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Corresponding author(s): Harris H. Wang

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.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Flow cytometry was performed using InCyte 3.1 software on the Guava easyCyte HT flow cytometer. BD FACSDiva software was used for FACS on the BD FACSAria II cell sorter. NIS-Elements-AR software was used for fluorescence microscopy. Gen5 software was used to operate the plate reader for measurement of GFP expression in isolate strains.
Data analysis	All 16S data were processed using the UPARSE pipeline and the RDP classifier (USEARCH v.10.0.240) and subsequently analyzed in R, using the calculations stated in the Methods section. For whole genome sequencing assembly, we used SPAdes (v.3.9.1) software to generate contigs and then performed sequence analysis using BLAST, PlasmidFinder(v.1.3), and Geneious (v.7.1.5). FCS Express 6 was used for formatting FACS plots.

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 upon request. 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 data and analysis code are available from the corresponding author upon request

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	Sample sizes of mice were chosen to ensure that the effect of treatment with the engineered bacteria was robust and replicable. At least 3 mice were used for each treated group, and at least 2 mice were used for control groups.
Data exclusions	No data were excluded from the analysis
Replication	All attempts at replication were successful. We ran multiple iterations of the study using different cohorts of mice, with multiple mice in each treatment group (see samples size above).
Randomization	Mice were randomly allocated to different treatments. We ensured that animals shipped to the animal facility in different cages were mixed appropriately in order to avoid microbiome cage bias.
Blinding	Blinding does not apply to this study because the investigators needed to identify the cages of mice for subsequent FACS sorting and analysis.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Unique biological materials

Policy information about availability of materials

Obtaining unique materials	All strains used in the study are available upon request from the corresponding author.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	7-8 week old C57BL/6 female mice from Taconic and Charles River Laboratories were used.

Wild animals	No wild animals were used.
Field-collected samples	The study did not involve samples collected from the field.

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	Bacteria were extracted from murine feces as described in the Methods section by resuspension in PBS and filtration. The bacteria were run directly on the flow cytometer/cell sorter without additional treatment.
Instrument	BD FACSAria II, Guava easyCyte HT
Software	BD FACSAriaII was operated using BD FACSDiva. Guava easyCyte HT was operated using InCyte3.1. FCS Express 6 software was used to format FACS plots.
Cell population abundance	Representative population abundances pre- and post-sorting are shown in the manuscript. The purity of samples is addressed in the manuscript, as autofluorescent cells were filtered out of the post-sort population.
Gating strategy	FSC/SSC gates were determined by comparison of fecal bacterial samples and in vitro cultures of E. coli against the PBS background to gate in the signal for live bacteria and exclude noise. GFP and mCherry gates were set by comparing GFP+/mCherry+ E. coli, GFP+/mCherry- E. coli, GFP-/mCherry+ E. coli, and GFP-/mCherry- E. coli. To minimize sorting of autofluorescent fecal bacteria, we adjusted the fluorescence gates to stringently gate out the natural murine gut bacterial community.

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