

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 eBURST V3 (eburst.mlst.net/V3/mlst_datasets/),

Data analysis Image J ver. 1.43u (National Institutes of Health, USA), Clustal Omega (www.ebi.ac.uk/Tools/msa/clustalo/), Simple Phylogeny (www.ebi.ac.uk/Tools/services/web_simple_phylogeny/toolform.ebi), and CLC genomic workbench

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 generated or analysed during this study are included in this published article (and its supplementary information files).

Human clinical studies were registered at the Japan UMIN Clinical Trials Registry (UMIN000024338 for Fig. 5 and Supplementary Fig. 4, and UMIN000020807 for

Fig. 6).

DNA sequence of rRNA have been deposited in Genbank (accession number; MK182799).

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession SJRZ00000000. The version described in this paper is version DDBJ/ENA/GenBank under the accession SJRZ00000000.

The E. faecalis YM0831 (0831-07) has been deposited in National Institute of Technology and Evaluation (Deposit number: P-02309, NITE, Tokyo, Japan).

Plasmid (pMan operon) have been deposited in Addgene (Deposit number; 76594).

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](https://www.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	More than three samples. The data are shown as the mean \pm SEM. Unless otherwise noted, the significance of differences was calculated using a two-tailed Student's t-test at the significance level $P < 0.05$.
Data exclusions	No data were excluded from the analyses.
Replication	The reproducibility of the experimental findings were checked. Human clinical studies were not checked the reproducibility.
Randomization	Random
Blinding	The investigator (Dr. Setsuo Hasegawa, MD) and doctors in Osaki Hospital Tokyo Heart Center, Tokyo, Japan was blinded.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Unique biological materials
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Human research participants

Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Caco-2 cells
Authentication	American Type Cell Collection (ATCC, Manassas, VA, USA)
Mycoplasma contamination	Caco-2 cells were tested negative for mycoplasma contamination by the ATCC.
Commonly misidentified lines (See ICLAC register)	<i>Name any commonly misidentified cell lines used in the study and provide a rationale for their use.</i>

Animals and other organisms

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

Laboratory animals	Silkworms. Fertilized silkworm eggs (Bombyx mori, Hu · Yo x Tukuba · Ne) were purchased from Ehime sericulture incorporated company (Ehime, Japan).
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Wild animals

Provide details on animals observed in or captured in the field; report species, sex and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.

Field-collected samples

For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics

Population characteristics were described in supplementary Table 4.

Recruitment

Participants were randomly recruited at Osaki Hospital Tokyo Heart Center, Tokyo, Japan, and all subjects provided written informed consent before initiation of any study procedures.