

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 (<i>n</i>) 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	Bright-field whole-slide images were acquired on an Aperio digital slide scanner (Leica Biosystems), and on a Hamamatsu NanoZoomer 2.0-HT whole-slide scanner using NDP.scan (Version 3.4.2). Automated immunohistochemistry was run on a Leica BOND-RX stainer. Confocal fluorescence images were acquired on a Zeiss spinning-disk confocal microscope using ZEN Lite (Version 3.8.99) (Zeiss). Immunoblot chemiluminescence images were acquired using a ChemiDoc Imaging System (BIO-RAD) and Image Lab Touch Software (BIO-RAD, version 2.3.0.07). Quantitative PCR data were obtained with the Bio-Rad CFX96 Real-Time System and Bio-Rad CFX Manager (BIO-RAD, version 3.1.1517.0823). Flow cytometry data were acquired on a BD LSR II UV (BD Biosciences). Flow cytometry data were acquired on a BD LSR II UV flow cytometer (BD Biosciences) using BD FACSDiva software (BD Biosciences). Cell sorting was performed on a MoFlo XDP cell sorter (Beckman Coulter). GC-MS data were acquired on an Agilent 7890B/5977B system using Agilent MassHunter GC/MS Acquisition (version B.07.05.2479). Luminescence, absorbance and fluorescence plate reader measurements were collected on a SpectraMax M5 plate reader (Agilent) using SoftMax Pro (Molecular Devices, version 7.0).
Data analysis	Statistical analyses were done using GraphPad Prism 9.0 and 10.5.0 (GraphPad). RNA-seq reads were aligned with HISAT2 (version 2.2.1) and differential expression was performed with DESeq2 (version 1.44.0) by Novogene Corporation. Gene set enrichment analysis and over-representation analysis were performed in R v4.4.2 using clusterProfiler v4.14.6, enrichplot v1.26.6 and the org.Mm.eg.db annotation database (version 3.20.0). Colocalization was quantified in Fiji using the Coloc2 plugin (version 2.1.0). Flow cytometry data were analyzed using FlowJo v10. Confocal images were analyzed using Zen Lite software (version 3.8.99) and Fiji ImageJ 1.54g; Java 1.8.0_345. Histological analyses were performed using MetFinder. MetFinder is freely available at metfinder.org for academic and non-commercial research use, and has no publicly reported version number. GC-MS analysis script is available at https://github.com/Sethjparker/IntegrateNetCDF_WithCorrect under MIT license.

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](#)

RNA-seq data have been deposited to the Gene Expression Omnibus (GEO) data repository with accession numbers GSE324743 and GSE324997. Mass spectrometry data have been deposited in the MassIVE repository under accession number MSV000102778. Source data for all main and Extended Data figures, including exact P values, are provided with this paper. The KEGG FoxO signaling pathway gene set (mmu04068) used for GSEA is publicly available at https://www.genome.jp/dbget-bin/www_bget?path:mmu04068. Uncropped immunoblot images are provided in Supplementary Fig. 1. Human tissue specimens were obtained under a materials transfer agreement from the UNMC Rapid Autopsy Program and are subject to institutional restrictions. The org.Mm.eg.db mouse genome annotation database is publicly available at DOI: 10.18129/B9.bioc.org.Mm.eg.db. All other data supporting the findings of this study are available within the paper and its Supplementary Information. Further information and requests for reagents should be directed to the corresponding author, Alec C. Kimmelman (Alec.Kimmelman@nyulangone.org).

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	The specimens were provided to the investigators in a de-identified manner without accompanying information on sex or gender.
Reporting on race, ethnicity, or other socially relevant groupings	The specimens were provided to the investigators in a de-identified manner without accompanying information on race, ethnicity or other socially relevant groupings. Therefore, analyses based on these characteristics were not performed.
Population characteristics	Human PDAC liver metastasis specimens and normal liver specimens were obtained through the Rapid Autopsy Program at the University of Nebraska Medical Center. The specimens were provided to the investigators in a de-identified manner without accompanying clinical or genotypic information. Therefore, covariate-relevant population characteristics were unavailable and were not analysed.
Recruitment	Snap-frozen and FFPE sections of liver tissues from de-identified PDAC patients and healthy individuals were procured from the Rapid Autopsy Program at University of Nebraska Medical Center (in compliance with IRB 091-01).
Ethics oversight	The study was approved by the University of Nebraska Medical Center Institutional Review Board under protocol 091-01, and informed consent for rapid autopsy and research use of the specimens was obtained from all participants.

