Supplementary Material

Global meta-analysis of associations between ambient temperature and pathogen-specific respiratory infections

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List of abbreviations

OHAT	Office of Health Assessment and Translation
IV	Influenza virus
HPIV	Human parainfluenza virus
RSV	Respiratory syncytial virus
ARI	Acute respiratory infection
GBD	Global Burden of Diseases, Injuries, and Risk Factors Study
DALYs	disability-adjusted life years
RTIs	Respiratory tract infections
HMPV	Human metapneumovirus
HRV	Human rhinovirus
HAdV	Human adenovirus
HBoV	Human bocavirus
MERS-CoV	Middle East Respiratory Syndrome Coronavirus
SARS-CoV	Severe acute respiratory syndrome coronavirus
SARS-CoV-2	Severe acute respiratory syndrome coronavirus 2
HCoV	Human coronavirus
EV	Enterovirus
M. pneumoniae	*Mycoplasma pneumoniae*
C. pneumoniae	*Chlamydophila pneumoniae*
S. pneumoniae	*Streptococcus pneumoniae*
S. pyogenes	*Streptococcus pyogenes pharyngiti*
H. influenzae	*Haemophilus influenzae*
L. pneumoniae	*Legionella pneumoniae*
M. catarrhalis	*Moraxella catarrhalis*
P. aeruginosa	*Pseudomonas aeruginosa*
CBM	China Biology Medicine
WHO	World Health Organization

Table S1. PRISMA Checklist

Section and Topic	Item #	Checklist item	Location where item is reported
TITLE			
Title	1	Identify the report as a systematic review.	1
ABSTRACT			
Abstract	2	See the PRISMA 2020 for Abstracts checklist.	1-2
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of existing knowledge.	3-4
Objectives	4	Provide an explicit statement of the objective(s) or question(s) the review addresses.	4
METHODS			
Eligibility criteria	5	Specify the inclusion and exclusion criteria for the review and how studies were grouped for the syntheses.	4-5
Information sources	6	Specify all databases, registers, websites, organisations, reference lists and other sources searched or consulted to identify studies. Specify the date when each source was last searched or consulted.	5
Search strategy	7	Present the full search strategies for all databases, registers and websites, including any filters and limits used.	5
Selection process	8	Specify the methods used to decide whether a study met the inclusion criteria of the review, including how many reviewers screened each record and each report retrieved, whether they worked independently, and if applicable, details of automation tools used in the process.	5
Data collection process	9	Specify the methods used to collect data from reports, including how many reviewers collected data from each report, whether they worked independently, any processes for obtaining or confirming data from study investigators, and if applicable, details of automation tools used in the process.	6
Data items	10a	List and define all outcomes for which data were sought. Specify whether all results that were compatible with each outcome domain in each study were sought (e.g. for all measures, time points, analyses), and if not, the methods used to decide which results to collect.	6
	10b	List and define all other variables for which data were sought (e.g. participant and intervention characteristics, funding sources). Describe any assumptions made about any missing or unclear information.	6
Study risk of bias assessment	11	Specify the methods used to assess risk of bias in the included studies, including details of the tool(s) used, how many reviewers assessed each study and whether they worked independently, and if applicable, details of automation tools used in the process.	7
Effect measures	12	Specify for each outcome the effect measure(s) (e.g. risk ratio, mean difference) used in the synthesis or presentation of results.	8
Synthesis methods	13a	Describe the processes used to decide which studies were eligible for each synthesis (e.g. tabulating the study intervention characteristics and comparing against the planned groups for each synthesis (item #5)).	8
	13b	Describe any methods required to prepare the data for presentation or synthesis, such as handling of missing summary statistics, or data conversions.	8
	13c	Describe any methods used to tabulate or visually display results of individual studies and syntheses.	8

Section and Topic	Item #	Checklist item	Location where item is reported
	13d	Describe any methods used to synthesize results and provide a rationale for the choice(s). If meta-analysis was performed, describe the model(s), method(s) to identify the presence and extent of statistical heterogeneity, and software package(s) used.	8-9
	13e	Describe any methods used to explore possible causes of heterogeneity among study results (e.g. subgroup analysis, meta-regression).	8-9
	13f	Describe any sensitivity analyses conducted to assess robustness of the synthesized results.	8-9
Reporting bias assessment	14	Describe any methods used to assess risk of bias due to missing results in a synthesis (arising from reporting biases).	7-8
Certainty assessment	15	Describe any methods used to assess certainty (or confidence) in the body of evidence for an outcome.	7-8
RESULTS			
Study selection	16a	Describe the results of the search and selection process, from the number of records identified in the search to the number of studies included in the review, ideally using a flow diagram.	9
	16b	Cite studies that might appear to meet the inclusion criteria, but which were excluded, and explain why they were excluded.	9
Study characteristics	17	Cite each included study and present its characteristics.	9
Risk of bias in studies	18	Present assessments of risk of bias for each included study.	10
Results of individual studies	19	For all outcomes, present, for each study: (a) summary statistics for each group (where appropriate) and (b) an effect estimate and its precision (e.g. confidence/credible interval), ideally using structured tables or plots.	9-12
Results of syntheses	20a	For each synthesis, briefly summarise the characteristics and risk of bias among contributing studies.	9-12
	20b	Present results of all statistical syntheses conducted. If meta-analysis was done, present for each the summary estimate and its precision (e.g. confidence/credible interval) and measures of statistical heterogeneity. If comparing groups, describe the direction of the effect.	9-12
	20c	Present results of all investigations of possible causes of heterogeneity among study results.	9-12
	20d	Present results of all sensitivity analyses conducted to assess the robustness of the synthesized results.	9-12
Reporting biases	21	Present assessments of risk of bias due to missing results (arising from reporting biases) for each synthesis assessed.	12
Certainty of evidence	22	Present assessments of certainty (or confidence) in the body of evidence for each outcome assessed.	12-13
DISCUSSION			
Discussion	23a	Provide a general interpretation of the results in the context of other evidence.	13-14
	23b	Discuss any limitations of the evidence included in the review.	14-16

Section and Topic	Item #	Checklist item	Location where item is reported
	23c	Discuss any limitations of the review processes used.	15-16
	23d	Discuss implications of the results for practice, policy, and future research.	16
OTHER INFORMATION			
Registration and protocol	24a	Provide registration information for the review, including register name and registration number, or state that the review was not registered.	1
	24b	Indicate where the review protocol can be accessed, or state that a protocol was not prepared.	5
	24c	Describe and explain any amendments to information provided at registration or in the protocol.	5
Support	25	Describe sources of financial or non-financial support for the review, and the role of the funders or sponsors in the review.	Title page
Competing interests	26	Declare any competing interests of review authors.	Title page
Availability of data, code and other materials	27	Report which of the following are publicly available and where they can be found: template data collection forms; data extracted from included studies; data used for all analyses; analytic code; any other materials used in the review.	/

From: Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, et al. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. BMJ 2021;372:n71. doi: 10.1136/bmj.n71

For more information, visit: http://www.prisma-statement.org/

Table S2. Search strategy: terms, databases, limitations and number of articles for review

PubMed database	
#1	("temperature"[MeSH Terms] OR "temperature"[All Fields] OR "temperatures"[All Fields] OR "temperature s"[All Fields] OR "ambient temperature"[All Fields] OR "seasurface temperature"[All Fields] OR ("climate"[MeSH Terms] OR "climate"[All Fields] OR "climates"[All Fields] OR "climate s"[All Fields] OR "climatic"[All Fields] OR "climatically"[All Fields]) OR ("weather"[MeSH Terms] OR "weather"[All Fields] OR "weatherability"[All Fields] OR "weatherable"[All Fields] OR "weathered"[All Fields] OR "weathering"[All Fields] OR "weathers"[All Fields]) OR ("meteorologic"[All Fields] OR "meteorological"[All Fields] OR "meteorologically"[All Fields]) OR "climate change"[All Fields] OR "meteorolog*"[All Fields] OR "extreme weather"[All Fields] OR "hot weather"[All Fields] OR "cold weather"[All Fields] OR "meteorological factor"[All Fields] OR "climatic factor"[All Fields] OR "global warming"[All Fields])
#2	("Bacterial Pneumonia"[All Fields] OR "pneumonia bacterial"[All Fields] OR "Bacterial Pneumonias"[All Fields] OR "Bacterial Infections and Mycoses"[All Fields] OR "Bacterial Infections"[All Fields] OR "pneumonia pneumococcal"[All Fields] OR "pneumonia staphylococcal"[All Fields] OR "Streptococcus pneumoniae"[All Fields] OR "Chlamydial Pneumonia"[All Fields] OR "pneumonia mycoplasma"[All Fields] OR "Mycoplasma pneumoniae"[All Fields] OR "Schizoplasma pneumoniae"[All Fields] OR "Chlamydophila pneumoniae"[All Fields] OR "Lower respiratory tract"[All Fields] OR "upper respiratory tract"[All Fields] OR "Human Rhinovirus"[All Fields] OR "Human Enterovirus"[All Fields] OR "Respiratory Tract Infections"[All Fields] OR "Respiratory System Infections"[All Fields] OR "Respiratory System Infection"[All Fields] OR "Upper Respiratory Tract Infections"[All Fields] OR "Upper Respiratory Infections"[All Fields] OR "Upper Respiratory Tract Infection"[All Fields] OR "respiratory infections"[All Fields] OR "respiratory virus"[All Fields] OR "Respiratory syncytial virus"[All Fields] OR "Respiratory Syncytial Viruses"[All Fields] OR "RSV"[All Fields] OR "Chimpanzee Coryza Agent"[All Fields] OR ("adenoviridae"[MeSH Terms] OR "adenoviridae"[All Fields] OR "adenoviruses"[All Fields] OR "adenoviruse"[All Fields]) OR "Human Adenovirus"[All Fields] OR Enterovirus [All Fields] OR "Human Adenoviruses"[All Fields] OR "APC Viruses"[All Fields] OR "APC Virus"[All Fields] OR ("orthomyxoviridae"[MeSH Terms] OR "orthomyxoviridae"[All Fields] OR "orthomyxoviruses"[All Fields]) OR ("orthomyxoviridae"[MeSH Terms] OR "orthomyxoviridae"[All Fields] OR "myxoviruses"[All Fields]) OR "Influenza viruses"[All Fields] OR "Influenza A virus"[All Fields] OR "Influenza A viruses"[All Fields] OR "Orthomyxovirus Type A"[All Fields] OR "Influenza Viruses Type A"[All Fields] OR "Influenza B virus"[All Fields] OR "influenza B viruses"[All Fields] OR "Influenza Viruses Type B"[All Fields] OR "Influenza B 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"Coryza Virus"[All Fields] OR ("coronavirus"[MeSH Terms] OR "coronavirus"[All Fields] OR "coronaviruses"[All Fields]) OR "SARS coronavirus"[All Fields] OR "severe acute respiratory syndrome related coronavirus"[All Fields] OR "severe acute respiratory syndrome related coronavirus"[All Fields] OR "HCoV-SARS"[All Fields] OR "SARS Virus"[All Fields] OR ("severe acute respiratory syndrome related coronavirus"[MeSH Terms] OR ("severe"[All Fields] AND "acute"[All Fields] AND "respiratory"[All Fields] AND "syndrome related"[All Fields] AND "coronavirus"[All Fields]) OR "severe acute respiratory syndrome related coronavirus"[All Fields] OR "sarbecovirus"[All Fields]) OR ("severe acute respiratory syndrome related coronavirus"[MeSH Terms] OR ("severe"[All Fields] AND "acute"[All Fields] AND "respiratory"[All Fields] AND "syndrome related"[All Fields] AND "coronavirus"[All Fields]) OR "severe acute respiratory syndrome related coronavirus"[All Fields] OR "sarbecoviruses"[All Fields]) OR "Severe 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	Fields]) OR "Sore Throats"[All Fields] OR "Acute viral laryngitis"[All Fields] OR "acute pharyngitis"[All Fields] OR "acute epiglottitis"[All Fields] OR ("epiglottal"[All Fields] OR "epiglottis"[MeSH Terms] OR "epiglottis"[All Fields] OR "epiglottic"[All Fields] OR "epiglottitis"[MeSH Terms] OR "epiglottitis"[All Fields] OR "epiglottitides"[All Fields]) OR ("bronchitis"[MeSH Terms] OR "bronchitis"[All Fields] OR "bronchitides"[All Fields]) OR ("larynges"[All Fields] OR "laryngitis"[MeSH Terms] OR "laryngitis"[All Fields] OR "laryngitides"[All Fields] OR "larynx"[MeSH Terms] OR "larynx"[All Fields] OR "laryngeal"[All Fields]) OR ("legionellosis"[MeSH Terms] OR "legionellosis"[All Fields] OR "legionelloses"[All Fields]) OR "Lung Abscess"[All Fields] OR ("blastomycosis"[MeSH Terms] OR "blastomycosis"[All Fields] OR "blastomycoses"[All Fields]) OR "pneumonia pneumocystis"[All Fields] OR ("pharyngitis"[MeSH Terms] OR "pharyngitis"[All Fields] OR "pharyngitides"[All Fields]) OR ("nasopharyngitis"[MeSH Terms] OR "nasopharyngitis"[All Fields]) OR "Retropharyngeal Abscess"[All Fields] OR ("pleurisy"[MeSH Terms] OR "pleurisy"[All Fields] OR "pleurisies"[All Fields]) OR ("pleuropneumonia"[MeSH Terms] OR "pleuropneumonia"[All Fields] OR "pleuropneumonias"[All Fields] OR "pleuropneumoniae"[All Fields]) OR ("pneumonia"[MeSH Terms] OR "pneumonia"[All Fields] OR "pneumonias"[All Fields] OR "pneumoniae"[All Fields] OR "pneumoniae s"[All Fields]) OR ("bronchopneumonia"[MeSH Terms] OR "bronchopneumonia"[All Fields] OR "bronchopneumonias"[All Fields] OR "bronchopneumoniae"[All Fields]) OR ("pleuropneumonia"[MeSH Terms] OR "pleuropneumonia"[All Fields] OR "pleuropneumonias"[All Fields] OR "pleuropneumoniae"[All Fields]) OR ("rhinitis"[MeSH Terms] OR "rhinitis"[All Fields] OR "rhinitides"[All Fields]) OR ("rhinoscleroma"[MeSH Terms] OR "rhinoscleroma"[All Fields] OR "rhinoscleromas"[All Fields]) OR "Severe Acute Respiratory Syndrome"[All Fields] OR ("paranasal sinuses"[MeSH Terms] OR ("paranasal"[All Fields] AND "sinuses"[All Fields]) OR "paranasal sinuses"[All Fields] OR "sinuses"[All Fields] OR "sinusal"[All Fields] OR "sinuse"[All Fields] OR "sinusitis"[MeSH Terms] OR "sinusitis"[All Fields] OR "sinusitides"[All Fields]) OR "Allergic Fungal Sinusitis"[All Fields] OR "Ethmoid Sinusitis"[All Fields] OR "Frontal Sinusitis"[All Fields] OR "Maxillary Sinusitis"[All Fields] OR "Sphenoid Sinusitis"[All Fields] OR ("supraglottitis"[MeSH Terms] OR "supraglottitis"[All Fields]) OR ("epiglottal"[All Fields] OR "epiglottis"[MeSH Terms] OR "epiglottis"[All Fields] OR "epiglottic"[All Fields] OR "epiglottitis"[MeSH Terms] OR "epiglottitis"[All Fields] OR "epiglottitides"[All Fields]) OR ("tracheitis"[MeSH Terms] OR "tracheitis"[All Fields]) OR ("silicotuberculosis"[MeSH Terms] OR "silicotuberculosis"[All Fields]) OR "Whooping Cough"[All Fields])
#3	#1 AND #2
Cochrane Central Register of Controlled Trials	
#1	MeSH descriptor: [Temperature] explode all trees
#2	MeSH descriptor: [Climate Change] explode all trees
#3	MeSH descriptor: [Weather] explode all trees
#4	#1 or #2 or #3
#10	(temperature or "ambient temperature" or "seasurface temperature" or climate or weather or meteorological or "climate change" or Meteorolog* or "extreme weather" or "meteorological factor" or "hot weather" or "cold weather" or "climatic factor" or "global warming"):ti,ab,kw
#11	#9 or #10
#12	MeSH descriptor: [Respiratory Tract Infections] explode all trees
#13	MeSH descriptor: [Pneumonia, Bacterial] explode all trees
#14	MeSH descriptor: [Respiratory Syncytial Viruses] explode all trees
#15	MeSH descriptor: [Mycoplasma pneumoniae] explode all trees
#16	MeSH descriptor: [Adenoviridae] explode all trees
#17	#12 or #13 or #14 or #15 or #16
#18	("Bacterial Pneumonia" or "Pneumonia, Bacterial" or "Bacterial Pneumonias" or "Bacterial Infections and Mycoses" or "Bacterial Infections" or "Pneumonia, Pneumococcal" or "Pneumonia, Staphylococcal" or "Streptococcus pneumoniae" or "Chlamydial Pneumonia" or "Pneumonia, Mycoplasma" or "Mycoplasma pneumoniae" or "Schizoplasma pneumoniae" or "Chlamydophila pneumoniae" or "Lower respiratory tract" or "upper respiratory tract" or "Human Rhinovirus" or "Human Enterovirus" or "Respiratory Tract Infections" or "Respiratory System Infections" or "Respiratory System Infection" or "Upper Respiratory Tract Infections" or "Upper Respiratory Infections" or "Upper Respiratory Tract Infection" or "respiratory infections" or "respiratory virus" or "Respiratory syncytial virus" or "Respiratory Syncytial Viruses" or "RSV" or "Chimpanzee Coryza Agent" or Adenoviruses or "Human Adenovirus" or "Human Adenoviruses" or "APC Viruses" or "APC Virus" or Orthomyxoviruses or Myxoviruses or "Influenza viruses" or "Influenza A virus" or "Influenza A viruses" or "Orthomyxovirus Type A" or "Influenza Viruses Type A" or "Influenza B virus" or "influenza B viruses" or "Influenza Viruses Type B" or "Influenza B virus" or "Influenzavirus C" or "Influenza C Virus" or "Influenza C Viruses" or "Human parainfluenza viruses" or "Parainfluenza Virus 2, Human" or "Parainfluenza Virus Type 2" or "Croup-Associated Viruses" or "Croup Associated Viruses" or "Human parainfluenza virus 2" or "Croup-Associated Virus" or "Croup Associated Virus" or "HPIV" or Metapneumovirus or Metapneumoviruses or "Human Metapneumoviruses" or "Human Metapneumovirus" or "HMPV" or Rhinoviruses or "Human Rhinovirus" or "Common Cold Virus" or "Common Cold Viruses" or "Coryza Virus" or Coronaviruses or "SARS coronavirus" or "Severe acute respiratory syndrome-related coronavirus" or "Severe acute respiratory syndrome related coronavirus" or "HCoV-SARS" or "SARS Virus" or Sarbecovirus or Sarbecoviruses or "Severe acute respiratory syndrome coronavirus" or "Severe Acute Respiratory Syndrome Virus" or"SARS-Cov-2" or "HcoV" or "NL63" or "OC43" or "229E" or "HKU1"or Enterovirus or "Human bocaviruses" or "Coxiella burnetii" or "Chlamydophila psittaci" or "Legionella pneumophila" or "Staphylococcus aureus" or "Haemophilus influenzae" or "Pseudomonas

	aeruginosa" or "Klebsiella pneumoniae" or "Proteus mirabilis" or "Providencia stuartii" or "Moraxella catarrhalis" or "Streptococcus hemolyticus" or "Streptococcus anginosus" or "streptococcus pneumoniae" or "Gram-positive cocci" or "Gram-negative bacteria" or "gram-negative bacillus" or "pseudomonas aeruginosa" or Candida or "Corynebacterium diphtheriae" or "Bordetella pertussis" or "M.tuberculosis" or "Acute bronchitis" or "acute angina" or "acute tonsillitis" or tonsillitis or "Sinus Infections" or "Viral Pneumonias" or "Acute Coryza" or "Acute viral pharyngitis" or Pharyngitides or "Sore Throats" or "Acute viral laryngitis" or "acute pharyngitis" or "acute epiglottitis" or Epiglottitides or Bronchitis or Laryngitis or Legionellosis or "Lung Abscess" or Blastomycosis or "Pneumonia, Pneumocystis" or Pharyngitis or Nasopharyngitis or "Retropharyngeal Abscess" or Pleurisy or Pleuropneumonia or Pneumonia or Bronchopneumonia or Pleuropneumonia or Rhinitis or Rhinoscleroma or "Severe Acute Respiratory Syndrome" or Sinusitis or "Allergic Fungal Sinusitis" or "Ethmoid Sinusitis" or "Frontal Sinusitis" or "Maxillary Sinusitis" or "Sphenoid Sinusitis" or Supraglottitis or Epiglottitis or Tracheitis or Silicotuberculosis or "Whooping Cough"):ti,ab,kw
#19	#17 or #18
#20	#11 and #19
Scopus	
#1	(TITLE-ABS-KEY ((temperature OR "ambient temperature" OR "seasurface temperature" OR climate OR weather OR meteorological OR "climate change" OR meteorolog* OR "extreme weather" OR "meteorological factor" OR "climatic factor" OR "hot weather" OR "cold weather" OR "global warming")) AND TITLE-ABS-KEY (("Bacterial Pneumonia" OR "Pneumonia, Bacterial" OR "Bacterial Pneumonias" OR "Bacterial Infections and Mycoses" OR "Bacterial Infections" OR "Pneumonia, Pneumococcal" OR "Pneumonia, Staphylococcal" OR "Streptococcus pneumoniae" OR "Chlamydial Pneumonia" OR "Pneumonia, Mycoplasma" OR "Mycoplasma pneumoniae" OR "Schizoplasma pneumoniae" OR "Chlamydophila pneumoniae" OR "Lower respiratory tract" OR "upper respiratory tract" OR "Human Rhinovirus" OR "Human Enterovirus" OR "Respiratory Tract Infections" OR "Respiratory System Infections" OR "Respiratory System Infection" OR "Upper Respiratory Tract Infections" OR "Upper Respiratory Infections" OR "Upper Respiratory Tract Infection" OR "respiratory infections" OR "respiratory virus" OR "Respiratory syncytial virus" OR "Respiratory Syncytial Viruses" OR "RSV" OR "Chimpanzee Coryza Agent" OR adenoviruses OR "Human Adenovirus" OR "Human Adenoviruses" OR "APC Viruses" OR "APC Virus" OR orthomyxoviruses OR myxoviruses OR "Influenza viruses" OR "Influenza A virus" OR "Influenza A viruses" OR "Orthomyxovirus Type A" OR "Influenza Viruses Type A" OR "Influenza B virus" OR "influenza B viruses" OR "Influenza Viruses Type B" OR "Influenza B virus" OR "Influenzavirus C" OR "Influenza C Virus" OR "Influenza C Viruses" OR "Human parainfluenza viruses" OR "Parainfluenza Virus 2, Human" OR "Parainfluenza Virus Type 2" OR "Croup-Associated Viruses" OR "Croup Associated Viruses" OR "Human parainfluenza virus 2" OR "Croup-Associated Virus" OR "Croup Associated Virus" OR "HPIV" OR metapneumovirus OR metapneumoviruses OR "Human Metapneumoviruses" OR "Human Metapneumovirus" OR "HMPV" OR rhinoviruses OR "Human Rhinovirus" OR "Common Cold Virus" OR "Common Cold Viruses" OR "Coryza Virus" OR coronaviruses OR "SARS coronavirus" OR "Severe acute respiratory syndrome-related coronavirus" OR "Severe acute respiratory syndrome related coronavirus" OR "HCoV-SARS" OR "SARS Virus" OR "SARS-Cov-2" OR "HcoV" OR "NL63" OR "OC43" OR "229E" OR "HKU1" OR sarbecovirus OR sarbecoviruses OR "Severe acute respiratory syndrome coronavirus" OR "Severe Acute Respiratory Syndrome Virus" OR "Human bocaviruses" OR "Coxiella burnetii" OR "Chlamydophila psittaci" OR "Legionella pneumophila" OR "Staphylococcus aureus" OR "Haemophilus influenzae" OR enterovirus OR "Pseudomonas aeruginosa" OR "Klebsiella pneumoniae" OR "Proteus mirabilis" OR "Providencia stuartii" OR "Moraxella catarrhalis" OR "Streptococcus hemolyticus" OR "Streptococcus anginosus" OR "streptococcus pneumoniae" OR "Gram-positive cocci" OR "Gram-negative bacteria" OR "gram-negative bacillus" OR "pseudomonas aeruginosa" OR candida OR "Corynebacterium diphtheriae" OR "Bordetella pertussis" OR "M.tuberculosis" OR "Acute bronchitis" OR "acute angina" OR "acute tonsillitis" OR tonsillitis OR "Sinus Infections" OR "Viral Pneumonias" OR "Acute Coryza" OR "Acute viral pharyngitis" OR pharyngitides OR "Sore Throats" OR "Acute viral laryngitis" OR "acute pharyngitis" OR "acute epiglottitis" OR epiglottitides OR bronchitis OR laryngitis OR legionellosis OR "Lung Abscess" OR blastomycosis OR "Pneumonia, Pneumocystis" OR pharyngitis OR nasopharyngitis OR "Retropharyngeal Abscess" OR pleurisy OR pleuropneumonia OR pneumonia OR bronchopneumonia OR pleuropneumonia OR rhinitis OR rhinoscleroma OR "Severe Acute Respiratory Syndrome" OR sinusitis OR "Allergic Fungal Sinusitis" OR "Ethmoid Sinusitis" OR "Frontal Sinusitis" OR "Maxillary Sinusitis" OR "Sphenoid Sinusitis" OR supraglottitis OR epiglottitis OR tracheitis OR silicotuberculosis OR " Whooping Cough")))
EMBASE	
#1	temperature:ab,ti OR 'ambient temperature':ab,ti OR 'seasurface temperature':ab,ti OR rain*:ab,ti OR climate:ab,ti OR weather:ab,ti OR meteorological:ab,ti OR 'climate change':ab,ti OR 'extreme weather':ab,ti OR 'meteorological factor':ab,ti OR 'hot weather':ab,ti OR 'cold weather':ab,ti OR snow:ab,ti OR 'climatic factor':ab,ti OR 'global warming':ab,ti
#2	'bacterial pneumonia':ab,ti OR 'pneumonia, bacterial':ab,ti OR 'bacterial pneumonias':ab,ti OR 'bacterial infections':ab,ti OR mycoses:ab,ti OR 'bacterial infections':ab,ti OR 'pneumonia, pneumococcal':ab,ti OR 'pneumonia, staphylococcal':ab,ti OR 'chlamydial pneumonia':ab,ti OR 'pneumonia, mycoplasma':ab,ti OR 'mycoplasma pneumoniae':ab,ti OR 'schizoplasma pneumoniae':ab,ti OR 'chlamydophila pneumoniae':ab,ti OR 'lower respiratory tract':ab,ti OR 'upper respiratory tract':ab,ti OR 'human enterovirus':ab,ti OR 'respiratory tract infections':ab,ti OR 'respiratory system infections':ab,ti OR 'respiratory system infection':ab,ti OR 'upper respiratory tract infections':ab,ti OR 'upper respiratory infections':ab,ti OR 'upper respiratory tract infection':ab,ti OR 'respiratory infections':ab,ti OR 'respiratory virus':ab,ti OR 'respiratory syncytial virus':ab,ti OR 'respiratory

