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Corresponding author(s): Randy M. Bruno

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	For array recording, open-source software (OpenEphys) was used. The behavior was implemented using custom code, which is available upon request.
Data analysis	Open-source software was used for whisker measurements (Clack et al 2012) and spike sorting and clustering (Kilosort and Phy). All other analyses were performed with custom MATLAB programs, which 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 computer code and data are available from the corresponding author upon reasonable 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

Life sciences study design

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

Sample size	(1) Inactivation of barrel cortex during behavior -- optogenetic inactivation and lesions Previous studies reported transient inactivation decreased performance to chance levels (50% performance, e. g., O'Connor et al., 2010, Guo et al., 2014, Sachidhanandam et al., 2013). Based on the mean and standard deviation of normal performance levels of trained animals (81.4% +/- 7.4%), power analysis yielded a minimum n of 3 to detect a change in performance to chance levels with a significance value of P = 0.05. In this study, n = 10 Emx-eNphR, n = 7 control animals, and n = 5 PV-ChR mice were included in the study. For lesion studies, n = 8 and n=9 mice were tested for each group (1 and 3-day rest groups). (2) Learning with lesions Based on the average learning speed of previously trained animals (25 +/- 8.6 sessions), power analysis indicated a sample size of 5 would be needed to detect a 2-fold increase in learning speed. In this study, we included 11 unlesioned, and 9 lesioned animals.
Data exclusions	Based on preestablished criteria, several conditions led to exclusion of data: (1) animals that were able to perform the detection task (>60% correct performance) after all whiskers were trimmed were deemed to be using other sensory modalities to perform the task and excluded from further analysis. (2) For the learning experiments, if animals lost their C2 whisker during training, subjects were excluded from further analysis. For cortical lesions included in learning experiments, animals that had inadvertent lesions beyond cortex, extending below the white matter tract were excluded from analysis.
Replication	All attempts at replication were successful.
Randomization	For learning experiments, cohorts of 10-15 mice from multiple litters were trained at a time. Animals were chosen at random, such that roughly half of the animals from the same litter (and home cage) received cortical lesions, while the other half received sham-operations. The first cohort was trained in 2016 by one trainer, and the experiment was repeated in 2017 by a second trainer.
Blinding	For learning experiments, the human trainers were blind to which animals received lesions. For analysis of the extent of lesion (cortex only vs. cortex plus subcortical areas (usually the striatum), histology images from all animals were scored blindly by 5 "experts" who had 3 or more years of mouse histology experience. Subjects were blind to the animal identity and outcome of the experiments (i.e., recovered behaviorally or whether they learned the task, if for learning experiments).

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

Antibodies

Antibodies used	Mouse anti-NeuN Antibody, clone A60 (Millpore MAB377)
Validation	The anti-mouse NeuN was used in Figure 1a to label neurons relative to Emx1-cre positive cells. This monoclonal antibody clone has been validated for specificity in numerous publications (2000+, see https://www.citeab.com/antibodies/226230-mab377-anti-neun-antibody-clone-a60/publications).

Animals and other organisms

Laboratory animals	All animals used in this study (Emx1-cre, RCL-eNpHR3.0/YFP, Nr5a1-cre, PV-cre, and RCL-ChR2/YFP) were maintained on a C57 background. Animal ages ranged from P40 to P250 (average P111 +/- 50 days standard deviation) at the start of training. 65% of the subjects were female; 35% were male.
Wild animals	No wild animals were involved in the study.
Field-collected samples	No field-collected samples were used in the study.