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](https://www.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	No sample size calculation was done either for in vivo studies. For in vivo studies, sample sizes were determined based on our preliminary experiments. In our experience, n = 5-10 mice per group is sufficient to detect meaningful biological differences with good reproducibility. For in vitro experiments, no statistical methods were used to predetermine sample sizes. Sample sizes were determined based on preliminary experiments to estimate the expected variability and effect size.
Data exclusions	No animals were excluded from the prespecified in vivo analyses, except, where applicable, for animals that died before the planned endpoint. Samples or image regions were excluded from specific histological analyses when extensive necrosis, tissue disruption, or poor section quality precluded reliable quantification.
Replication	To replicate our biologically meaningful findings, experiments were repeated independently at least twice. This is indicated in the associated figure legend for each result. We also utilized orthogonal approaches to validate our findings (e.g., different cell lines, different inhibitors, genetic and pharmacological inhibition, primary and transformed cells, murine and human metastasis specimens).
Randomization	Prior to treatment initiation and selecting animals for downstream pipelines, mice bearing liver metastasis were randomized. Liver weights

Randomization

were not measured at the time of randomization.

For the AAV–CRISPR experiments, age-matched homozygous Rosa26-LSL-Cas9-EGFP female mice were randomly assigned to receive sgScr, sgPhgdh or sgCxcr2 AAV. Tumour cells were implanted from a single common cell suspension per genotype across all groups within an experiment. Tissue sections and image fields selected for quantification were chosen at random with respect to experimental group. For in vitro experiments, allocation of wells to condition was arbitrary and all conditions were seeded from a common cell suspension; randomization is not applicable to cell culture experiments in which the intervention is applied to the entire culture. Covariates were controlled by using age-matched, sex-matched animals of a single genetic background housed under identical conditions.

Blinding

Investigators were not blinded to group allocation during data collection, as knowledge of treatment group was required for correct execution of surgical and drug-dosing procedures and for animal husbandry. To mitigate the resulting risk of bias, primary endpoints were chosen to be objective or were quantified using predefined procedures: liver and tumour weights were measured only at the experimental endpoint after euthanasia; metastatic tumour burden was quantified by MetFinder, an automated deep learning classifier applied identically to all whole-slide images; and PGP9.5-positive areas were quantified in Fiji using identical predefined image-processing parameters across all images. PHGDH IHC intensity was quantified using a fixed-threshold Positive Pixel Count algorithm following manual region annotation. For human specimen analysis, PHGDH staining was scored without knowledge of the corresponding CXCL5 ELISA results.

For survival studies, mice were monitored daily and euthanised on reaching humane endpoints that were defined before the start of the experiment and applied identically across groups; endpoint determination was performed by investigators aware of group allocation, which we note as a limitation.

In vitro studies were not blinded because experimental and surrogate counting wells needed to be assigned and treated similarly during treatment.

