

Reporting Summary

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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

Metagenomes were collected from MG-RAST: <http://www.mcs.anl.gov/project/mg-rast-metagenomics-rast-server>, and the SRA database, and information on their source (published work) is referred in Supplementary Table 15.

Data analysis

All the software used for data analysis is available online:
 R software - version 3.5.1 - packages: vegan, ggplot2, heatmap3, bipartite, picante, MASS.
 NetCmpt - Kreimer, A., Doron-Faigenboim, A., Borenstein, E. & Freilich, S. NetCmpt: a network-based tool for calculating the metabolic competition between bacterial species. *Bioinformatics* 28, 2195-2197, doi:10.1093/bioinformatics/bts323 (2012).
 CoNet - version 1.1.1 beta and Cytoscape - version 3.7.1.
 QIIME2 - <https://qiime2.org/>
 DADA2 - package in R
 FastTree, 2.1 version
 MEGA, 6.0 version

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

A data availability statement is provided in the main manuscript, Line 452-456:

Data availability. Sequencing data can be found at the NCBI (SRA) database under the study accession code SRP118834 and SUB396945. Non-sequencing data are available in Supplementary Data Tables 1, 16 and 17.

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

Ecological, evolutionary & environmental sciences study design

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

Study description	The animal trial included a 6 week experiment with 3 sampling points (1st, 2nd and last week). Four different diets (in triplicate groups) consisting of different nutrient levels (protein and fat), as described in the Methods section, were administered in juvenile European sea bass. At the end of the trial, 9 randomly selected animals per group were sampled and their intestine was dissected into 3 parts (pyloric caeca, midgut, hindgut; See Figure 1). Thus, 3 intestinal samples were collected per each individual fish - a total of 36 fish - and subjected to 16S rRNA gene amplicon sequencing analysis (after DNA extraction).
Research sample	Each gut part of an individual fish represents a research sample. These samples were taken from European sea bass (<i>Dicentrarchus labrax</i>) intestinal tract that were brought to the laboratory from a commercial hatchery (Maagan Michael, Israel), originating from the same population (same parents). The age of the animals was approximately 6-7 months (approximately 10 g in weight). At this stage, the animals are all sexually immature.
Sampling strategy	As the focus of our broad analysis around different microbial species distribution and their potential relationship to physiological functions, we aimed at a representative sample size that would cover the different microbial taxa in the different fish gut parts. For this purpose, we did a rarefaction curve taking different sample sizes and read depths and we reached a visible sample rarefaction plateau (Supplementary Figure S1).
Data collection	Throughout the trial all treatments were handled in a similar manner by the same trained research technician of the institute. Samples for each time point were collected during the same day, by trained scientific personnel. After anesthesia using clove oil, fish from each tank were randomly selected and their guts were dissected using sterile instruments and separated into pyloric caeca, foregut and hindgut. Samples were taken both for DNA extraction and bacteria isolation kept in glycerol.
Timing and spatial scale	The animal experimental trial lasted in total 6 weeks. Samples were taken after week 1, 2, and at the end point (6th week). The experimental setup consisted of three systems, each containing six 250-l tanks and a central main biofilter of 350 l, where the fish were kept throughout both the whole experimental trial and the acclimatization period (1 month before).
Data exclusions	Four sample were discarded due to insufficient sequencing depths. After quality filtering, reads that were much below a 4000 sequence depth were excluded. This sequence depth was selected based on the rarefaction curves, reaching the minimum depth for a plateau.
Reproducibility	The animal experiment was performed successfully in triplicate groups for each treatment. Concerning the microbial interaction trials (liquid and agar media), the trials were performed successfully in triplicates (96-well plates and agar plates, respectively).
Randomization	Concerning the animal experiment, animals (fish) were randomly allocated and were in equal numbers in each experimental group (diet). The size of the animals was measured and animals deviating from the mean were removed, in order not to have significantly different size between the groups. The samples used for the analysis originated from randomly selected fish from each experimental group. The experimental setup consisted of three systems, each containing six 250-l tanks and a central main biofilter of 350 l. The experimental feed was given in triplicate for each diet with random assignment. Each of the diets was represented in each of the three systems used to assess the influence of biofilter on intestinal bacterial community. Moreover, ANOSIM did not reveal any clustering of samples according to biofilter (Supplementary Table 18).
Blinding	The experimental procedure was applied by research technicians who were unaware to the meaning of the different treatments and was therefore unaffected by it. Additionally, the investigators analyzed the data using the same computational tools and procedures and therefore make blinding irrelevant.
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
☐	☒ 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

For the study, European sea bass (*Dicentrarchus labrax*) were involved, brought to the laboratory from a commercial hatchery (Maagan Michael, Israel), originating from the same population. The age of the animals was approximately 6-7 months (approximately 10 g in weight). At this stage, the animals are all sexually immature.

Wild animals

The study did not involve wild animals.

Field-collected samples

The study did not involve samples collected from the field.

Ethics oversight

The experimental procedures used in the present study were approved by the Animal Policy and Welfare Committee of the Agricultural Research Organization (approval number IL-241/10) and were in accordance with the guidelines of the Israel Council on Animal Care.

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