	syncytial viruses':ab,ti OR 'rsv':ab,ti OR 'chimpanzee coryza agent':ab,ti OR adenoviruses:ab,ti OR 'human adenovirus':ab,ti OR 'human adenoviruses':ab,ti OR 'apc viruses':ab,ti OR 'apc virus':ab,ti OR orthomyxoviruses:ab,ti OR myxoviruses:ab,ti OR 'influenza viruses':ab,ti OR 'influenza a virus':ab,ti OR 'influenza a viruses':ab,ti OR 'orthomyxovirus type a':ab,ti OR 'influenza viruses type a':ab,ti OR 'influenza b viruses':ab,ti OR 'influenza viruses type b':ab,ti OR 'influenza b virus':ab,ti OR 'influenzavirus c':ab,ti OR 'influenza c virus':ab,ti OR 'influenza c viruses':ab,ti OR 'human parainfluenza viruses':ab,ti OR 'parainfluenza virus 2, human':ab,ti OR 'parainfluenza virus type 2':ab,ti OR 'croup-associated viruses':ab,ti OR 'croup associated viruses':ab,ti OR 'human parainfluenza virus 2':ab,ti OR 'croup-associated virus':ab,ti OR 'croup associated virus':ab,ti OR 'hpiv':ab,ti OR metapneumovirus:ab,ti OR metapneumoviruses:ab,ti OR 'human metapneumoviruses':ab,ti OR 'human metapneumovirus':ab,ti OR 'hmpv':ab,ti OR rhinoviruses:ab,ti OR 'human rhinovirus':ab,ti OR 'common cold virus':ab,ti OR 'common cold viruses':ab,ti OR 'coryza virus':ab,ti OR coronaviruses:ab,ti OR 'sars coronavirus':ab,ti OR 'severe acute respiratory syndrome-related coronavirus':ab,ti OR 'Enterovirus':ab,ti OR 'severe acute respiratory syndrome related coronavirus':ab,ti OR 'hcov-sars':ab,ti OR 'sars virus':ab,ti OR sarbecovirus:ab,ti OR sarbecoviruses:ab,ti OR 'severe acute respiratory syndrome coronavirus':ab,ti OR 'severe acute respiratory syndrome virus':ab,ti OR 'HcoV':ab,ti OR 'NL63':ab,ti OR 'OC43':ab,ti OR '229E':ab,ti OR 'HKU1':ab,ti OR 'human bocaviruses':ab,ti OR 'coxiella burnetii':ab,ti OR 'chlamydophila psittaci':ab,ti OR 'legionella pneumophila':ab,ti OR 'staphylococcus aureus':ab,ti OR 'haemophilus influenzae':ab,ti OR 'klebsiella pneumoniae':ab,ti OR 'proteus mirabilis':ab,ti OR 'providencia stuartii':ab,ti OR 'moraxella catarrhalis':ab,ti OR 'streptococcus hemolyticus':ab,ti OR 'streptococcus anginosus':ab,ti OR 'streptococcus pneumoniae':ab,ti OR 'gram-positive cocci':ab,ti OR 'gram-negative bacteria':ab,ti OR 'gram-negative bacillus':ab,ti OR 'pseudomonas aeruginosa':ab,ti OR candida:ab,ti OR 'corynebacterium diphtheriae':ab,ti OR 'bordetella pertussis':ab,ti OR 'm.tuberculosis':ab,ti OR 'acute bronchitis':ab,ti OR 'acute angina':ab,ti OR 'acute tonsillitis':ab,ti OR tonsillitis:ab,ti OR 'sinus infections':ab,ti OR 'viral pneumonias':ab,ti OR 'acute coryza':ab,ti OR 'acute viral pharyngitis':ab,ti OR pharyngitides:ab,ti OR 'sore throats':ab,ti OR 'acute viral laryngitis':ab,ti OR 'acute pharyngitis':ab,ti OR 'acute epiglottitis':ab,ti OR epiglottitides:ab,ti OR bronchitis:ab,ti OR laryngitis:ab,ti OR legionellosis:ab,ti OR 'lung abscess':ab,ti OR blastomycosis:ab,ti OR 'pneumonia, pneumocystis':ab,ti OR pharyngitis:ab,ti OR nasopharyngitis:ab,ti OR 'retropharyngeal abscess':ab,ti OR pleurisy:ab,ti OR pneumonia:ab,ti OR bronchopneumonia:ab,ti OR pleuropneumonia:ab,ti OR rhinitis:ab,ti OR rhinoscleroma:ab,ti OR 'severe acute respiratory syndrome':ab,ti OR sinusitis:ab,ti OR 'allergic fungal sinusitis':ab,ti OR 'ethmoid sinusitis':ab,ti OR 'frontal sinusitis':ab,ti OR 'maxillary sinusitis':ab,ti OR 'sphenoid sinusitis':ab,ti OR supraglottitis:ab,ti OR epiglottitis:ab,ti OR tracheitis:ab,ti OR silicotuberculosis:ab,ti OR 'whooping cough':ab,ti
#3	#1 AND #2
Web of Science	
#1	TS= (temperature or "ambient temperature" or “seasurface temperature” or climate or weather or meteorological or “climate change” or “extreme weather” or “meteorological factor” or “hot weather” or “cold weather” or “climatic factor” or “global warming”)
#2	TS= (“Bacterial Pneumonia” or “Pneumonia, Bacterial” or “Bacterial Pneumonias” or “Bacterial Infections and Mycoses” or “Bacterial Infections” or “Pneumonia, Pneumococcal” or “Pneumonia, Staphylococcal” or “Streptococcus pneumoniae” or “Chlamydial Pneumonia” or “Pneumonia, Mycoplasma” or “Mycoplasma pneumoniae” or “Schizoplasma pneumoniae” or “Chlamydophila pneumoniae” or “Lower respiratory tract” or “upper respiratory tract” or “Human Rhinovirus” or “Human Enterovirus” or “Respiratory Tract Infections” or “Respiratory System Infections” or “Respiratory System Infection” or “Upper Respiratory Tract Infections” or “Upper Respiratory Infections” or “Upper Respiratory Tract Infection” or “respiratory infections” or “respiratory virus” or “Respiratory syncytial virus” or “Respiratory Syncytial Viruses” or “RSV” or “Chimpanzee Coryza Agent” or Adenoviruses or “Human Adenovirus” or “Human Adenoviruses” or “APC Viruses” or “APC Virus” or Orthomyxoviruses or Myxoviruses or “Influenza viruses” or “Influenza A virus” or “Influenza A viruses” or “Orthomyxovirus Type A” or “Influenza Viruses Type A” or “Influenza B virus” or “influenza B viruses” or “Influenza Viruses Type B” or “Influenza B virus” or “Influenzavirus C” or “Influenza C Virus” or “Influenza C Viruses” or “Human parainfluenza viruses” or “Parainfluenza Virus 2, Human” or “Parainfluenza Virus Type 2” or “Croup-Associated Viruses” or “Croup Associated Viruses” or “Human parainfluenza virus 2” or “Croup-Associated Virus” or “Croup Associated Virus” or “HPIV” or Metapneumovirus or Metapneumoviruses or “Human Metapneumoviruses” or “Human Metapneumovirus” or “HMPV” or Rhinoviruses or “Human Rhinovirus” or “Common Cold Virus” or “Common Cold Viruses” or “Coryza Virus” or Coronaviruses or “SARS coronavirus” or “Severe acute respiratory syndrome-related coronavirus” or “Severe acute respiratory syndrome related coronavirus” or “HCoV-SARS” or “SARS Virus” or “SARS-Cov-2” or “HcoV” or “NL63” or “OC43” or “229E” or “HKU1” or Sarbecovirus or Sarbecoviruses or “Severe acute respiratory syndrome coronavirus” or “Severe Acute Respiratory Syndrome Virus” or “Human bocaviruses” or Enterovirus or “Coxiella burnetii” or “Chlamydophila psittaci” or “Legionella pneumophila” or “Staphylococcus aureus” or “Haemophilus influenzae” or “Pseudomonas aeruginosa” or “Klebsiella pneumoniae” or “Proteus mirabilis” or “Providencia stuartii” or “Moraxella catarrhalis” or “Streptococcus hemolyticus” or “Streptococcus anginosus” or “streptococcus pneumoniae” or “Gram-positive cocci” or “Gram-negative bacteria” or “gram-negative bacillus” or “pseudomonas aeruginosa” or Candida or “Corynebacterium diphtheriae” or “Bordetella pertussis” or “M.tuberculosis” or “Acute bronchitis” or “acute angina” or “acute tonsillitis” or tonsillitis or “Sinus Infections” or “Viral Pneumonias” or “Acute Coryza” or “Acute viral pharyngitis” or Pharyngitides or “Sore Throats” or “Acute viral laryngitis” or “acute pharyngitis” or “acute epiglottitis” or Epiglottitides or Bronchitis or Laryngitis or Legionellosis or “Lung Abscess” or Blastomycosis or “Pneumonia, Pneumocystis” or Pharyngitis or Nasopharyngitis or “Retropharyngeal Abscess” or Pleurisy or Pleuropneumonia or Pneumonia or Bronchopneumonia or Pleuropneumonia or Rhinitis or Rhinoscleroma or

	"Severe Acute Respiratory Syndrome" or Sinusitis or "Allergic Fungal Sinusitis" or "Ethmoid Sinusitis" or "Frontal Sinusitis" or "Maxillary Sinusitis"or "Sphenoid Sinusitis" or Supraglottitis or Epiglottitis or Tracheitis or Silicotuberculosis or "Whooping Cough")
#3	#1 AND #2

Chinese National Knowledge Infrastructure (CNKI)	
#1	SU=（温度+环境温度+海表温度+气候+天气+气象+气候变化+极端天气+高温+炎热天气+寒冷天气+气象因素+气候因素+全球变暖）*（呼吸道感染+肺炎支原体+肺炎衣原体+呼吸道病毒+流感病毒+鼻病毒+腺病毒+呼吸道合胞病毒+人类冠状病毒+博卡病毒+肠道病毒+人偏肺病毒+副流感病毒+严重急性呼吸综合征相关冠状病+严重急性呼吸综合征冠状病毒+革兰氏阳性球菌+溶血性链球菌+草绿色链球菌+肺炎链球菌+金黄色葡萄球菌+革兰氏阴性杆菌+流感嗜血杆菌+嗜麦芽窄食单胞菌+肺囊虫+肺炎克雷伯菌+铜绿假单胞菌+革兰氏阴性球菌+化脓性链球菌+卡他莫拉菌+嗜肺军团菌+鲍曼不动杆菌+念珠菌+结核分枝杆菌+结核杆菌+白喉棒状杆菌+百日咳鲍特菌+细菌性感染和真菌病+细菌性感染+肺炎葡萄球菌+下呼吸道感染+上呼吸道感染+急性支气管炎+急性咽峡炎+急性疱疹性咽峡炎+急性扁桃体炎+急性鼻窦炎+细菌性肺炎+病毒性肺炎+非典型肺炎+普通感冒+急性病毒性咽炎+急性病毒性喉炎+急性咽炎+急性会厌炎+咽炎）
VIP	
#1	U= (温度 OR 环境温度 OR 海表温度 OR 气候 OR 天气 OR 气象 OR 气候变化 OR 极端天气 OR 高温 OR 炎热天气 OR 寒冷天气 OR 气象因素 OR 气候因素 OR 全球变暖) AND（呼吸道感染 OR 肺炎支原体 OR 肺炎衣原体 OR 呼吸道病毒 OR 流感病毒 OR 鼻病毒 OR 腺病毒 OR 呼吸道合胞病毒 OR 人类冠状病毒 OR 肠道病毒 OR 博卡病毒 OR 人偏肺病毒 OR 副流感病毒 OR 严重急性呼吸综合征相关冠状病 OR 严重急性呼吸综合征冠状病毒 OR 革兰氏阳性球菌 OR 溶血性链球菌 OR 草绿色链球菌 OR 肺炎链球菌 OR 嗜麦芽窄食单胞菌 OR 肺囊虫 OR 金黄色葡萄球菌 OR 革兰氏阴性杆菌 OR 流感嗜血杆菌 OR 肺炎克雷伯菌 OR 铜绿假单胞菌 OR 革兰氏阴性球菌 OR 卡他莫拉菌 OR 嗜肺军团菌 OR 鲍曼不动杆菌 OR 念珠菌 OR 结核分枝杆菌 OR 结核杆菌 OR 白喉棒状杆菌 OR 百日咳鲍特菌 OR 化脓性链球菌 OR 细菌性感染和真菌病 OR 细菌性感染 OR 肺炎葡萄球菌 OR 下呼吸道感染 OR 上呼吸道感染 OR 急性支气管炎 OR 急性咽峡炎 OR 急性疱疹性咽峡炎 OR 急性扁桃体炎 OR 急性鼻窦炎 OR 细菌性肺炎 OR 病毒性肺炎 OR 非典型肺炎 OR 普通感冒 OR 急性病毒性咽炎 OR 急性病毒性喉炎 OR 急性咽炎 OR 急性会厌炎 OR 咽炎）
WanFang	
#1	题名或关键词：(温度 OR 环境温度 OR 海表温度 OR 气候 OR 天气 OR 气象 OR 气候变化 OR 极端天气 OR 高温 OR 炎热天气 OR 寒冷天气 OR 气象因素 OR 气候因素 OR 全球变暖) AND（呼吸道感染 OR 肺炎支原体 OR 肺炎衣原体 OR 呼吸道病毒 OR 流感病毒 OR 鼻病毒 OR 腺病毒 OR 呼吸道合胞病毒 OR 人类冠状病毒 OR 肠道病毒 OR 博卡病毒 OR 人偏肺病毒 OR 副流感病毒 OR 严重急性呼吸综合征相关冠状病 OR 严重急性呼吸综合征冠状病毒 OR 革兰氏阳性球菌 OR 溶血性链球菌 OR 草绿色链球菌 OR 肺炎链球菌 OR 嗜麦芽窄食单胞菌 OR 肺囊虫 OR 金黄色葡萄球菌 OR 革兰氏阴性杆菌 OR 流感嗜血杆菌 OR 肺炎克雷伯菌 OR 铜绿假单胞菌 OR 革兰氏阴性球菌 OR 卡他莫拉菌 OR 嗜肺军团菌 OR 鲍曼不动杆菌 OR 念珠菌 OR 结核分枝杆菌 OR 结核杆菌 OR 白喉棒状杆菌 OR 百日咳鲍特菌 OR 化脓性链球菌 OR 细菌性感染和真菌病 OR 细菌性感染 OR 肺炎葡萄球菌 OR 下呼吸道感染 OR 上呼吸道感染 OR 急性支气管炎 OR 急性咽峡炎 OR 急性疱疹性咽峡炎 OR 急性扁桃体炎 OR 急性鼻窦炎 OR 细菌性肺炎 OR 病毒性肺炎 OR 非典型肺炎 OR 普通感冒 OR 急性病毒性咽炎 OR 急性病毒性喉炎 OR 急性咽炎 OR 急性会厌炎 OR 咽炎）
Chinese BioMedical Literature Database (CBM)	
#1	("温度"[不加权:扩展] OR "气象学概念"[不加权:扩展]) OR "气候"[不加权:扩展]) OR "天气"[不加权:扩展] OR "极端天气"[不加权:扩展] OR "天气和发病"[不加权:扩展]) OR "气象学概念"[不加权:扩展])
#2	"温度" [常用字段:智能] OR"环境温度" [常用字段:智能] OR"海表温度" [常用字段:智能] OR "气候" [常用字段:智能] OR "天气" [常用字段:智能] OR "气象" [常用字段:智能] OR "气候变化" [常用字段:智能] OR "极端天气" [常用字段:智能] OR "高温" [常用字段:智能] OR "炎热天气" [常用字段:智能] OR "寒冷天气" [常用字段:智能] OR "气象因素" [常用字段:智能] OR "气候因素" [常用字段:智能] OR "全球变暖" [常用字段:智能]
#3	#1 OR #2
#4	("呼吸道感染"[不加权:扩展] OR "肺炎支原体"[不加权:扩展] OR "肺炎衣原体"[不加权:扩展] OR "呼吸道合胞病毒"[不加权:扩展] OR "冠状病毒 OC43, 人"[不加权:扩展] OR "人博卡病毒"[不加权:扩展] OR "革兰氏阳性球菌"[不加权:扩展] OR "肠道病毒属"[不加权:扩展] OR "肠道病毒感染"[不加权:扩展] OR "嗜麦芽窄食单胞菌"[不加权:扩展] OR "草绿色链球菌"[不加权:扩展] OR "金黄色葡萄球菌"[不加权:扩展] OR "肺炎克雷伯菌"[不加权:扩展] OR "铜绿假单胞菌"[不加权:扩展] OR "白色念珠菌"[不加权:扩展])
#5	("呼吸道感染" [常用字段:智能] OR"肺炎支原体" [常用字段:智能] OR"肺炎衣原体" [常用字段:智能] OR"呼吸道病毒" [常用字段:智能] OR"流感病毒" [常用字段:智能] OR"鼻病毒" [常用字段:智能] OR"腺病毒" [常用字段:智能] OR "呼吸道合胞病毒" [常用字段:智能] OR "人类冠状病毒" [常用字段:智能] OR "博卡病毒" [常用字段:智能] OR "肠道病毒" [常用字段:智能] OR "人偏肺病毒" [常用字段:智能] OR "副流感病毒" [常用字段:智能] OR "严重急性呼吸综合征相关冠状病" [常用字段:智能] OR "严重急性呼吸综合征冠状病毒" [常用字段:智能] OR "革兰氏阳性球菌" [常用字段:智能] OR "溶血性链球菌" [常用字段:智能] OR "草绿色链球菌" [常用字段:智能] OR "肺炎链球菌" [常用字段:智能] OR "金黄色葡萄球菌" [常用字段:智能] OR "革兰氏阴性杆菌" [常

	用字段:智能] OR "嗜麦芽窄食单胞菌" [常用字段:智能] OR "肺囊虫" [常用字段:智能] OR "流感嗜血杆菌" [常用字段:智能] OR "肺炎克雷伯菌" [常用字段:智能] OR "铜绿假单胞菌" [常用字段:智能] OR 革兰氏阴性球菌" [常用字段:智能] OR "卡他莫拉菌" [常用字段:智能] OR "嗜肺军团菌" [常用字段:智能] OR "鲍曼不动杆菌" [常用字段:智能] OR "念珠菌" [常用字段:智能] OR "结核分枝杆菌" [常用字段:智能] OR "结核杆菌" [常用字段:智能] OR "化脓性链球菌" [常用字段:智能] OR "白喉棒状杆菌" [常用字段:智能] OR "百日咳鲍特菌" [常用字段:智能] OR "细菌性感染" [常用字段:智能] OR "肺炎葡萄球菌" [常用字段:智能] OR "下呼吸道感染" [常用字段:智能] OR "上呼吸道感染" [常用字段:智能] OR "急性支气管炎" [常用字段:智能] OR "急性咽峡炎" [常用字段:智能] OR "急性疱疹性咽峡炎" [常用字段:智能] OR "急性扁桃体炎" [常用字段:智能] OR "急性鼻窦炎" [常用字段:智能] OR "细菌性肺炎" [常用字段:智能] OR "病毒性肺炎" [常用字段:智能] OR "非典型肺炎" [常用字段:智能] OR "普通感冒" [常用字段:智能] OR "急性病毒性咽炎" [常用字段:智能] OR "急性病毒性喉炎" [常用字段:智能] OR "急性咽炎" [常用字段:智能] OR "急性会厌炎" [常用字段:智能]OR 咽炎" [常用字段:智能]）
#6	#4 OR #5
#7	#3 AND #6

Search terms and protocol

PubMed, Scopus, Embase, the Cochrane Library, Web of Science, China National Knowledge Infrastructure, Wanfang Data, Weipu Database, and China Biology Medicine (CBM) for observational studies were comprehensively searched. we identified studies that explored the effect of relationship between temperature and morbidity, hospital admissions, outpatient visits, mortality, or reported cases of respiratory infection surveillance. Zotero and Covidence tools were used for screening. Additionally manual-searched the literature through forward and backward citation tracing using CoCites to obtain remaining studies

Procedure:

1. Search the terms in the table below
2. Download references
3. Import document management software
3. 3. Review all paper titles for eligibility
4. Make record of how many research results were found and how many papers were retrieved by each platform
5. Remove duplicates; record the number of records before and after
6. Screen these abstracts for eligibility- sometimes a screen of the full paper
7. Select the list of final papers for review, sending these references and the number of papers reviewed at each stage to other reviewer
8. All authors agree on which studies are ultimately included

PECO Statement

***Panel*: Population-Exposure-Comparators-Outcomes framework**
Population assessing respiratory disease risk among the general population **Exposure** per 1°C increase in temperature (defined as daily/weekly/monthly/ mean/min/max temperature) **Comparators** Comparable populations not exposed to the relevant ambient temperature **Outcomes** the risk of morbidity due to pathogen-specific respiratory infections

Table S3. Conversion of effect estimates

If RR values were not directly provided in the study, we performed the following transformations.

Effect estimates	Conversion
Excessrisk (ER)	RR=（ER÷100）+1
Percentage change	Divide by 100 plus 1
Beta coefficients	exp (beta)
Correlation coefficient r	We use the following steps to calculate a confidence interval for the population correlation coefficient based on the sample size n and the sample correlation coefficient r. In order to normalize the distribution of r and to make the variance independent of p, Fisher (1921) proposed the z-transformation $z_r = \ln((1 + r)/(1 - r)) / 2$ Find the upper and lower limits of the logarithm $L = z_r - (z\ 1-\alpha/2 / \sqrt{}\ n-3)$ $U = z_r + (z\ 1-\alpha/2 / \sqrt{}\ n-3)$ Find the confidence interval Confidence interval = $[(e^{2L} -1)/(e^{2L} +1), (e^{2U} -1)/(e^{2U} +1)]$ Then, correlation coefficient convert to effect sizes (OR), refer to the method of Lenhard 2022. Lenhard, W. & Lenhard, A. (2022). Computation of effect sizes. Retrieved from: https://www.psychometrica.de/effect_size.html. Psychometrica. DOI: 10.13140/RG.2.2.17823.9232
OR, SE	Calculate 95% CI: L= OR-1.96 x SE U= OR+1.96 x SE If the value is negative and does not conform to normal distribution, log conversion is performed： L= exp(log(OR) - 1.96 x log(SE)) U= exp(log(OR) + 1.96 x log(SE))

Table S4. Risk of Bias Assessment in individual studies

Adapted from: Office of Health Assessment and Translation (OHAT) Risk of Bias Rating Tool for Human and Animal Studies

Bias domains	Questions and criteria	Risk level assessment
Exposure assessment	This includes measurement error or measurement limitations. **Major considerations are:** • Is the exposure data source clearly described, not provided, or difficult to interpret? • Were the temporal and spatial resolution of temperature measurements appropriate (e.g. more than one weather station, meteorological bureau)? • daily temperature measurements were available? • Were missing data present and/or imputed? • Were selected lag(s) appropriate based on biological plausibility and other factors?	**Definitely low** risk of bias (++): There is direct evidence of low risk of bias practices (the true average population exposure at temperature has high confidence). **Probably low** risk of bias (+): There is indirect evidence that the method assessment is robust, it is deemed that deviations from low risk of bias method for these criteria during the study would not appreciably bias results, including consideration of direction and magnitude of bias. **Probably high** risk of bias (-): There is indirect evidence of high risk of bias practices, there is insufficient information (e.g., not reported or "NR"), or two out of the three listed considerations are not applied (e.g. use of single weather station). **Definitely high** risk of bias (--): There is direct evidence of high risk of bias practices, or all listed **considerations** are not applied.
Outcome assessment	**This includes measurement error or measurement limitations.** **Major considerations are:** • outcome measurements were not influenced by knowledge of the exposure (data were from different databases) • Was Laboratory-confirmed source for pathogen-specific studies and/or clinical diagnosis appropriate? • Was selected date or timing of outcome appropriate (i.e. close to illness onset) • Was missing data present and/or imputed?	**Definitely low** risk of bias **(++):** Outcome was Laboratory-confirmed pathogen-specific respiratory infection and the selected timing approximates the occurrence of symptoms. **Probably low** risk of bias **(+):** Outcome was clinical diagnosis using standard criteria (e.g. WHO definition and International Classification System – ICD code) and the selected timing approximates the occurrence of symptoms. **Probably high** risk of bias (-): outcome was not based on standard diagnosis criteria, there is evidence that suggests the existence of misclassification bias, or there is insufficient information (e.g. not reported) provided. **Definitely high** risk of bias (--): Outcome was based on self-reports (e.g. parents or family members) and selected timing was inappropriate.
Confounding bias	**Major considerations are:** Did the study appropriately adjusted/accounted for all important well studied potential confounders (e.g. time, seasonality, other weather parameters, and model specifications, lag effect)? •Design or analysis accounted for potential confounding or modifying •Consideration of other exposures that might bias results	**Definitely low** risk of bias (++): Study accounted for all important confounders which were measured consistently. **Probably low** risk of bias (+): Study accounted for most of confounding and is not expected to introduce bias. **Probably high** risk of bias (-): Study adjusted for some but not all of confounding and is expected to introduce bias. **Definitely high** risk of bias (--): Study did not account for potential confounders or were inappropriately measured.
Selection bias	**Major considerations are:** Was selection of participants into the study done in a manner that might introduce bias in the study? • Was similar baseline characteristics, application of inclusion/exclusion criteria, recruitment strategy? • Was all data available collected? • Was there any form of randomisation of selection of individual cases?	**Definitely low** risk of bias (++): Similar baseline characteristics, the descriptions of the selection of participants were sufficiently detailed to support the assertion that risk of selection effects was minimal. **Probably low** risk of bias (+): Insufficient information about selection of participants to permit a judgment of low risk of bias but there is indirect evidence that suggests low risk of bias. **Probably high** risk of bias (-): Insufficient information about selection of participants to permit a judgment of high risk of bias and there is

		indirect evidence that suggests high risk of bias. **Definitely high** risk of bias (--): Direct indications from descriptions of the participant selection of high risk of bias.
Incomplete outcome data	**Major considerations are:** • missing data of outcome measures? • missing data of exposures?	**Definitely low** risk of bias (++): no missing data present or missing data does not affect the real results **Probably low** risk of bias (+): indirect evidence that suggests low risk of bias (e.g., <10% missing data, or missing data related to outcome). **Probably high** risk of bias (-):indirect evidence that suggests high risk bias (e.g., ≥10% missing data without imputed using appropriate method, while rational for attrition explained in the study). **Definitely high** risk of bias (--): missing outcome data are related to true outcome (e.g., substantial missing exposure data (≥10%), rationale for missing data not explained in the study).
Selective reporting	**Major considerations are:** Was selection of participants into the study done in a manner that might introduce bias in the study? • Selective reporting of entire studies, outcomes, or analyses. • Systematic differences between reported and unreported findings. • Can include potential for bias in reporting through source of funding	**Definitely low** risk of bias (++): Complete report of the entire study results and analysis. **Probably low** risk of bias (+): There is not enough information to judge the risk of low bias, but there is indirect evidence of low risk of bias. (i.e., effect estimates presented for less than all hypotheses tested as per aims; but evidence suggests that effect estimates unlikely to be seriously biased). **Probably high** risk of bias (-): There is not enough information to judge the risk of high bias, but there is indirect evidence of high risk of bias. **Definitely high** risk of bias (--): There is a high risk of selectively reporting entire studies, results, or analyses.
Conflict of interest	**Major considerations are:** Potential source of bias in reporting through source of funding • Source of funding (government, academic institution, commercial institution, or no funding? • Is conflict of interest declared?	**Definitely low** risk of bias (++): the study was not funded or funded by government or academic institutions or non-profit organizations, and the authors declare no conflict of interest **Probably low** risk of bias (+): insufficient information to judge for low risk, but indirect evidence suggests study was free of financial interest **Probably high** risk of bias (-): insufficient information to judge for high risk, but indirect evidence suggests study was not free of financial interest **Definitely high** risk of bias (--): study was supported by a commercial institution with a financial interest in the findings, and the authors declare a conflict of interest)
Other bias	Bias due to other problems not covered elsewhere	**Definitely low** risk of bias (++): No other bias **Probably low** risk of bias (+): insufficient information to judge for low risk, but indirect evidence suggests study was free of other problems **Probably high** risk of bias (-): insufficient information to judge for high risk, but indirect evidence suggests study was not free of other problems **Definitely high** risk of bias (--): at least one important risk of bias (e.g., selective reporting of subgroups, a potential source of bias related to the specific study design used, study has been claimed to have been fraudulent)

Table S5. Overall risk of bias rating

Overall Rating	Combinations (three key components of exposure assessment, outcome assessment, and confounding bias)
Definitely high (DH)	Definitely high + Definitely High + (Definitely high / Probably high / Probably low / Definitely low) Definitely high + Probably high + Probably high
Probably high (PH)	Definitely high + Probably high + (Probably low / Definitely low) Probably high + Probably high + (Probably high / Probably low/Definitely low)
Probably low (PL)	Probably high+(Probably low/Definitely low) + (Probably low / Definitely low) Probably low + Probably low + Definitely Low
Definitely Low (DL)	Probably low + Definitely low + Definitely low Definitely low + Definitely low + Definitely low

Table S6. Assessing confidence in the Body of Evidence (adapted from Johnson et al. 2014)

Evaluation factors	Criteria
Risk of bias	Study limitations include a significant risk of bias across the body of evidence.
Indirectness	The research evidence was not similar to the primary objective, i.e., participants, exposure, comparison, Outcome (PECO); Indirect evidence.
Inconsistency	High heterogeneity (I^2); variability in results; inconsistent magnitude and direction of effect magnitude.
Imprecision	Small sample size and wide confidence intervals.
Publication bias	The funnel plot is obviously asymmetrical; Egger's test or Begg's tests show that publication bias exists. Trim and Fill procedure was used to estimate potentially missing studies.
Large magnitude of effect	The rating was upgraded if modeling suggested that confounding alone was unlikely to explain associations that were judged to be of large magnitude.
Dose response	If dose-response relationships in one or more studies and/or dose-response across studies are consistent, the rating was upgraded.
Confounding minimizes effect	Upgraded if the consideration of all plausible residual confounders or biases would underestimate the effect or suggest a spurious effect when results show no effect.

