1.19.3), Pandas (1.2.4), scikit-image (0.16.2), scikit-learn (0.24.2), matplotlib (3.4.1), seaborn (0.11.1), opencv (3.4.2.17) were used for data analysis and visualization.

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 raw imaging data for the CRISPRmap screens mentioned in the manuscript were deposited into the Bioimage Archive database under accession number S-BIAD985 and are available at the following URL: https://www.ebi.ac.uk/biostudies/BioImages/studies/S-BIAD985. ClinVar database for variant characterization is available at https://www.ncbi.nlm.nih.gov/clinvar/.

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	In the CRISPRmap screens performed on cultured cells, we imaged on average at least 300 cells per guide per treatment condition. This number is determined based on our pilot experiments to ensure enough statistical power to perform guider-to-control comparison of optical phenotypes. Sample sizes in other experiments were chosen based on the statistical requirements (two-sided Mann-Whitney U test or student t-test).
Data exclusions	In the DDR364 base-editing screens, guides with Rule set 2 on-target score below the threshold described in the article were excluded from the analysis of statistical significance changes and the clustering of guides targeting functionally related genes. This is supported by evidence provided in the article and the previous base-editing study (Cuella-Martin, R. et al. 2021. Cell.). In all CRISPRmap screens, cells did not pass the barcode QC criteria described in the article were excluded from further analysis of optical phenotypes. This is to ensure high-fidelity genotyping as we established in our pilot experiments.
Replication	All CRISPRmap screens on cultured cells were replicated in corresponding pilot studies for barcode readout and phenotype imaging, then major screens covering the number of cells meet the sample size criteria were performed and depicted in the article. We validated the phenotypes identified in the DDR364 base-editing screens using 9 individually transduced guides, as described in the article. In vivo CRISPRmap screens were replicated on three technical replicates with representative experiments depicted. Biological or technical replicated were indicated in the figure legend, methods, or associated text, when appropriate.
Randomization	Randomizations were applied when appropriate. In the CRISPRmap base-editing screens, cells seeded on the same plate were randomly assigned with treatments. By the design of our assay, guide/barcode distribution is random throughout cells in a given well.
Blinding	Blinding was not applicable in this study as the researchers need to know the treatment groups for sample preparation and analysis, however, grouping assignment bias was controlled on the control treatment group, in which the exact procedures were carried out as in the other treatment groups.

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	*Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).*
Research sample	*State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.*
Sampling strategy	*Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.*
Data collection	*Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.*
Timing	*Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.*
Data exclusions	*If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Non-participation	*State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.*
Randomization	*If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.*

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	*Briefly describe the study. For quantitative data include treatment factors and interactions, design structure (e.g. factorial, nested, hierarchical), nature and number of experimental units and replicates.*
Research sample	*Describe the research sample (e.g. a group of tagged Passer domesticus, all Stenocereus thurberi within Organ Pipe Cactus National Monument), and provide a rationale for the sample choice. When relevant, describe the organism taxa, source, sex, age range and any manipulations. State what population the sample is meant to represent when applicable. For studies involving existing datasets, describe the data and its source.*
Sampling strategy	*Note the sampling procedure. Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.*
Data collection	*Describe the data collection procedure, including who recorded the data and how.*
Timing and spatial scale	*Indicate the start and stop dates of data collection, noting the frequency and periodicity of sampling and providing a rationale for these choices. If there is a gap between collection periods, state the dates for each sample cohort. Specify the spatial scale from which the data are taken*
Data exclusions	*If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Reproducibility	*Describe the measures taken to verify the reproducibility of experimental findings. For each experiment, note whether any attempts to repeat the experiment failed OR state that all attempts to repeat the experiment were successful.*
Randomization	*Describe how samples/organisms/participants were allocated into groups. If allocation was not random, describe how covariates were controlled. If this is not relevant to your study, explain why.*
Blinding	*Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.*

