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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	ScanImage, Custom VR code (in MATLAB), Custom code (in MATLAB), BlackRock Microsystems Cerebus software
Data analysis	Suite2p, KlustaSuite, Custom analysis code (in MATLAB)

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

The data and custom code from this study 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

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	As is common in neurophysiology, we did not precompute a required sample-size. Rather, we recorded from a large number of neurons across multiple animals, and analyzed their activity and determined the significance of the resulting analyses. For the two-photon experiments: these experiments provide data from hundreds of neurons each recording session. We recorded in 18 recording sessions, giving us a sample size larger than needed to make our points. For electrophysiology: we chose electrodes that would record from >15 neurons from V1 and >20 neurons from CA1, which allowed us to decode animal position. We repeated this measurement in 4 animals and 8 recording sessions in total to obtain a sample size in the same order of magnitude obtained in the two-photon experiments.
Data exclusions	No data were excluded from analysis.
Replication	We repeated the experiments and analyses across multiple animals in this study. All our attempts at replication were successful. Models were verified with cross-validation.
Randomization	Within each animal, we split behavioral trials into even and odd, and analyzed the two separately. Models were verified with cross-validation.
Blinding	The experiments and the initial analysis pipeline (region-of-interest identification for imaging, and spike sorting for electrophysiology) were performed without knowledge of each cell's contribution to the effects reported in the paper.

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

Animals and other organisms

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

Laboratory animals	Mouse -- C57BL6/J -- 4 Male -- implanted at 4-8 weeks Mouse -- Camk2a-tTA;tetO-G6s -- 3 Female -- implanted at 4-10 weeks Mouse -- Emx1- Cre;Camk2a-tTA;Ai93 -- 1 Male, 2 Female -- implanted at 4-10 weeks
Wild animals	No wild animals were used in this study
Field-collected samples	No field-collected samples were used in this study