From:: Johnson, P. I., Sutton, P., Atchley, D. S., Koustas, E., Lam, J., Sen, S., Robinson, K. A., Axelrad, D. A., & Woodruff, T. J. (2014). The Navigation Guide - evidence-based medicine meets environmental health: systematic review of human evidence for PFOA effects on fetal growth. Environmental health perspectives, 122(10), 1028–1039. https://doi.org/10.1289/ehp.1307893

Table S7. Strength of evidence definitions for human evidence according to the Navigation Guide (adapted from Johnson et al., 2014)

Strength rating	Definition
Sufficient evidence	A positive relationship is observed between exposure and outcome, where chance, bias, and confounding can be ruled out with reasonable confidence. The available evidence includes results from one or more well-designed, well conducted studies, and the conclusion is "unlikely to be strongly affected by the results of future studies."
Limited evidence	A positive relationship is observed between exposure and outcome, where chance, bias, and confounding cannot be ruled out with reasonable confidence. Confidence in the relationship is constrained by factors such as "the number, size, or quality of individual studies" or "inconsistency of findings across individual studies." As more information becomes available, the observed effect could change, and this change may be large enough to alter the conclusion.
Inadequate evidence	"The available evidence is insufficient to assess effects" of the exposure. The evidence is insufficient because of "the limited number or size of studies," low quality of individual studies, or "inconsistency of findings across individual studies." More information may allow an assessment of effects.
Lack of evidence	No relationship is observed between exposure and outcome; and chance, bias, and confounding can be ruled out with reasonable confidence. The available evidence includes consistent results from more than one well-designed, well conducted study at the full range of exposure levels that humans are known to encounter, and the conclusion is unlikely to be strongly affected by the results of future studies. The conclusion is limited to the age at exposure and/or other conditions and levels of exposure studied.

From:: Johnson, P. I., Sutton, P., Atchley, D. S., Koustas, E., Lam, J., Sen, S., Robinson, K. A., Axelrad, D. A., & Woodruff, T. J. (2014). The Navigation Guide - evidence-based medicine meets environmental health: systematic review of human evidence for PFOA effects on fetal growth. Environmental health perspectives, 122(10), 1028–1039. https://doi.org/10.1289/ehp.1307893

Table S8. Full texts excluded on basis of eligibility

Reference	Title	Reason
Sohn S 2019	'Pneumonia Weather': Short-term Effects of Meteorological Factors on Emergency Room Visits Due to Pneumonia in Seoul, Korea	Target the disease, not the pathogen
Bishop-Williams KE 2017	A protocol for a systematic literature review: comparing the impact of seasonal and meteorological parameters on acute respiratory infections in Indigenous and non-Indigenous peoples	Effect estimates are not applicable
Chen J 2021	Ambient Temperature Is an Independent Risk Factor for Acute Tonsillitis Incidence	Target the disease, not the pathogen
Wenfang G	Assessing the effects of meteorological factors on daily children's respiratory disease hospitalizations: A retrospective study	Effect estimates are not applicable
Zhang Lei 2017	Analysis of Mycoplasma pneumoniae infection among children with respiratory tract infection in hospital in Chengdu from 2013 to 2015	Outcome not applicable
Zhang L 2021	Analysis of mycoplasma pneumoniae infection among children with respiratory tract infections in hospital in Chengdu from 2014 to 2020	Outcome not applicable
Fang J 2021	Association between ambient temperature and childhood respiratory hospital visits in Beijing, China: a time-series study (2013-2017)	Target the disease, not the pathogen
Liu Y 2015	Association between Temperature Change and Outpatient Visits for Respiratory Tract Infections among Children in Guangzhou, China	Effect estimates are not applicable
Ruchiraset A 2020	Association of climate factors and air pollutants with pneumonia incidence in Lampang province, Thailand: findings from a 12-year longitudinal study	Target the disease, not the pathogen
Zhang Y 2015	Burden of respiratory syncytial virus infections in China: Systematic review and meta-analysis	Outcome not applicable
Ashmita Gosai 2009	Climate and respiratory disease in Auckland, New Zealand	Target the disease, not the pathogen
Ghia C 2021	Disease Burden Due to Respiratory Syncytial Virus in Indian Pediatric Population: A Literature Review.	Outcome not applicable
Álvaro-Meca A 2022	Environmental factors linked to hospital admissions in young children due to acute viral lower respiratory infections: A bidirectional case-crossover study	Focusing on lower respiratory tract infections
Falagas ME 2008	Effect of meteorological variables on the incidence of respiratory tract infections	Target the upper and lower respiratory tract infections
Jang JY 2021	Effect of diurnal temperature range on emergency room visits for acute upper respiratory tract infections	Improper temperature
Xie MY 2017	Effect of diurnal temperature range on the outpatient visits for acute bronchitis in children: a time-series study in Hefei, China	Target the disease
Álvaro-Meca A 2022	Environmental factors linked to hospital admissions in young children due to acute viral lower respiratory infections: A bidirectional case-crossover study	Target the lower respiratory tract infection
Li Y 2019	Global patterns in monthly activity of influenza virus, respiratory syncytial virus, parainfluenza virus, and metapneumovirus: a systematic analysis	Outcome not applicable
Hossain MZ 2019	Sociodemographic, climatic variability and lower respiratory tract infections: a systematic literature review	Outcome not applicable
Choe YJ 2019	Seasonality of respiratory viruses and bacterial pathogens	Not specific to bacteria
Nastos PT 2006	Weather impacts on respiratory infections in Athens, Greece	Target the disease
Simmering JE 2017	Weather-Dependent Risk for Legionnaires' Disease, United States	Outcome not applicable
TNS 2012	The seasonal variations of respiratory syncytial virus infections in Turkey: a 2-year epidemiological study	Outcome not applicable
Gleason JA 2016	Under the Weather: Legionellosis and Meteorological Factors	Outcome not applicable
Karagiannis I 2009	Warm, wet weather associated with increased Legionnaires' disease incidence in The Netherlands	Target the disease, not the pathogen

Brandsema PS 2014	Summer increase of Legionnaires' disease 2010 in The Netherlands associated with weather conditions and implications for source findin	Target the disease, not the pathogen
Han XY 2019	Solar and Climate Effects Explain the Wide Variation in Legionellosis Incidence Rates in the United States	Outcome not applicable/Temperature not applicable
Conza L 2013	Meteorological factors and risk of community-acquired Legionnaires' disease in Switzerland: an epidemiological study	Temperature not applicable
Fisman DN 2005	It's not the heat, it's the humidity: wet weather increases legionellosis risk in the greater Philadelphia metropolitan area	Outcome not applicable
Ng V 2008	Going with the flow: legionellosis risk in Toronto, Canada is strongly associated with local watershed hydrology	Temperature not applicable
Yuan L 2011	Relationship between Influenza and Meteorological Conditions in Tianjin	Target the disease, not the pathogen
Paynter S 2013	Sunshine, rainfall, humidity and child pneumonia in the tropics: time-series analyses	Temperature not applicable
WU Zhi-qiang 2022	A single-center study on the relationship between meteorological factors and the number of visits for respiratory diseases in children	Outcome not applicable
JIAN Wanlin 2023	A Stratified Comparative Study on the Meteorological Factors Impacting Respiratory Diseases in the Two Counties of Eastern and Western China	Target the disease, not the pathogen
Paynter S 2014	Respiratory syncytial virus seasonality in tropical Australia	effect estimates not applicable
Michelozzi P 2009	High temperature and hospitalizations for cardiovascular and respiratory causes in 12 european cities	effect estimates not applicable
Shao Lin 2009	Extreme high temperatures and hospital admissions for respiratory and cardiovascular diseases	Outcome not applicable
Habeebullah TM 2021	Impact of outdoor and indoor meteorological conditions on the COVID-19 transmission in the western region of Saudi Arabia	did not have convertible estimates
Donzelli G 2022	Role of meteorological factors on SARS-CoV-2 infection incidence in Italy and Spain before the vaccination campaign. A multi-city time series study	effect estimates not applicable
Kaplin A 2021	Evidence and magnitude of the effects of meteorological changes on SARS-CoV-2 transmission	did not have convertible estimates
Mandal CC 2022	Combinatorial influence of environmental temperature, obesity and cholesterol on SARS-CoV-2 infectivity	did not have convertible estimates
Li Ruiying 2018	Study of the Influence of Meteorological Condition on Children Lower Respiratory Tract Infection and the Prediction Model in Qinhuangdao	Outcome not applicable
Dufloo J 2024	Temperature impacts SARS-CoV-2 spike fusogenicity and evolution	did not have convertible estimates
Thi Khanh HN 2023	The impact of ambient temperature and air pollution on SARS-CoV2 infection and Post COVID-19 condition in Belgium (2021-2022)	Under the combined influence of ambient temperature and air pollution/Not a single temperature effect
Kim J 2023	How Does Climate Change Affect the Upper Airway?	No effect estimation
Grover EN 2024	Does behavior mediate the effect of weather on SARS-CoV-2 transmission? Evidence from cell-phone data	No effect estimation
Lee H 2024	Impact of ambient temperature on respiratory disease: a case-crossover study in Seoul	Target the disease, not the pathogen
Maciorowski D 2021	Environmental factors and their role in the transmission of SARS-CoV-2. Biosaf Health.	No effect estimation
Kaplin A 2021	Evidence and magnitude of the effects of meteorological changes on SARS-CoV-2 transmission	effect estimates not applicable
Nichols GL 2021	Coronavirus seasonality, respiratory infections and weather	Temperature not applicable
Tian Y 2023	Ambient temperature variability and hospital admissions for pneumonia: A nationwide study	Target the disease, not the pathogen
Makrufardi F 2024	Extreme temperatures increase the risk of pediatric pneumonia: a systematic review and meta-analysis	Target the disease, not the pathogen

Miyayo SF 2021	Analysis of Pneumonia Occurrence in Relation to Climate Change in Tanga, Tanzania	Outcome not applicable

Table S9. Basic characteristics of 137 included studies

Study	Location	Study period	Time sample	Population	Ages	Reporting frequency	Climate	Case source	Exposure (°C)	Pathogen	Income	Overall bias
Raymundo (2023)[1]	Oahu, USA	2016.05-2019.05	37	7143	<6 y	Monthly	A	Reported cases	T_{mean}	EV/HRV	High	PL
Annabel (2023)[2]	Bukit Timah, Singapore	2009-2019	4016	7329	<5 y	Daily	A	Influenza infection	T_{mean}	IVA, IVB	High	DH
Chee (2023)[3]	Kuala Lumpur, Malaysia	2017-2021	60	2950	<12 y	Monthly	A	Hospitalized for ARI	T_{mean}	RSV	Upper-middle	PH
Keita (2023)[4]	47 prefectures in Japan	2014-2019	312	721709	all	Weekly	C	Reported cases	T_{mean}	RSV	High	PL
Ping-Ing (2023)[5]	Taiwan, China	1995-2005, 2000-2005	206	1740	<18 y	Monthly	A/C	Reported bronchiolitis/pneumonia	T_{mean}	RSV	High	PL
Meng (2023)[6]	Singapore	2009-2019	4016	15715	<5 y	Daily	A	Reported cases	T_{mean}, T_{max}, T_{min}	RSV	High	PL
You (2022)[7]	Gwangju, Korea	2016-2019	48	4195	all	Monthly	D	Hospitalized with ARI	T_{mean}	IV, HAdV, PIV, RSV, HCoV, HRV, HBoV, HMPV, EV	High	PH
Zhang (2022)[8]	Jiangyin, China	2015-2020	72	12294	28 d-14 y	Monthly	C	Hospitalized for ARTI	T_{mean}	RSV, IVA, IVB, HPIV 1-3, HAdV	Upper-middle	PH
Yuan (2022)[9]	Chendu, China	2016-2019	48	5127	28 d-14 y	Monthly	C	Hospitalized for ARI	T_{mean}	*M. pneumoniae*	Upper-middle	PH
Na (2022)[10]	Nantong, China	2017-2019	156	51665	<14 y	Weekly	C	Reported pneumonia cases	T_{mean}	*M. pneumoniae*	Upper-middle	PL
Pan (2022)[11]	Shenzhen, China	2009-2015	2555	5744	all	Daily	C	Influenza	T_{mean}, T_{max}, T_{min}	IVA, IVB	Upper-middle	DL
Huang (2022)[12]	Suzhou, China	2016-2019	48	7940	1 m-15 y	Monthly	C	Hospitalized for ARI	T_{mean}	*H. influenzae*	Upper-middle	PH
Ming (2022)[13]	Wenzhou, China	2008-2017	121	89898	1–3 y	Monthly	C	Hospitalized with ARI	T_{mean}	HPIV-3	Upper-middle	PL
You (2022)[14]	13 European countries	2010-2019	521	30965	<5 y	Weekly	Multiple	Hospitalized with ARI	T_{mean}	RSV	High	DH
Sung (2022)[15]	Changwon, Korea	2020.1.20-04.29	100	3234	all	Daily	C	Reported cases	T_{mean}	SARS-CoV-2	High	PL

Lisa (2022)[16]	Helsinki, Finland	2020.08.01-2021.05.31	62	48013	all	Daily	C	Reported cases	T_{mean}	SARS-CoV-2	High	PL
Keita (2022)[17]	Six Japanese prefectures	2020.05-2022.03	699	2982262	all	Daily	C	Notified cases	T_{mean}	SARS-CoV-2	High	PH
Cheng (2022)[18]	Macao, China	2014-2017	1460	4880	1 m-14 y	Daily	C	Hospitalized for ARI	T_{mean}	EV/HRV, HAdV, RSV-A, RSV-B, IVA, IVB, HPIV, HMPV, HBoV, HCoV	High	DL
Zhi (2021)[19]	Suzhou, China	2016-2018	36	1157	1-15 y	Monthly	C	Hospitalized with LRTI	T_{mean}	RSV	Upper-middle	DH
Eun (2021)[20]	Cheonan, Korea	2012-2018	2556	9010	1–9 y	Daily	D	Reported RI	T_{mean}	HPIV 1-3	High	PL
Aleix (2021)[21]	52 Spanish provinces	Weeks 10-16 of 2020	7	2418250	all	Weekly	C	Reported cases	T_{mean}, T_{max}, T_{min}	SARS-CoV-2	High	PL
Liu (2021)[22]	Moscow	2020.03.11-06.22	103	Not reported	all	Daily	D	Reported cases	T_{mean}, T_{max}, T_{min}	SARS-CoV	High	PH
Na (2021)[23]	Tianjin, China	2015.06-2019.02	44	63821	0-16 y	Monthly	D	Hospitalized for ARI	T_{mean}	*M. pneumoniae*	Upper-middle	DL
Wu (2021)[24]	Haikou, China	2018-2020	36	309	5.05 m	Monthly	A	Hospitalized for RTI	T_{mean}	RSV, RSV-A, RSV-B	Upper-middle	PL
Chen (2021)[25]	Guangdong, China	2020.01.21-02.26	36	1347	all	Daily	C	Reported cases	T_{mean}	SARS-CoV-2	Upper-middle	PL
Stacy (2021)[26]	Singapore	2009-2019	4016	6393	<5 y	Daily	A	Reported cases	T_{mean}	HPIV	High	PL
Eun (2021)[27]	Cheonan, Korea	2012-2018	85	9010	<10 y	Monthly	D	Reported RTI	T_{mean}	HAdV	High	PL
Can (2021)[28]	China	2004-2017	522	1986536	all	Weekly	C/D	Reported cases	T_{mean}	IVA/H1N1pdm09, IVA/H3N2, IVB	Upper-middle	PH
Chan (2021)[29]	Hong Kong, China	1993-1997	60	9635	<5 y	Monthly	C	Admission with RI	T_{mean}	RSV	High	PL
Dong (2021)[30]	Cheonan, Korea	2012-2018	85	1920	all	Monthly	D	Hospital with RI	T_{mean}	HRV	High	DH
Therese (2021)[31]	Nairobi, Kenya	2007–2013	85	17261	all	Monthly	A	Reported influenza-like illness	T_{mean}	RSV, HPIV 1-3, HAdV	Upper-middle	PL
Lei (2021)[32]	Chengdu, China	2014-2020	85	22882	1 m-17 y	Monthly	C	Hospitalized with RTI	T_{mean}	*M. pneumoniae*	Upper-middle	PL
Mohamed (2021)[33]	Safat, Kuwait	2020.02.24-05.30	96	176	all	Daily	A	Reported cases	T_{mean}	SARS-CoV-2	High	PH

Liu (2021)[34]	Chongqing, China	2009.06-2019.06	3681	3107	1 m-18 y	Daily	C	Hospitalized for ARI	T_{mean}, T_{max}, T_{min}	RSV	Upper-middle	PL
Rosalie (2021)[35]	Amsterdam, The Netherlands	2003-2016	170/730	2161	≤ 24 m	Monthly/ Weekly	C	Admissions for bronchiolitis	T_{mean}, T_{max}, T_{min}	RSV	High	PL
Jang (2020)[36]	Cheonan, Korea	2012-2018	2556	9010	<10 y	Daily	D	Reported cases	T_{mean}	HCoV- 229E, HCoV-OC43	High	PL
Ilada (2020)[37]	Bangkok, Thailand	2012-2018	85	8209	≤ 5 y	Monthly	A	Reported ILI cases	T_{mean}	RSV	Upper-middle	PH
Asmaa (2020)[38]	Riyadh, Saudi Arabia	2012.10-2018.12	75	712	all	Monthly	A	Reported cases	T_{mean}	MERS-CoV	High	DL
Sheikh (2020)[39]	Bukit Timah, Singapore	2005-2015	4016	9905	< 30 m	Daily	A	Reported cases	T_{mean}, T_{max}, T_{min}	RSV	High	PL
Shiv (2020)[40]	Fifty U.S. states and Washington D.C.	2020.1.22-2020.3.4	42	974	all	Daily	Multiple	Reported cases	T_{max}	SARS-CoV-2	High	PL
Zhang (2020)[41]	Suzhou, China	2014-2017	48	7525	2.51±15.93 m	Monthly	C	Hospitalized for CAP	T_{mean}	HPIV- 3	Upper-middle	PH
Simone (2020)[42]	Milan; Florence; Trento, Italy	2020.03.08-2020.06.19	103	Not reported	all	Daily	C/D	Reported cases	T_{mean}, T_{max}, T_{min}	SARS-CoV-2	High	PL
Kong (2020)[43]	Wuhan, China	2020.01.20-02.11	22	Not reported	all	Daily	C	Reported cases	T_{mean}	SARS-CoV-2	Upper-middle	PH
Giselmo (2020)[44]	Maranhao, Brazil	2018.04-2019.03	12	151	2–12 y	Monthly	A	Hospitalized with RTI	T_{mean}, T_{max}, T_{min}	RSV, HRV	Upper-middle	PL
Li (2020)[45]	Shanghai, China	2017.07-2019.06	104	29135	0-18 y	Weekly	C	Reported cases	T_{mean}, T_{max}, T_{min}	IVA, IVB	Upper-middle	PH
Rory (2019)[46]	Edinburgh, Scotland, UK	2009.04-2015.11	81	52060	all ages	Monthly	C	Hospitalized with RTI	T_{mean}	HPIV 1-3, RSV, HMPV, IVA, IVB, HRV, HAdV	High	PL
Huang (2019)[47]	Zhongshan, China	2014.09-2016.08	24	13705	1 m-14 y	Monthly	C	Hospitalized with CAP	T_{mean}	*M. pneumoniae*, *C. pneumoniae*, *M. catarrhalis*, IVA, IVB, HAdV, HPIV, RSV, *H. influenzae*, *S.pneumoniae*	Upper-middle	PH
Pan (2019)[48]	Panzhihua, China	2006-2015	121	6892	all	Monthly	C	Influenza infection	T_{mean}	IVA, IVB	Upper-middle	DL

He (2019)[49]	Suzhou, China	2012-2015	48	8711	＜18 y	Monthly	C	Hospitalized for RTI	T_{mean}	HBoV	Upper-middle	PL
Wu (2019)[50]	Wu zhishan, China	2015-2016	24	1597	1 m-14 y	Monthly	A	Hospitalized for ARI	T_{mean}	*M. pneumoniae*	Upper-middle	PH
Wei (2019)[51]	Jinan, China	2013-2016	208	9170	all	Weekly	D	Reported cases	T_{mean}	IVA/H1N1pdm09, IVA/H3N2, IVB	Upper-middle	PL
Yong (2019)[52]	Seoul, Korea	2007- 2016	521	23694	<18 y	Weekly	D	Hospitalized for ARI	T_{mean}, T_{max}, T_{min}	HMPV	High	PL
Katerina (2019)[53]	Liverpool, UK	2011.11-2017.03	65	374	18-50 y	Monthly	C	Reported cases	T_{mean}, T_{max}, T_{min}	*S. pneumoniae*	High	PL
Magali (2018)[54]	Dijon, France	2011-2016	90	4300	all	Weekly	C	Hospitalized for ARI	T_{mean}	HMPV, RSV	High	PL
Wen-Kuan (2018)[55]	Guangzhou, China	2009.07-2016.06	85	11399	≤14 y	Monthly	C	Hospitalized for ARI	T_{mean}	HBoV-1	Upper-middle	PL
Morley (2018)[56]	Gold Coast, Australia	2007.07-2016.06	469	15387	<5 y	Weekly	C	Hospitalized with ARI	T_{mean}, T_{max}, T_{min}	RSV	High	PL
Hermann (2018)[57]	Garoua, Cameroon	2014-2016	36	1666	0-5 y	Monthly	D	Reported influenza cases	T_{mean}	IVA, IVB	Lower-middle	PL
Ines (2018)[58]	Sousse, Northern Africa	2003–2015	158	5131	≤ 5 y	Monthly	B	Hospitalized for bronchiolitis	T_{mean}	RSV	Lower-middle	PL
Jung (2018)[59]	Seoul, Korea	2005-2012	97	9113	< 3 y	Monthly	D	Hospitalized with bronchiolitis/pneumonia	T_{mean}	RSV	High	PL
Adriana (2018)[60]	Toronto, Canada	2010-2015	312	44362	1 m-108 y	Weekly	D	Reported cases	T_{mean}	IVA, IVB	High	PL
Benjamin (2018)[61]	Nha Trang, central Vietnam	2007.01.29-2012.4.26	63	2998	all	Monthly	A	Hospitalized with ARI	T_{mean}	IVA, IVB, RSV, HMPV, HPIV 1-4, HRV, HCoV-229E, HCoV-OC43, HAdV, HBoV	Lower-middle	PL
Zhou (2018)[62]	Suzhou, China	2013-2015	36	5994	17 d-15 y	Monthly	C	Hospitalized for ARI	T_{mean}	HRV	Upper-middle	DH
Jang (2017)[63]	Cheonan, Korea	2006.12-2014.02	88	6279	<1 y	Monthly	D	Reported cases	T_{mean}	RSV	High	PL
Terezinha (2017)[64]	Sao Paulo, Brazil	1996-2010	182	Not reported	<5 y	Monthly	C	Hospitalized with bronchiolitis/pneumonia	T_{mean}	RSV	Upper-middle	PL

Wang (2017)[65]	Suzhou, China	2006-2013	97	15098	1 m-14 y	Monthly	C	Hospitalized with ARI	T_{mean}	*M. pneumoniae*	Upper-middle	PL
Gwladys (2017)[66]	Yaounde´, Cameroon	2009.01-2015.10	360	5216	all	Weekly	A	Reported ILI/ARI cases	T_{mean}	IVA, IVB	Lower-middle	DH
Yan (2017)[67]	Suzhou, China	2013-2015	36	6194	<14 y	Monthly	C	Hospitalized with LRTI	T_{mean}	HRV	Upper-middle	PL
Tian (2017)[68]	Hangzhou, China	2015	365	36500	4.3-52.8 m	Daily	C	Reported pneumonia cases	T_{mean}, T_{max}, T_{min}	RSV, *M. pneumoniae*	Upper-middle	PH
Zhou (2017)[69]	Huangshi, China	2016	12	2326	1 m-14 y	Monthly	C	Hospitalized for ARI	T_{mean}	HRV	Upper-middle	PL
Raffaella (2017)[70]	Rome, Italy	2004-2014	133	723	< 1 y	Monthly	C	Hospitalized for acute bronchiolitis	T_{mean}	RSV	High	PL
Wei (2016)[71]	Shanghai, China	2011.08-2014.12	41	2819	2 m-12 y	Monthly	C	Hospitalized with ARI	T_{mean}	IFV, HPIV 1-4, EV, RSV, HCoV, HAdV, HMPV, HBoV, HRV	Upper-middle	PL
Qing (2016)[72]	Hangzhou, China	2015	365	36500	4.3 m	Daily	C	Hospitalized with ARI	T_{mean}, T_{max}, T_{min}	RSV	Upper-middle	DH
PSOTER (2016)[73]	48 states of USA	2003-2009	2556	3463	<7 y	Daily	A/B/C/D	Reported cases	T_{mean}	*P.aeruginosa*	High	PH
Nicklas (2016)[74]	Gothenburg, Sweden	2010.10-2013.07	147	20062	<18 y	Weekly	C	Hospitalized for RTI	T_{mean}	IVA, IVB, RSV, HRV, EV, HCoV, HMPV, HAdV, HPIV 1–4, HBoV, *C. pneumoniae*, *M. pneumoniae*	High	DH
Shi (2016)[75]	Zhengzhou, China	2012.01-2015.01	36	2323	18-94 y	Monthly	D	Hospitalized for ARI	T_{mean}	*M. pneumoniae*	Upper-middle	PH
Chen (2016)[76]	Yancheng, China	2014-2015	24	3672	1 m-10 y	Monthly	C	Hospitalized for ARI	T_{mean}	RSV, IVA, IVB, HPIV 1-3, HAdV	Upper-middle	PH
Sobral (2020)[77]	USA	2019.12-2020.03	118	Not reported	all	Daily	Multiple	Reported cases	T_{mean}, T_{max}, T_{min}	SARS-CoV-2	High	PL
Jaqueline (2016)[78]	Curitiba, Brazil	2012-2013	24	755	all	Monthly	C	Hospitalized for ARI	T_{mean}	HRV	Upper-middle	PL
Tiina (2016)[79]	Kajaani, Finland	2004.07-2005.01	214	386	all	Daily	C	Reported cases	T_{mean}	HRV	High	DH

