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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 <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

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St	at	121	$1 \cap S$

n/a	Confirmed
	\square 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.
\boxtimes	A description of all covariates tested
\boxtimes	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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
\boxtimes	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
\boxtimes	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 <i>d</i> , Pearson's <i>r</i>), 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

Electrophysiological signals were collected by Plexon system. Gaze position was monitored using ISCAN system. All other experimental parameters were recorded using a custom software Kofiko (https://github.com/shayo/Kofiko) (version: Feb/4/2014). The electrode trajectories were planned using custom software (https://github.com/shayo/Planner) (Revision 93 Feb/19/2014).

Data analysis

Functional imaging data are processed with Freesurfer and FSL. Multichannel recorded electrophysiological data was automatically sorted by Kilosort2 (github.com/MouseLand/Kilosort2) and manually refined in Phy (github.com/cortex-lab/phy). Custom code written in MATLAB was used for analysis. The code that reproduce the core results are available at https://doi.org/10.5281/zenodo.10460607. All other code is available from the lead corresponding author upon reasonable 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 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 <u>availability of data</u>

All manuscripts must include a <u>data availability statement</u>. 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

The data set of neural responses to thousand monkey face set are available at https://doi.org/10.5281/zenodo.10460607.

PrimFace database: http://visiome.neuroinf.jp/primface

FERET database: https://www.nist.gov/itl/products-and-services/color-feret-database

CVL Face Database: http://www.lrv.fri.uni-lj.si/facedb.html

MR2 face database: https://osf.io/skbq2/

Chicago Face Database: https://www.chicagofaces.org/

CelebA CelebFaces Attributes Dataset: https://mmlab.ie.cuhk.edu.hk/projects/CelebA.html

FEI Face Database: fei.edu.br/~cet/facedatabase.html PICS Psychological Image Collection at Stirling: pics.stir.ac.uk Caltech faces 1999: https://data.caltech.edu/records/6rjah-hdv18

Essex Face Recognition Data: http://cswww.essex.ac.uk/mv/allfaces/faces95.html

The MUCT Face Database: www.milbo.org/muct

All other data are available from the lead corresponding author upon reasonable request.

Research involving human participants, their data, or biological material

Policy information about studies w	<u>(ith numan participants or numan data</u> . See also policy information about <u>sex, gender (identity/presentation)</u>
and sexual orientation and race, et	hnicity and racism.
Reporting on sex and gender	N/A

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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 r	naking your selection.

Ecological, evolutionary & environmental sciences

Life sciences Behavioural & social sciences Ecological, evolutio

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	Sample sizes were chosen in a manner commensurate with similar previous studies.
Data exclusions	We recorded from every neuron encountered. Only visual responsive units were considered for further analysis.
Replication	Results were replicated across 2-3 different animals for each experiment independently.
Randomization	The visual stimuli were shown in a random order. Organisms random allocation is not relevant to this study, different subjects were used to repeat the same experimental condition.
Blinding	Investigators were not blinded to experimental groups due to the nature of the experiments.

Reporting for specific materials, systems and methods

		of materials, experimental systems and methods used in many studies. Here, indicate whether each material, are not sure if a list item applies to your research, read the appropriate section before selecting a response.
Materials & experime	ntal systems	Methods
Materials & experimental systems n/a Involved in the study		n/a Involved in the study
Antibodies		ChIP-seq
Eukaryotic cell lines		Flow cytometry
Palaeontology and a	rchaeology	MRI-based neuroimaging
Animals and other or	ganisms	
Clinical data		
Dual use research of	concern	
Plants		
Animals and other	research orga	inisms
		; <u>ARRIVE guidelines</u> recommended for reporting animal research, and <u>Sex and Gender in</u>
Laboratory animals	Seven male rhesus maca	ques (Macaca mulatta) of 5-13 years old were used in this study.
Wild animals	The study did not involve wild animals.	
Reporting on sex	This study was conducted using only male animals.	
Field-collected samples	The study did not involve field-collected samples.	
Ethics oversight	All procedures conformed to local and US National Institutes of Health guidelines, including the US National Institutes of Health Guide for Care and Use of Laboratory Animals. All experiments were performed with the approval of the Caltech and UC Berkeley Institutional Animal Care and Use Committee.	
lote that full information on th	e approval of the study p	rotocol must also be provided in the manuscript.
Magnetic resonan	ce imaging	
Experimental design		
Design type	Block design	
of the non-face		asted 24 s blocks (each image lasted 500 ms). In each run, the face block was repeated four times and each face blocks was shown once. A block of grid-scrambled noise patterns was presented between each stimulus t the beginning and end of each run. Each scan lasted 408 seconds.
		re position was monitored using an infrared eye tracking system (ISCAN). Juice reward was delivered every nange for maintaining fixation on a small spot (0.2 degree)
Acquisition		
Imaging type(s) Functional and		and anatomical imaging
Field strength 3 Tesla		
mm isotropic v voxels were 1		d anatomical volumes were measured with MP-RAGE sequence(TR 2,300 ms; IR 1,100 ms; TE 3.37 ms; 0.5 ic voxels) . EPI volumes were acquired in an AC88 gradient insert (Siemens) TR was 2000 ms,TE was 17 ms, $1 \times 1 \times 1$ mm with an no gap between slices. Matrix size was (96, 96, 64) (read [x], phase [y], slice [z]), the was 96 × 96 mm in-plane. Flip angle was 80°
Area of acquisition	Whole brain	n

Preprocessing

Diffusion MRI

Preprocessing software

Used

Not used

Analysis of functional volumes was performed using the FreeSurfer Functional Analysis Stream (Massachusetts General Hospital). Volumes were corrected for motion and undistorted based on acquired field map.

Normalization

No normalization needed as analysis only compare data from the same scan.

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Normalization template	We did not normalize any imaging data into template. All the analysis were done in the single subject's original space.	
Noise and artifact removal	We remove the linear or quadratic trends in the timeseries.	
Volume censoring	Motion noises were removed by putting the motion parameters as the regressors in the GLM analysis.	
Statistical modeling & infere	ence	
Model type and settings	The analysis used only first-level analysis.	
Effect(s) tested	d We ran t-tests between different conditions within each single subject.	
Specify type of analysis: Whole brain ROI-based Both		
Statistic type for inference All the analyses were done using voxel-wise inference.		
(See Eklund et al. 2016)		
Correction	We did not apply any multiple-comparison correction in the fMRI imaging analysis.	
Models & analysis		
n/a Involved in the study		
Functional and/or effective connectivity		
Graph analysis		
Multivariate modeling or predictive analysis		