Did the study involve field work? ☐ Yes ☐ No

Field work, collection and transport

Field conditions	*Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).*
Location	*State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).*
Access & import/export	*Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible manner and in compliance with local, national and international laws, noting any permits that were obtained (give the name of the issuing authority, the date of issue, and any identifying information).*
Disturbance	*Describe any disturbance caused by the study and how it was minimized.*

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	All antibodies used in the study are listed below in the Validation section.
Validation	Name: Rat monoclonal anti-human CD326 (EpCAM); Supplier: BioLegend Cat# 312502, RRID:AB_2890747; Clone: W18060B Validated by BioLegend and: 1. Strnad J, et al. 1989. Cancer Res. 49:314. 2. Munz M, et al. 2004. Oncogene 23:5748. 3. Rao CG, et al. 2005. Int. J. Oncol. 27:49. Name: Rabbit polyclonal anti-RPA2; Supplier: Bethyl Laboratories Cat# A300-244A; RRID:AB_185548 Validated by Bethyl Laboratories and: Xiao W, et al. 2021. Nat Commun. 12: 4373. Joséphine G, et al. 2023. Cell Reports. 42, 9. James O, et al. 2022. Cell Reports 41, 111670. Name: Rabbit monoclonal anti-ATM; Supplier: Cell Signaling Technology Cat# 2873; RRID:AB_2062659; Clone: D2E2 Validated by Cell Signaling Technology and: Fröhlich L, et al. 2023. Cancer Res Commun. 3,9 1743-1755. Jianli Z, et. al. 2023. Oncotarget. 14 597-611. And other publications listed on: https://www.cellsignal.com/products/primary-antibodies/atm-d2e2-rabbit-mab/2873 Name: Rabbit polyclonal anti-53BP1; Supplier: Bethyl laboratories Cat# A300-272A; RRID:AB_185520 Validated by Bethyl laboratories and: Stephen A, et al. 2023. Mol. Cell. 83, 16. Julie G, et al. 2019. Oncotarget. 10, 41. Name: Rad18 (D2B8) XP Rabbit mAb #9040 (BSA and Azide Free); Supplier: Cell Signaling Technology Cat# 9040; RRID:AB_2756446; Clone D2B8 Validated by Cell Signaling Technology and: Liangliang R, et al. 2023. Cell Death Dis. 14, 8. Ruyuan Yu, et. al. 2022. Nucleic Acids Res. 50, 14. And other publications listed on: https://www.cellsignal.com/products/primary-antibodies/rad18-d2b8-xp-rabbit-mab/9040 Name: Rabbit polyclonal anti-RAD51 (affinity-pure, ChIp grade); Supplier: Bioacademia Cat# 70-012; RRID:AB_1056187 Validated by Bioacademia and: Masae I, et al. 2022. Mol Cell Biol. 42, 11.

Diego D, et al. 2023. BioRxiv. https://doi.org/10.1101/2023.05.22.541781.

Name: Mouse monoclonal anti-BRCA1 (BSA and Azide Free); Supplier: Santa Cruz Biotechnology Cat# sc-6954; RRID:AB_626761; Clone: D-9
Validated by Santa Cruz Biotechnology and:
Ozgencil, M. et al. 2023. Life Sci Alliance. 6.
Zou, RS. et al. 2023. Nat Methods. 20: 706-713.
Bassi, N. et al. 2023. BMC Cancer. 23: 368.
And other publications listed on: https://www.scbt.com/p/brca1-antibody-d-9

Name: Mouse monoclonal anti-ɣ-H2AX; Supplier: BioLegend Cat# 613402; RRID:AB_315795; Clone: 2F3
Validated by BioLegend and:
Chomiak AA, et al. 2022. iScience. 25:104354.
Li M, et al. 2011. Mol Cell Biol. 31:2090.
Kuefner M, et al. 2012. Radiology. 264:59:00
And other publications listed on: https://www.biolegend.com/en-us/products/purified-anti-h2a-x-phospho-ser139-antibody-1990

Name: Rabbit monoclonal anti-Cyclin A2 (BSA and Azide Free); Supplier: Cell Signaling Technology Cat# 29113SF, RRID:AB_3075524; Clone: E6D1J
Validated by Cell Signaling Technology.