Gamba-Sanchez (2016)[80]	Bogota, Colombia	2009-2013	60	13488	<3 y	Monthly	C	Reported cases	T_{mean}	RSV	Upper-middle	DL
Rodriguez-Martinez (2015)[81]	Bogota, Colombian	2010.01-2011.04	16	3931	<3 y	Monthly	C	Hospitalized for ARI	T_{mean}	RSV	Upper-middle	DL
Geng (2015)[82]	Suzhou, China	2001-2011	133	42664	3 d-15 y	Monthly	C	Hospitalized for ARI	T_{mean}	RSV	Upper-middle	PL
Daniel (2015)[83]	Mallorca, Spain	2006-2011	312	60659	1– 15 y	Weekly	C	Reported pharyngitis cases	T_{mean}	*S. pyogenes*	High	PL
Lu (2015)[84]	Suzhou, China	2010-2014	60	1803	≤28 d	Monthly	C	Hospitalized with LRTI	T_{mean}	RSV	Upper-middle	PL
Cui (2015)[85]	Chaoshan, China	2010.12-2011.11	364	1074	0–16 y	Daily	C	Hospitalized for ARI	T_{mean}	RSV, IVA, IVB, HCoV, HMPV, HPIV 1-4, HRV, EV, HAdV, HBoV	Upper-middle	DH
Lin (2015)[86]	Quanzhou, China	2013	12	6020	0-15 y	Monthly	C	Hospitalized for ARI	T_{mean}	RSV, HAdV, IVA, IVB, HPIV, *M. pneumoniae, C.pneumoniae, L. pneumophila*	Upper-middle	PL
Yan (2015)[87]	Shanghai, China	2011-2013	36	2526	0-12 y	Monthly	C	Hospitalized for ARI	T_{mean}	HPIV 1-4	Upper-middle	PL
Huang (2015)[88]	Suzhou, China	2013	12	1926	1-140 m	Monthly	C	Hospitalized for ARI	T_{mean}	HRV	Upper-middle	PH
Ni (2014)[89]	Suzhou, China	2006-2011	72	10596	1-13 y	Monthly	C	Hospitalized for ARI	T_{mean}	*M. pneumoniae*	Upper-middle	PL
Sun (2014)[90]	Suzhou, China	2006-2010	60	8143	1-180 m	Monthly	C	Hospitalized with ARI	T_{mean}	*M. catarrhalis*	Upper-middle	PL
Onozuka (2014)[91]	Fukuoka, Japan	2006-2012	365	30215	all	Weekly	C	Reported cases	T_{mean}, T_{max}, T_{min}	RSV	High	PH
Zheng (2014)[92]	Suzhou, China	2001-2011	133	42104	1 m-14 y	Monthly	C	Hospitalized with ARI	T_{mean}	RSV, IVA, IVB, HPIV 1-3, HAdV	Upper-middle	PH
Chen (2014)[93]	Suzhou, China	2009-2012	48	7626	<14 y	Monthly	C	Hospitalized with LRTI	T_{mean}	HBoV	Upper-middle	PL
Chen (2013)[94]	Suzhou, China	2006	12	1598	1 m-13 y	Monthly	C	Hospitalized for ARI	T_{mean}	*M. pneumoniae, C. pneumoniae*	Upper-middle	PL
Tang (2013)[95]	Suzhou, China	2009	12	1883	1 m-10 y	Monthly	C	Hospitalized for RTI	T_{mean}	RSV	Upper-middle	PH

Wan (2013)[96]	Suzhou, China	2007-2011	60	28871	3 d-15 y	Monthly	C	Reported cases	T_{mean}	RSV	Upper-middle	PH
Wang (2013)[97]	Guilin, China	2011-2012	24	1342	30 d-14 y	Monthly	C	Hospitalized for ARI	T_{mean}	*M. pneumoniae*	Upper-middle	PL
Zheng (2013)[98]	Luoyang, China	2011	12	256	8-23 m	Monthly	D	Hospitalized for ARI	T_{mean}	*M. pneumoniae*	Upper-middle	PL
Yin (2013)[99]	Suzhou, China	2006-2009	48	8368	1 m-14 y	Monthly	C	Hospitalized for ARI	T_{mean}	*M. pneumoniae*	Upper-middle	PL
Chen (2013)[100]	Suzhou, China	2006-2010	60	8157	1 m-14 y	Monthly	C	Hospitalized with RTI	T_{mean}	*M. pneumoniae*	Upper-middle	DH
Li (2013)[101]	Zhuhai, China	2010	12	924	1 m-78 y	Monthly	C	Reported ILI cases	T_{mean}	IVA/H3N2, IVA/H1N1pdm09, IVB, HPIV 1-3, RSV, HMPV, HAdV	Upper-middle	PL
Wang (2013)[102]	Suzhou, China	2006 - 2009	48	6655	30 d-10 y	Monthly	C	Hospitalized for ARI	T_{mean}	HMPV	Upper-middle	PL
Chen (2012)[103]	Suzhou, China	2009-2010	24	998	1-24 m	Monthly	C	Hospitalized for bronchiolitis	T_{mean}	RSV, HBoV, HPIV-3, IVA, HAdV, HMPV, *M. pneumoniae*	Upper-middle	PH
Chee-Sieng (2012)[104]	Kuala Lumpur, Malaysia	1982-2008	328	10269	≤5 y	Monthly	A	Hospitalized with RTI	T_{mean}	RSV	Upper-middle	PL
Chen (2012)[105]	Suzhou, China	2006-2010	60	8197	1-120 m	Monthly	C	Hospitalized for ARI	T_{mean}	HAdV	Upper-middle	PH
TNS (2012)[106]	Turkey four regions	2008.05-2010.09	29	3464	<2 y	Monthly	C/D	bronchiolitis/pneumonia	T_{mean}	RSV	Upper-middle	PL
Daniel Hervás (2012)[107]	Mallorca, Spain	1995-2006	146/625	2384	≤ 2 y	Monthly/ Weekly	C	Hospitalized for bronchiolitis	T_{mean}, T_{max}, T_{min}	RSV	High	PL
Susana (2012)[108]	Valencia, Spain	2006-2009	48	243	> 18 y	Monthly	C	Hospitalized for CAP	T_{mean}	*S.pneumoniae*, *L. pneumophila*	High	PH
Ji (2011)[109]	Suzhou, China	2006-2009	48	6655	1 m -10 y	Monthly	C	Hospitalized for ARI	T_{mean}	RSV, IVA, IVB, HPIV 1-3, HAdV, HMPV, HBoV	Upper-middle	PL
Sun (2011)[110]	Suzhou, China	2006-2009	48	6655	1-120 m	Monthly	C	Hospitalized for RI	T_{mean}	HPIV-3	Upper-middle	PH
Wang (2011)[111]	Suzhou, China	2006-2009	48	6599	1-120 m	Monthly	C	Hospitalized for ARI	T_{mean}	HMPV	Upper-middle	PH
Loh (2011)[112]	Bukit Timah, Singapore	2003.08–2008.12	65	44026	0–5 y	Weekly	A	Hospitalized with RTI	T_{mean}, T_{max}, T_{min}	IVA, IVB, RSV, HPIV 1–3, HAdV	High	PL
Cristiana (2010)[113]	Salvador, Brazil	2003.09-2005.05	20	184	<5 y	Monthly	A	Reported pneumonia cases	T_{mean}	IVA, IVB, RSV, HPIV 1-3, HAdV, *H.*	Upper-middle	PL

										influenzae, S. pneumoniae, M. pneumoniae, C. pneumoniae, M. catarrhalis		
Cao (2010)[114]	Beijing, China	2009.08.03-11.08	97	Not reported	all	Daily	D	Reported ILI cases	T_{mean}	IVA/H1N1pdm09	Upper-middle	PH
Jean-Baptist (2009)[115]	Rheinland-Pfalz, Mainz	2001-2006	312	3044	≤16 y	Weekly	C	Hospitalized for ARI	T_{mean}	IVA, HAdV, HMPV, HRV, CoV, *M. pneumoniae, C. pneumoniae*	High	PH
Noyola (2009)[116]	San Luis Potosí, Mexico	2002.10-2006.05	191	1393	<18 y	Weekly	D	Hospitalized with LRTI	T_{mean}	RSV	High	PH
Maria (2009)[117]	Kathmandu, Nepal	2004.06-2007.06	37	887	2-35 m	Monthly	A	Reported pneumonia cases	T_{mean}	RSV, IVA, IVB, HPIV 1-3, HMPV	Lower	PL
Onozuka (2009)[118]	Fukuoka,Tokyo, Japan	1999-2007	469	13056	<15 y	Weekly	C	Reported pneumonia cases	T_{mean}	*M. pneumoniae*	High	PL
Tang (2009)[119]	Hong Kong, China	2000.05–2007.12	93	8539	<18 y	Monthly	C	Hospitalized for RTI	T_{mean}	IVA, IVB, RSV	High	PL
Onozuka (2008)[120]	Fukuoka, Japan	1999-2007	432	13056	all	Weekly	C	Reported cases	T_{mean}	*M. pneumoniae*	Upper-middle	PH
Asma (2008)[121]	Doha, Qatar	2002.01-2007.09	69	3121	≤ 2 y	Monthly	A	Reported cases	T_{mean}	RSV	High	PL
Yuan (2006)[122]	Beijing, China	2003.04.03 - 06.11	69	2522	all	Daily	C	Reported cases	T_{mean}, T_{max}, T_{min}	SARS-CoV-2	Upper-middle	PL
Bi (2006)[123]	Beijing and Hong Kong, China	2003.04.21-05.20	29	Not reported	all	Daily	C/D	Notified cases	T_{mean}, T_{max}, T_{min}	SARS-CoV	Upper-middle	PL
Wang (2005)[124]	Hangzhou, China	2001-2003	36	13642	1 m-13 y	Monthly	C	Hospitalized for pneumonia	T_{mean}	RSV	Upper-middle	PL
Feng (2005)[125]	Guangzhou, Hong Kong, Toronto, Singapore, Taiwan, Beijing	2003.01.01-05.18	137	581	all	Daily	A/C/D	Reported cases	T_{mean}, T_{max}, T_{min}	SARS-CoV	Upper-middle/High	PH
Mariana (2004)[126]	Buenos Aires, Argentina	1998 –2002	60	18561	<5 y	Monthly	C	Hospitalized with ARI	T_{mean}	RSV, HPIV, IVA, IVB, HAdV	High	PL

Huang (2004)[127]	Guangdong, China	2003.01-05	129	1491	all	Daily	C	Reported cases	T_{mean}, T_{max}, T_{min}	SARS-CoV	Upper-middle	PH
Hailin (2019)[128]	Wenzhou, China	2008-2017	121	89898	<18 y	Monthly	C	Hospitalized with RTI	T_{mean}	RSV	Upper-middle	PL
Liu (2019)[129]	Guangzhou, China	2009.07-2016.06	85	11398	≤14 y	Monthly	C	Hospitalized with ARI	T_{mean}	RSV, HPIV, HMPV	Upper-middle	DL
Natalia (2016)[130]	Athens, Greece	2002-2013	146	7516	0-14 y	Monthly	C	Hospitalized with ARI	T_{mean}	RSV	High	PH
Omer (2008)[131]	Lombok, Indonesia	2000-2002	1095	2878	< 2 y	Daily	A	Reported pneumonia cases	T_{mean}, T_{max}, T_{min}	RSV	Upper-middle	DH
Patrick (2015)[132]	Kuala Lumpur, Malaysia	1982-1997	194	5691	< 2 y	Monthly	A	Reported bronchiolitis and pneumonia	T_{mean}	RSV	Upper-middle	DL
Santiago (2004)[133]	Leon, Spain	1995.10-2000.06	247	221	< 18 y	Weekly	C	Hospitalized with bronchitis/bronchiolitis/pneumonia	T_{mean}, T_{max}, T_{min}	RSV	High	PH
Silvia (2013)[134]	Bologna, Italy	2007-2010	208	327	< 2 y	Weekly	C	Reported cases	T_{min}	RSV	High	PL
Virginia (2015)[135]	Nine states (Arizona, California, Colorado, Iowa, Massachusetts, Maryland, New Jersey, Washington, and Wisconsin), United States	1989-2009	255	Not reported	all	Monthly	C	Reported acute bronchiolitis	T_{mean}, T_{max}, T_{min}	RSV	High	PL
Zhang (2013)[136]	Suzhou, China	2001-2011	133	42664	3 d -15 y	Monthly	C	Hospitalized with ARI	T_{mean}	RSV	Upper-middle	PH
Tamara (2009)[137]	Amsterdam, Netherlands	1998-2005	417	10672	< 6 m	Weekly	C	Reported cases	T_{min}	RSV	High	PL

Note: *d: day(s), wk: week(s), m: month(s), y: year(s); $T_{mean:}$ mean temperature, $T_{max:}$ maximum temperature; $T_{min:}$ minimum temperature; TNS: Turkish Neonatal Society; C: Temperate; A: Tropical; B: Arid; D: Continental; ILI: Influenza-like illness; LRTI: lower respiratory tract infection; ARI: acute respiratory infection; CAP: Community acquired pneumonia; VRI: viral respiratory infection; RSV: Respiratory syncytial virus; IAV: influenza A virus; IBV: influenza B virus; HAdV: human adenovirus; HPIV: human parainfluenza virus; HMPV: human metapneumovirus; HBoV: human bocavirus; HRV: human rhinovirus; EV: enterovirus; HCoV: human coronavirus; EV/HRV: enterovirus/human rhinovirus; MERS-CoV: Middle East Respiratory Syndrome Coronavirus; SARS-CoV: Severe Acute Respiratory Syndrome Coronavirus; *M. pneumoniae: Mycoplasma pneumoniae; S. pneumoniae: Streptococcus pneumoniae; C. pneumoniae: Chlamydophila pneumoniae; L. pneumophila: Legionella pneumophila; H. influenzae : Haemophilus influenzae; M. catarrhalis: Moraxella catarrhalis; P. aeruginosa: Pseudomonas aeruginosa; S. pyogenes: Streptococcus pyogenes* pharyngitis

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Table S10. Global distribution of common respiratory tract specific pathogen infections studies and sites (applied to the Figure 2)

Country	Number of studies	Number of sites
Leon, Spain	1	1
Valencia, Spain	1	1
Mallorca, Spain	2	1
52 Spanish provinces	1	1
Yaounde, Cameroon	1	1
Garoua, Cameroon	1	1
Riyadh, Saudi Arabia	1	1
Nha Trang, central Vietnam	1	1
Sousse, Northern Africa	1	1
Turkey four regions: Marmara, Mediterranean and Aegean region; Black Sea region; East Anatolian region; Middle Anatolian region	1	4
Kathmandu, Nepal	1	1
Nairobi, Kenya	1	1
Doha, Qatar	1	1
Safat, Kuwait	1	1
Lombok, Indonesia	1	1
Bangkok, Thailand	1	1
Athens, Greece	1	1
Toronto, Canada	1	1
Gold Coast, Australia	1	1
Buenos Aires, Argentina	1	1
Moscow	1	1
Dijon, France	1	1
Gothenburg, Sweden	1	1
Kajaani, Finland	1	1
Helsinki, Finland	1	1
Bukit Timah, Singapore	3	1
Singapore	2	1
Bologna, Italy	1	1
Milan; Florence; Trento, Italy	1	3
Rome, Italy	1	1
Amsterdam, the Netherlands	2	1
Nine states (Arizona, California, Colorado, Iowa, Massachusetts, Maryland, New Jersey, Washington, and Wisconsin) , United States	1	9
Rhode Island, USA	1	1
Oahu, USA	1	1
48 states of USA	1	1
Kuala Lumpur, Malaysia	3	1
San Luis Potosí, Mexico	1	1
Rheinland-Pfalz, Mainz	1	1
Curitiba, Brazil	1	1
Sao Paulo, Brazil	1	1
Maranhao, Brazil	1	1

Salvador, Brazil	1	1
Edinburgh, UK	1	1
Liverpool, UK	1	1
Bogota, Colombian	2	1
Cheonan, Korea	5	1
Changwon, Korea	1	1
Gwangju, Korea	1	1
Seoul, Korea	2	1
Fukuoka,Tokyo, Japan	3	1
Six Japanese prefectures (Hokkaido, Tokyo, Aichi, Osaka, Fukuoka, and Okinawa)	1	6
46 Okinawa prefecture, Japan	1	1
47 prefectures in Japan	1	1
13 European countries (Austria, Denmark, Estonia, France, Germany, Greece, Ireland, Netherlands, Poland, Portugal, Slovenia, Spain, United Kingdom)	1	13
Fifty U.S. states and Washington D.C.	1	1
Guangzhou, Hong Kong, Toronto, Singapore, Taiwan, Beijing	1	6
Guangzhou, China	2	1
Guangdong, China	1	1
Zhongshan, China	1	1
Zhuhai, China	1	1
Chaoshan, China	1	1
Shenzhen, China	1	1
Guangzhou, Jiangmen, Foshan, Shenzhen, Zhaoqing, and Zhongshan in Guangdong Province, China	1	6
Hong Kong, China	2	1
Beijing and Hong Kong, China	1	2
Beijing, China	2	1
Shanghai, China	3	1
Wenzhou, China	2	1
Hangzhou, China	3	1
Chengdu, China	2	1
Macao, China	1	1
Chongqing, China	1	1
Panzhihua, China	1	1
Wu zhishan, China	1	1
Henan, China	1	1
Luoyang, China	1	1
Zhengzhou, China	1	1
Jinan, China	1	1
Nantong, China	1	1
Taiwan, China	1	1
Quanzhou, China	1	1
Guilin, China	1	1
Huangshi, China	1	1
Tianjin, China	1	1

Haikou, China	1	1
Yancheng, China	1	1
Jiangyin, China	1	1
Wuhan, China	1	1
Suzhou, China	26	1

Table S11. Risk of bias (RoB) Assessment for each study (n=137)

Study	Exposure assessment	Outcome assessment	Confounding bias	Selection bias	Incomplete missing data	Selective outcome reporting	Conflict of interest	Other bias
Santiago (2004)	PL	PL	DL	DL	DL	DL	DL	PH
Zhang (2013)	PL	PL	PH	DL	PL	DL	PL	PL
Liu (2019)	PL	DL	DL	DL	DL	DL	DL	DL
Natalia (2016)	PL	DL	PL	PL	PH	DL	DL	DL
Silvia (2013)	PL	DL	PL	PL	DL	DL	PL	PL
Tamara (2009)	PH	DL	DL	DL	DL	DL	DL	PL
Omer (2008)	PL	DL	PL	PL	DL	DH	PL	PL
Virginia (2015)	PL	PL	PL	DL	PL	PL	DL	DL
Patrick (2015)	PL	DL	DL	DL	DL	DL	DL	DL
Hailin (2019)	PL	PL	DL	PL	PL	PL	PL	DL
Zheng (2014)	PL	PL	DL	DL	DL	PH	DL	DL
Ming (2022)	DL	PL	PL	DL	PL	DL	DL	DL
Eun (2021)	PL	DL	DL	DL	DL	DL	DL	DL
Ilada (2020)	DL	PH	DL	DL	DL	DL	DL	PL
Nicklas (2016)	DL	PL	DH	DL	DH	PH	DL	DL
Jean-Baptist (2009)	PL	PL	PH	PH	DL	DL	DL	DL
Noyola (2009)	DL	PL	PL	PL	PL	PL	PH	DL
Rodriguez-Martinez (2015)	PL	DL	DL	DL	DL	DL	DL	DL
Young (2019)	PH	PL	DL	DL	DL	DL	DL	PL
Zhi (2021)	PL	DH	PL	DH	DL	DL	DL	DL

Huang (2022)	PL	PL	PL	PL	PL	PL	PH	DL
Gamba-Sanchez (2016)	PL	DL	DL	DL	DL	DL	DL	DL
Cheng (2022)	DL	DL	DL	DL	DL	DL	DL	DL
Jang (2020)	PL	PL	DL	PL	PL	DL	DL	PL
Chee (2023)	PH	DL	DL	DL	DL	DL	DL	DL
Wen-Kuan (2018)	PL	PL	DL	PL	DL	PL	DL	DL
Li (2020)	PL	PH	DL	PL	DL	PL	PL	DL
Chen (2014)	PL	PL	DL	PL	DL	PL	DL	DL
Chen (2013)	PL	PL	DL	PL	DL	PL	DL	DL
Liu (2021)	PH	DL	DL	DL	DL	DL	DL	DL
Wang (2005)	DL	DL	PL	DL	PL	PL	DL	PL
Chen (2014)	PH	DL	DL	DL	DL	DL	DL	DL
Giselmo (2020)	PL	DL	DL	PL	PL	PL	DL	DL
Chen (2013)	PL	DL	DH	PH	PL	DL	DL	DL
Rory (2019)	PL	DL	DL	PL	DL	PL	DL	DL
Onozuka (2009	PL	DL	DL	PL	PL	DL	DL	DL
Keita (2022)	PL	PH	PH	DL	DL	PL	DL	DL
Mohamed (2021)	PL	PL	PH	DL	PL	PH	DL	DL
Yuan (2006)	PL	DL	PL	PL	PL	PL	DL	DL
Tian (2017)	PL	PH	DL	DL	DL	DL	DL	DL
Tiina (2016)	PL	PL	DL	DL	DH	DL	DL	DL
Cui (2015)	PL	DL	DH	DL	DH	DL	DL	DL
Yan (2017)	PL	DL	PL	DL	PL	DL	DL	DL

Lei (2021)	PL	PL	PL	PL	DL	DL	PL	DL
Jaqueline (2016)	PL	DL	PL	PL	PL	DL	DL	DL
Lu (2015)	PL	PL	PL	DL	PL	DL	DL	DL
Ji (2011)	PL	DL	PL	DL	PL	DL	DL	DL
Geng (2015)	PL	DL	PL	DL	PL	PL	DL	DL
Daniel (2015)	PL	DL	PL	PL	PL	DL	DL	DL
Cristiana (2010)	DL	PL	DL	DL	PL	PL	DL	DL
Susana (2012)	PH	PL	DL	DL	DL	DL	DL	DL
Maria (2009)	DL	DL	PL	PL	PL	PL	PL	DL
Katerina (2019)	PL	PL	DL	DL	DL	PL	PL	DL
Magali (2018)	PL	PL	DL	DL	DL	PL	DL	DL
Loh (2011)	PL	PL	DL	DL	DL	PL	DL	DL
Yong (2019)	PL	PL	DL	DL	PL	PL	DL	DL
Shi (2016)	PH	PL	DL	DL	DL	DL	PL	DL
Therese (2021)	DL	PL	PL	DL	DL	DL	PL	DL
Li (2013)	DL	PL	PL	PL	PL	DL	PL	DL
TNS (2012)	DL	PL	DL	DL	PL	DL	PL	DL
Wang (2013)	PL	PL	PL	DL	PL	PL	PL	DL
Daniel Hervás (2012)	PL	PL	DL	DL	PL	DL	DL	DL
Asma (2008)	PL	PL	DL	PL	PL	DL	PL	PL
Raffaella (2017)	PL	PL	DL	DL	PL	DL	PL	DL
Sheikh (2020)	PL	PL	DL	DL	PL	DL	PL	PL
Ines (2018)	DL	PL	DL	PL	PL	PL	PL	DL

Sun (2014)	DL	PL	DL	DL	PL	PL	PL	DL
You (2022)	PH	PL	DL	DL	PL	PL	PL	DL
Jung (2018)	DL	PL	DL	DL	PL	PL	PL	DL
Adriana (2018)	DL	PL	DL	DL	PL	PL	PL	DL
Chee-Sieng (2012)	DL	PL	DL	DL	PL	PL	PL	DL
Huang (2019)	PH	PL	DL	DL	DL	DL	DL	DL
Wei (2019)	PL	PL	DL	DL	PL	DL	PL	PL
Tang (2009)	PL	PL	DL	DL	PL	DL	PL	DL
Morley (2018)	PL	PL	DL	DL	PL	DL	PL	DL
Hermann (2018)	PL	PL	DL	DL	PL	DL	PL	DL
Rosalie (2021)	PL	PL	DL	DL	DL	DL	PL	DL
Wei (2016)	PL	PL	PL	DL	DL	DL	PL	DL
Keita (2023)	PL	PL	DL	DL	DL	DL	PL	DL
Qing (2016)	PL	PL	DL	DH	PL	DL	PL	DL
Jang (2017)	DL	PL	DL	DL	PL	DL	PL	PL
You (2022)	PL	PL	PL	DH	PL	DL	PL	DL
Terezinha (2017)	PL	PL	DL	DL	PL	DL	PL	DL
Raymundo (2023)	PL	PL	DL	DL	PL	DL	PL	DL
Wang (2017)	PL	DL	DL	DL	PL	DL	PL	DL
Gwladys (2017)	PL	PL	DL	DL	DH	DL	PL	DL
Annabel (2023)	PL	PL	PL	DH	DH	DL	PL	DL
Aleix (2021)	PL	PL	DL	DL	PL	DL	PL	DL

Bi (2006)	PL	DL	DL	DL	PL	DL	PL	DL
Mariana (2004)	PL	PL	DL	DL	PL	DL	PL	DL
Pan (2022)	PH	PL	DL	PL	DL	DL	PL	DL
Asmaa (2020)	DL	PL	DL	DL	DL	DL	PL	DL
Pan (2019)	DL	PL	DL	DL	DL	DL	PL	DL
Can (2021)	DL	PL	DL	DL	DH	DL	PL	DL
Na (2022)	DL	PL	DL	DL	PL	DL	PL	DL
Stacy (2021)	PL	DL	DL	DL	PL	DL	PL	DL
Eun (2021)	PL	PL	DL	DL	PL	DL	PL	DL
Ping-Ing (2023)	PL	PL	DL	DL	PL	DL	PL	DL
Chan (2021)	PL	PL	DL	DL	PL	DL	PL	DL
Dong (2021)	DL	PL	DL	DL	DH	DL	PL	DL
Onozuka (2014)	DL	PH	DL	DL	DL	DL	PL	DL
Benjamin (2018)	PL	PL	DL	DL	PL	DL	PL	DL
Shiv (2020)	DL	PL	DL	PL	DL	DL	DL	DL
PSOTER (2016)	PH	PL	DL	PL	DL	DL	DL	DL
Meng (2023)	DL	PL	DL	PL	DL	DL	DL	DL
Lin (2015)	DL	PL	DL	DL	DL	PL	DL	DL
Wang (2013)	DL	PL	DL	PL	DL	DL	DL	DL
Chen (2012)	PH	PL	DL	PL	DL	DL	DL	DL
Sun (2011)	PH	PL	DL	PL	PL	DL	DL	DL
Onozuka (2008)	PH	PL	DL	PL	DL	DL	DL	DL

Zhou (2018)	PH	DL	OH	DL	DL	DL	DL	DL
Wu (2019)	PH	DL	DL	DL	DL	DL	DL	DL
Zhou (2017)	PL	DL	DL	DL	PL	DL	DL	DL
Na (2021)	PL	DL	DL	DL	DL	DL	DL	DL
Huang (2015)	PH	DL	DL	PH	DL	DL	DL	DL
Wang (2011)	PH	DL	DL	DL	PL	DL	DL	DL
Yuan (2022)	PH	PL	DL	DL	DL	DL	DL	DL
Ni (2014)	PL	PL	DL	DL	DL	DL	DL	DL
Yin (2013)	PL	PL	PL	PL	DL	DL	DL	DL
Zheng (2013)	PL	PL	DL	PL	DL	DL	DL	DL
Sobral (2020)	PL	PL	DL	PL	DL	DL	DL	DL
Wu (2021)	PL	PL	DL	PL	DL	DL	DL	DL
Tang (2013)	PH	DL	DL	PL	DL	DL	DL	DL
Wan (2013)	PH	DL	DL	DL	DL	DL	DL	DL
Chen (2016)	PH	DL	PL	PL	DL	DL	DL	DL
Zhang (2022)	PH	PH	DL	PH	DL	DL	DL	DL
He (2019)	PL	DL	DL	PL	DL	DL	DL	DL
Yan (2015)	PL	DL	DL	PL	DL	DL	DL	DL
Zhang (2020)	PH	DL	DL	PL	DL	DL	DL	DL
Cao (2010)	PL	PH	DL	PL	DL	DL	DL	DL
Chen (2021)	PL	DL	DL	PL	DL	DL	DL	DL
Feng (2005)	PH	DL	DL	PL	DL	DL	DL	DL

