

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
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

Software developed:
MATLAB GUI (graphical user interface) was used to build the sorting platform.

Data analysis

No software was used.

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

The datasets generated or analyzed in this protocol are available from the corresponding authors upon request.

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

Life sciences study design

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

Sample size	The sample size was constrained by cells analysed during the sorting. We used all samples measured during the sorting in our developed platform.
Data exclusions	No data were excluded from the analyses.
Replication	All experiments were conducted with at least three replicates. All attempts at replication were successful.
Randomization	The sample from the each culture tube was randomly collected and used for the sorting.
Blinding	Our sorting platform works in a fully automated manner. We were totally blinded to group allocation during data collection and/or analysis.

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		Methods	
n/a	Involved in the study	n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies	<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines	<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology	<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms		
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<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data		

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	For the mouse colon microbial community sample, the colon contents of a 6–8 week old C57BL/6J mouse was harvested in an anaerobic tent. Randomization and blinding are not applicable as animals were not distributed into groups.
Wild animals	The study did not involve wild animals.
Field-collected samples	The marine sediment samples were collected from the Pacific Ocean off the coast of Vancouver, Canada. The samples were maintained in the dark and at room temperature until further processing in the laboratory. A small spatula of sediment (0.5 g) was transferred to the vitamin-supplemented ASW medium (50 mL) supplemented by 1 mM NaNO ₂ and incubated in the dark at 28 °C without agitation. Nitrite concentration was monitored at weekly intervals and when depleted, 10% volume of culture was transferred into fresh medium with 1 mM NaNO ₂ . Four sequential transfers were performed before Raman-activated cell sorting (RACS) to increase the initially low abundance of taxa of interest (cytochrome c-expressing cells) within the community.
Ethics oversight	The mouse colon specimens were collected under approval from the Institutional Ethics Committee of the University of Veterinary Medicine, Vienna, in accordance with Austrian laws (BMWF-66.006/0002-II/10b/2010).

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