

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

Data collection was carried out through the DATASUS portal (<https://datasus.saude.gov.br/>) and the "Microdados de Vigilância em Saúde" portal of the Espírito Santo State Health Secretariat (<https://app.wiki.saude.es.gov.br/pt-br/vigilanciasaude/sistema-de-informacao-e-dados/microdados>).

Data analysis

A descriptive analysis was performed for the total number of confirmed dengue cases, hospitalizations, and deaths over the study period. Code for data processing is available at: <https://codeocean.com/capsule/2090307/tree>

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 data supporting the findings of this study are available from the DATASUS at [<https://datasus.saude.gov.br/>] and the “Microdados de Vigilância em Saúde” portal of the Espírito Santo State Health Secretariat (<https://app.wiki.saude.es.gov.br/pt-br/vigilanciasaude/sistema-de-informacao-e-dados/microdados>).

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	The findings were based solely on biological sex; data regarding gender were not collected.
Reporting on race, ethnicity, or other socially relevant groupings	Race and ethnicity data were retrieved from administrative records within the Brazilian National Disease Surveillance System (SINAN). Although accessed through administrative databases, these variables are originally collected via standardized self-reporting at the time of notification, following the official categories defined by the Brazilian Institute of Geography and Statistics (IBGE).
Population characteristics	The study population comprises 14,215,369 laboratory-confirmed and clinical-epidemiological diagnosed dengue cases reported in Brazil between 2014 and 2024. The cohort includes individuals of all age groups, ranging from <1 to >100 years old. The variables analyzed included sociodemographic characteristics (age, sex, municipality of residence), clinical features (systemic signs and symptoms of dengue), disease outcomes (hospitalization, severity, and death), and final case classification of confirmed cases. No genotypic or clinical treatment data were available in this nationwide administrative dataset.
Recruitment	As this is a retrospective cohort study, participants were not actively recruited. Instead, data were retrieved from the public, nationwide database maintained by the Brazilian Ministry of Health, the Notifiable Diseases Information System (SINAN).
Ethics oversight	<i>Identify the organization(s) that approved the study protocol.</i>

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 statistical method was used to predetermine sample size. The sample size was determined by the total number of dengue cases reported to the Brazilian National Notifiable Diseases Information System (SINAN) during the study period (2014–2024).
Data exclusions	Data exclusion criteria were pre-established. To ensure the specificity of the findings, entries classified as 'discarded' (non-confirmed) or 'under investigation' in the SINAN database were excluded from the final analysis. Only laboratory-confirmed or clinically-epidemiologically confirmed cases were included in the cohort.
Replication	The robustness of the findings was ensured through rigorous data cleaning protocols and sensitivity analyses across different regions and years. All statistical scripts were peer-reviewed internally by the research team to ensure reproducibility and consistency of the results. All attempts at internal replication were successful.
Randomization	Not applicable
Blinding	Not applicable

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

Methods

- 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

- 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
- Study protocol
- Data collection
- Outcomes

Plants

- Seed stocks
- Novel plant genotypes
- Authentication