Liu (2021)	PL	DL	DL	PL	DL	DL	DL	DL
Kong (2020)	PL	PH	DL	PL	DL	DL	DL	DL
Huang (2004)	PH	DL	DL	PL	DL	DL	DL	DL
Sung (2022)	PL	DL	DL	PL	DL	DL	DL	DL
Lisa (2022)	PL	PL	DL	PL	DL	DL	DL	DL
Simone (2020)	PL	DL	DL	PL	DL	DL	DL	DL

Note: PL- Probably Low risk; PH- Probably High risk; DH- Definitely High risk; DL- Definitely Low risk

Table S12. Summary of included studies corresponding to each pathogen

Pathogen	Study
Viral infection	
RSV	
Respiratory syncytial virus -A	Zhi (2021) [19] Cheng (2022)[18] Jang (2017)[63] Wu (2021)[24]
Respiratory syncytial virus -B	Zhi (2021) [19] Cheng (2022)[18] Jang (2017)[63] Wu (2021)[24]
Respiratory syncytial virus - unsubtyped	Santiago (2004)[133] Zhang (2013)[136] Liu (2019)[129] Natalia (2016)[130] Silvia (2013)[134] Omer (2008)[131] Virginia (2015)[135] Patrick (2015)[132] Hailin (2019)[128] Zheng (2014)[92] Ilada (2020)[37] Nicklas (2016)[74] Jean-Baptist (2009)[115] Noyola (2009)[116] Rodriguez-Martinez (2015)[81] Gamba-Sanchez (2016)[80] Chee (2023)[3] Chen (2012)[103] Liu (2021)[34] Giselmo (2020)[44] Rory (2019)[46] Tian (2017)[68] Cui (2015)[85] Lu (2015)[84] Cristiana (2010)[113] Maria (2009)[117] Magali (2018)[54] Therese (2021)[31] Li (2013)[101] Daniel Hervás (2012)[107] Asma (2008)[121] Raffaella (2017)[70] Sheikh (2020)[39] Ines (2018)[58] You (2022)[7] Chee-Sieng (2012)[104] Rosalie (2021)[35] Wei (2016)[71] Keita (2023)[4] Qing (2016)[72] Terezinha (2017)[64] You (2022)[14] Mariana (2004)[126] Ping-Ing (2023)[5] Chan (2021)[29] Onozuka (2014)[91] Benjamin (2018)[61] Meng (2023)[6] TNS (2012)[106] Wang (2005)[124] Geng (2015)[82] Jung (2018)[59] Lin (2015)[86] Tang (2013)[95] Wan (2013)[96] Chen (2016)[76] Zhang (2022)[8] Ji (2011)[109]
Overall respiratory syncytial virus (RSV)	Zhi (2021) [19] Cheng (2022)[18] Jang (2017)[63] Wu (2021)[24] Santiago (2004)[133] Zhang (2013)[136] Liu (2019)[129] Natalia (2016)[130] Silvia (2013)[134] Omer (2008)[131] Virginia (2015)[135] Patrick (2015)[132] Hailin (2019)[128] Zheng (2014)[92] Ilada (2020)[37] Nicklas (2016)[74] Jean-Baptist (2009)[115] Noyola (2009)[116] Rodriguez-Martinez (2015)[81] Gamba-Sanchez (2016)[80] Chee (2023)[3] Chen (2012)[103] Liu (2021)[34] Giselmo (2020)[44] Rory (2019)[46] Tian (2017)[68] Cui (2015)[85] Lu (2015)[84] Cristiana (2010)[113] Maria (2009)[117] Magali (2018)[54] Therese (2021)[31] Li (2013)[101] Daniel Hervás (2012)[107] Asma (2008)[121] Raffaella (2017)[70] Sheikh (2020)[39] Ines (2018)[58] You (2022)[7] Chee-Sieng (2012)[104] Rosalie (2021)[35] Wei (2016)[71] Keita (2023)[4] Qing (2016)[72] Terezinha (2017)[64] You (2022)[14] Mariana (2004)[126] Ping-Ing (2023)[5] Chan (2021)[29] Onozuka (2014)[91] Benjamin (2018)[61] Meng (2023)[6] TNS (2012)[106] Wang (2005)[124] Geng (2015)[82] Jung (2018)[59] Lin (2015)[86] Tang (2013)[95] Wan (2013)[96] Chen (2016)[76] Zhang (2022)[8] Ji (2011)[109]
IV	
Influenza virus A	Zheng (2014)[92] Jean-Baptist (2009)[115] Cheng (2022)[18] Li (2020)[45] Chen (2012)[103] Rory (2019)[46] Cui (2015)[85] Maria (2009)[117] Adriana (2018)[60] Gwladys (2017)[66] Annabel (2023)[2] Mariana (2004)[126] Benjamin (2018)[61] Ji (2011)[109] Zhang (2022)[8] Lin (2015)[86] Chen (2016)[76]
Influenza virus A/H1N1pdm09	Li (2013)[101] Wei (2019)[51] Pan (2019)[48] Pan (2022)[11] Can (2021)[28] Cao (2010)[114]
Influenza virus A/H3N2	Li (2013)[101] Adriana (2018)[60] Wei (2019)[51] Pan (2019)[48] Can (2021)[28]
Influenza virus B	Zheng (2014)[92] Nicklas (2016)[74] Jean-Baptist (2009)[115] Cheng (2022)[18] Li (2020)[45] Rory (2019)[46] Maria (2009)[117] Li (2013)[101] Adriana (2018)[60] Gwladys (2017)[66] Mariana (2004)[126] Pan (2022)[11] Ji (2011)[109] Lin (2015)[86] Chen (2016)[76] Zhang (2022)[8] Can (2021)[28] Wei (2019)[51]
Influenza virus B/Victoria	Pan (2019)[48]
Influenza virus B/Yamagata	Pan (2019)[48]
Influenza virus -unsubtyped	You (2022)[7] Adriana (2018)[60] Gwladys (2017)[66] Wei (2016)[71]
Overall influenza virus (IV)	Zheng (2014)[92] Jean-Baptist (2009)[115] Li (2020)[45] Chen (2014)[93] Rory (2019)[46] Cui (2015)[85] Maria (2009)[117] Adriana (2018)[60] Gwladys (2017)[66] Annabel (2023)[2] Mariana (2004)[126] Benjamin (2018)[61] Cao (2010)[114] Ji (2011)[109] Li (2013)[101] Wei (2019)[51] Pan (2022)[11] Can (2021)[28] Nicklas (2016)[74] Cheng (2022)[18] Lin (2015)[86] Chen (2016)[76] Zhang (2022)[8] Pan (2019)[48] You (2022)[7] Wei (2016)[71]
HPIV	
Human parainfluenza virus -1	Eun (2021)[20] Jean-Baptist (2009)[115] Ji (2011)[109] Maria (2009)[117] Chen (2016)[76] Zheng (2014)[92]
Human parainfluenza virus -2	Eun (2021)[20] Ji (2011)[109] Maria (2009)[117] Zheng (2014)[92] Chen (2016)[76]
Human parainfluenza virus -3	Chen (2016)[76] Cui (2015)[85] Eun (2021)[20] Jean-Baptist (2009)[115]

	Ji (2011)[109] Maria (2009)[117] Ming (2022)[13] Zheng (2014)[92] Sun (2011)[110] Chen (2016)[76] Zhang (2022)[8] Zhang (2020)[41]
Human parainfluenza virus -4	Cui (2015)[85]
Human parainfluenza virus -unsubtyped	Huang (2019)[47] Li (2013)[101] Therese (2021)[31] Stacy (2021)[26] Wei (2016)[71] Yan (2015)[87] Cheng (2022)[18] Liu (2019)[129] Mariana (2004)[126] You (2022)[7] Lin (2015)[86]
Overall human parainfluenza virus (HPIV)	Eun (2021)[20] Jean-Baptist (2009)[115] Ji (2011)[109] Maria (2009)[117] Chen (2016)[76] Zheng (2014)[92] Maria (2009)[117] Ming (2022)[13] Sun (2011)[110] Zhang (2022)[8] Zhang (2020)[41] Cui (2015)[85] Huang (2019)[47] Li (2013)[101] Therese (2021)[31] Stacy (2021)[26] Wei (2016)[71] Yan (2015)[87] Cheng (2022)[18] Liu (2019)[129] Mariana (2004)[126] You (2022)[7] Lin (2015)[86]
HMPV	
Human metapneumoviruses (HMPV)	Rory (2019)[46] Nicklas (2016)[74] Liu (2019)[129] Jean-Baptist (2009)[115] Chen (2012)[103] Maria (2009)[117] Magali (2018)[54] Yong (2019)[52] Li (2013)[101] Wang (2013)[102] You (2022)[7] Ji (2011)[109] Cheng (2022)[18] Wang (2011)[111]
HRV	
Human rhinovirus (HRV)	Jean-Baptist (2009)[115] Giselmo (2020)[44] Cui (2015)[85] Tiina (2016)[79] Yan (2017)[67] Jaqueline (2016)[78] You (2022)[7] Dong (2021)[30] Benjamin (2018)[61] Zhou (2018)[62] Zhou (2017)[69] Huang Huang (2015)[88]
HAdV	
Human adenovirus (HAdV)	Zheng (2014)[92] Nicklas (2016)[74] Jean-Baptist (2009)[115] Cheng (2022)[18] Chen (2014)[93] Rory (2019)[46] Therese (2021)[31] Li (2013)[101] You (2022)[7] Mariana (2004)[126] Eun (2021)[27] Ji (2011)[109] Lin (2015)[86] Chen (2012)[105] Chen (2016)[76] Zhang (2022)[8]
HBoV	
Human bocavirus -1	Wen-Kuan (2018)[55]
Human bocavirus -unsubtyped	Cui (2015)[85] Cheng (2022)[18] Chen (2014)[93] You (2022)[7] Nicklas (2016)[74] Chen (2012)[103] Ji (2011)[109] He (2019)[49]
Overall human bocavirus virus (HBoV)	Cui (2015)[85] Cheng (2022)[18] Wen-Kuan (2018)[55] Chen (2014)[103] You (2022)[7] Nicklas (2016)[74] Chen (2014)[103] Ji (2011)[109] He (2019)[49]
EV	
Enterovirus (EV)	You (2022)[7] Cui (2015)[85] Jean-Baptist (2009)[115] Wei (2016)[71]
CoV	
HCoV -229E	Jang (2020)[36]
HCoV -OC43	Jang (2020)[36]
HCoV -unsubtyped	You (2022)[7] Jean-Baptist (2009)[115] Nicklas (2016)[74] Cui (2015)[85] Wei (2016)[71]
MERS-CoV	Asmaa (2020)[38]
SARS-CoV-2	Shiv (2020)[40] Aleix (2021)[21] Keita (2022)[17] Chen (2021)[25] Sung (2022)[15] Lisa (2022)[16] Kong (2020)[43] Simone (2020)[42]
SARS-CoV	Bi (2006)[123] Feng (2005)[125] Liu (2021)[22] Huang (2004)[127]
HRV/EV	
Human rhinovirus/enterovirus (HRV/EV)	Cheng (2022)[18] Raymundo (2023)[1]
Bacterial infection	
Streptococcus pneumoniae	Susana (2012)[108] Cristiana (2010)[113] Katerina (2019)[53] Onozuka (2009)[118]
Streptococcus pyogenes pharyngitis	Daniel (2015)[83]
Moraxella catarrhalis	Huang (2019)[47] Sun (2014)[90]
Pseudomonas aeruginosa	PSOTER (2016)[73]
Legionella pneumophila	Susana (2012)[108] Lin (2015)[86]
Haemophilus influenzae	Huang (2022)[12]
Mycoplasma pneumoniae	Jean-Baptist (2009)[115] Chen (2012)[103] Chen (2013)[94] Huang (2019)[47] Tian (2017)[68] Na (2022)[10] Wang (2017)[65] Lei (2021)[32] Onozuka (2008)[120] Yuan (2022)[9] Lin (2015)[86] Wang (2013)[97] Wu (2019)[50] Na (2021)[23] Ni (2014)[89] Yin (2013)[99] Zheng (2013)[98] Shi (2016)[75], Chen (2013)[100]

Chlamydia pneumoniae	Huang (2019)[47] Chen (2013)[94] Jean-Baptist (2009)[115] Lin (2015)[86]
Note: Studies that were included in systematic reviews but not in meta-analyses: Mohamed (2021)[33] Morley (2018)[56] Hermann (2018)[57] Loh (2011)[112] Yuan (2006)[122] Tang (2009)[119] Sobral (2020)[77] Tamara (2009)[137]	

Table S13. Meta-regression results

Outcome	Covariates	Coef.	Std. Err.	Z	P>|z|	Ci.lb	Ci.ub
RSV	**National income level**						
	High	.2724197	0.4951057	0.55	0.583	-.7095057	1.254345
	Upper-middle	-.3211209	0.4932868	-0.65	0.517	-1.299439	0.657197
	Lower-middle	-.1973232	1.780681	-0.11	0.912	-3.728884	-3.728884
	Low	1.765932	2.549974	0.69	0.489	-3.231925	6.763789
	WHO-region						
	Africa	.8373415	1.45493	0.58	0.565	-2.014268	3.688951
	Americas	.3209991	1.064084	0.30	0.763	-1.764567	2.406565
	Eastern Mediterranean	-1.275594	1.838391	-0.69	0.488	-4.878774	2.327586
	Europe	-.9819557	.5239502	-1.87	0.064	-2.021087	.0571759
	South-East Asia	1.765932	2.549974	0.69	0.489	-3.231925	6.763789
	Western Pacifc	0.7205144	0.4944524	1.46	0.148	-.2601152	1.701144
	Study Design						
	cohort	-.8153311	.4878452	-1.67	0.095	-1.77149	.140828
	case-control	.8004486	1.203324	0.67	0.506	-1.558023	3.158921
	cross-sectional	-.0459937	.5319277	-0.09	0.931	-1.088553	.9965654
	case-crossover	-.3570562	1.784618	-0.20	0.841	-3.854844	3.140732
	time-series	1.268819	.6338912	2.00	**0.045**	.0264152	2.511223
	Age	1.188387	0.7958024	1.49	0.138	-.3898992	2.766673
IV	**National income level**						
	High	-.5391765	.4383816	-1.23	0.219	-1.398389	.3200357
	Low	.3938516	1.213169	0.32	0.745	-1.983917	2.77162
	Upper-middle	.4604176	.426858	1.08	0.281	-.3762086	1.297044
	WHO-region						
	Africa	.8025995	.9249863	0.87	0.386	-1.01034	2.615539
	Americas	-.4676699	.5736834	-0.82	0.415	-1.592069	.6567289
	Europe	-.0751581	.0119288	-6.30	**0.000**	-.0985382	-.051778
	South-East Asia	.3938516	1.213169	0.32	0.745	-1.983917	2.77162
	Western Pacifc	.3576141	.4337681	0.82	0.410	-.4925558	1.207784
	Study Design						
	cohort	-.078567	.0118534	-6.63	**0.000**	-.1017992	-.0553349
	cross-sectional	-.4525397	.3953467	-1.14	0.252	-1.227405	.3223255
	case-crossover	2.617493	1.729004	1.51	0.130	-.7712925	6.006278
	time-series	-.5498703	.389102	-1.41	0.158	-1.312496	.2127556
	Age	.5640363	.3840765	1.47	0.142	-.1887397	1.316812
PIV	**National income level**						
	High	-1.278616	.5058212	-2.53	**0.011**	-2.270007	-.2872246
	Low	.9196676	.9207501	1.00	0.318	-.8849693	2.724305
	Upper-middle	.8291939	.4922186	1.68	0.092	-.1355368	1.793925
	WHO-region						
	Africa	-.7801076	.9954686	-0.78	0.433	-2.73119	1.170975
	Americas	-2.247165	1.454936	-1.54	0.122	-5.098788	.6044577
	Europe	-1.340657	.9798861	-1.37	0.171	-3.261198	.5798848
	South-East Asia	.9196676	.9207501	1.00	0.318	-.8849693	2.724305
	Western Pacifc	.6947843	.565879	1.23	0.220	-.4143182	1.803887
	Study Design						
	case-control	1.068844	.8694856	1.23	0.219	-.6353161	2.773005
	cohort	.7647135	.6160566	1.24	0.214	-.4427353	1.972162
	case-crossover	-1.124318	1.514906	-0.74	0.458	-4.093479	1.844843
	cross-sectional	1.503414	.4132066	3.64	**0.000**	.6935438	2.313284
	time-series	.8719242	.5420643	1.61	0.108	-.1905024	1.934351
	ecological	-.9416197	1.381015	-0.68	0.495	-3.648359	1.76512
	Age	-.2108411	.8557342	-0.25	0.805	-1.888049	1.466367
HMPV	**National income level**						
	High	.4654326	.4281547	1.09	0.277	-.3737352	1.3046
	Low	.1921004	1.005379	0.19	0.848	-1.778406	2.162607
	Upper-middle	-.5276054	.4393033	-1.20	0.230	-1.388624	.3334133
	WHO-region						
	Europe	-.1917908	.4546588	-0.42	0.673	-1.082906	.699324
	Western Pacifc	.1413122	.4406817	0.32	0.748	-.7224082	1.005033
	South-East Asia	.1921004	1.005379	0.19	0.848	-1.778406	2.162607
	Study Design						
	cohort	.9778105	.3358525	2.91	**0.004**	.3195517	1.636069
	case-crossover	-.339844	.9568592	-0.36	0.722	-2.215254	1.535565
	cross-sectional	-.6637794	.4392632	-1.51	0.131	-1.524719	.1971607
	time-series	-.681461	.537519	-1.27	0.205	-1.734979	.3720568
	Age	.0597434	.0614445	0.97	0.331	-.0606855	.1801724
HRV	**National income level** *(High vs Upper-middle)*	-1.528162	.8748558	-1.75	0.081	-3.242848	.1865236
	WHO-region	-1.796305	.847199	-2.12	**0.034**	-3.456785	-.1358255

	(Europe vs Western Pacifc)						
	Study Design						
	case-control	.6886622	1.646415	0.42	0.676	-2.538252	3.915577
	case-crossover	-.941739	1.122595	-0.84	0.402	-3.141984	1.258506
	cross-sectional	.910875	.9192012	0.99	0.322	-.8907263	2.712476
	cohort	.5377858	1.383341	0.39	0.697	-2.173513	3.249084
	time-series	-2.493636	1.643218	-1.52	0.129	-5.714284	.7270108
	Age	-1.67809	.9866331	-1.70	0.089	-3.611856	.2556748
HAdVs	**National income level** *(High vs Upper-middle)*	1.844764	.5307367	3.48	**0.001**	.8045392	2.884989
	WHO-region						
	Africa	-.4373683	1.014488	-0.43	0.666	-2.425729	1.550992
	Americas	-2.15672	1.392943	-1.55	0.122	-4.886838	.5733973
	Europe	-1.442254	.7782993	-1.85	0.064	-2.967693	.0831848
	Western Pacifc	1.647847	.5619552	2.93	**0.003**	.5464347	2.749259
	Study Design						
	cohort	-1.211562	.7724662	-1.57	0.117	-2.725568	.3024437
	case-crossover	-.9328839	1.473294	-0.63	0.527	-3.820487	1.954719
	cross-sectional	1.465095	.5827668	2.51	**0.012**	.3228926	2.607296
	time-series	-.4536482	.7224517	-0.63	0.530	-1.869628	.9623311
	Age	-.6745164	.7700138	-0.88	0.381	-2.183716	.8346829
HBoV	**National income level** *(High vs Upper-middle)*	.5216799	.7176844	0.73	0.467	-.8849556	1.928315
	WHO-region *(Europe vs Western Pacifc)*	1.16555	.7904104	1.47	0.140	-.3836257	2.714726
	Study Design						
	cohort	-.6837422	.1137644	-6.01	**0.000**	-.9067163	-.4607682
	case-crossover	.5538944	1.034743	0.54	0.592	-1.474165	2.581954
	cross-sectional	1.15892	.5094783	2.27	**0.023**	.160361	2.157479
	time-series	-.4482961	.8900741	-0.50	0.614	-2.192809	1.296217
	Age	.5538944	1.034743	0.54	0.592	-1.474165	2.581954
EV	**National income level** *(High vs Upper-middle)*	.9369969	.2057731	4.55	**0.000**	.5336889	1.340305
	WHO-region *(Europe vs Western Pacifc)*	1.132873	.2167625	5.23	**0.000**	.7080263	1.557719
	Study Design						
	cohort	.9369969	.2057731	4.55	**0.000**	.5336889	1.340305
	case-crossover	1.101775	.9500641	1.16	0.246	-.7603166	2.963866
	time-series	-1.132873	.2167625	-5.23	**0.000**	-1.557719	-.7080263
	Age	1.101775	.9500641	1.16	0.246	-.7603166	2.963866
SARS-CoV-2	**National income level** *(High vs Upper-middle)*	-.0344442	.0104926	-3.28	**0.001**	-.0550093	-.0138792
	WHO-region						
	Americas	.0116355	.0093826	1.24	0.215	-.0067541	.0300251
	Europe	-.2472766	.1011741	-2.44	**0.015**	-.4455742	-.048979
	Western Pacifc	-.0093421	.009325	-1.00	0.316	-.0276188	.0089345
	Study Design						
	cohort	.0255756	.0072157	3.54	**0.000**	.0114331	.039718
	case-crossover	-.275535	.0114296	-24.11	**0.000**	-.2979366	-.2531335
	time-series	.9746894	.3969559	2.46	**0.014**	.1966701	1.752709
HCoV	**National income level** *(High vs Upper-middle)*	2.015627	1.031223	1.95	0.051	-.0055333	4.036786
	WHO-region *(Europe vs Western Pacifc)*	2.057392	.9107748	2.26	**0.024**	.2723064	3.842478
	Study Design						
	cohort	2.125852	1.004709	2.12	**0.034**	.1566589	4.095045
	case-crossover	-2.200029	1.600112	-1.37	0.169	-5.33619	.9361322
	time-series	-1.442606	1.580981	-0.91	0.362	-4.541272	1.656059
	Age	-2.200029	1.600112	-1.37	0.169	-5.33619	.9361322
SARS-CoV	**National income level** *(High vs Upper-middle)*	-.3785387	.7851233	-0.48	0.630	-1.917352	1.160275
	WHO-region *(Europe vs Western Pacifc)*	-1.766721	.613975	-2.88	**0.004**	-2.97009	-.5633517
	Study Design *(cross-sectional vs time-series analysis)*	-.2922677	.9553481	-0.31	0.760	-2.164716	1.58018

S. pneumoniae	**National income level** *(High vs Upper-middle)*	-1.34663	.6411379	-2.10	**0.036**	-2.603237	-.0900225
	WHO-region						
	Americas	-.7572833	1.182572	-0.64	0.522	-3.075082	1.560515
	Europe	-.531455	.1121689	-4.74	**0.000**	-.751302	-.311608
	Western Pacifc	.564659	.1103552	5.12	**0.000**	.3483667	.7809513
	Study Design *(cohort vs time-series analysis)*	.564659	.1103552	5.12	**0.000**	.3483667	.7809513
M. pneumoniae	**National income level** *(High vs Upper-middle)*	1.390195	2.402839	0.58	0.563	-3.319282	6.099673
	WHO-region *(Europe vs Western Pacifc)*	1.770413	3.320054	0.53	0.594	-4.736772	8.277599
	Study Design						
	cohort	-1.225525	1.43057	-0.86	0.392	-4.02939	1.57834
	cross-sectional	1.900281	1.456086	1.31	0.192	-.9535947	4.754157
	time-series	-1.390195	2.402839	-0.58	0.563	-6.099673	3.319282
	Age	-2.350963	2.385202	-0.99	0.324	-7.025874	2.323947
C. pneumoniae	**National income level** *(High vs Upper-middle)*	5.287783	.2139942	24.71	**0.000**	4.868363	5.707204
	WHO-region *(Europe vs Western Pacifc)*	5.287783	.2139942	24.71	**0.000**	4.868363	5.707204
	Study Design						
	cohort	5.296347	.2115122	25.04	**0.000**	4.881791	5.710903
	cross-sectional	-2.004481	3.697434	-0.54	0.588	-9.251319	5.242357
	time-series	-5.287783	.2139942	-24.71	**0.000**	-5.707204	-4.868363

Crl = credible interval. RSV: Respiratory syncytial virus; IV: influenza virus; HAdV: human adenovirus; HPIV: human parainfluenza virus; HMPV: human metapneumovirus; HBoV: human bocavirus; HRV: human rhinovirus; EV: enterovirus; HCoV: human coronavirus; SARS-CoV: Severe Acute Respiratory Syndrome Coronavirus; *S. pneumoniae*: *Streptococcus pneumoniae*; *M. pneumoniae: Mycoplasma pneumoniae; S. pneumoniae: C. pneumoniae: Chlamydophila pneumoniae*

Table S14: Summary of the assessment of the quality and strength of the evidence on ambient temperature as a risk factor for incidence of viral, mycoplasma and chlamydia respiratory infections

Reference	Ambient temperature	Respiratory syncytial virus (RSV) (n = 62)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	-1	Most studies carry a substantial risk of bias.
Indirectness	0	The studies assessed population, exposure, and outcome of interest morbidity was appropriate outcome, studies conducted in the population of interest, mostly direct measures of exposure.
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity.
Imprecision	0	We judged that the incidence CI of meta-analyses was narrow enough.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	1	Most studies report dose-response patterns that are broadly similar, with incidence increasing or decreasing with ambient temperature above a certain threshold.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is "moderate")	*Moderate*	Moderate+(1)+(-1) = Moderate. Downgrading/upgrading resulted in moderate rating for the quality of evidence.
Summary of findings	n/a	Overall moderate quality of the evidence of the reduction in the incidence of RSV infection associated with ambient temperature exposure (see results from meta-analyses in Figure S2).
Strength considerations		
Quality of body of evidence	n/a	*Moderate*
Direction of effect estimate	n/a	Direction largely as expected: increased temperature reduced incidence.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are generally consistent, and most studies have a low risk of bias, especially studies with large sample sizes, but several have large confidence intervals. It is unlikely that a new study would have an effect estimate that would make the results of the meta-analysis null or insignificant.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Sufficient	Based on our analysis and interpretation of the evidence, we conclude that there is an association between temperature exposure and RSV incidence, and we are reasonably confident that opportunity, bias, and confounding factors can be excluded as explanations for this association. The available evidence includes the results of one or more well-designed, well-conducted studies, and we believe that our conclusions are unlikely to strongly influence the outcomes of future studies.
Reference	Ambient temperature	Influenza viruses (IV) (n = 27)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	-1	Some studies are at risk of bias.

Indirectness	0	The studies assessed population, exposure, and outcome of interest
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis did not appear to be strongly influenced by the individual studies. measures are consistent in the direction of overall effect estimates.
Imprecision	0	We judged that the incidence CI of meta-analyses was narrow enough.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	1	Most studies report dose-response patterns that are broadly similar, with incidence increasing or decreasing with ambient temperature above a certain threshold.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is ”moderate”)	*Moderate*	Moderate+(1)+(-1) = Moderate. Downgrading/upgrading resulted in moderate rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	We found that most of the reduction in the incidence of IFV infection associated with ambient temperature exposure (see results from meta-analyses in Figure S3).
Strength considerations		
Quality of body of evidence	n/a	*Moderate*
Direction of effect estimate	n/a	Direction largely as expected: increased temperature reduced incidence.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are generally consistent, and most studies have a low risk of bias, especially studies with large sample sizes, but several have large confidence intervals. It is unlikely that a new study would have an effect estimate that would make the results of the meta-analysis null or insignificant.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Sufficient	Based on our analysis and interpretation of the evidence, we conclude that there is an association between temperature exposure and IFV incidence, and we are reasonably confident that opportunity, bias, and confounding factors can be excluded as explanations for this association. The available evidence includes the results of one or more well-designed, well-conducted studies, and we believe that our conclusions are unlikely to strongly influence the outcomes of future studies.