Name: Mouse monoclonal anti-H2A.X Phospho (Ser139) (Alexa Fluor 647 Conjugate); Supplier: BioLegend Cat# 613408, RRID:AB_2295046; Clone: 2F3
Validated by BioLegend and:
Georges RO, et al. 2022. Nat Commun. 13:6230.
de Jong MRW, et al. 2019. Cancers (Basel). 1.66875.
Kang J, et al. 2015. Proc Natl Acad Sci U S A. 112: E4236-E4245.
And other publications listed on: https://www.biolegend.com/en-us/products/alexa-fluor-647-anti-h2a-x-phospho-ser139-antibody-3503

Name: Rabbit monoclonal anti-phospho-Histone H3 (Alexa Fluor 555 Conjugate); Supplier: Cell Signaling Technology Cat# 3475, RRID:AB_10694639
Validated by Cell Signaling Technology and:
ShuYing X, et. al. 2020. J Mol Cell Biol. 12, 1.
Rumana R, et. al. 2019. Sci Data. 6, 1.
And other publications listed on: https://www.cellsignal.com/products/antibody-conjugates/phospho-histone-h3-ser10-d2c8-xp-rabbit-mab-alexa-fluor-555-conjugate/3475

Name: Rabbit monoclonal anti-Cyclin B1 (BSA and Azide Free); Supplier: Cell Signaling Technology Cat# 65173SF, RRID:AB_3075525; Clone: D5C10
Validated by Cell Signaling Technology.

Name: Rabbit monoclonal anti-p53 (Alexa Fluor 488 Conjugate); Supplier: Cell Signaling Technology Cat# 5429, RRID:AB_10695458: Clone: 7F5
Validated by Cell Signaling Technology and:
Yuki S, et. al. 2021. FEBS Open Bio.
Jennifer E, et. al. 2019. Methods Mol Biol.
Chao F, et. al. 2019. Int J Biol Sci.
And other publications listed on: https://www.cellsignal.com/products/antibody-conjugates/p53-7f5-rabbit-mab-alexa-fluor-488-conjugate/5429

Name: Rabbit monoclonal anti-p21 Waf1/Cip1 (Alexa Fluor 555 Conjugate); Supplier: Cell Signaling Technology Cat# 8493, RRID:AB_10860074: Clone: 12D1
Validated by Cell Signaling Technology and:
Sumiko W, et. al. 2019. Cytotechnology.
Jia-Ren L, et. al. 2018. Elife.
And other publications listed on: https://www.cellsignal.com/products/antibody-conjugates/p21-waf1-cip1-12d1-rabbit-mab-alexa-fluor-555-conjugate/8493

Name: Rabbit monoclonal anti-Cleaved PARP (Asp214) (Alexa Fluor 647 Conjugate); Supplier: Cell Signaling Technology Cat# 6987, RRID:AB_10858215; Clone: D64E10
Validated by Cell Signaling Technology and:
Yelyzaveta S, et. al. 2023. Nat Commun.
Gro R, et. al. 2019. Front Oncol.
And other publications listed on: https://www.cellsignal.com/products/antibody-conjugates/cleaved-parp-asp214-d64e10-xp-174-rabbit-mab-alexa-fluor-174-647-conjugate/6987

Name: Rabbit monoclonal anti-Ki-67 (BSA and Azide Free); Supplier: Cell Signaling Technology Cat# 34330, RRID:AB_2942026: Clone: D3B5
Validated by Cell Signaling Technology.

