

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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	The 16S sequence was analyzed using the program DADA2 v.1.12.1 167 and R v.3.6.1 168 to infer amplicon sequence variants (ASVs). Complete code was modified from Lee, M (2019). https://astrobiomike.github.io/amplicon/dada2_workflow_ex For the shotgun metagenomic sequence data, manual binning and curation was performed following the genome-resolved metagenomic workflow implemented in anvio v.6.2. (https://merenlab.org/2016/06/22/anvio-tutorial-v2/) Gut brain modules (GBMs) were inferred using Omixer-RPM v.0.3.2 (https://github.com/raeslab/omixer-rpm).
Data analysis	Diversity estimates and hypothesis testing for both 16S and shotgun sequence data were modeled using the breakaway package v.4.6.16, DivNet package v.0.3.5 and corncob v.0.1.0. (https://github.com/adw96)

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](#)

The sequence data that support the findings of this study are available in European Nucleotide Archive (ENA) at <https://www.ebi.ac.uk/ena/>, study accession number PRJEB29232.

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	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Ecological, evolutionary & environmental sciences study design

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

Study description	Metagenome sequence data was generated and analysed from 123 faecal samples collected from the Belyayev fox cohort, in order to explore for correlations between
Research sample	123 fecal samples from captive silver foxes (<i>Vulpes vulpes</i>). The samples represent two collection years (2015: tame (n=10); aggressive (n=10); 2017: tame (n=51); aggressive (n=52)).
Sampling strategy	Samples had been previously taken and stored frozen as a matter of routine cohort documentation, prior to provision to this study. In our study we analysed all samples that were available.
Data collection	Frozen faecal samples were provided by A. Kukekova to L. Puetz, who then extracted DNA, generated 16s and shotgun metagenomic data, and performed computational analysis on the samples.
Timing and spatial scale	Samples represent two collection years, 2015 and 2017.
Data exclusions	No data was excluded
Reproducibility	Analyses were performed on multiple samples per behavioural cohort, to explore for consistent differences in the microbiome between cohort.
Randomization	Allocation was not random, rather based on behavioural cohort.
Blinding	Not relevant - samples provided had been specifically allocated to the two cohorts.

Did the study involve field work? ☐ Yes ☒ No

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	Farm bred populations of red fox (<i>Vulpes vulpes</i>).
Wild animals	Did not involve wild animals
Reporting on sex	Both sexes were used in the study.
Field-collected samples	Did not involve field collected samples
Ethics oversight	Faecal samples were collected from foxes maintained at the experimental farm of the Institute of Cytology and Genetics (ICG) in Novosibirsk, Russia. All animal procedures at the ICG complied with standards for humane care and use of laboratory animals by foreign institutions.

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

Plants

Seed stocks	NA
Novel plant genotypes	NA
Authentication	NA