Reference	Ambient temperature	Human parainfluenza virus (HPIV) (n = 23)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	-1	There is a risk of bias in some studies.
Indirectness	0	The studies assessed population, exposure, and outcome of interest
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of

		HPIV infection do not appear to be strongly influenced by an individual study. measures are consistent in the direction of overall effect estimates.
Imprecision	0	We judged that the incidence CI of meta-analyses was narrow enough.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	1	Most studies report dose-response patterns that are broadly similar, with incidence increasing or decreasing with ambient temperature above a certain threshold.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is "moderate")	*Moderate*	Moderate+(1)+(-1) = Moderate. Downgrading/upgrading resulted in moderate rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	We found that most of the reduction in the incidence of HPIV infection associated with ambient temperature exposure (see results from meta-analyses in Figure S4).
Strength considerations		
Quality of body of evidence	n/a	*Moderate*
Direction of effect estimate	n/a	The direction of effect estimates largely showed an increasing trend in HPIV infection with increasing high temperatures.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are generally consistent, and most studies have a low risk of bias, especially studies with large sample sizes, but several have large confidence intervals. It is unlikely that a new study would have an effect estimate that would make the results of the meta-analysis null or insignificant.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Sufficient	Based on our analysis and interpretation of the evidence, we conclude that there is an positive association between temperature exposure and HPIV incidence, and we are reasonably confident that opportunity, bias, and confounding factors can be excluded as explanations for this association. The available evidence includes the results of one or more well-designed, well-conducted studies, and we believe that our conclusions are unlikely to strongly influence the outcomes of future studies.

Reference	Ambient temperature	Human metapneumovirus (hMPV) (n = 14)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	-1	Some studies carry a certain risk of bias.
Indirectness	0	The studies assessed population, exposure, and outcome of interest
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of respiratory infection do not appear to be strongly influenced by an individual study.
Imprecision	-1	Except six studies, the 95% CIs of the studies possessed notably narrow confidence intervals.

Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	1	Most studies report dose-response patterns that are broadly similar, with incidence increasing or decreasing with ambient temperature above a certain threshold.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is "moderate")	*Low*	Moderate+(-1)+(-1)+(1) = Low. Downgrading/upgrading resulted in low rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	We found that most of the reduction in the incidence of hMPV infection associated with ambient temperature exposure (see results from meta-analyses in Figure S5).
Strength considerations		
Quality of body of evidence	n/a	*Low*
Direction of effect estimate	n/a	The direction of effect estimates largely showed an decreasing trend in hMPV infection with increasing temperatures.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are generally consistent, and most studies have a low risk of bias, especially studies with large sample sizes, but several have large confidence intervals. It is unlikely that a new study would have an effect estimate that would make the results of the meta-analysis null or insignificant.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Sufficient	Based on our analysis and interpretation of the evidence, we conclude that there is an negative association between temperature exposure and hMPV incidence, and we are reasonably confident that opportunity, bias, and confounding factors can be excluded as explanations for this association. The available evidence includes the results of one or more well-designed, well-conducted studies, and we believe that our conclusions are unlikely to strongly influence the outcomes of future studies.

Reference	Ambient temperature	Human rhinovirus (HRV) (n = 12)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	-1	There is a substantial risk of bias across most studies.
Indirectness	0	The studies assessed population, exposure, and outcome of interest.
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of respiratory infection do not appear to be strongly influenced by an individual study. The results of all four metaanalyses for change in the respiratory infection. measures are consistent in the direction of overall effect estimates.
Imprecision	-1	We judged that the incidence CI of 3 studies was wide.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		

Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	0	Random effects contain uniformity and are not statistically significant.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is ”moderate”)	*Very low*	Moderate+(-1)+(-1) = Very low. Downgrading/upgrading resulted in very low rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	The random effect result contains unity and were statistically insignificant. (see results from meta-analyses in Figure S6).
Summary of qualitative findings	n/a	Studies not included in the meta-analyses presented mixed results, mostly insignificant associations.
Strength considerations		
Quality of body of evidence	n/a	*Very low*
Direction of effect estimate	n/a	No association was found and the results were inconclusive.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are often inconsistent, and most studies have a risk of bias, and some have large confidence intervals, which makes the results uncertain for the future.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Limited	Based on our analysis and interpretation of the evidence, we conclude that there is no association between temperature exposure and HRV morbidity.

Reference	Ambient temperature	Human adenovirus (HAdV) (n = 16)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	-1	There is a risk of bias in some studies.
Indirectness	0	The studies assessed population, exposure, and outcome of interest.
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of respiratory infection do not appear to be strongly influenced by an individual study. The results of all four metaanalyses for change in the respiratory infection. measures are consistent in the direction of overall effect estimates.
Imprecision	-1	We judged that the incidence CI of 4 studies was wide.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	0	Random effects contain uniformity and are not statistically significant.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is ”moderate”)	*Very low*	Moderate+(-1)+(-1) = Very low. Downgrading/upgrading resulted in very low rating for the quality of evidence.

Summary of findings from meta-analysis	n/a	Random effect contains unity and were statistically insignificant (see results from meta-analyses in Figure S7).
Strength considerations		
Quality of body of evidence	n/a	*Very low*
Direction of effect estimate	n/a	No association was found and the results were inconclusive.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are often inconsistent, and some studies have a risk of bias and some have large confidence intervals.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Limited	Based on our analysis and interpretation of the evidence, we conclude that there is no association between temperature exposure and incidence, and that future studies may change our results.

Reference	Ambient temperature	Human bocavirus (HBoV) (n = 9)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	0	There is no indication that there is substantial risk of bias across the body of available evidence.
Indirectness	0	The studies assessed population, exposure, and outcome of interest
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of respiratory infection do not appear to be strongly influenced by an individual study. The results of all four metaanalyses for change in the respiratory infection. measures are consistent in the direction of overall effect estimates.
Imprecision	-1	The number of studies is small, the sample size is insufficient, and the incidence CI of 5 studies was wide.
Publication bias	0	We found no reason to suspect publication bias.The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	1	Most studies report dose-response patterns that are broadly similar, with incidence increasing or decreasing with ambient temperature above a certain threshold.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is ”moderate”)	*Moderate*	Moderate+(1)+(-1) = Moderate. Downgrading/upgrading resulted in moderate rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	We found that most of the increase in the incidence of HBoV infection associated with ambient temperature exposure (see results from meta-analyses in Figure S8).
Strength considerations		
Quality of body of evidence	n/a	*Moderate*
Direction of effect estimate	n/a	Direction largely as expected: higher risk of incidence at high ambient temperatures.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are generally consistent, and most

		studies have a low risk of bias, especially studies with large sample sizes, but several have large confidence intervals. It is unlikely that a new study would have an effect estimate that would make the results of the meta-analysis null or insignificant.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Limited	Based on our analysis and interpretation of the evidence, we conclude that there is an positive association between temperature exposure and HBoV incidence, and we are reasonably confident that opportunity, bias, and confounding factors can be excluded as explanations for this association. The available evidence includes the results of one or more well-designed, well-conducted studies, and we believe that our conclusions are unlikely to strongly influence the outcomes of future studies.

Reference	Ambient temperature	Enterovirus (EV) (n = 4)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	0	There is no indication that there is substantial risk of bias across the body of available evidence.
Indirectness	0	The studies assessed population, exposure, and outcome of interest
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of EVs infection do not appear to be strongly influenced by an individual study. The results of all four meta-analyses for change in the respiratory infection. measures are consistent in the direction of overall effect estimates.
Imprecision	-1	The number of studies is small and the sample size is insufficient.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	0	No dose-response relationship was found.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is ”moderate”)	*Low*	Moderate+(-1)= Low. Downgrading/upgrading resulted in low rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	We found that most of the reduction in the incidence of respiratory infection associated with ambient temperature exposure (see results from meta-analyses in Figure S9).
Strength considerations		
Quality of body of evidence	n/a	*Low*
Direction of effect estimate	n/a	The overall low quality evidence showed no association between temperature exposure and EVs morbidity.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure results of interest, influence directions are inconsistent, the number of studies is small, and one study has a large confidence interval.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and

		physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Sufficient	Based on our analysis and interpretation of the evidence, we conclude that there is no association between temperature exposure and EVs incidence, and that the addition of future studies may change the current results.

Reference	Ambient temperature	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (n =8)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	0	There is no indication that there is substantial risk of bias across the body of available evidence.
Indirectness	0	The studies assessed population, exposure, and outcome of interest.
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of respiratory infection do not appear to be strongly influenced by an individual study. measures are consistent in the direction of overall effect estimates.
Imprecision	-1	We judged that the incidence CI of one study was wide and the remaining CI was narrow enough.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	1	Most studies report dose-response patterns that are broadly similar, with incidence increasing or decreasing with ambient temperature above a certain threshold.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is ”moderate”)	*Moderate*	Moderate+(1)+(-1) = Moderate. Downgrading/upgrading resulted in moderate rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	We found that most of the reduction in the incidence of respiratory infection associated with ambient temperature exposure (see results from meta-analyses in Figure S10).
Strength considerations		
Quality of body of evidence	n/a	*Moderate*
Direction of effect estimate	n/a	The direction of effect estimates largely showed an decreasing trend in COVID-19 infection with increasing high temperatures.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are usually consistent, and studies have a low risk of bias, especially studies with large sample sizes, but some studies have large confidence intervals. A new study is unlikely to have an effect estimate that would render the results of the meta-analysis invalid or not significant.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Sufficient	Based on our analysis and interpretation of the evidence, we conclude that there is an negative association between temperature exposure and COVID-19 incidence, and we are reasonably confident that opportunity, bias, and confounding factors can be excluded as explanations for this association. The available evidence includes the results of one or more well-designed, well-conducted studies, and we believe that our

		conclusions are unlikely to strongly influence the outcomes of future studies.
Reference	Ambient temperature	Severe acute respiratory syndrome coronavirus (SARS-CoV) (n=4)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	-1	There is a risk of bias in some studies.
Indirectness	0	The studies assessed population, exposure, and outcome of interest.
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of respiratory infection do not appear to be strongly influenced by an individual study. The results of all four meta-analyses for change in the respiratory infection. measures are consistent in the direction of overall effect estimates.
Imprecision	-1	The number of studies is small and the sample size is insufficient.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	1	Most studies report dose-response patterns that are broadly similar, with incidence increasing or decreasing with ambient temperature above a certain threshold.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is ”moderate”)	*Low*	Moderate+(1)+(-1)+(-1) = Low. Downgrading/upgrading resulted in low rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	Low quality evidence did not show that the incidence of SARS infection was related to ambient temperature exposure (see results from meta-analyses in Figure S11).
Strength considerations		
Quality of body of evidence	n/a	*Low*
Direction of effect estimate	n/a	The direction of effect estimates did not show an association between temperature and SARS infection, and the results were inconclusive.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are generally consistent, and most studies have a low risk of bias, but several have large confidence intervals. It is unlikely that a new study would have an effect estimate that would make the results of the meta-analysis null or insignificant.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Limited	Based on our analysis and interpretation of the evidence, we did not find an association between temperature exposure and SARS morbidity, and the available evidence is insufficient.
Reference	Ambient temperature	Human coronavirus (HCoV) (n=5)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	0	There is no indication that there is substantial risk of bias across the body of available evidence.

Indirectness	0	The studies assessed population, exposure, and outcome of interest.
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of HCoV infection do not appear to be strongly influenced by an individual study. Measures are consistent in the direction of overall effect estimates.
Imprecision	-1	The number of studies is small and the sample size is insufficient.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	1	Most studies report dose-response patterns that are broadly similar, with incidence increasing or decreasing with ambient temperature above a certain threshold.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is "moderate")	*Moderate*	Moderate+(1)+(-1) = Moderate. Downgrading/upgrading resulted in moderate rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	We found that most of the reduction in the incidence of HCoV infection associated with ambient temperature exposure (see results from meta-analyses in Figure S12).
Strength considerations		
Quality of body of evidence	n/a	*Moderate*
Direction of effect estimate	n/a	Direction largely as expected: increased temperature reduced incidence.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are generally consistent, and most studies have a low risk of bias, but several have large confidence intervals. It is unlikely that a new study would have an effect estimate that would make the results of the meta-analysis null or insignificant.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Sufficient	Based on our analysis and interpretation of the evidence, we conclude that there is an negative association between temperature exposure and HCoV incidence, and we are reasonably confident that opportunity, bias, and confounding factors can be excluded as explanations for this association. The available evidence includes the results of one or more well-designed, well-conducted studies, and we believe that our conclusions are unlikely to strongly influence the outcomes of future studies.

Reference	Ambient temperature	MERS-CoV (n =1)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	0	No risk of bias was found.
Indirectness	0	The studies assessed population, exposure, and outcome of interest.
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods,

		lag structure considered, model) and not be driven by unexpected heterogeneity.
Imprecision	-1	The number of studies is small and the sample size is insufficient.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	1	As ambient temperature increases, morbidity increases in dose-response patterns.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is "moderate")	*Moderate*	Moderate+(1)+(-1) = Moderate. Downgrading/upgrading resulted in moderate rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	We found that the increased incidence of respiratory infections was associated with ambient temperature exposure (see results from meta-analyses in Figure S9).
Strength considerations		
Quality of body of evidence	n/a	*Moderate*
Direction of effect estimate	n/a	The incidence of respiratory pathogens increased with the increase of temperature.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are usually consistent, studies have low risk of bias, small sample sizes, and large confidence intervals. The emergence of a new study may invalidate or make significant the results of the meta-analysis.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Sufficient	Based on our analysis and interpretation of the evidence, we conclude that there is an association between temperature exposure and incidence, and we have reason to believe that chance, bias, and confounding factors can be excluded as explanations for this association. The available evidence includes the results of only one well-designed study, and our conclusions are unlikely to strongly influence the results of future studies.

Reference	Ambient temperature	Human rhinovirus/enterovirus (HRV/EV) (n = 2)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	0	There is no indication that there is substantial risk of bias across the body of available evidence.
Indirectness	0	The studies assessed population, exposure, and outcome of interest
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of HRVs/EVs infection do not appear to be strongly influenced by an individual study.
Imprecision	-1	The number of studies is small and the sample size is insufficient.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.

Dose response	1	Most studies report dose-response patterns that are broadly similar, with incidence increasing or decreasing with ambient temperature above a certain threshold.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is "moderate")	*Moderate*	Moderate+(1)+(-1) = Moderate. Downgrading/upgrading resulted in moderate rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	We found that the increase in the incidence of HRVs/EVs infection associated with ambient temperature rise (see results from meta-analyses in Figure S13).
Strength considerations		
Quality of body of evidence	n/a	*Moderate*
Direction of effect estimate	n/a	Direction largely as expected: higher risk of incidence at high ambient temperatures.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are generally consistent, and most studies have a low risk of bias, especially studies with large sample sizes, but several have large confidence intervals. It is unlikely that a new study would have an effect estimate that would make the results of the meta-analysis null or insignificant.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Limited	Based on our analysis and interpretation of the evidence, we conclude that there is a positive association between temperature exposure and the incidence of HRV/EVs, but this contains only a small amount of available evidence.

n/a, not applicable. "0" quality rating indicates there were no upgrades or downgrades for each factor being evaluated across the body of evidence; –1=downgrade; +1=upgrade.

Table S15: Summary of the assessment of the quality and strength of the evidence on ambient temperature as a risk factor for incidence of bacterial respiratory infections

Reference	Ambient temperature					
	Streptococcus pneumoniae	*Streptococcus pyogenes pharyngiti*	*Moraxella catarrhalis*	*Pseudomonas aeruginosa*	*Legionella pneumoniae*	*Haemophilus influenzae*
Initial rating Quality factor	Moderate	Moderate	Moderate	Moderate	Moderate	Moderate
i. Downgrade						
Risk of bias across studies	-1	-1	0	-1	0	-1
Indirectness	0	0	0	0	0	0
Inconsistency	0	n/a	-1	n/a	-1	n/a
Imprecision	-1	-1	-1	-1	-1	0
Publication bias	0	0	0	0	0	0
ii. Upgrade						
Large magnitude of effect	0					
Dose response	0	+1	0	+1	+1	0
Confounding minimizes effect	0	0	0	0	0	0

iii. Summary of the quality assessment						
Overall quality of evidence (initial rating is ”moderate”)	*Very Low*	*Low*	*Very Low*	*Moderate*	*Low*	*Low*
Summary of findings from meta-analysis	n/a	n/a	n/a	n/a	n/a	n/a
Summary of qualitative findings	n/a	n/a	n/a	n/a	n/a	n/a
Strength considerations						
Quality of body of evidence	n/a	n/a	n/a	n/a	n/a	n/a
Direction of effect estimate	n/a	n/a	n/a	n/a	n/a	n/a
Confidence in effect estimate	n/a	n/a	n/a	n/a	n/a	n/a
Other compelling attributes of the data that may influence certainty	n/a	n/a	n/a	n/a	n/a	n/a
Overall strength of evidence	Limited	Limited	Limited	Limited	Limited	Limited

n/a, not applicable. “0” quality rating indicates there were no upgrades or downgrades for each factor being evaluated across the body of evidence; –1=downgrade; +1=upgrade.

Table S16: Summary of the assessment of the quality and strength of the evidence on ambient temperature as a risk factor for incidence of mycoplasma and chlamydia respiratory infections

Reference	Ambient temperature	Mycoplasma pneumoniae (n =19)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	-1	There is a substantial risk of bias across most studies.
Indirectness	0	The studies assessed population, exposure, and outcome of interest
Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of respiratory infection do not appear to be strongly influenced by an individual study. Measures are consistent in the direction of overall effect estimates.
Imprecision	-1	We judged that the incidence CI of one study was wide.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	0	No significant dose-response relationship was found.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is ”moderate”)	*Very low*	Moderate+(-1)+(-1)=Very low. Downgrading/upgrading resulted in very low rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	The quality of evidence was generally low, and the incidence of Mycoplasma pneumoniae infections was not associated with ambient temperature (see results from meta-analyses in Figure S17).
Summary of qualitative findings	n/a	Studies not included in the meta-analyses presented mixed results, mostly insignificant associations.
Strength considerations		
Quality of body of evidence	n/a	*Low*
Direction of effect estimate	n/a	The direction of effect estimates did not show an association between temperature and mycoplasma infection, and the results were inconclusive.
Confidence in effect estimate	n/a	Ambient temperature studies directly measure outcomes of interest, influence directions are inconsistent, and due to these methodological deficiencies, it cannot be ruled out that new studies may show different estimates of effects.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Limited	Based on our analysis and interpretation of the evidence, we conclude that there is no association between temperature exposure and morbidity.
Reference	Ambient temperature	Chlamydophila pneumoniae (n =4)
Quality factor	Rating	Basis
i. Downgrade		
Risk of bias across studies	-1	There is a risk of bias in some studies.
Indirectness	0	The studies assessed population, exposure, and outcome of interest.

Inconsistency	0	The magnitude of effect estimates likely to differ because of differences in study methods (study design, statistical methods, lag structure considered, model) and not be driven by unexpected heterogeneity. The results of the meta-analysis for incidence of respiratory infection do not appear to be strongly influenced by an individual study.
Imprecision	-1	The number of studies is small and the sample size is insufficient.
Publication bias	0	We found no reason to suspect publication bias. The search was comprehensive, and the studies were generally consistent among their findings, regardless of size or funding source.
ii. Upgrade		
Large magnitude of effect	0	We did not consider the estimated effects large.
Dose response	0	Most studies have found no effect of temperature on chlamydophila pneumoniae morbidity.
Confounding minimizes effect	0	No evidence found to suggest that possible residual confounders would reduce effect estimates.
iii. Summary of the quality assessment		
Overall quality of evidence (initial rating is ”moderate”)	*Very low*	Moderate+(1)+(-1)+(-1) = Very low. Downgrading/upgrading resulted in very low rating for the quality of evidence.
Summary of findings from meta-analysis	n/a	Very low-quality evidence suggests that the incidence of chlamydophila pneumoniae infections is not associated with ambient temperature exposure (see meta-analysis results in Figure S18).
Summary of qualitative findings	n/a	Studies not included in the meta-analyses presented mixed results, mostly insignificant associations.
Strength considerations		
Quality of body of evidence	n/a	*Very low*
Direction of effect estimate	n/a	Effect estimates showed no significant difference in temperature and respiratory infections, making the results inconclusive.
Confidence in effect estimate	n/a	No trend was observed in overall random effects, and the number of studies included in the meta-analysis was small, making the results uncertain for the future.
Other compelling attributes of the data that may influence certainty	n/a	Differences in study design, exposure measures, statistical methods, consideration of lagged effects, and background factors, including completeness of incidence statistics, population exposure levels and vulnerability, and differences in physical and physiological adaptations of study populations, make interpretation and comparison difficult.
Overall strength of evidence	Limited	No association was observed, the quality of evidence was "very low", and a small number of studies led to "limited" evidence to draw conclusions about the association between respiratory infections and temperature.

n/a, not applicable. “0” quality rating indicates there were no upgrades or downgrades for each factor being evaluated across the body of evidence; –1=downgrade; +1=upgrade.

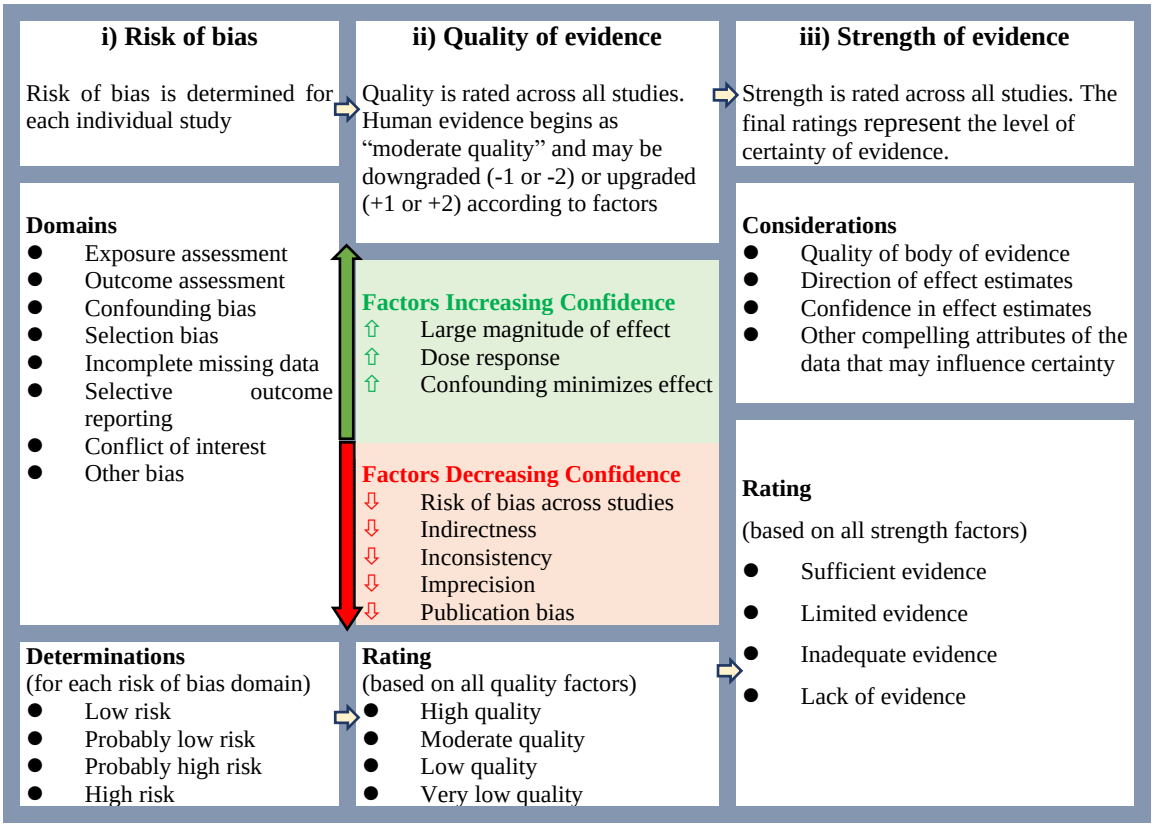


Figure X1 | Overview of Navigation Guide systematic review methodology used for rating the quality and strength of the human evidence.

Picture shows three parts of evidence evaluation, namely risk of bias, quality of evidence, and strength of evidence, respectively showing the subdomains and determinations/ratings of evaluation.

