nature research

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Last updated by author(s): May 20, 2019

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 *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	Illumina sequencing data was collected with MiSeq Control Software v2.6. Images were acquired with Nikon Elements AR 5.11.00.
Data analysis	USEARCH 9.2.64 was used for sequencing data analysis. Taxonomic classification of OTUs was performed with RDP classifier release 11.5. Net Relatedness Index was calculated using code adapted from Qiime 1.9.1 relatedness_library.py script and input neighbor joining tree was calculated with MUSCLE 3.8.31. Custom code utilized to demultiplex barcoded MaP-seq data is available at https://github.com/ravisheth/mapseq. Jupyter 1.0.0, Python 2.7, Pandas 0.19.2, NumPy 1.15.4, Matplotlib 2.2.3, seaborn 0.9.0, scikit-bio 0.4.2, SciPy 1.1.0, NetworkX 1.11, and PyGraphviz 1.3.1 were utilized for data analysis and figure generation.

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 sequencing data is available at NCBI SRA under PRJNA541181. OTU tables can be accessed at http://github.com/ravisheth/mapseq.

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	No sample size calculations were performed as the number clusters analyzed depended on the yield from the experiment; sample sizes are listed in figure legends where applicable.
Data exclusions	Data exclusion was based on sequencing coverage or cluster yield with predetermined criteria to remove technical artifacts as described in the Methods section.
Replication	All mouse samples were profiled in technical replicate. To assess reproducibility of the technique, technical replicates were analyzed (Supplementary Figure 6). Biological replicates were also performed and analyzed for various mouse samples (Supplementary Figure 7, 10, 11, 16, 17 etc.). Further information on MaP-seq datasets can be found in Supplementary Table 5. All attempts at replication were successful.
Randomization	Where relevant mice were allocated randomly to different experimental groups.
Blinding	Blinding was not possible during experiments as HF and LF diets visually appear different. All analyses of MaP-seq data were performed with the same parameters and criteria across different conditions, minimizing bias.

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
☐	☒	Animals and other organisms
☒	☐	Human research participants
☒	☐	Clinical data

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	6-8 week-old female C57BL6/J mice were utilized from Taconic or Jackson as indicated in the text.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve field-collected samples.
Ethics oversight	All mouse procedures were approved by the Columbia University Medical Center Institutional Animal Care and Use Committee (protocol AC-AAAR1513) and complied with all relevant regulations.

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