Name: Monoclonal Rat anti-Tenascin C; Supplier: R and D Systems Cat# MAB2138, RRID:AB_2203818; Clone # 578
Validated by R and D Systems and:
Morganti M, et al. 1990. Exp. Neurol. 109:98.
Husmann, K. et al. 1992. J. Cell Biol. 116:1475.
And other publications listed on: https://rndsystems.com/products/human-mouse-tenascin-c-antibody-578_mab2138#product-

citations

Name: Rat monoclonal anti-Fibroblast Marker (Alexa Fluor® 488 Conjugate); Supplier: Santa Cruz Biotechnology Cat# sc-73355, RRID:AB_1122890; Clone: ER-TR7
Validated by Santa Cruz Biotechnology and:
Ugur, M. et al. 2023. Immunity. 56: 1778-1793.e10.
González-Chávez, SA. et al. 2023. Cells. 12.
And other publications listed on: https://www.scbt.com/p/fibroblast-marker-antibody-er-tr7?gad_source=1&gclid=EAIaIQobChMIn7K8i5CigwMVXW0PAh26yQeeEAAYASAAEgJIfvD_BwE

Name: Goat polyclonal anti-CD31(Alexa Fluor® 488 Conjugate); Supplier: R and D Systems Cat# FAB3628G, RRID:AB_10972784
Validated by R and D Systems and:
Zhang D, et al. 2021. Nat Commun. 12(1):3964.
Liu X, et al. 2023. Nat Commun. 12(1):1832.
And other publications listed on: https://www.rndsystems.com/products/mouse-rat-cd31-pecam-1-alexa-fluor-488-conjugated-antibody_fab3628g#product-citations

Name: Mouse monoclonal anti-Lamin A/C; Supplier: Sigma-Aldrich Cat# MABT1341, RRID:AB_3075526; Clone: 4C11
Validated by Sigma-Aldrich and:
Kamikawa Y, et al. 2023. Cell Death Discov. 9, 233.

Name: Goat anti-Rat IgG (H+L) Cross-Adsorbed Secondary Antibody (DyLight 755 Conjugate); Supplier: Thermo Fisher Scientific Cat# SA5-10023, RRID:AB_2556603
Validated by Thermo Fisher Scientific.

Name: Rabbit monoclonal anti-STAT1; Supplier: Cell Signaling Technology Cat# 14994, RRID:AB_2737027; Clone: D1K9Y
Validated by Cell Signaling Technology and:
Jian-Ping R, et. al. 2023. Virulence.
Shih-Ching L, et. al. 2023. Nat Commun.
And other publications listed on: https://www.cellsignal.com/products/primary-antibodies/stat1-d1k9y-rabbit-mab/14994

Name: Mouse monoclonal anti-IRF-3 (Alexa Fluor 555 Conjugate); Supplier: Cell Signaling Technology Cat# 73147, RRID:AB_2799834; Clone; D9J5Q
Validated by Cell Signaling Technology.

Name: Rabbit monoclonal anti-NF-κB p65 (Alexa Fluor 488 conjugate); Supplier: Cell Signaling Technology Cat# 49445, RRID:AB_2799359; Clojne: D14E12
Validated by Cell Signaling Technology and:
Yanhui T, et. al. 2022. Front Pharmacol.
Yanhui T, et. al. 2020. Br J Pharmacol.
And other publications listed on: https://www.cellsignal.com/products/antibody-conjugates/nf-kb-p65-d14e12-xp-rabbit-mab-alexa-fluor-488-conjugate/49445

Name: Mouse monoclonal anti-BRCA2; Supplier: Millipore Cat# OP95, RRID:AB_2067762; Clone: 2B
Validated by Millipore and:
Andres, J.L., et al. 1998. Oncogene 16, 2229.
Chen, J., et al. 1998. Mol. Cell 2, 317.
Chen, P.L., et al. 1998. Proc. Natl. Acad. Sci. USA 95, 5287.
And other publications listed on: https://www.merckmillipore.com/CN/zh/product/Anti-BRCA2-Ab-1-Mouse-mAb-2B,EMD_BIO-OP95

Name: Rat monoclonal anti-Tubulin; Supplier: Novus Biologicals Cat# NB 600-506, RRID:AB_343284; Clone: YL1/2
Validated by Novus Biologicals and:
Huang J, et al. 2020. Nat Commun.
Miyamoto T, et al. 2020. EMBO J.
And other publications listed on: https://novusbio.com/products/alpha-tubulin-antibody-yl1-2_nb600-506#PublicationSection

Name: Rabbit monoclonal anti-Phospho KAP-1 (S824); Supplier: Bethyl Laboratories Cat# A700-013, RRID:AB_2891814; Clone: BL-246-7B5
Validated by Bethyl Laboratories.

