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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	Data were compiled from published studies and publicly available datasets, including data from WHO, UNICEF and the World Bank. No custom software was developed specifically for primary data collection.
Data analysis	All statistical analyses and modelling were conducted using R (version 4.3.3). Custom R scripts were developed for country-specific RSV burden estimation, including risk-factor-based incidence prediction, hospitalisation modelling, mortality estimation, uncertainty quantification and model validation. Analysis code is available at https://github.com/slren95/RSV_burden_by_country_LMIC.

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 used in this study are publicly available and have been appropriately cited. The corresponding data sources are detailed in the Methods and Supplementary Material, which also provides the country-specific RSV burden estimates generated in this study.

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	This study estimated RSV disease burden by age group and country using previously published and publicly available data. Sex- and gender-specific analyses were not performed because the modelling framework focused on age-specific burden estimates and the available input data did not consistently support sex-disaggregated analyses.
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable. This study used country-level and age-specific data to estimate RSV disease burden. Individual-level information on race or ethnicity was not collected or analysed, and no race- or ethnicity-specific analyses were performed.
Population characteristics	The study population comprised children younger than five years across 135 low- and middle-income countries, based on the 2019 World Bank income classification. Disease burden was estimated for infants aged 0–<6 months and 6–<12 months and children aged 12–<60 months, with additional estimates for infants aged 0–<12 months and children aged 0–<60 months.
Recruitment	Not applicable. No participants were directly recruited. The study was based on secondary analysis and modelling of previously published and publicly available data.
Ethics oversight	No new human participants were recruited, and no identifiable individual-level data were collected. The study was based on secondary analysis of previously published and publicly available data.

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 135 low- and middle-income countries classified according to the 2019 World Bank income classification. All countries meeting the study eligibility criteria were included. No formal sample size calculation was performed, as this was a modelling study aiming to provide country-specific RSV burden estimates across all eligible countries.
Data exclusions	Countries were included according to the 2019 World Bank income classification. The inclusion and exclusion criteria for the empirical studies and data used to inform model parameters are described in the Methods and Supplementary Material.
Replication	Model performance was evaluated through internal and external validation against empirical estimates of RSV disease burden. The validation procedures and results are described in the Methods and Supplementary Material.
Randomization	Not applicable. This was an observational data-based modelling study, and no participants, countries or samples were randomly allocated to experimental groups.
Blinding	Not applicable. This study involved secondary data analysis and statistical modelling, with no experimental group allocation or intervention. Blinding was therefore 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

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	Not applicable.
Novel plant genotypes	Not applicable.
Authentication	Not applicable.