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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	Relevant data was collected by Microsoft Excel 2017.
Data analysis	Data analysis was conducted by using the SPSS software v29.0 and R v4.4.1.

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

Data is deposited in National Microbiology Data Center (NMDC) with the accession number NMDC40064186 (https:/nmdc.cn/resource/genomics/sra/detai1/NMDC40064186).

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 information was collected as part of the clinical characteristics from hospital medical records. The study included 662 male and 517 female participants. Subgroup analyses based on sex and gender were conducted to demonstrate the clinical characteristics.
Reporting on race, ethnicity, or other socially relevant groupings	Race and ethnicity information were not collected as it was not relevant to the research objectives.
Population characteristics	The study included a total of 1179 participants including 662 male and 517 female. Baseline characteristics of the participants were collected, including comorbidities: 436 individuals had diabetes mellitus, 222 had pulmonary disease, 427 had digestive diseases, 377 had urological diseases, 64 had rheumatic diseases, 440 had cerebrovascular diseases, 239 had cancer, and 40 had non-solid tumors. Additionally, health insurance information was recorded, with 923 participants covered under superior insurance, 161 under non-superior insurance, and 95 with unknown insurance status. The participants long-term residence categories were also documented, with 998 individuals residing in urban areas, 159 in rural areas, and 22 with unknown residence.
Recruitment	Patients who isolated Klebsiella pneumoniae (Kp) verified by whole genome sequencing (WGS) were enrolled.
Ethics oversight	The protocol for this study was approved by the Peking University Third Hospital Medical Science Research Ethics Committee.

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	The study included a total of 1179 participants. The sample size was determined by the total number of patients who met the inclusion criteria during the study period. As this was a retrospective observational study, a formal power calculation was not performed. Patients who isolated Klebsiella pneumoniae (Kp) verified by whole genome sequencing (WGS) were enrolled, and enough medical records were included in the analysis.
Data exclusions	Patients were excluded if they did not have enough medical records, if isolates were not verified as Klebsiella pneumoniae (Kp) by whole genome sequencing (WGS), or if the WGS data failed quality control.
Replication	The findings are supported by robust inclusion criteria, comprehensive data collection, and verification of Klebsiella pneumoniae (Kp) isolates through whole genome sequencing (WGS), ensuring the reliability and reproducibility.
Randomization	No randomization was applied in this study. Propensity score matching (PSM) was conducted to balance baseline characteristics between patient groups.
Blinding	Blinding was not applicable to this study as it was a retrospective study.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	This is a retrospective study.
Study protocol	The protocol for this study was approved by the Peking University Third Hospital Medical Science Research Ethics Committee.
Data collection	Data were retrospectively collected from the electronic medical record system between 2017 and 2023. Collected data included demographic information, comorbidities, laboratory results, treatment records, and outcomes. Klebsiella pneumoniae (Kp) isolates were confirmed through whole genome sequencing (WGS).
Outcomes	The primary outcomes of this study were 14-day, 28-day, and 90-day mortality rates. The secondary outcomes included: 14-day, 28-day, and 90-day poor prognosis rates, incidence of sepsis and septic shock.

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.*