nature portfolio

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Reporting Summary

Nature Portfolio 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 Portfolio policies, see our Editorial Policies 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	Video data was collected on on the Ubuntu 22.04 OS, using custom code written in python (v3.10) and based primarily on the Spinnaker API (v3.0.0.118) for operating Blackfly S USB3 cameras, available from Teledyne FLIR. This code is available at https://github.com/hatsopoulos-lab/marmoset-camera_control_code. Neural data was collected using the program Central, which is part of the Cerebus Windows Suite available from Blackrock Neurotech.
Data analysis	Data processing and analysis was computed using custom code available on Github at https://github.com/hatsopoulos-lab/marmoset-data_processing and https://github.com/hatsopoulos-lab/marmoset-trajectory_and_network_encoding_model, respectively. Additionally, Deeplabcut (v2.2.1) was used to estimate pose from video data. SpikeInterface was used for automated spike-sorting and phy (v2.0b1) was used for manual curation of sorted spikes. Data was packaged in NWB format using pynwb (v2.1.0). Data was processed in a conda environment using python v3.9.5 and analyzed in a conda environment using python v.3.11.5.

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Data from marmoset MG is available at INSERT_LINK**. Data availability for marmoset TY is delayed due to the dataset's use in manuscripts currently in preparation.
** This dataset will be deposited on DANDI and the link inserted here prior to final acceptance. A temporary link will be made available to reviewers.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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

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

Life sciences study design

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

Sample size	The sample size of n=2 marmosets was selected as this is the standard in non-human primate research. Neural and behavioral sample sizes were determined by array quality and by each marmoset subject's engagement in the experimental task.
Data exclusions	The only data exclusion that occurred was exclusion of a few low-quality neural units (units with average firing rate < 2 spikes/sec and units with signal-to-noise ratio < 3). Additionally, two units for monkey MG were excluded because they exhibited significant signal dropout (more than half of the data collection session). All exclusions are demonstrated in the available code.
Replication	After producing all primary figures and associated data, we reorganized and simplified the code and re-ran all analysis from scratch. All results were replicated.
Randomization	Reaching events were separated into two groups for analysis and association with two separate functional networks. Reaches were assigned

Randomization	randomly. We also conducted many train/test splits (in most cases, n=500), in which 80% of data was randomly selected with replacement for each split and the remaining 20% was held out for testing.
Blinding	All randomization was conducted using a different randomization seed in python. The seed was generated using the range() function in python without any investigator knowledge of the output of a given seed value.

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
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	TY: common marmoset, Callithrix jacchus, 10 years, 370g, male. MG: common marmoset, Callithrix jacchus, 8 years, 350g, female.
Wild animals	The study did not involve wild animals.
Reporting on sex	We included one male and one female in the study. We did not consider sex in the study because it is not expected that neuronal computations in primary cortex would depend on sex at the level of our study. Findings were replicated across the two subjects of different sex.
Field-collected samples	The study did not include field-collected sample.
Ethics oversight	All methods were approved by the Institutional Animal Care and Use Committee of the University of Chicago.

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

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*