Figure S1. Random-effects meta-analysis of respiratory syncytial virus (RSV) estimates (62 studies)

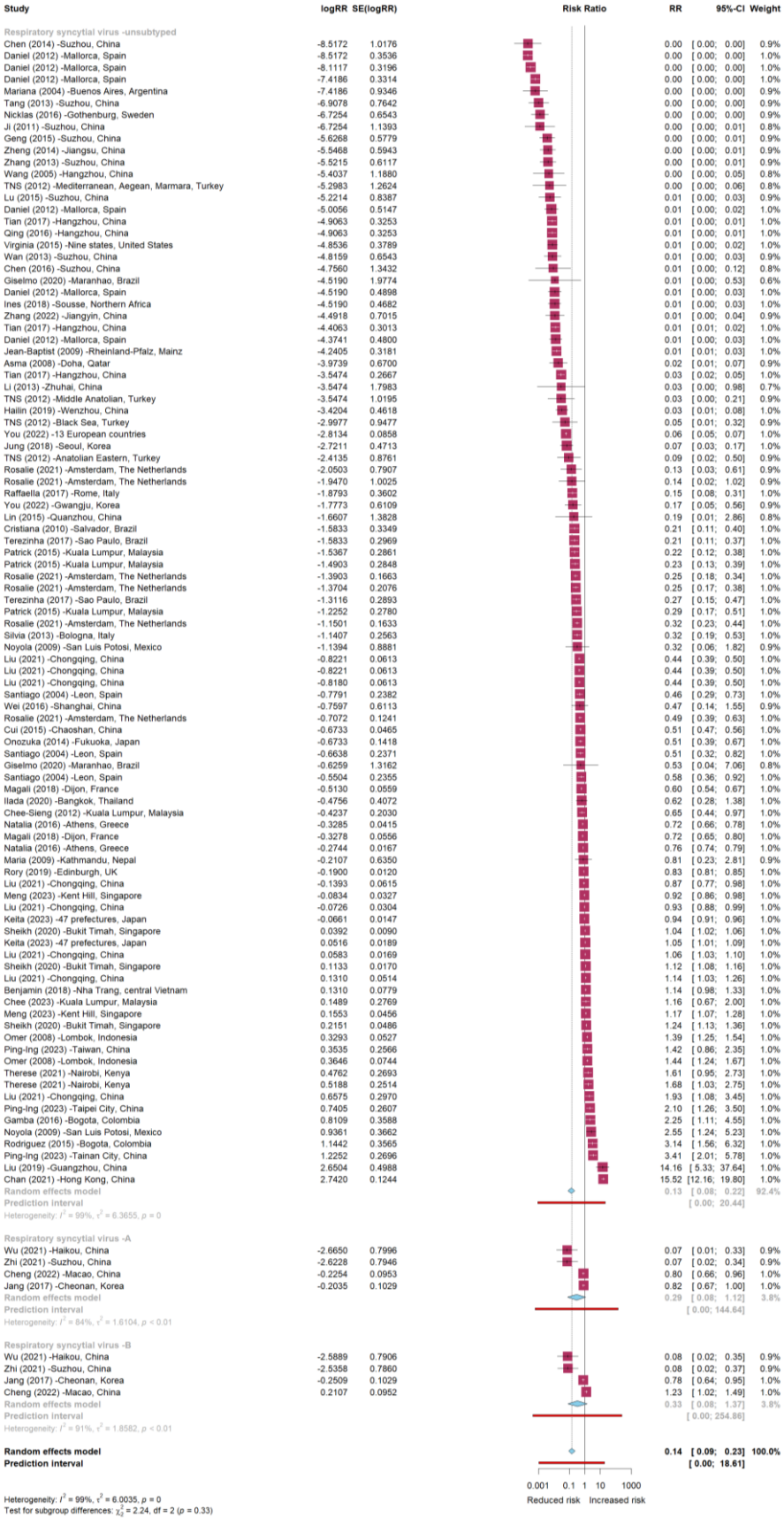


Figure S1-1. Subgroup analysis of respiratory syncytial virus (RSV) meta-analysis by Köppen-Geiger climate

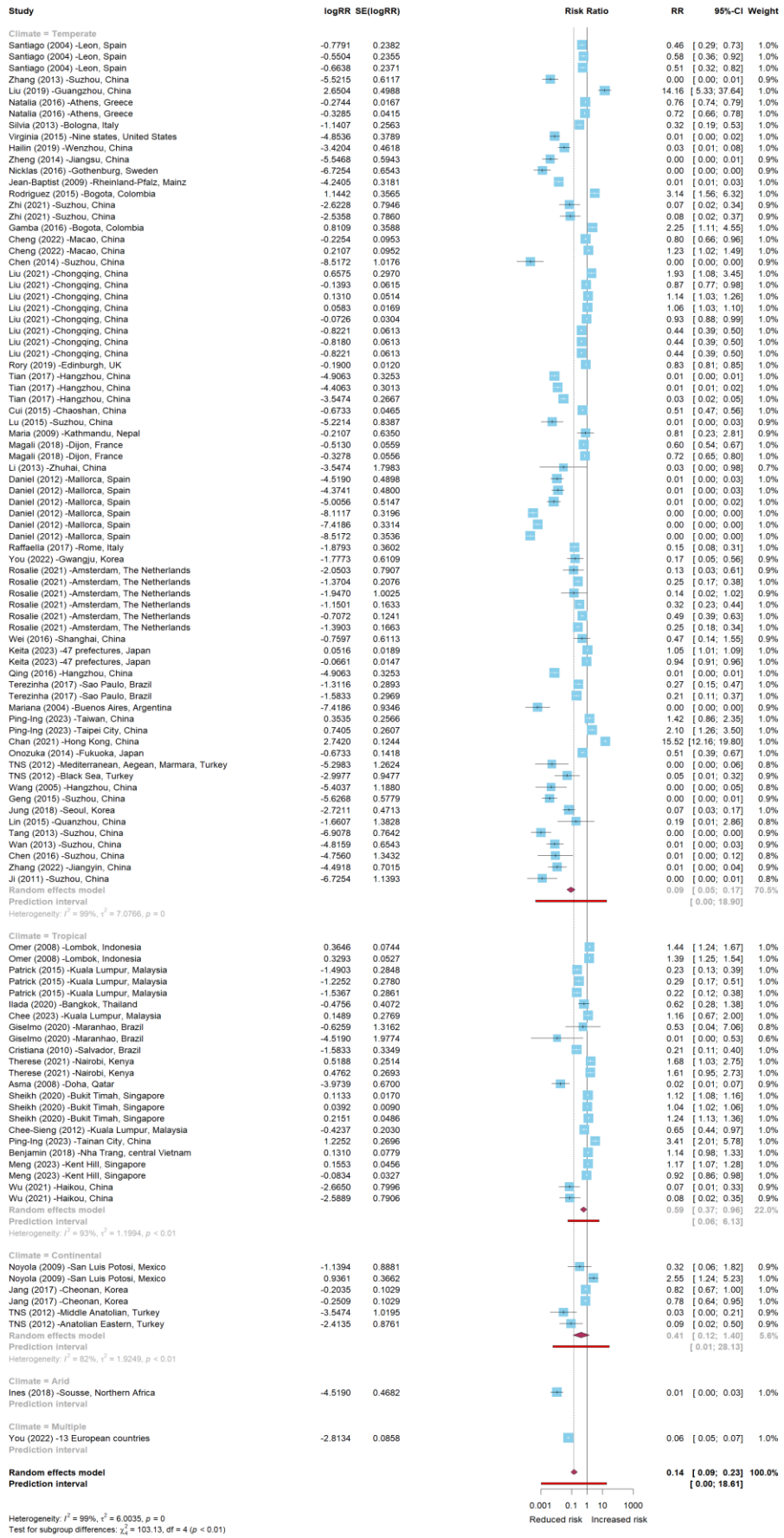


Figure S1-2. Subgroup analysis of respiratory syncytial virus (RSV) meta-analysis by World Bank income category

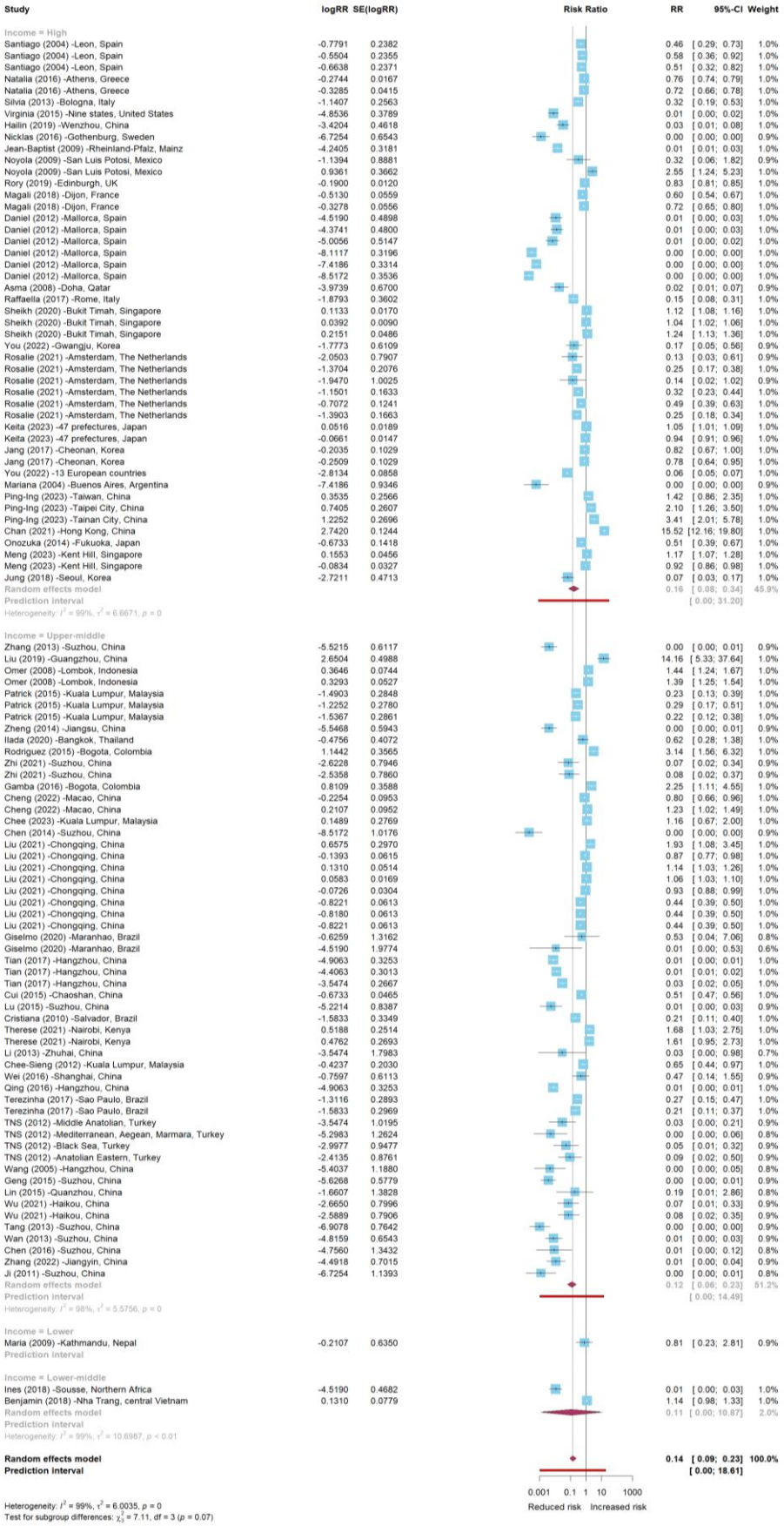


Figure S1-3. Subgroup analysis of respiratory syncytial virus (RSV) meta-analysis by temporal resolution

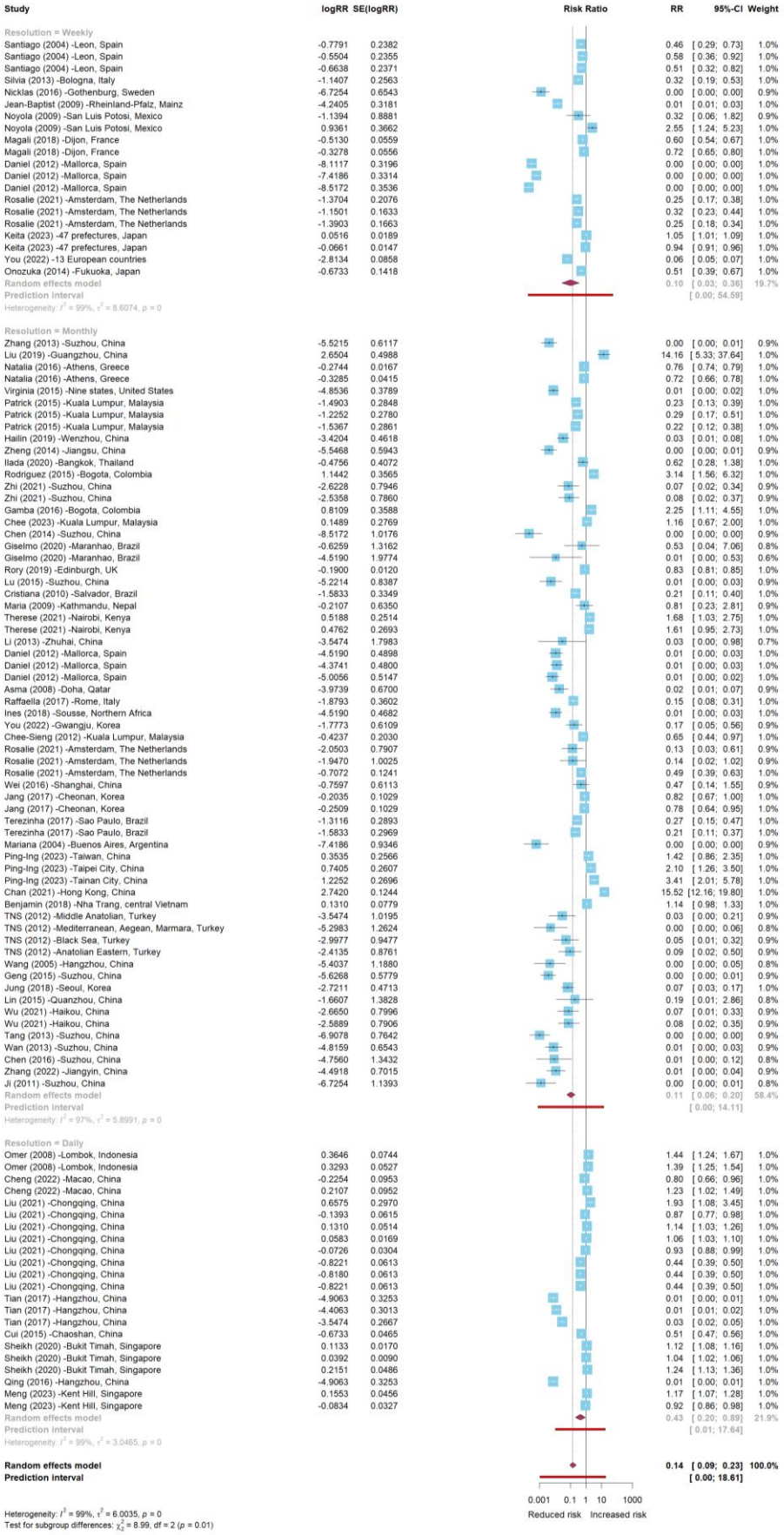


Figure S1-4. Subgroup analysis of respiratory syncytial virus (RSV) meta-analysis by exposure measure

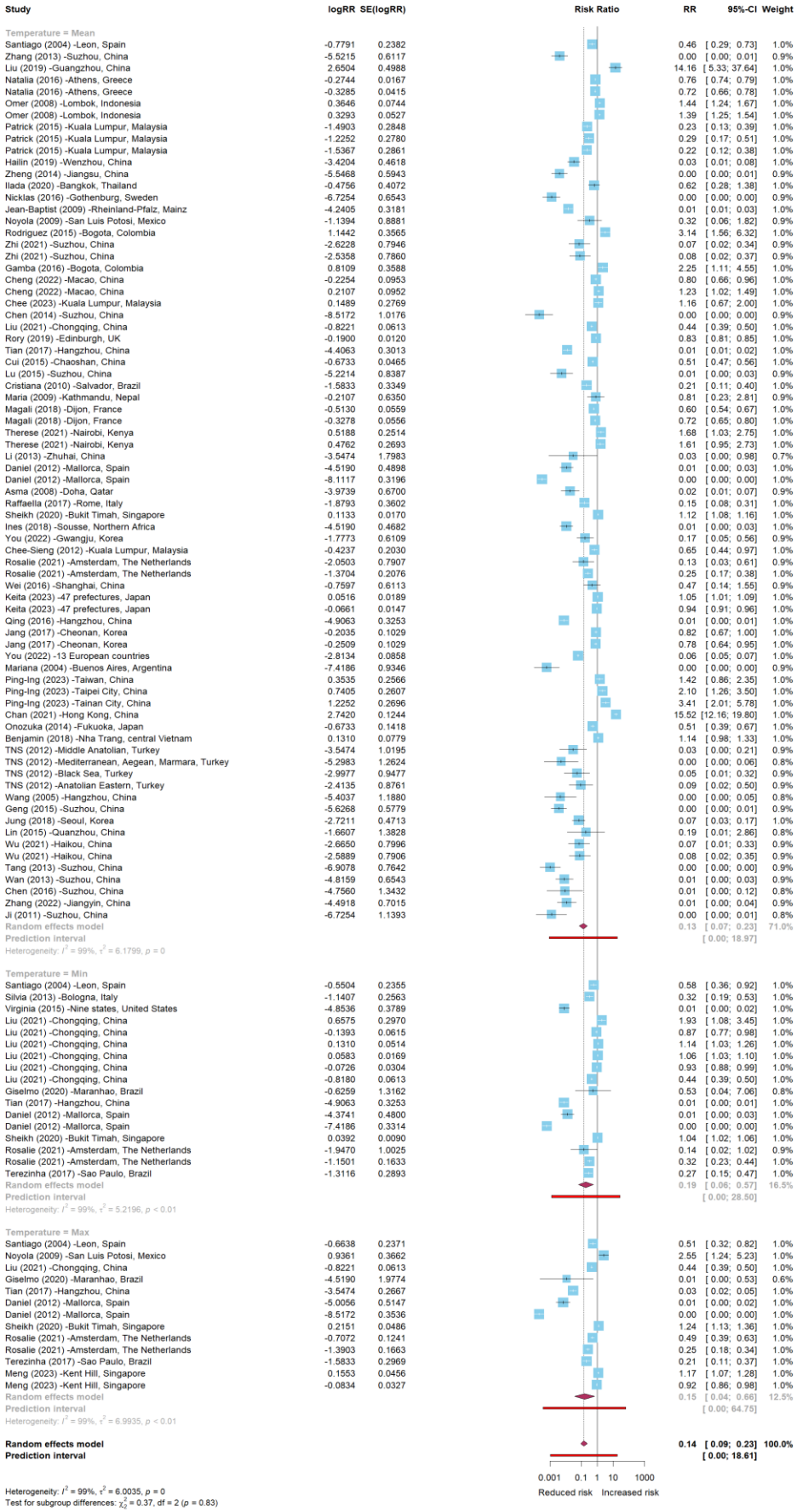


Figure S1-5. Subgroup analysis of respiratory syncytial virus (RSV) meta-analysis by modelling approach

Figure S1-6. Subgroup analysis of respiratory syncytial virus (RSV) meta-analysis by lag type

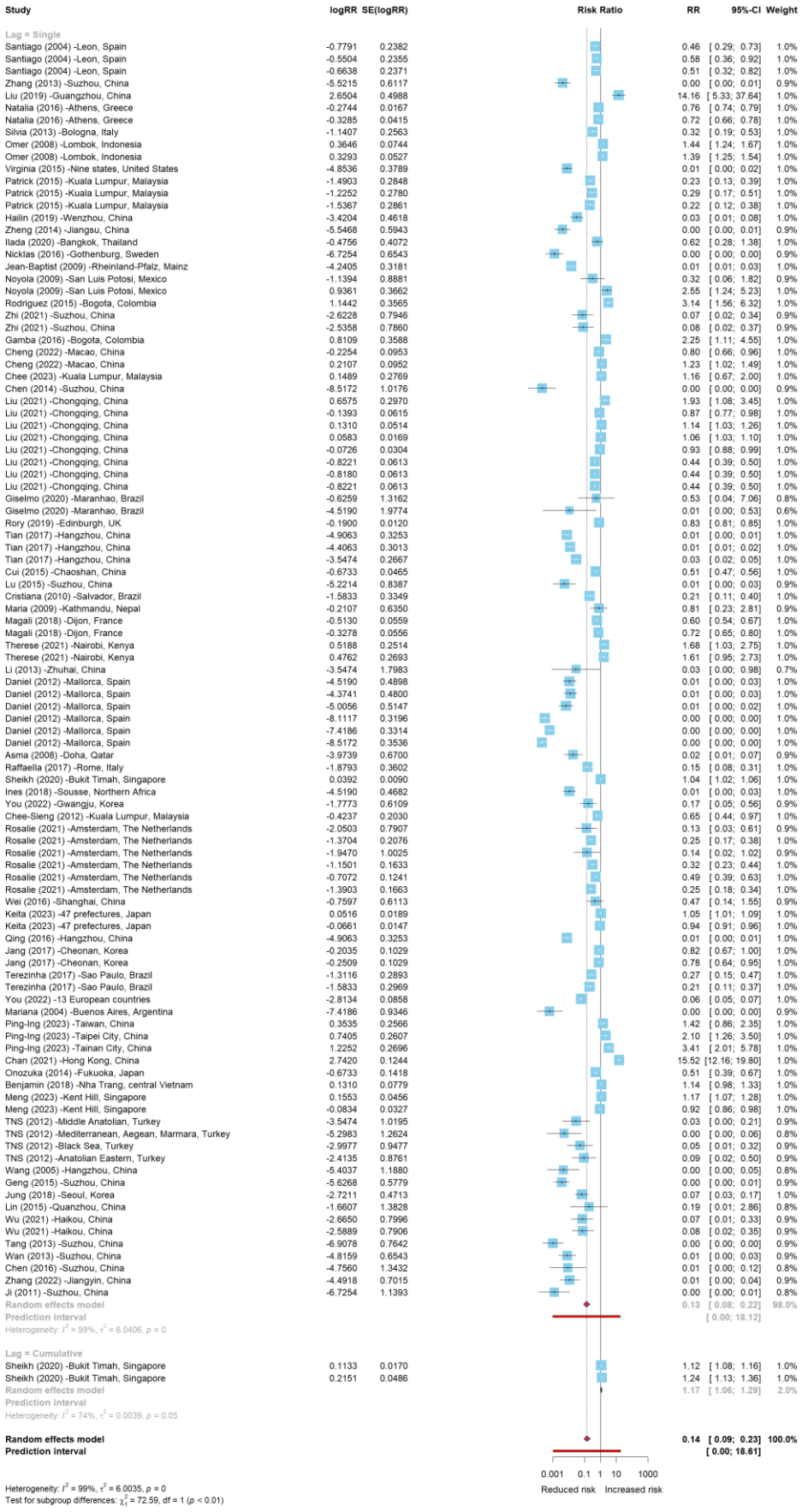


Figure S1-7. Leave-one-out analysis of respiratory syncytial virus (RSV) meta-analysis

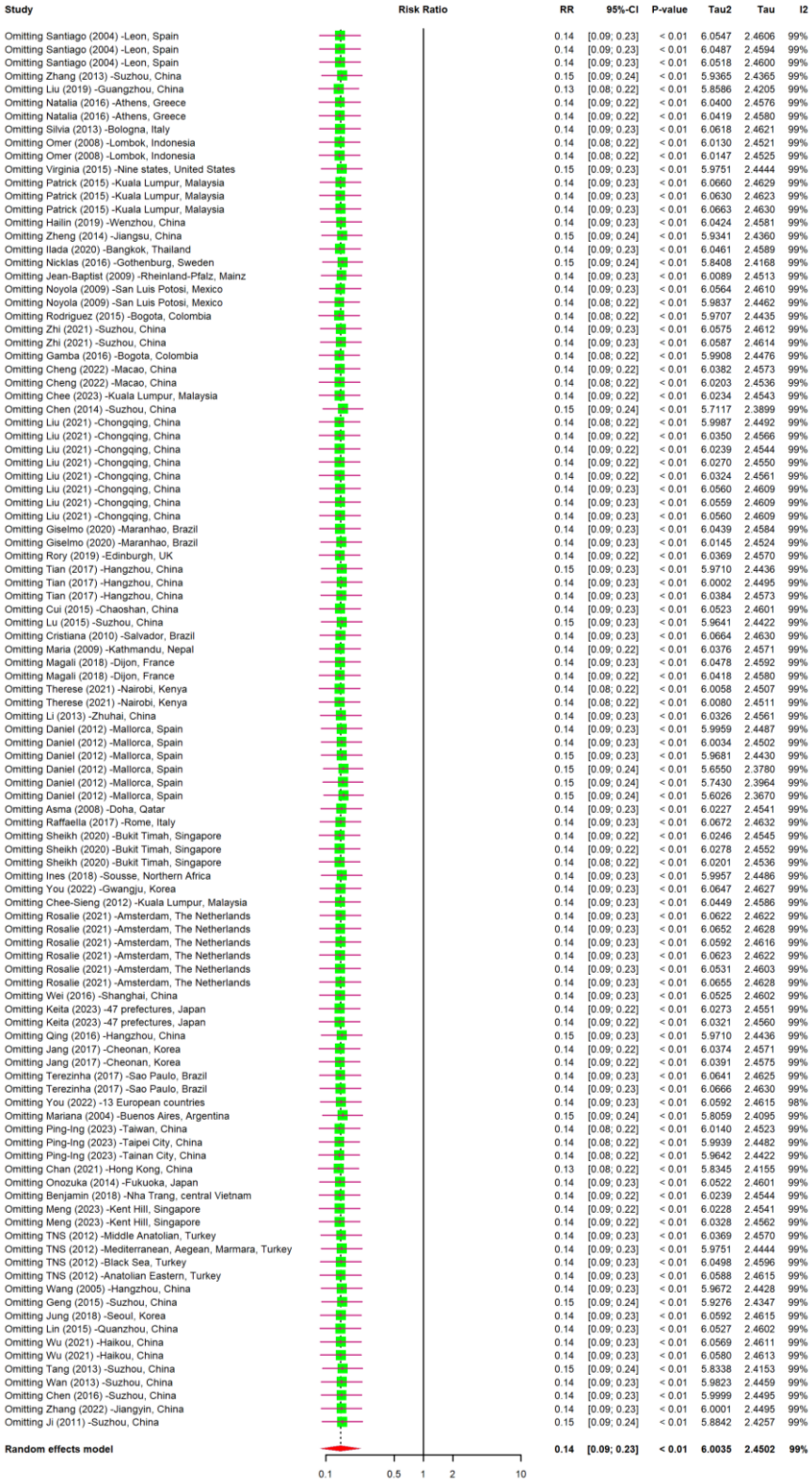
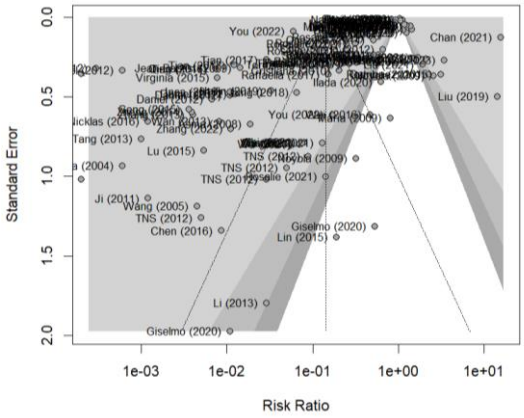


Figure S1-8. Funnel plot of respiratory syncytial virus (RSV) estimates



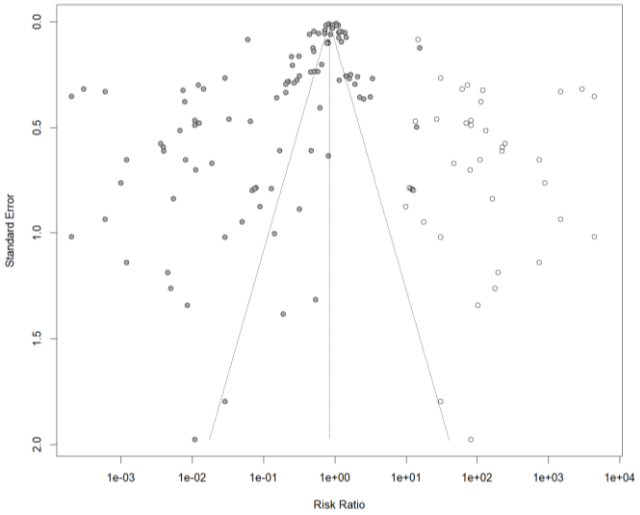
Linear regression test of funnel plot asymmetry

Egger's test result: t = -6.36, df = 103, p-value < 0.0001

Sample estimates:

bias	se.bias	intercept	se.intercept
-5.1657	0.8258	0.0354	0.0397

Figure S1-9. Trim and fill of respiratory syncytial virus (RSV) meta-analysis



Number of studies: k = 145 (with 40 added studies)

Adjusted estimates: RR= 0.8329 [0.4510; 1.5382], Z= -0.58, *P*= 0.5591

Quantifying heterogeneity: tau^2 = 13.7945 [11.1059; 17.9865]; tau = 3.7141 [3.3326; 4.2411],

I^2 = 98.9% [98.8%; 99.0%]; H = 9.50 [9.21; 9.80]

Figure S2. Random-effects meta-analysis of influenza virus (IV) estimates (27 studies)

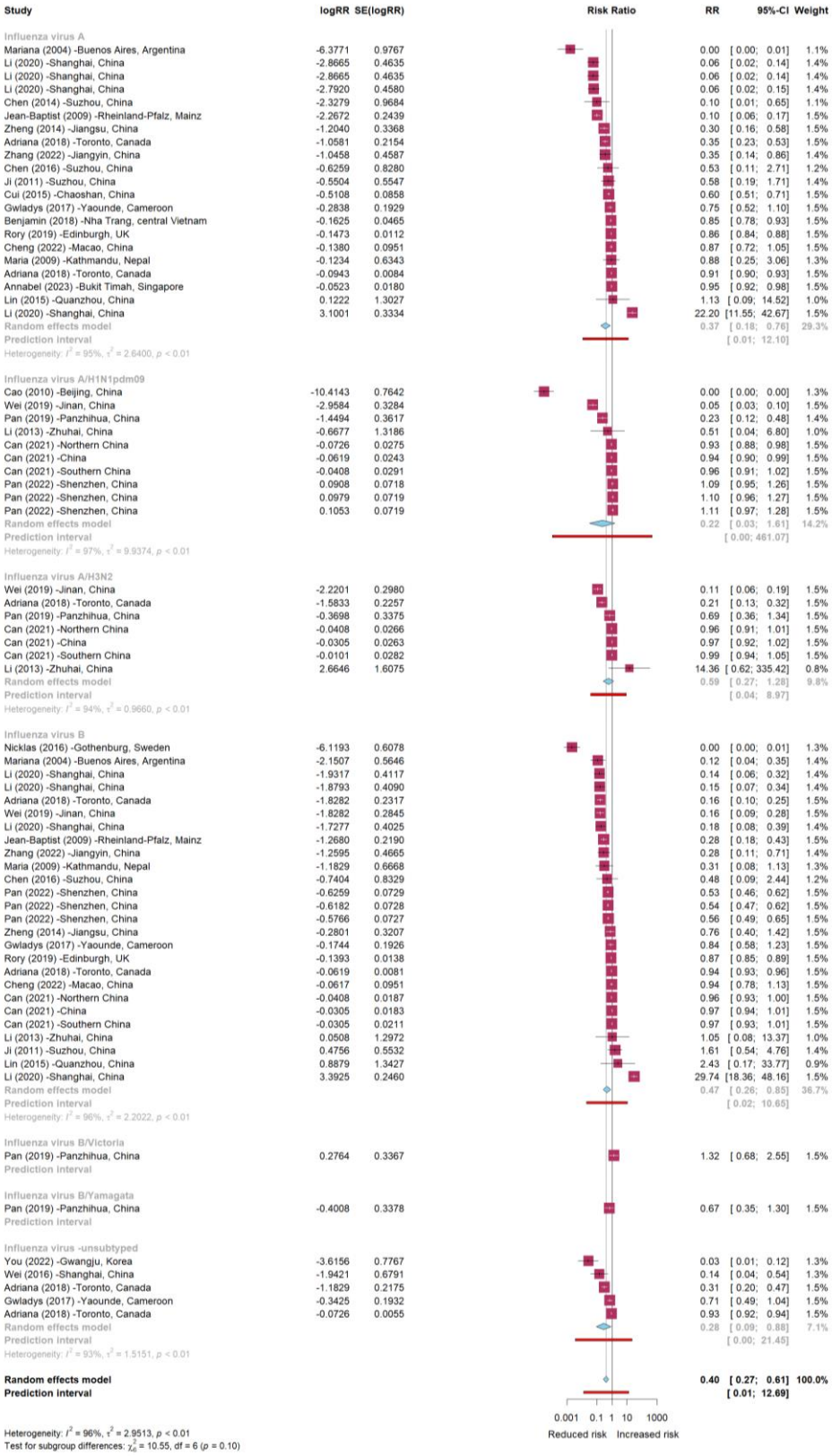


Figure S2-1. Subgroup analysis of influenza virus (IV) meta-analysis by Köppen-Geiger climate

