nature portfolio

Corresponding author(s): Ruggero La Rosa

Last updated by author(s): Jun 2, 2026

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 to collect data.
Data analysis	GraphPad Prism 8 version 8.4.3, JMP Pro version 17, LasX software (Leica).

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

All data supporting the findings in this manuscript are either provided in the supplementary data file or upon request from the corresponding author.

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	Sex and gender are not applicable to this study, as no human participants or primary human samples were involved. Experiments were conducted using an immortalized human airway epithelial cell line.
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable. This study does not involve human participants or population-based analyses. Experiments were performed using bacterial strains and an established human airway epithelial cell line.
Population characteristics	Not applicable. This study does not involve human participants or population-based analyses. Experiments were performed using bacterial strains and an established human airway epithelial cell line.
Recruitment	Not applicable. No human participants were recruited for this study.
Ethics oversight	The use of stored clinical Pseudomonas aeruginosa isolates was approved by the local ethics committee at the Capital Region of Denmark (Region Hovedstaden; registration number H-21078844). No human participants or identifiable personal data were involved in this study.

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	Sample sizes were not predetermined using statistical methods. Instead, they were chosen based on standard practice in experimental infection studies using airway epithelial models and are consistent with those used in previous studies employing similar approaches. These sample sizes were sufficient to ensure reproducibility and to detect robust differences between conditions.
Data exclusions	No data were excluded.
Replication	Each experiment included at least three independent biological replicates, as indicated in the Methods and figure legends. Key findings were reproducible across independent experiments and across multiple clinical strain backgrounds.
Randomization	Randomization was not required, as experiments involved predefined bacterial strains and controlled in vitro infection conditions, without allocation of subjects or samples to different treatment groups.
Blinding	Blinding was not applied, as experiments involved direct comparisons between predefined bacterial strains under controlled conditions. Sample identity was inherently linked to strain preparation during infection experiments, making blinding impractical. Outcome measures were based on objective quantitative readouts, minimizing potential bias.

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

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Non-smoker–derived immortalized human bronchial basal cell line BCi-NS1.1 (doi: 10.1186/1465-9921-14-135). Source: Professor Ronald G. Crystal (Weill Cornell Medical College, New York, USA).
Authentication	BCi-NS1.1 is a well-characterized human bronchial epithelial cell line that has been previously described in the literature and is widely used for differentiated airway epithelial cultures. No additional authentication testing was performed in this study. The identity and characteristics of the cell line are described in the original publication and subsequent studies using this model.
Mycoplasma contamination	No mycoplasma contamination was observed during the course of this study.
Commonly misidentified lines (See ICLAC register)	The BCi-NS1.1 airway epithelial cell line used in this study is not listed in the International Cell Line Authentication Committee (ICLAC) database of commonly misidentified cell lines.

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*