

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

- 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

Med-Associates Med-PC custom code was used to collect behavioral data, Quanteon 1.0 FAST software was used for amperometry data collection

Data analysis

All data were processed using Microsoft Excel 2013 (Redmond, WA), then compiled and statistically analyzed with GraphPad Prism v6.07 (La Jolla, CA) and SPSS v24 (IBM Corp, Chicago, IL). A custom-written python script was used for lickometer data analysis, synaptosoft mini analysis v6.0.7 was used for glutamate transient analysis.

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 data that support the findings of this study are available from the corresponding author.

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	The number of animals proposed per group was informed by power analyses performed on previously-collected data to generate group sizes that will ensure minimally sufficient statistical power (0.9) to detect statistically significant differences between groups (0.05), using mixed ANOVA and appropriate post-hoc tests adjusted for multiple comparisons. Sample size also included expected attrition due to misplaced fibers/cannula and virus.
Data exclusions	Data was excluded if biosensor, cannula, viral expression, or optic fiber placement was off-target. The criteria were established prior to data collection and reported in the Methods section.
Replication	All experiments were run in at least 2 cohorts of subjects for internal replication. All attempts at replication were successful.
Randomization	For deprivation state and drug group assignments, subjects were counterbalanced based on the average lever-press rate during the last two instrumental training session. For viral vector infusions, two weeks prior to behavioral procedures, rats were randomly assigned to viral group
Blinding	Investigators were not blinded in glutamate receptor antagonist or chemogenetic experiments because they were required to administer drug. Behavioral experimenter was blinded to viral conditions in optogenetic experiments.

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	anti-HA, 1:500, Biolegend, San Diego, CA, cat. no. 901501, lot:B220768 goat anti-mouse IgG, Alexa 594 conjugate, 1:1000, Invitrogen, cat. no. A11005, Lot: GR303504-1
Validation	anti-HA has been validated by manufacturer using immunofluorescence and immunoprecipitation. Relevant citations can be found on manufacturer's website: https://www.biolegend.com/en-us/products/purified-anti-ha-11-epitope-tag-antibody-11374 goat anti-mouse IgG, Alexa 594 conjugate relevant citations can be found on manufacturer's website: https://www.thermofisher.com/antibody/product/Goat-anti-Mouse-IgG-H-L-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A-11005

Animals and other organisms

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

Laboratory animals	Male, Long Evans rats (aged 8-10 weeks at the start of the experiment; Charles River Laboratories, Wilmington, MA) were used.
Wild animals	This study did not involve wild animals.

Field-collected samples

This study did not involve samples collected from the field.

Ethics oversight

All procedures were conducted in accordance with the NIH Guide for the Care and Use of Laboratory Animals and were approved by the UCLA Institutional Animal Care and Use Committee.

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