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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 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<br>*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<br>*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 | We listed all softwares used in the experiments and for analysis in the Methods section. We used a custom TDT program, OpenEx (Tucker-Davis Technologies) to collect the fiberphotometry signal and send a trigger signal to the pulse generator for optogenetics, and StreamPix5 (Norpix) for multiple camera recording. We used the customade Matlab code to track movement of mice. Epifluorescent images were captured with a virtual slide scanner (Olympus, VS120). Confocal images were captured with Zen program from LSM 510 or700 (Zeiss). Differential interference contrast imaging to obtain the whole-cell recording (Slicesscope Pro 6000, Scentifica). Electrophysiological signals were recorded using an Axopatch 700B amplifier (Molecular Devices). The tissue samples for RNA-Seq were laser-dissected using a LMD6000 fluorescence microscope system (Leica microsystems). The cDNA libraries in RNA-Seq were sequenced with Illumina HiSeq 4000 using high output mode. |
| Data analysis | We listed all softwares used in the experiments and for analysis in the Methods section. We used customized code written in MATLAB 2013 to annotate behavior an to track the location of animals (https://github.com/pdollar/toolbox) and further analyze the time-locked photometry signal by a customized code. Attack events in a randomly selected set of videos were annotated using Deeplabcut and Simba (Mathis. et al., 2018 Nat. Neurosci., Nilson et al., 2020 bioRxiv). Epifluorescent and confocal microscopic imaging data were analyzed by ZEN2009 Light Edition and ImageJ1.52P with custom settings. Whole-cell patch clamp data were analyzed with Igor Pro (Wavemetrics). Sequencing reads were aligned to the mouse genomes (build mm10/GRCm38) using the splice-aware STAR aligner and then the counts for each gene were generated using featureCounts. Differential gene expression analysis were performed using the limma R package with normalized gene reads through an open-source software iDEP (http://ge-lab.org/idep/). All statistical analysis were performed using GraphPad Prism 7 or MATLAB2018a. The custom codes will be available from corresponding authors upon reasonable request. |

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.

## 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

The data that support the findings of this study are available from the corresponding author upon reasonable request. All codes described in this study are available from the corresponding authors upon request. The accession code for RNA-Seq data is GSE151798.

