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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	No software was used.
Data analysis	For analysis of 16S rRNA amplicon reads, freely available online tutorials were used. For QIIME2, see: https://docs.qiime2.org/2018.2/tutorials/moving-pictures/. For DADA2, see: https://benjjneb.github.io/dada2/tutorial.html.

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

Illumina sequences obtained in the present study were deposited in the Sequence Read Archives (SRA) NCBI database under accession number SRP148888. Sanger sequences were deposited in Genbank under accession numbers MH759762-MH759768.

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

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-size calculation was not performed. It is impossible to predict the magnitude of the variation between animals for a particular parameter based on our current knowledge. The group sizes determined for each experimental design (at least 4 animals per treatment group) represent the minimal number of animals needed to detect a difference in means.
Data exclusions	Mice that were euthanized early due to health concerns were excluded from the analysis, except for experiments determining lethal morbidity after challenge.
Replication	Most experiments were independently repeated at least twice. All attempts to replicate the experiments were successful.
Randomization	Animals were randomly assigned to groups (cages) prior to any experimentation (see methods section: Specific-pathogen free mouse husbandry).
Blinding	Microbiota sample preparation and analysis performed in a blinded manner.

Materials & experimental systems

Policy information about availability of materials

n/a	Involved in the study
☒	☐ Unique materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☐	☒ Research animals
☒	☐ Human research participants

Research animals

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

Animals/animal-derived materials	Male and female Swiss Webster were used for experiments involving germ-free animals with ages ranging 6 to 12 weeks. Female mice from Charles River (C57BL/6NCrl), Envigo (C57BL/6NHsd), Taconic (C57BL/6NTac) and Jackson (C57BL/6J and C57BL/6NJ) were purchased and infections were carried out concurrently when animals reached 8 to 12 weeks of age. Full husbandry and experimental details provided in methods sections: Mouse lines, Specific-pathogen free mouse husbandry, S. Tm infection in C57BL/6 mice, Germ-free mouse husbandry, and S. Typhimurium infections in Germ-free Swiss Webster mice.

Method-specific reporting

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ Magnetic resonance imaging