Name: Rabbit monoclonal anti-N-Cadherin (Alexa Fluor 647 Conjugate); Supplier: Cell Signaling Technology Cat# 99377, RRID:AB_2800316; Clone: D4R1H
Validated by Cell Signaling Technology.

Name: Rabbit monoclonal anti-Vimentin (Alexa Fluor 555 Conjugate); Supplier: Cell Signaling Technology Cat# 9855, RRID:AB_10859896; Clone: D21H3
Validated by Cell Signaling Technology and:
Jennifer E, et. al. 2019. Methods Mol Biol.
Jia-Ren L, et. al. 2018. Elife.
And other publications listed on: https://www.cellsignal.com/products/antibody-conjugates/vimentin-d21h3-xp-rabbit-mab-alexa-fluor-555-conjugate/9855

Name: Rabbit monoclonal anti-E-Cadherin (Alexa Fluor 488 Conjugate); Supplier: Cell Signaling Technology Cat# 3199, RRID:AB_10691457; Clone: 24E10
Validated by Cell Signaling Technology and:
Kelly V, et. al. 2022. Sci Rep.

Xueman L, et. al. 2020. Invest Ophthalmol Vis Sci.
And other publications listed on: https://www.cellsignal.com/products/antibody-conjugates/e-cadherin-24e10-rabbit-mab-alexa-fluor-488-conjugate/3199

Name: Rat monoclonal anti-SOX2; Supplier: Thermo Fisher Scientific; Cat# 14-9811-82, RRID:AB_2865466; Clone: Btjce
Validated by Thermo Fisher Scientific and:
Amanda A., et. al. 2017. Nat. Methods.
And other publications listed on: https://www.thermofisher.com/antibody/product/SOX2-Antibody-clone-Btjce-Monoclonal/14-9811-82

Name: Rabbit monoclonal anti-Oct-4A; Supplier: Cell Signaling Technology Cat# 2840, RRID:AB_2167691; Clone: C30A3
Validated by Cell Signaling Technology and:
Looijenga, L.H. et al. 2003. Cancer Res.
Pan, G. and Thomson, J.A. 2007. Cell Res.
And other publications listed on: https://www.cellsignal.com/products/primary-antibodies/oct-4a-c30a3-rabbit-mab/2840

Name: Mouse monoclonal anti-Nanog; Supplier: Cell Signaling Technology Cat# 4893, RRID:AB_10548762; Clone: 1E6C4
Validated by Cell Signaling Technology and:
Margarita D., et al. 2024. Front Mol Neurosci.
Chun-Lei S., et al. 2023. J Cancer.
And other publications listed on: https://www.cellsignal.com/products/primary-antibodies/nanog-1e6c4-mouse-mab/4893

Name: Mouse monoclonal anti-NeuN; Supplier: Millipore Sigma; Cat# 4893, RRID:AB_2298772; Clone: A60
Validated by Millipore Sigma and:
Stacey T., et al. 2006. J Neurosci.
And other publications listed on: https://www.sigmaaldrich.com/US/en/product/mm/mab377

