nature portfolio

Corresponding author(s): Arpana Gupta

Last updated by author(s): 06/19/23

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.

Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study.
For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

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 collectio Data: no software and code was used that is not readily available or open sourced

analysis:

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

Deidentified individual participant data (brain) can be shared upon request and will be made available through the Center's pain repository portal (https://www.painrepository.org/). To access the data, participants will fill out a user agreement, upon which access to the data will be made available through a secure password protected portal. The raw microbiome sequences can be accessed NIH NCBI BioProject (BioProject ID: PRJNA946906).

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	Sex was reported by discrimination (Table 1) and all analyses accounted for sex by using it as a covariate
Reporting on race, ethnicity, or other socially relevant groupings	Race was reported by discrimination levels (Table 1) and all analyses accounted for race by using it as a covariate
Population characteristics	Population characteristics are summarized in Table 1 as divided by discrimination group. There were no significant differences in sex, age, BMI, education, marital status, income, and diet except SES.
Recruitment	Generally healthy participants were recruited from the Los Angeles area
Ethics oversight	All procedures complied with institutional guidelines and were approved by the IRB at UCLA's Office of Protection for Research Subjects. All participants provided written informed consent.

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	
Data exclusions	
Replication	
Randomization	
Blinding	

Behavioural & social sciences study design

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

Study description	data are quantitative
Research sample	107 individuals (87 women who were premenopausal and scanned during the follicular phase of the menstrual cycle.
Sampling strategy	This was a sample of convenience so long as they met inclusion/exclusion criteria until projected sample size of 100 was reached
Data collection	using survey questionnaires methods, and biological markers (MRI and stool)
Timing	2016-2020
Data exclusions	Exclusions: major medical/neurological conditions, current or past psychiatric illnesses, comorbidities such as vascular disease, diabetes, weight loss/abdominal surgeries, substance use disorders, tobacco dependence, or metal implants; were pregnant or breastfeeding; performed extreme strenuous exercise, > 400 pounds were excluded due to weight constraints of the MRI scanner.
Non-participation	Analyses only included those participants who completed the MRI functional scans
Randomization	Non-randomization as cross-sectional study without intervention

Ecological, evolutionary & environmental sciences study design

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

Study description	
Research sample	
Sampling strategy	
Data collection	
Timing and spatial scale	
Data exclusions	
Reproducibility	
Randomization	
Blinding	

Did the study involve field work? ☐ Yes ☒ No

Field work, collection and transport

Field conditions	
Location	
Access & import/export	
Disturbance	

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

Antibodies

Antibodies used	
Validation	

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	
Authentication	
Mycoplasma contamination	
Commonly misidentified lines (See ICLAC register)	

Palaeontology and Archaeology

Specimen provenance	
Specimen deposition	
Dating methods	

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight	

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

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	
Wild animals	
Reporting on sex	
Field-collected samples	
Ethics oversight	

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	NA as not a clinical trial
Study protocol	NA
Data collection	Reported
Outcomes	Reported

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☐	☐	Public health
☐	☐	National security
☐	☐	Crops and/or livestock
☐	☐	Ecosystems
☐	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
X	☐	Demonstrate how to render a vaccine ineffective
X	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
X	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
X	☐	Increase transmissibility of a pathogen
X	☐	Alter the host range of a pathogen
X	☐	Enable evasion of diagnostic/detection modalities
X	☐	Enable the weaponization of a biological agent or toxin
X	☐	Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	
Novel plant genotypes	
Authentication	

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	
Files in database submission	
Genome browser session (e.g. UCSC)	

Methodology

Replicates	
Sequencing depth	
Antibodies	
Peak calling parameters	
Data quality	
Software	

Flow Cytometry

Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	
Instrument	
Software	
Cell population abundance	
Gating strategy	

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type	Functional stimulus with whole brain
Design specifications	Blocks of 6, comprising unaltered or pixelated images, with a total of 18 blocks (each image shown for 3s). A black screen with a white crosshair was displayed for 12 s before the first block of images, between each block, and after the final block
Behavioral performance measures	Willingness to eat the food in the scanner
Imaging type(s)	Food stimulus organized into 5 groups: unhealthy (high calorie) savory, unhealthy (high calorie) sweet, healthy (low calorie) savory, healthy (low calorie) sweet, and non-food
Field strength	3.0T Prisma
Sequence & imaging parameters	TE/TR=28ms/2000ms, flip angle=77°, scan duration=10m6s, FOV=220mm, slices=40, and slice thickness=4.0mm
Area of acquisition	Whole Brain

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	FEAT version 6 included in the FMRIB Software Library (FSL).
Normalization	5-mm full-width at half-maximum (FWHM) Gaussian kernel
Normalization template	Montreal Neurological Institute (MNI) standard space using affine transformation through FSL's Linear Image Registration Tool (FLIRT)
Noise and artifact removal	Preprocessing included motion correction, brain extraction, 100-s high-pass filtering and spatial smoothing
Volume censoring	NA

Statistical modeling & inference

Model type and settings	5 contrasts used depending on food type (including reverse contrasts), imputed into random-effects group-level analyses using FSL's Local Analysis of Mixed Effects (FLAME1) in a whole-brain analysis with outlier deweighting
Effect(s) tested	Group-level (high discrimination vs. low discrimination) unpaired t-tests were performed in FEAT using a mixed-effects model with BMI, age, sex, race, diet and SES as covariates

Specify type of analysis: ☒ Whole brain ☒ ROI-based ☒ Both

Statistic type for inference

(See Eklund et al. 2016)

T -tests

Correction

All statistical maps were family-wise error (FWE) cluster-corrected for multiple comparisons (cluster height threshold: Z>2.3; cluster significance: p<0.05).

Models & analysis

n/a	Involved in the study
[ ]	[x] Functional and/or effective connectivity
[x]	[ ] Graph analysis
[x]	[ ] Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Functional responses to food cue stimulus

Graph analysis

NA

Multivariate modeling and predictive analysis

NA