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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.

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	All biochemical assays were measured using SoftMax Pro 7.0.3; qPCRs were run with StepOnePlus real-time PCR system; Liver histological pictures were taken with DP Controller and DP Manager (Olympus); Phage electronic microscopy pictures were taken using Maxim DL5; Plates were scanned using EPSON 4990 Photo; All pictures were viewed using ImageJ
Data analysis	Bacteriophage sequencing and phage tree: Albacore v2.3.4 (ONT), Porechop v0.2.3, Unicycler v0.4.7 pipeline, Pilon v1.22, CLC Genomics Workbench 4.9, NCBI Prokaryotic Genome Annotation Pipeline, in-house PERL script using Xfig, Phage_Finder, MASH program, GGRaSP and APE R-package, iTOL tree viewer 16S sequencing: MOTHUR-based 16S rDNA analysis workflow E. faecalis genome sequencing and tree: abricate v0.8.10 , Prokka, Roary, RAxML, iTOL Statistical analyses: R statistical software 3.5.1, GraphPad Prism v6.01

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

Raw 16S sequence reads can be found in the NCBI SRA associated with Bioproject PRJNA525701. Bacteriophage raw sequence reads and annotated genomes are

available at NCBI under the following consecutive BioSample IDs (SAMN11089809 – SAMN11089827). Genome sequence data of E. faecalis strains isolated in this study were registered at ENA under Study PRJEB25007.

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

Life sciences study design

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

Sample size	No power analyses or other calculations were used to predetermine sample sizes. Sample sizes were chosen based on prior literature using similar experimental paradigms (Nat Commun. 2017;8:2137; Gut. 2019;68:1504-1515)
Data exclusions	No data were excluded
Replication	In vivo experiments: more than two technical replicates (from different cohorts, on different dates), as well as biological replicates were performed to ensure data reproducibility; In vitro experiments: three independent experiments and also replicates were performed on different dates to ensure data reproducibility. All replications were successful.
Randomization	Mice of similar age and weight were randomly assigned to experimental and control groups.
Blinding	The investigators were not blinded during cell and animal experiment assays.

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	Female and male C57BL/6 mice (age, 9–12 weeks) (strain: wild type, Atp4asl/sl)
Wild animals	No wild animals were involved in the study.
Field-collected samples	No field-collected samples were involved in the study
Ethics oversight	All animal studies were reviewed and approved by the Institutional Animal Care and Use Committee of the University of California, San Diego.

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	Alcoholic hepatitis patients were from multiple centers from United States, Mexico and Europe, with the age ranged from 30 to

Population characteristics	75. Alcohol use disorder patients and non-alcoholic controls were from United States and Europe, with the age ranged from 27 to 74. Both genders were included in all populations. Detailed descriptions in Methods, Extended Data Tables 1 and 2
Recruitment	Patients with alcohol use disorder fulfilling the DSM IV criteria (J Abnorm Psychol. 1997;106:545-553) were recruited from an alcohol withdrawal unit in San Diego, USA and Brussels, Belgium where they followed a detoxification and rehabilitation program. Alcoholic hepatitis patients were enrolled from the InTeam Consortium (ClinicalTrials.gov identifier number: NCT02075918) from centers in the USA, Mexico, United Kingdom, France and Spain. Detailed inclusion and exclusion criteria are listed in Methods
Ethics oversight	The protocol was approved by the Ethics Committee of Hôpital Huriez (Lille, France), Universidad Autonoma de Nuevo Leon (Monterrey, México), Hospital Universitari Vall d'Hebron (Barcelona, Spain), King's College London (London, UK), Yale University (New Haven, USA), University of North Carolina at Chapel Hill (Chapel Hill, USA), Weill Cornell Medical College (New York, USA), Columbia University (New York, USA), University of Wisconsin (Madison, USA), VA San Diego Healthcare System (San Diego, USA) and Université Catholique de Louvain (Brussels, Belgium).

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