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	Primary antibodies (IHC/IF): anti-PHGDH (rabbit polyclonal, Sigma-Aldrich Prestige, HPA021241; 1:100); anti-albumin (Abcam, ab106582; 1:200); anti-cytokeratin 19/CK19 (rat monoclonal, clone TROMA-III, Developmental Studies Hybridoma Bank; 1:100); anti-Ki-67 (rabbit polyclonal, Abcam, ab15580; 1:400); anti-FOXO3A (rabbit monoclonal, clone 75D8, Cell Signaling Technology, 2497; 1:200); anti-PGP9.5/UCHL1 (rabbit monoclonal, clone EPR4118, Abcam, ab108986; 1:350). Primary antibodies (immunoblot): anti-PHGDH (Sigma-Aldrich, HPA021241; 1:1,000); anti-AKT (rabbit monoclonal, clone C67E7, Cell Signaling Technology, 4691; 1:1,000); anti-phospho-AKT (Ser473) (rabbit polyclonal, Cell Signaling Technology, 9271; 1:1,000); anti-mouse CXCL5/LIX (R&D Systems, MAB433-100; 1:300); anti-CXCR2 (rabbit polyclonal, Invitrogen, PA1-31217; 1:1,000); anti-FOXO3A (clone 75D8, Cell Signaling Technology, 2497S; 1:1,000); anti-phospho-FOXO3A (Ser315) (Proteintech, 28755-1-AP; 1:500); anti-phospho-FOXO3A (Ser253) (Invitrogen, PA5-36816; 1:500); anti-β-actin (mouse monoclonal, clone AC-15, Sigma-Aldrich, A5441; 1:1,000). ChIP: anti-FOXO3 (clone 75D8, Cell Signaling Technology, 2497; 1:200), with normal rabbit IgG supplied in the SimpleChIP Enzymatic Chromatin IP Kit (Cell Signaling Technology, 9003) as isotype control.
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Secondary antibodies: HRP-conjugated anti-mouse IgG (Cell Signaling Technology, 7076S; 1:5,000) and HRP-conjugated anti-rabbit IgG (Cell Signaling Technology, 7074S; 1:5,000) for immunoblot. Chromogenic IHC detection used the VECTASTAIN Elite ABC-HRP kit (Vector Laboratories, PK-6100) with DAB (Vector Laboratories, SK-4100). Automated PGP9.5 IHC used the anti-rabbit HRP-conjugated polymer and DAB supplied in the Leica BOND Polymer Refine Detection System (Leica, DS9800). Fluorescent secondary antibodies include Goat anti-rabbit IgG, Alexa Fluor™ 647 (1:300, Invitrogen, catalog no. A-21245), Goat anti-rabbit IgG, Alexa Fluor™ 594 (1:300, Invitrogen, catalog no. A-11037), Goat anti-rat IgG, Alexa Fluor™ 488 (1:300, Invitrogen, catalog no. A-11006), anti-mouse IgG, Alexa Fluor™ 568 (1:300, Thermo Fisher Scientific, catalog no. A11004).

Blocking reagents: 2.5% normal horse serum (Vector Laboratories, MP-7800-15) for IHC and 10% normal goat serum (Vector Laboratories, S-1000-20) for IF.

Validation

All antibodies were used at the application and species for which they are validated by the manufacturer; manufacturer validation data and citation records are available on the respective product pages.

PHGDH (HPA021241): validated in-house by loss of hepatocyte signal in AAV-CRISPR sgPhgdh livers (immunoblot on sorted EGFP+ hepatocytes, Extended Data Fig. 2). The antibody is an Enhanced Validation Prestige Antibody with orthogonal RNA-seq and independent-antibody validation in the Human Protein Atlas. FOXO3A (CST 2497, 75D8): validated in-house by loss of signal in Foxo3a-knockout AML12 cells generated with two independent sgRNAs (immunoblot, Extended Data Fig. 6a) and by gain of signal upon reconstitution with Flag-FOXO3A. Manufacturer-validated for WB, IHC-P, IF and ChIP in human, mouse and rat. CXCR2 (Invitrogen PA1-31217): validated in-house by loss of signal in Cxcr2-knockout AML12 cells and in AAV-CRISPR sgCxcr2 hepatocytes (immunoblot, Extended Data Fig. 6i). CXCL5/LIX (R&D MAB433-100): validated in-house by loss of signal in Cxcl5-knockout HY19636 cells generated with two independent sgRNAs, and by neutralisation of rCXCL5 activity in functional assays. The same clone is the capture/detection reagent in the validated R&D mouse CXCL5 DuoSet ELISA. Phospho-FOXO3A (Ser253, Invitrogen PA5-36816) and phospho-FOXO3A (Ser315, Proteintech 28755-1-AP): phospho-specificity was supported by loss of signal upon PI3K inhibition with BKM120 consistent with manufacturer validation. AKT (CST 4691) and phospho-AKT Ser473 (CST 9271): widely used, manufacturer-validated for mouse and human by WB; phospho-specificity demonstrated in-house by loss of signal upon BKM120 treatment. PGP9.5/Uchl1 (Abcam ab108986): manufacturer-validated for IHC-P in mouse and human tissue; staining pattern in this study was restricted to fibres with neuronal morphology, and a no-primary control section was included in every run. CK19 (TROMA-III), albumin (ab106582) and Ki-67 (ab15580): used as lineage and proliferation markers; specificity was confirmed by the expected restriction of staining to PDAC cells, hepatocytes and cycling cells respectively. β -actin (A5441, AC-15): loading control, manufacturer-validated across species; single band at expected molecular weight. Secondary-antibody-only controls were performed for all immunofluorescence experiments.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)

