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
- Cytobank software (Beckman Coulter, Indianapolis, IN)
- Nikon Elements Software (Version 5.21.05)
- GraphPad Prism (Version 9.2.0)
- Seven Bridges Genomics platform [https://igor.sbgenomics.com]
- Seurat

Data analysis
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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.
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/mx-reporting-summary-flat.pdf.

Life sciences study design

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

- Sample size: Each experiment was performed with at least 4 technical replicates.
- Data exclusions: NA
- Replication: Each experiment was performed with at least 3 technical replicates. Reproducibility was achieved as documented by statistical analyses. Sample size was based on assessment of power analysis using SigmaStat software. Data collected from each study from at least 4 in vitro technical replicates unless otherwise stated was analyzed by obtaining the mean + standard error of the mean (SEM) and significance of the results were then tested using commercially available software (GraphPad Prism, GraphPad software, San Diego, CA).
- Randomization: NA
- Blinding: Investigators were blinded in the analyses.

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: Describe all antibodies used in the study, as applicable, provide supplier name, catalog number, clone name, and lot number.

Validation

Use of well-validated reagents from manufacturer-recommended vendors and, once the assays are optimized, consistent use of reagents from the same vendor and quality will be key to maintaining consistency of results. For qRT-PCR assay, previously published validated primer sets will be used. All antibodies will be purchased from commercial vendors, which have been subjected to the quality controls of manufacturers. In addition, key antibodies will be verified using samples known to have the specific antigens, and also samples which are absent of those specific antigens by flow cytometry. Validated flow cytometry reagents will be purchased and revalidated for project specific assays. Cell culture grade and validated cell purification reagents will be purchased from Sigma-Aldrich.
Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)  
Patient derived pituitary adenomas  
Patient derived induced pluripotent stem cells.

Authentication  
Each line will be sent for Karyotyping to ensure no karyotypic abnormalities are observed and contributing to the phenotype observed in vitro. Organoid culture procedures will strictly follow the established laboratory protocols within the Churko laboratory. The organoid differentiation and morphology will be monitored by microscopic observation, as well as the expression of marker genes by the Zavros laboratory using established protocols presented in the proposal. Organoids will be validated and authenticated by the Genomic Research Services University of Arizona Genetics Core.

Mycoplasma contamination  
All human iPSC lines were tested to be negative for mycoplasma contamination using the MycoAlert Mycoplasma testing kits (LT07-318, Lonza) and no karyotype abnormalities were found (KaryoStat+, Thermo).

Commonly misidentified lines  
(See ICLAC register)  
NA

Human research participants

Policy information about studies involving human research participants

Population characteristics  
Patients with planned transsphenoidal surgery for pituitary adenomas were identified in the outpatient neurosurgery clinics.

Recruitment  
Patients with planned transsphenoidal surgery for pituitary adenomas were identified in the outpatient neurosurgery clinics.

Ethics oversight  
Tissues were collected under the St. Joseph’s Hospital and Barrow Neurological Institute Biobank collection protocol PHXA-05T53038 and collection of outcomes data pro-tocol PHXA-0004-72-29 with the approval of the Institutional Review Board (IRB) and patient consent. Samples were de-identified and shipped to the Zavros laboratory (University of Arizona) for processing.

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.

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GFO.

☐ 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  
(eg. 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
### 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**
  
  Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.

- **Instrument**
  
  Data was acquired using the Cytek™ Aurora

- **Software**
  
  Cytobank software (Beckman Coulter, Indianapolis, IN).

- **Cell population abundance**
  
  NA cells were not sorted.

- **Gating strategy**
  
  Gating strategy is shown in Supplemental Figure 1

- 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)**
  

- **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

<table>
<thead>
<tr>
<th>n/a</th>
<th>Involved in the study</th>
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<tbody>
<tr>
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<td>Multivariate modeling or predictive analysis</td>
</tr>
</tbody>
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#### 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.