

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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

Behavior set up was programmed as a custom software written in LabVIEW 2011 (64 bit) using commercial library of functions from Phidgets and Zaber libraries. Two-photon calcium data was collected using HelioScan software. Whisker tracking was performed with Noldus EthoVision XT software.

Data analysis

Matlab R2015b (Mathworks), Graph Pad Prism v8 (GraphPad Software), ImageJ Fiji. Behavioral data (animal performance, licking rate, whisking angle) was analysed in Matlab using custom codes that are described in detail in the Methods on pg.15-16. Imaging data was motion corrected using NoRMCorre (Flatiron Institute) available on GitHub. Calcium data was extracted and preprocessed using a custom Toolbox in Matlab (OCIA, HelmchenLabSoftware) available on GitHub. Calcium data was deconvolved using a custom algorithm in Matlab (constrained-foopsi, epnev) available on GitHub. The GLM analysis was performed using the Glmnet Matlab package available on web.stanford.edu. The various indices (Selectivity Index, Reward history modulation Index) were computed using Matlab custom codes as described in detail in Methods. The script library for data analysis will be 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. 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 will be available from the corresponding author upon request. All analysis codes will be made available before publication via GitHub.

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	Sample sizes were chosen in accordance with the standard number of animals in comparable studies in the field. Three to six mice per group were used in each imaging experiment. A larger number of mice were used in purely behavioral experiments. The exact number of animals are given in the main text and also in figure legends.
Data exclusions	Mice that lost their hooks during the behavioural training period and longitudinal imaging were excluded from the analyses. Trials or parts of trials with uncorrected large XY-motion or large Z-motion were also excluded. Neurons were excluded from longitudinal analyses when it was not possible to track them in consecutive training phases. The criteria for exclusion of specific neurons in longitudinal recording experiments is given in the Methods section. Exclusion criteria was not pre-established.
Replication	All experiments were reproduced multiple times in multiple animals. All attempts of replication was successful.
Randomization	No randomization was performed as this is not strictly relevant to this study.
Blinding	CNO injection experiments were performed blindly together with WT control.

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

Methods

n/a	Involved in the study	n/a	Involved in the study
☒	☐ Antibodies	☒	☐ ChIP-seq
☒	☐ Eukaryotic cell lines	☒	☐ Flow cytometry
☒	☐ Palaeontology	☒	☐ MRI-based neuroimaging
☐	☒ Animals and other organisms		
☒	☐ Human research participants		
☒	☐ Clinical data		

Animals and other organisms

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

Laboratory animals	Adult transgenic male mice (1.5-3 months old) were used in this study. These mice were triple transgenic Rasgrf2-2AdCre; CamK2a-tTA;TITL-GCaMP6f animals. Details are in the Methods section.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve field-collected samples.
Ethics oversight	Methods were carried out according to the guidelines of the Veterinary Office of Switzerland and following approval by the Cantonal Veterinary Office in Zurich.

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