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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.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Labview 2010 was used to collect data both from head fixed mice (primarily fiber photometry signals from GCaMP-expressing mice) and to collect choice data during various choice tasks. FlyCapture2 was used to capture video of mice during choice tasks and novel object exploration.
Data analysis	MATLAB R2017B was used to analyze all data (photometry, choice data, and video data). Any codes used are available upon 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/reviewers upon request. 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 data and any code used for analysis are available upon request

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-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. In all cases, we aimed for a sample size typical of similar studies in the field. In the 6OHDA lesion experiment, we aimed for a sample size large enough to demonstrate behavioral differences between groups. We analyzed the data by animal (n = number of animals) rather than by session or trial to be conservative.
Data exclusions	No animals were excluded from the study: all analysis includes data from all animals. However, after applying D1 receptor antagonist, we limited our analysis to the first 60 trials performed by the mice in each session to prevent off-target effects of the drug, due to potential spread from injection site.
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) as much as possible.
Randomization	For the GCaMP recording experiments, GFP control animals and GCaMP experimental animals were selected at random by the experimenter. For the 6OHDA lesion experiments, another lab member randomly selected mice to be in either Saline or 6OHDA groups. For the D1 antagonist experiments, saline and 6OHDA sessions were done in a random order (randomized separately for each mouse).
Blinding	For the 6OHDA lesion studies, the experimenter was blind to the animals' identities (control or lesion) during data collection and analysis. The identities of the animals were revealed to the experimenter only after analysis was complete. For the D1 antagonist experiments, the experimenter was not blind, and knew which solution was being infused (i.e. saline or D1 antagonist).

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

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

Unique biological materials

Policy information about availability of materials

Obtaining unique materials	All materials used are commercially available, and vendors are listed in the relevant Methods sections.

Antibodies

Antibodies used	We used a rabbit anti-tyrosine hydroxylase (TH) antibody (AB152, EMD Millipore). The lot number for this antibody was 2458991. The dilution used was 1:500 and staining was performed for 2 days at 4 degrees Celsius.
Validation	The specificity of this antibody has been verified by the company (http://www.emdmillipore.com/US/en/product/Anti-Tyrosine-Hydroxylase-Antibody,MM_NF-AB152#overview).

Animals and other organisms

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

Laboratory animals	96 male mice between 3 and 6 months old were used for this study. Surgeries were performed when mice were 3 months old so that data could be collected when mice were between 4-6 months old. Dopamine transporter (DAT)-cre (B6.SJL-Slc6a3tm1.1(cre)Bkmn/J, Jackson Laboratory; RRID:IMSR JAX:006660) Heterozygous mice were used for recording signals from dopamine axons expressing GCaMP, for stimulation of dopamine axons expressing ChR2 and for histological examination of TS-projecting dopamine neurons using rabies virus. All mice were backcrossed with C57BL/6J (Jackson Laboratory) for many generations. C57BL/6J mice were used for ablation of TS-projecting dopamine neurons using 6-OHDA. Vglut2flox (Slc17a6tm1Lowl/J, Jackson Laboratory 012898)63 homozygous/DAT-cre heterozygous mice and their littermates (Vglut2flox homozygous mice) were used for novelty exploration behavioral tests. Animals were housed on a 12 hour dark/12 hour light cycle (dark from 07:00 to 19:00) and performed a task at the same time each day. All procedures were performed in accordance with the National Institutes of Health Guide for the Care and Use of Laboratory Animals and approved by the Harvard Animal Care and Use Committee.
Wild animals	No wild animals were used.
Field-collected samples	No field-collected samples were used.