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Corresponding author(s): Sai Chavala

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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.

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	Stepone V2.3,Applied Biosystems; LASX,Leica; ZEN2.3SP1,Zeiss; ZEN2.3, Zeiss; Enduro GDS,Labnet International.
Data analysis	ImageJ (NIH), ZEN lite, Leica Application, Suite X, GraphPad Prism v5.0, Origin2019

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. 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

Supporting RNASeq and ATACSeq data are deposited in the in the Gene Expression Omnibus under accession code GSE138520 (RNASeq) and GSE138521 (ATACSeq) respectively. Source data for Fig. 1-4 and Extended Data Fig. 1-3,5-8 are available within the manuscript files.

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

Life sciences study design

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

Sample size	Sample size were chosen based upon previously described studies. No statistical methods were used to predetermine sample sizes.
Data exclusions	No data were excluded.
Replication	Each experiment had at least three replicates, and was performed two or more times.
Randomization	Animals were randomly assigned to groups.
Blinding	Investigators were masked to group identity for light aversion experiments.

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	Axin2/conductin, Goat, Santa Cruz, 1:100 (IF), 1:200 (WB) SC-8570; Nrl, Mouse monoclonal, Santa Cruz, 1:100(IF), SC-398046; Crx, Mouse monoclonal, Santa Cruz, 1:200 (IF), SC-377138; Beta actin, Mouse, Thermo Scientific, 1:2000 (WB), MA5-15739; GFP, Chicken, Abcam, 1:400 (IF), Ab13970; Axin1, Goat, RD systems, 1:400 (WB), AF3287; Rhodopsin, Mouse, Millipore, 1:100 (IF), MAB5316; Recoverin, Rabbit, Abcam, 1:100 (IF), Ab64945; ChX10, Sheep, Millipore, 1:100 (IF), AB9016; BrdU, Mouse, Thermo scientific, 1:500 (IF), MA3071; NF-kB Mouse Cell Signaling 6µg (ChiP) 6956P; Pkc, Mouse, Santa Cruz, 1:100(IF), SC-8393; Synaptophysin, Rabbit, Abcam, 1:500 (IF), Ab14692; CtBP2 (ribeye), Rabbit, BD, 1:500(IF), 612044.
Validation	All of the antibodies used in this study were used according to supplied instructions by the manufacturer or referenced publication.

Animals and other organisms

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

Laboratory animals	For pupil reflex and light aversion experiments, CiPCs were injected in to P31 or P24 rd1 mice (Jackson Laboratory, 000656). Males and females were used approximately in an equal ratio. FSP1-Cre (Jackson Laboratory, 012641) and R26-LSL-tdTomato (Jackson Laboratory, Ai9) crossed embryos were used for a standard procedure for MEF preparation (Li et al., 2015). All studies and animal care were performed in accordance with relevant guidelines and regulations as approved by the animal care and use committee at University of North Texas Health Science Center and EyeCRO.
Wild animals	This study did not involve wild animals.
Field-collected samples	This study did not involve samples collected from the field.
Ethics oversight	All animal studies and animal care were performed in accordance with relevant guidelines and regulations and approved by the animal care and use committee at University of North Texas Health Science Center.

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

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	Chemically reprogrammed cell population was PBS-washed, trypsinized (0.25%) and passed through a 40µM nylon cell strainer (Fisher Scientific, 08-777-1) and suspended in PBS containing 3% bovine serum.
Instrument	Beckton-Dickinson LSRII Flow cytometer, Sony SH800 cell sorter
Software	BD FACSDIVA, Sony SH800, Flowjo
Cell population abundance	Approx 0.2% CiPCs were obtained from mouse embryonic fibroblasts and 0.9% were obtained from human fetal lung fibroblasts.
Gating strategy	Cells were first identified by FSC/SSC so that all cells are visible on the plot. FSC-H and FSC-A were used to identify single cells. Positive cell population was sorted out based upon green/red fluorescence expression.

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