The cell lines MiaPaCa2, PaTu-8902 (human) and AML 12 (murine) were obtained from the American Type Culture Collection (ATCC) or the DSMZ. Primary mouse PDAC cell line HY19636 was established from pancreatic tumors derived from female KPC GEMM (LSL-KrasG12D/+; Trp53flox/+; p48-Cre) tumors that were fully backcrossed into a C57BL/6 background. HEK293FT cells used for viral packaging were obtained from Thermo Fisher Scientific.

Authentication

Cell lines were periodically authenticated by short tandem repeat (STR) profiling, and low-passage cultures were maintained in a centralized laboratory cell bank.

Mycoplasma contamination

Cells were tested routinely for mycoplasma contamination by PCR. All cell lines used in this study tested negative for mycoplasma.

Commonly misidentified lines (See [ICLAC](#) register)

No commonly misidentified cell lines were used.

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	All animal studies were approved by the NYU Grossman School of Medicine IACUC under protocols IA16-00507 and IA16-01331. Female C57BL/6J mice used in this study were 8-10 weeks old and not involved in previous procedures. Rosa26-LSL-Cas9-EGFP mice on a C57BL/6J background were used at 6–8 weeks of age; female mice were used except in Extended Data Fig. 2e, in which male mice were used. All mice were maintained in the animal facility of the New York University Grossman School of Medicine. All mice were housed at 22 ± 1 °C, 30-70% relative humidity, in a temperature controlled facility with 12 hour day-night light cycles. Mice were cared for by the husbandry staff at NYULH DCM (division of comparative medicine), and diet and water were provided ad libitum unless otherwise specified in text.
Wild animals	No wild animals were used in the study.
Reporting on sex	Female 8–10-week-old C57BL/6J mice were used for syngeneic transplantation experiments, and female 8–10-week-old NCr nude mice were used for xenograft experiments with human PDAC cell lines. Rosa26-LSL-Cas9-EGFP mice on a C57BL/6J background were used at 6–8 weeks of age; female mice were used except in Extended Data Fig. 2e, in which male mice were used.
Field-collected samples	No field collected samples were used in the study.
Ethics oversight	All experiments involving laboratory animals were approved by the New York University Institutional Animal Care and Use Committee (IACUC) under protocol numbers IA16-00507 and IA16-01331. This is indicated in the methods section.

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

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

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.

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	For EdU incorporation analysis in PDAC cells, cells grown in direct co-culture with murine hepatocytes were harvested by trypsinization and fixed using the fixative provided with the kit.
Instrument	Cells were analyzed on a BD LSR II UV flow cytometer (BD Biosciences).
Software	BD FACSDiva software (BD Biosciences) was used for data acquisition. Data were analyzed using FlowJo v10.
Cell population abundance	The purity of cells was confirmed by flow cytometric analyses and was usually >90%.
Gating strategy	The gating strategy used for Fig. 2d is shown in Supplementary Fig. 2.
☐ 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

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

(See [Eklund et al. 2016](#))

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.