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☐ Initial submission ☐ Revised version ☒ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

No statistical methods were used to pre-determine sample sizes but our sample sizes are similar to those reported in previous publications (Lee et al., 2014; Lu et al., 2014)

2. Data exclusions

Describe any data exclusions.

no data were excluded.

3. Replication

Describe whether the experimental findings were reliably reproduced.

All attempts for the replication were successful.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

The animals and cell samples themselves were genetically targeted. Within each group, the mouse and cell is randomly selected.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

No blinding experiments because the experiments were simple and observative.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒	A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	A statement indicating how many times each experiment was replicated
☐	☒	The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☒	☐	A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒	The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒	A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒	Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	in vitro data were analyzed in Clampfit 10.8 and OriginPro 8.5; in vivo data were analyzed with custom algorithms in Matlab. Some comparison were performed online website: http://www.socscistatistics.com/tests/Default.aspx

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	no unique materials were used.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	rabbit polyclonal RFP (1:1000, Rockland) or chicken polyclonal anti-GFP (1:1000, Aves) for fluorophore preservation of mcherry starter cells and GFP rabies virus expression, mouse monoclonal anti-parvalbumin (1:1000 Sigma), rabbit polyclonal phospho-IkappaB (1:300, Cell Signaling), rabbit polyclonal VIP (1:250, Immunostar), rabbit polyclonal somatostatin-14 (1:500, Peninsula), mouse monoclonal GAD-67 (1:500, EMD Millipore), mouse monoclonal VGAT (1:500, synaptic systems), goat polyclonal ChAT (1:500, EMD Millipore), and rabbit polyclonal NeuN (1:1000, Abcam).

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	none of cell line were used
b. Describe the method of cell line authentication used.	none of cell line were used
c. Report whether the cell lines were tested for mycoplasma contamination.	none of cell line were used
d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	none of cell line were used

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	In order to genetically label and manipulate chandelier cells, we crossed Nkx2.1-CreER mice (The Jackson Laboratory stock 014552) with either Rosa26-lox-stop-lox-TdTomato (Ai14) reporter (The Jackson Laboratory stock 007905) or in house derived Rosa26- lox-stop-lox-Flp (LSL-Flp) mice26. To properly identify embryonic day 17.5 (E17.5) for tamoxifen (TM) inductions, Swiss Webster females (Taconic) were housed with Nkx2.1CreER;Ai14 (het/homo) males overnight and females were checked for vaginal plug by 8-9 am the following morning. Positive plug identification was timed at E0.5. To genetically label pavalbumin positive basket cells (PVBCs), we crossed PV-Cre mice (The Jackson Laboratory stock 008069) with Ai14 reporter. The ages of animals used were ranged from postnatal 28 to 3 months, indicated in the different experiments stated in Methods. Both male and female mice were employed without distinction in all the experiments.

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	this study did not involve human research participants