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Name: MCF7; Source: ATCC (Cat#HTB-22; RRID:CVCL_0031); Species: Human; Sex: Female Name: OE19; Source: Sigma-Aldrich (Cat#96071721, RRID:CVCL_1622); Species: Human; Sex: Male Name: 293FT; Source: Thermo Fisher Scientific (Cat# R70007, RRID:CVCL_6911); Species: Human; Sex: Female Name: HT1080/Cas9 AAVS1; Source: Genecopoeia (Cat# SL512, RRID:CVCL_C9F8); Species: Human; Sex: Male Name: SW620; Source: ATCC (Cat# CCL-227, RRID:CVCL_0547); Species: Human; Sex: Male Name: A-375, Source: ATCC (Cat# CRL-1619, RRID:CVCL_0132); Species: Human; Sex: Female Name: U-2 OS; Source: ATCC (Cat# HTB-96, RRID:CVCL_0042); Species: Human; Sex: Female Name: A549; Source: ATCC (Cat# CCL-185, RRID:CVCL_0023); Species: Human; Sex: Male Name: IMR-90; Source: ATCC (Cat# CCL-186, RRID:CVCL_0347); Species: Human; Sex: Female Name: KOLF2.1J; Source: The Jackson Laboratory; Bar Harbor; USA (RRID:CVCL_B5P3); Species: Human; Sex: Male Name: RUES2; Source: Rockefeller University; New York; USA (RRID:CVCL_B810); Species: Human; Sex: Female
Authentication	The cell lines were obtained from the sources listed above and authenticated by cell morphology in the lab. ATCC provided short tandem repeat (STR) profiling for authentication.
Mycoplasma contamination	The cell lines were tested for mycoplasma contamination about once a month. All cell lines tested negative for mycoplasma contaminiation.
Commonly misidentified lines (See ICLAC register)	The cell lines are not commonly misidentified.

Palaeontology and Archaeology

Specimen provenance	*Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information). Permits should encompass collection and, where applicable, export.*
Specimen deposition	*Indicate where the specimens have been deposited to permit free access by other researchers.*
Dating methods	*If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.*

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight	*Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.*

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

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	Adult NU/J mice (>6 weeks of age) were obtained from The Jack Laboratory (Bar Harbor, ME).
Wild animals	No wild animals were used in this study.
Reporting on sex	All experiments were performed on female NU/J mice.
Field-collected samples	No field-collected samples were used in this study.
Ethics oversight	Animal care and experimental procedures were performed in accordance with the "Guide for the Care and Use of Laboratory Animals" of the National Institute of Health and were approved by the Columbia University Institutional Animal Care and Use Committe (IACUC). The protocol for this study is AC-AABT8654.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	*Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.*
Study protocol	*Note where the full trial protocol can be accessed OR if not available, explain why.*
Data collection	*Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.*
Outcomes	*Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.*

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☒	☐	Public health
☒	☐	National security
☒	☐	Crops and/or livestock
☒	☐	Ecosystems
☒	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☒	☐	Demonstrate how to render a vaccine ineffective
☒	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐	Increase transmissibility of a pathogen
☒	☐	Alter the host range of a pathogen
☒	☐	Enable evasion of diagnostic/detection modalities
☒	☐	Enable the weaponization of a biological agent or toxin
☒	☐	Any other potentially harmful combination of experiments and agents

Plants

Seed stocks: N/A

Novel plant genotypes: N/A

Authentication: N/A

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: HT1080 cells were lentivirally infected with plasmid vectors carrying GFP or mTurquiose2 sequences were sorted.

Instrument: Sony MA900 Multi-Application Cell Sorter

Software: Cell Sorter Software 3.2.0

Cell population abundance	~2% of GFP positive cells and 1% of mTurquoise2 positive cells were retained.
Gating strategy	We used WT HT1080 cells as the negative control and ensured that under the gating strategy we applied, no cells from the WT control being characterized as GFP or mTurquoise2 positive. The figures were attached in the Supplementary Information at Source Data Files.

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

Magnetic resonance imaging

Experimental design

Design type	*Indicate task or resting state; event-related or block design.*
Design specifications	*Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.*
Behavioral performance measures	*State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).*

Acquisition

Imaging type(s)	*Specify: functional, structural, diffusion, perfusion.*
Field strength	*Specify in Tesla*
Sequence & imaging parameters	*Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.*
Area of acquisition	*State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.*

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software	*Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).*
Normalization	*If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.*
Normalization template	*Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.*
Noise and artifact removal	*Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).*
Volume censoring	*Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.*

Statistical modeling & inference

Model type and settings	*Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).*
Effect(s) tested	*Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.*

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference (See Eklund et al. 2016)	*Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*
Correction	*Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).*

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).

Graph analysis

Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).

Multivariate modeling and predictive analysis

Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.