

## 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

- |                                     |                                     |  |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A description of all covariates tested   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted<br><i>Give <math>P</math> values as exact values whenever suitable.</i>                            |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | 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 collection was performed using Matlab 2016a and the commercial software Hamamatsu HC Image. All source code and custom scripts used for collection will be made available at time of publication and are available to reviewers and editors during review.

Data analysis

All analysis was performed using Matlab 2016b. All source code and custom scripts for analysis will be made available at time of publication and are available to reviewers and editors during review.

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

All raw data and custom functions to produce each figure will be made available at time of publication and are available to reviewers and editors during review.

## 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	Sample sizes were estimated based on neuron yields from pilot studies and published anatomical descriptions of PV and CHI population densities. A compromised power analysis was performed using G*Power 3.1.9.2 ( <a href="http://www.gpower.hhu.de">http://www.gpower.hhu.de</a> ). We applied a two tailed Wilcoxon-Mann-Whitney test utilizing an $\beta/\alpha$ ratio=1.0, an effect size of 0.5. Additional assumptions included the expectations of 300neurons/recording and PV and CHI density of 2.5% of all cells. Applying these assumptions resulted in $\alpha$ and $\beta$ probabilities of <0.1 with 6+ subjects of each genotype background.
Data exclusions	No animals were excluded from this manuscript. A subset of traces (1.9%) were not analyzed because they contained both slow and fast calcium dynamics making automated selection of calcium events impractical. We found no evidence that these traces were more pronounced in any of the cell classes we identified (PV, MSN, or CHI). Please see Supplemental Methods Page 6, paragraph 5, for details.
Replication	No direct replication was performed although each animal was subject to calcium imaging 1-3 times and data was collapsed together for analysis.
Randomization	There were no treatment conditions to compare in this study. All recording sessions days were randomly performed with PV-cre and ChAT-cre genotyped animals intermixed across days.
Blinding	Partially: On recording days, animal backgrounds were known. Trace extraction and calcium signals were analyzed with the investigators unaware of which neurons belonged to each cell class or the genotype of the animal being analyzed.  For histology - sections were selected and images were taken from slides by a researcher not aware of genotype or antibody used. Cells were also counted and quantified from these sections by a researcher blinded to the genotype of the animal or antibody used.

## 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
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

### Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

## Antibodies

Antibodies used	Primary Antibodies against PV (rabbit anti-PV, SWANT PV25 1:1000, Primary anti-ChAT antibody, Millipore AB144P 1:500, Alexa Fluor 633 donkey anti-goat secondary antibody for ChAT staining (Life Technologies, A21082 1:200), Alexa Fluor 633 goat anti-rabbit secondary antibody for PV staining (Invitrogen A21070, 1:1000)
Validation	PV: <a href="https://www.swant.com/pdfs/PV27_Rabbit_anti_Parvalbumin.pdf">https://www.swant.com/pdfs/PV27_Rabbit_anti_Parvalbumin.pdf</a> : Absence of AB staining in PV knock out mice. Validated in mice and rat. Also see 1. Kretsinger R.H. (1981) Neurosci. Res. Progr. Bull. 19/8, MIT-Press 2. Celio M.R., Heizmann C.W. (1981) Nature 293: 300-302

3. Celio M.R., Heizmann C.W. (1982) Nature 297:504-506
4. Schwaller B., et al. (1999) Am. J. Physiol. 276. C395-403
5. \*Filice F, Celio M.R., Szabolcsi V. (2017) JCN, in press

ChAT: see website for validation studies: [http://www.emdmillipore.com/US/en/product/Anti-Choline-Acetyltransferase-Antibody,MM\\_NF-AB144P](http://www.emdmillipore.com/US/en/product/Anti-Choline-Acetyltransferase-Antibody,MM_NF-AB144P): Validated in mice and rats.

Secondaries: Validation:

<https://www.thermofisher.com/antibody/product/Donkey-anti-Goat-IgG-H-L-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A-21082>

<https://www.thermofisher.com/antibody/product/Goat-anti-Rabbit-IgG-H-L-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A-21070>

## Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals

Combined experiments included data from both ChAT-Cre mice (n=14; GM24Gsat) and PV-cre mice (n=14; B6;129P2-Pvalbtm1(cre)Arbr/J), 8–12 week old at the start of the experiments, both male and female, were used in this study (Chat-Cre: Mutant Mouse Resource Center, Davis, CA; and PV-cre: Jackson Laboratory, Maine)

Wild animals

N/A

Field-collected samples

N/A

Ethics oversight

All animal procedures were approved by the Boston University Institutional Animal Care and Use Committee

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