nature portfolio

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Reporting Summary

Nature Portfolio 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 Portfolio 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	Labview 2010 was used to collect data for fiber photometry and lick signals. ScanImage 4.0 was used to collect data for 2-photon microscopy imaging
Data analysis	MATLAB R2020a and 2015b were used to analyze photometry, 2-photon microscopy imaging and licking data. Suite2p was used for 2-photon imaging data analysis. Any codes used in this study are available from public repository (https://github.com/VTA-SNc/Amo2022). The model code is attached as a Supplementary Data.

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 Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The fluorometry data and 2-photon imaging data are shared at a public deposit source (doi:10.5061/dryad.hhmgqnkjw).

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 formal power analysis was carried out but our samples sizes are similar to those reported in previous publications (Menegas et al., 2017; Kim et al., 2020; Tsutsui-Kimura et al., 2020). We mostly analyzed the data by animal (n = number of animals). Some data are analyzed by sessions with different conditions. We analyzed data by neuron for cellular analysis of 2-photon imaging data (n = number of neurons).
Data exclusions	No animals were excluded from the study: all analysis includes data from all animals except for one session in the Extended Data Figure7f where we could not detect enough number of trough for analysis. Similarly, the neurons that do not have enough number of peaks for the analysis were excluded from analysis in 2-photon imaging (Figure 5 and Extended Data Figure 10).
Replication	Animals were not formally divided into separate groups for "proof of principle" and "replication". Instead, we pooled all data, and displayed data from each animal (along with the average and standard error or boxplot) as much as possible. Of note, major experimental data are took from more than 2 separate batch of experiments as indicated in the Methods (subsection: Behavior) and the observed tendency was conserved among the batches. Moreover, the phenomenon we are reporting was observed across different experiment types in this study.
Randomization	The study did not include the experiment requiring randomization as we did not compare the difference between groups.
Blinding	The study did not include the experiment requiring blinding as we did not compare the difference between groups.

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	anti-TH, rabbit polyclonal, AB152, Millipore Sigma; anti-DsRed, rabbit polyclonal, 632496, Takara; anti-GFP, chicken polyclonal, GFP-1010, AvesLabs
Validation	The specificity of this antibody has been verified by the company anti-TH: https://www.emdmillipore.com/US/en/product/Anti-Tyrosine-Hydroxylase-Antibody,MM_NF-AB152#overview anti-DsRed: https://www.takarabio.com/products/antibodies-and-elisa/fluorescent-protein-antibodies/red-fluorescent-protein-antibodies anti-GFP: https://www.aveslabs.com/products/green-fluorescent-protein-gfp-antibody

Animals and other organisms

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

Laboratory animals	20 both female and male mice, 2-14 months old were used in this study. We used heterozygote for DAT-Cre (Slc6a3tm1.1(cre)Bkmn; The Jackson Laboratory, 006660), DAT-tTA (Tg(Slc6a3-tTA)2Kftnk; this study), VGluT3-Cre (Slc17a8tm1.1(cre)Hze; The Jackson Laboratory, 028534), LSL-tdTomato (Gt(ROSA)26Sortm14(CAG-tdTomato)Hze; The Jackson Laboratory, 007914), and Ai148D (B6.Cg-Igs7tm148.1(tetO-GCaMP6f,CAG-tTA2)Hze/J; The Jackson Laboratory, 030328)51 transgenic lines. All mice were backcrossed with

	C57BL/6J (Jackson Laboratory) for several generations. Mice are housed on a 12 hr dark (7:00-19:00)/ 12 hr light (19:00-7:00) cycle. Experiments were performed in the dark period. Ambient temperature is kept at 75±5 F° and humidity is kept below 50%.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	The Harvard Animal Care and Use Committee

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