# 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

# Life sciences study design

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

| | |
|---|---|
| Sample size | No statistical methods were used to pre-determine sample sizes but our sample sizes in the data are similar with previous works in this field (Hashikawa et al., 2017 Nat Neurosci., Fang et al., 2018 Neuron). |
| Data exclusions | For single retrograde tracing experiments, 3/4 and 3/6 animals that showed correct unilateral targeting in MPN and VMHvl, respectively, were included in the final analysis. For dual retrograde CTB tracing experiments, 3/5 animals with correct targeting in both MPN and VMHvl were included. For microdissection of distinct subregions in the PA, 3/5 animals with correct targeting in both MPN and VMHvl were included in the final analysis. For microdissection of distinct subregions in the PA with retrograde tracing, 2/2 and 2/4 animals that showed correct unilateral targeting in MPN and VMHvl, respectively, were included in the final analysis. For dual-retrograde tracing, 3/7 animals that showed correct unilateral targeting in both MPN and VMHvl were included in the final analysis. For investigating the outputs of PAEsr1+MPN and PAEsr1 +VMHvl projectors, 3/5 animals that showed correct unilateral targeting in the MPN and correct virus expression in the PA and 3/5 animals that showed correct unilateral targeting in the VMHvl and correct unilateral virus expression in the PA were included in the final analysis. For investigating the inputs of PAEsr1+MPN and PAEsr1+VMHvl cells, 3/5 animals that showed correct unilateral targeting in the MPN and correct virus expression in the PA and 3/6 animals that showed correct unilateral targeting in the VMHvl and correct virus expression in the PA were included in the final analysis. For the slice recording experiment, 10/12 animals that showed correct unilateral targeting in MPN, VMHvl and PA were included in the final analysis. For fiber photometric recording of the PAEsr1+MPN (PAEsr1+VMHvl) population, 5/8 animals that showed correct unilateral targeting in the VMHvl and correct GCaMP6f expression and fiber placement in the PA were included in the final analysis. For pharmacogenetic inhibition of PAEsr1+ cells, 5/9 test animals that showed correct bilateral targeting of PA were included in the final analysis. For pharmacogenetic inhibition of PAEsr1+MPN or PAEsr1+VMHvl, 8/10 test animals that showed correct bilateral targeting in the MPN and correct bilateral virus expression in the PA were included in the final analysis. 8/10 test animals that showed correct bilateral targeting in the VMHvl and correct bilateral virus expression in the PA were included. For pharmacogenetic activation of PAEsr1+MPN or PAEsr1+VMHvl cells, 8/14 test animals that showed correct bilateral targeting in the VMHvl and correct bilateral virus expression and fiber placement in the PA were included in the final analysis. For optogenetic stimulation of PAEsr1+MPN or PAEsr1+VMHvl cells, 5/10 test animals that showed correct bilateral targeting in the MPN, correct bilateral expression of ChR2-EYFP in the PA and correct bilateral fiber placements in the PA were included in the final analysis. 5/16 test animals that showed correct bilateral targeting in the VMHvl, correct bilateral expression of ChR2-EYFP in the PA (> 100 positive cells in all sections) and bilateral fiber placements in the PA were included in the final analysis. |
| Replication | Experimental findings were reliably reproduced among all subjects in all experiments comprised of multiple cohorts. GCaMP6 recordings were conducted at least with 3 cohorts of animals. Pharmacogenetic experiments were conducted with 3 cohorts of animals. Optogenetic experiments were conducted with 2 cohorts of animals. |
| Randomization | For GCaMP6 recording and pharmacogenetic inactivation, animals were screened for both aggressive behaviors and sexual behaviors before the surgery and randomly assigned to experimental and control groups. For optogenetic and pharmacogenetic activation, experimental and control animals were randomly selected from naïve (no prior sexual experience or tested for aggression) animals. Intruder animals and objects were subsequently introduced into a subject's cage, after we confirmed the order of presentation didn't affect neural responses. |
| Blinding | The experiments were not done blindly in the study, since the experimental conditions (control vs experimental groups) were obvious to experimenters and the analyses were carried out objectively by using a recording system and not subjective to human bias.<br>During annotation and cell counting, the experimenter was blind to the GCaMP6 signal or behavioral responses. |

# 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

We listed all antibodies used with their catalog number in Methods section of "Immunohistochemistry". Primary antibodies : Rabbit anti-Esr1 (sc-542, Lot #F1715, Santa Cruz), Goat anti-cFos (sc-52-G, Santa Cruz), rabbit anti-GFP (A11122, Thermo Fisher) and Sheep anti-DIG (Sigma-Aldrich, 11207733910). Secondary antibodies: Donkey anti-rabbit Alexa 488/594 (R37118/R37119, Life Technologies) or Donkey anti-goat Alexa 488 (A11055, Life Technologies).

Validation

http://www.scbt.com/datasheet-52-c-fos-4-antibody.html
http://www.scbt.com/datasheet-542-eralpha-mc-20-antibody.html
https://www.thermofisher.com/order/genome-database/dataSheetPdf?producttype=antibody&productsubtype=antibody_primary&productId=A-11122&version=65

# Animals and other organisms

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

Laboratory animals

We described the subjects in Methods section (Mice). Mice were housed under a 12 h light-dark cycle (10 p.m. to 10 a.m. light), with food and water available ad libitum. Animals used for CTB retrograde tracing and RNA-Seq experiments were 14-16 week old wild-type C57BL/6N male purchased from Charles River. Male Esr1-2A-Cre (14-38 weeks, Jackson Stock No. 017911), male Vgat-ires-Cre × Ai6 (12-16 weeks, Jackson stock No. 016962 and 007906), male Vglut1-ires-Cre × Ai6 (12-16 weeks, Jackson stock No. 023527 and 007906) were used for functional, recording and histological experiments. Stimulus animals were adult C57BL/6N female and male or BALB/c male mice (> 8 weeks) purchased from Charles River. Stimulus animals were group housed. After surgery, all test animals were singly housed. All the experiments were performed during the dark cycle of the animals.

Wild animals

The study did not involve wild animals.

Field-collected samples

The study did not involve samples collected from the field.

Ethics oversight

All animal experiments were performed according to protocols approved by NYU IACUC protocols for the care and use of laboratory animals. We complied with all pertinent ethical regulations.

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