nature portfolio

Corresponding author(s): Oon Tek NG

Last updated by author(s): Jul 30, 2025

Reporting Summary

Nature Portfolio 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 Portfolio policies, see our Editorial Policies 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	No software was used
Data analysis	A detailed description of the tools used to analyse the data are available in the Methods section of the manuscript. A list is provided here as follows: Cutadapt v1.14, Guppy v3.2.6, MLST v2.23, MOB-suite v3.1.4, GenomeTester4, igraph v1.6.0, ComplexHeatmap, Prokka v1.14.6, Panaroo v1.5.0, ggtree v3.3.0, ggplot2 package v3.3.5, NCBI AMRFinderPlus v3.10.21, ABRicate v1.0.0, Bakta v1.11.0, NCBI Blastx v2.9.0-2, Blastn 2.9.0-2, PlasClass v0.1.1

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The Illumina short-read sequencing data generated in this study have been deposited in the NCBI Sequence Read Archive database under accession codes PRJNA757551 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA757551/] and PRJNA765801 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA765801/]. The Oxford

Nanopore Technologies long-read sequencing data generated in this study have been deposited in the NCBI Sequence Read Archive database under accession codes PRJNA801415 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA801415/] and PRJNA801416 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA801416/]. The hybrid assembly data generated in this study have been deposited in the GenBank database under accession codes PRJNA1171009 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1171009/], PRJNA1171156 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1171156/], PRJNA1171157 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1171157/] and PRJNA1171553 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1171553/]. The sample-specific hybrid assembly accession codes are provided in Supplementary Data 1. Three samples were not uploaded because they did not meet the GenBank assembly size criteria

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	N.A. (Information not reported in manuscript)
Reporting on race, ethnicity, or other socially relevant groupings	N.A. (Information not reported in manuscript)
Population characteristics	N.A. (Information not reported in manuscript)
Recruitment	From September 6, 2010 to April 28, 2015, all carbapenem-resistant Enterobacterales (CRE) isolates from inpatient clinical and surveillance cultures were collected across participating sites
Ethics oversight	The study was reviewed and approved by the ethics institutional review boards of National Health Group Singapore (DSRB reference: 2014/00617) which did not require that patients provide written informed consent. The waiver of informed consent was approved by the institutional ethics committee on the grounds that the study met two key criteria: (i) the study posed no more than minimal risk to the research participants, and (ii) waiver of informed consent did not adversely affect the rights and welfare of the research participants. To elaborate, this study only involved medical records' review and sequencing of isolates. No intervention to patient's care was conducted and the probability and magnitude of harm or discomfort anticipated in the research were not greater than those ordinarily encountered in daily life. Data collected was not sensitive in nature and was data that would be collected regardless of study participation, as part of standard clinically indicated procedures. Additionally, data collected was de-identified and anonymized. All identifying information from the isolates was removed before they were sent to the respective laboratories for sequencing. Data collection and sequencing of isolates did not affect the level of clinical care received by the subjects or any clinical decisions that the clinical team had already made.

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

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 sample size calculation was made. Retrospective cohort study design. From September 6, 2010 to April 28, 2015, all carbapenem-resistant Enterobacterales (CRE) isolates from inpatient clinical and surveillance cultures were collected across participating sites.
Data exclusions	The number and disposition of the isolates collected and the final population analysed in the study is detailed in the manuscript and Supplementary Information.
Replication	This retrospective cohort study adhered to the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) statement guidelines for reporting observational studies
Randomization	N.A. Retrospective cohort study design
Blinding	N.A. Retrospective cohort study design

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 and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Plants

Seed stocks	N.A.
Novel plant genotypes	N.A.
Authentication	N.A.