Figure S2-2. Subgroup analysis of influenza virus (IV) meta-analysis by World Bank income category

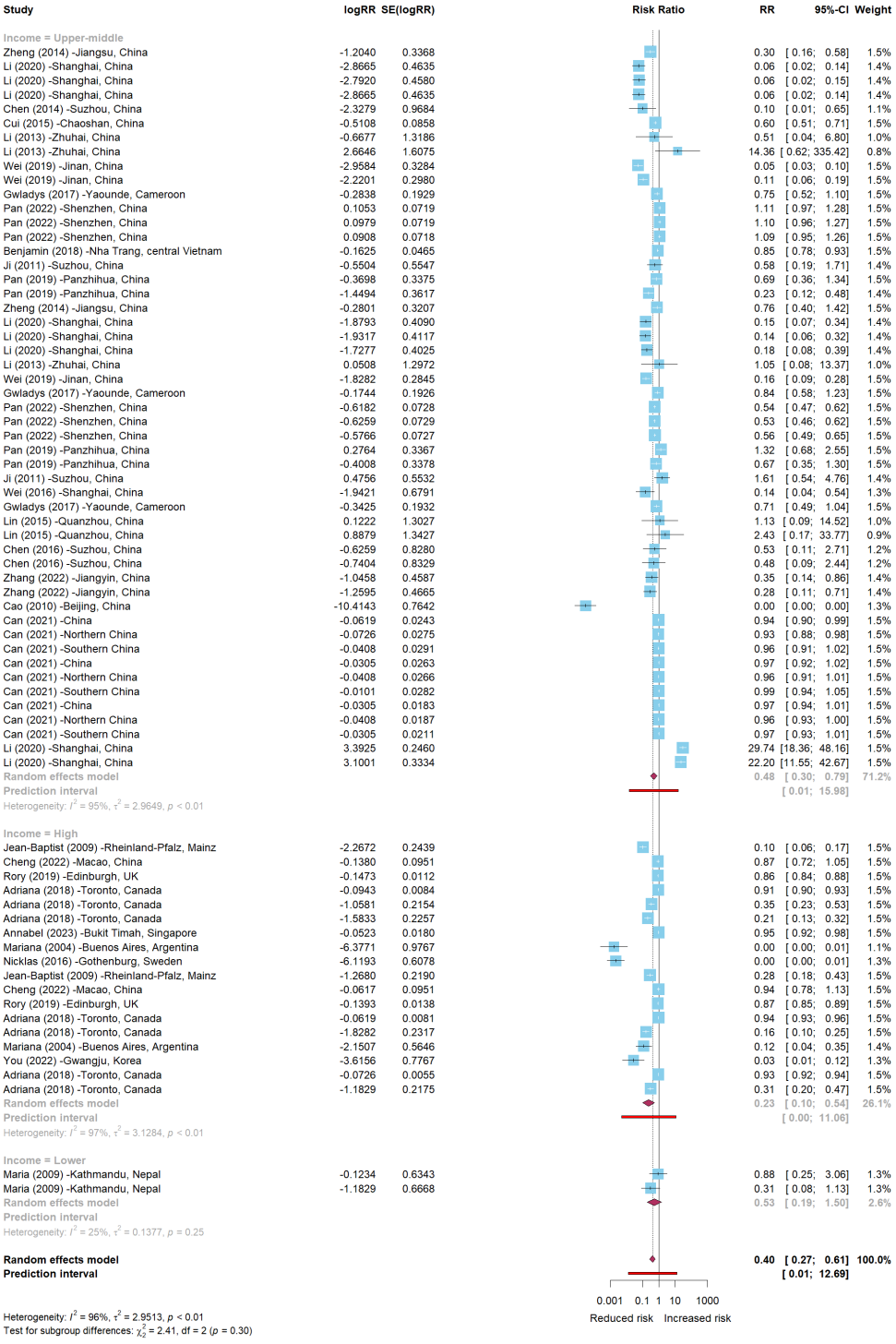


Figure S2-3. Subgroup analysis of influenza virus (IV) meta-analysis by temporal resolution

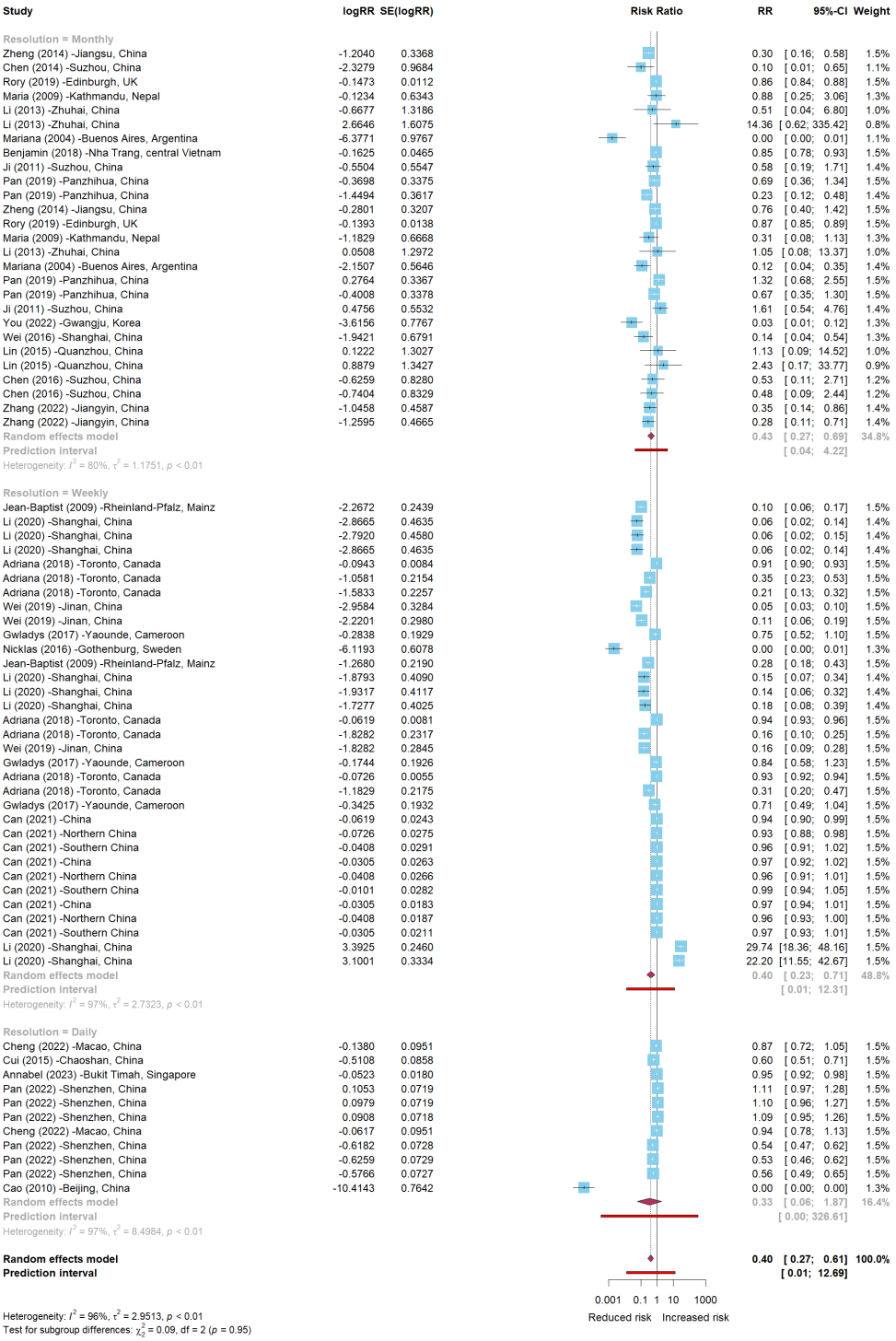


Figure S2-4. Subgroup analysis of influenza virus (IV) meta-analysis exposure measure

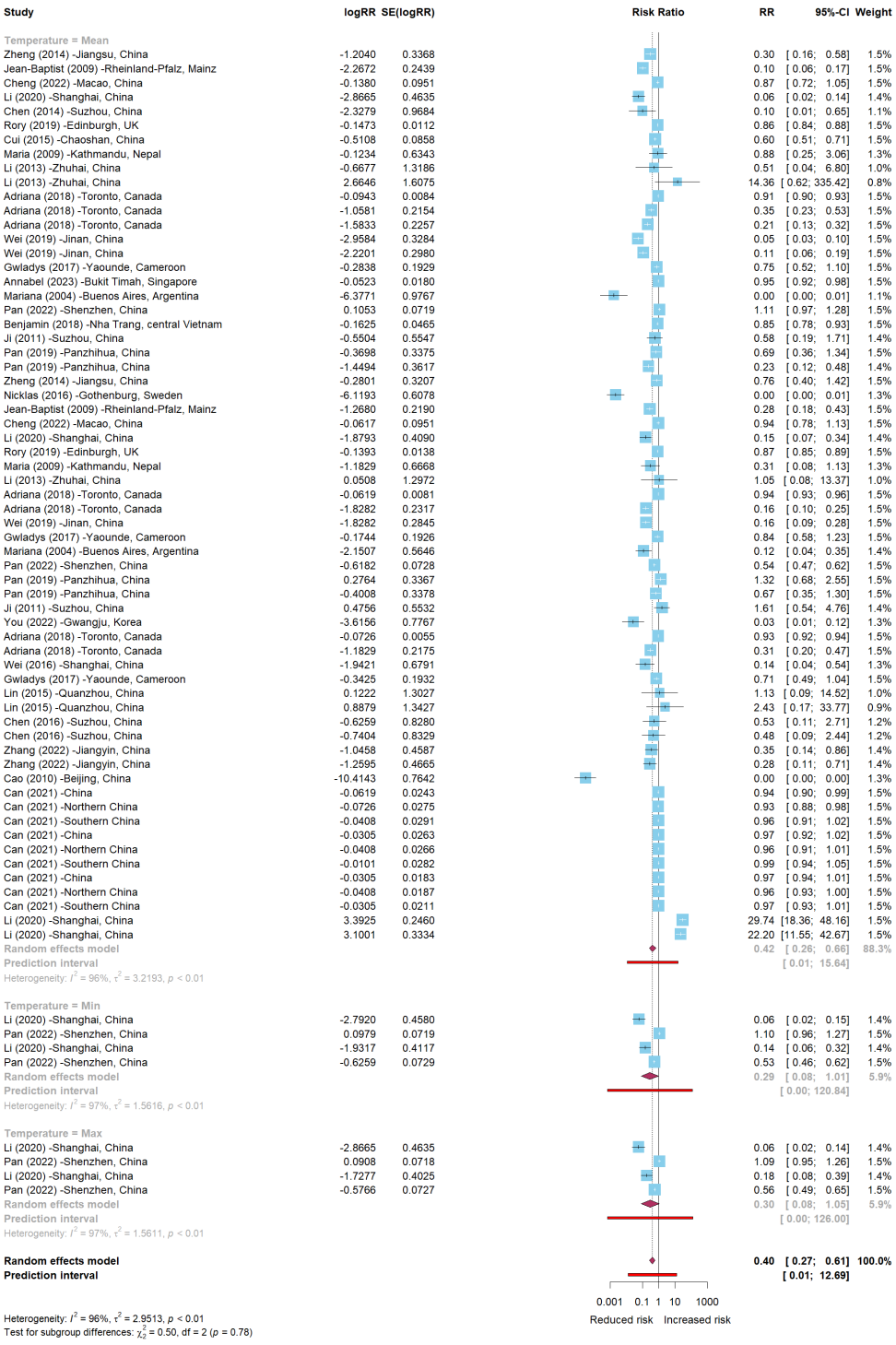


Figure S2-5. Subgroup analysis of influenza virus (IV) meta-analysis by modelling approach

Figure S2-6. Subgroup analysis of influenza virus (IV) meta-analysis by lag type

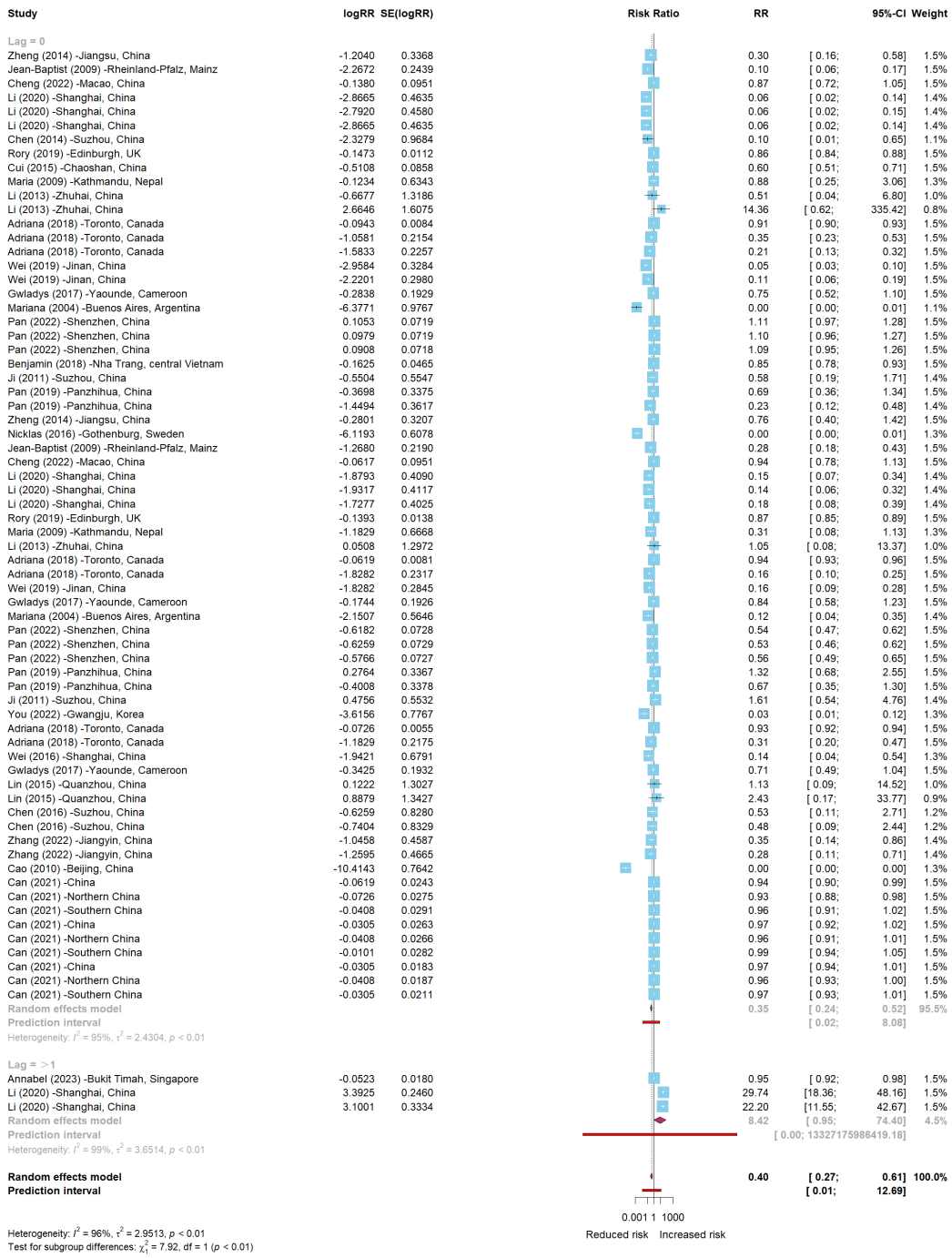


Figure S2-7. Leave-one-out analysis of influenza virus (IV) meta-analysis

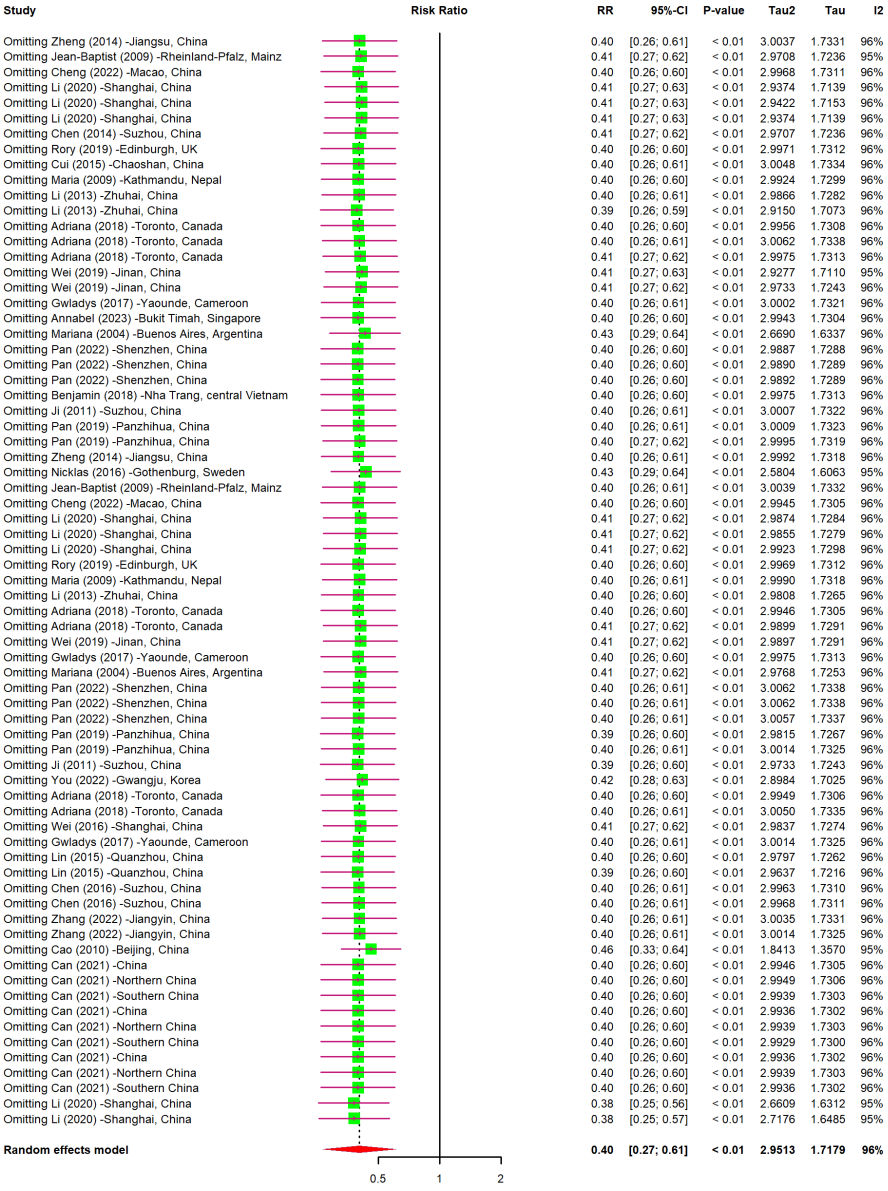


Figure S2-8. Sensitivity analysis by switching the relative risk for cold effects for Li et al 2020

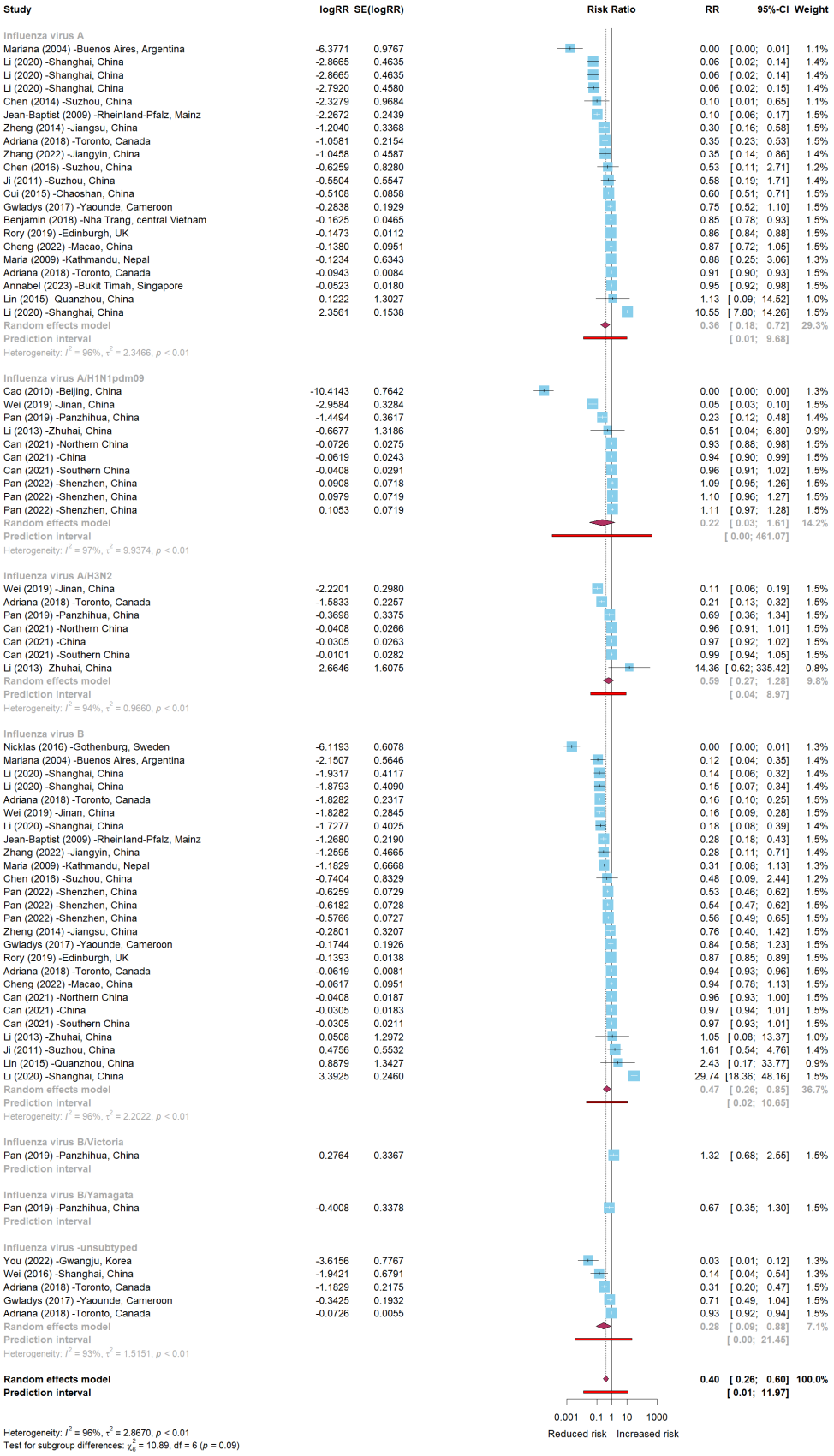
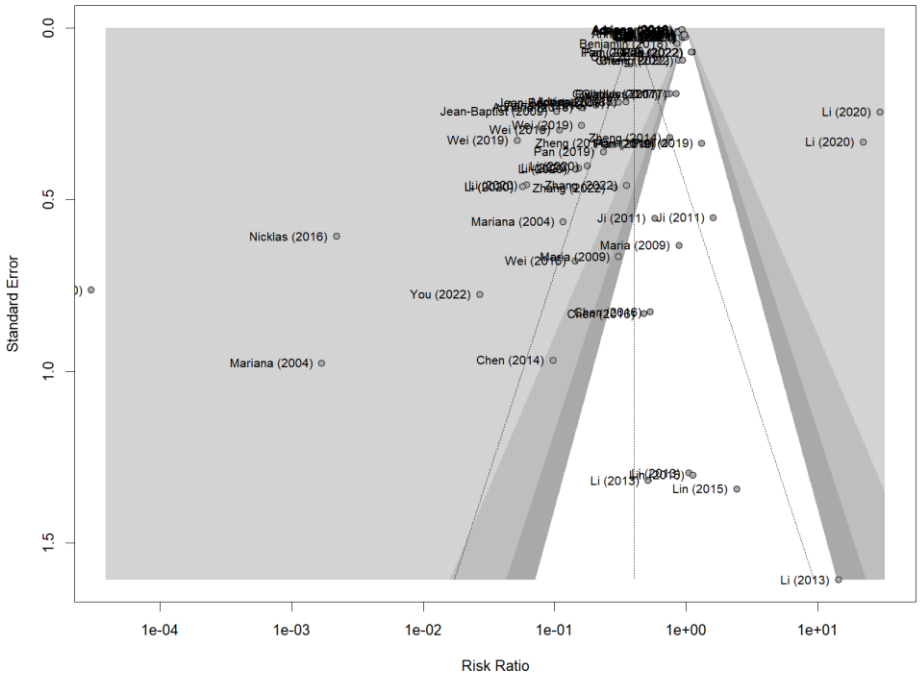


Figure S2-9. Funnel plot of influenza virus (IV) estimates



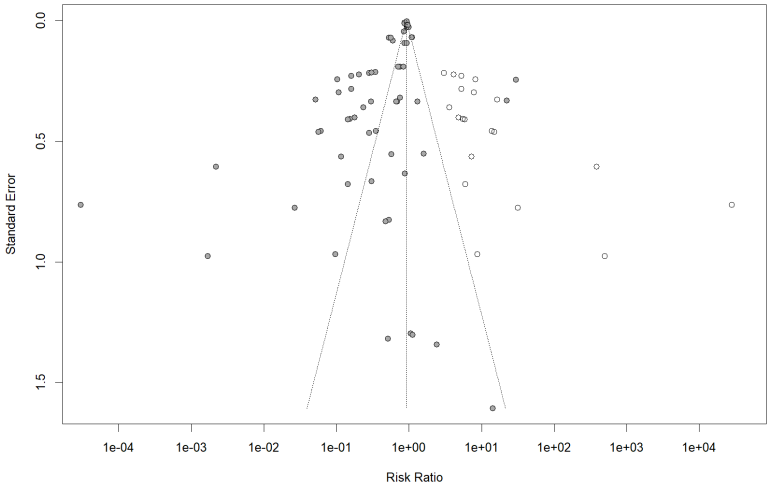
Linear regression test of funnel plot asymmetry

Egger's test result: t = -4.29, df = 69, p-value < 0.0001

Sample estimates:

bias	se.bias	intercept	se.intercept
-2.4900	0.5804	-0.0516	0.0156

Figure S2-10. Trim and fill of influenza virus (IV) meta-analysis



Number of studies: k = 92 (with 21 added studies)
Random effects model: RR= 0.9162 [0.5580; 1.5041], Z= -0.35, P=0.7292
Quantifying heterogeneity:
tau^2 = 5.6364 [4.3703; 8.2222]; tau = 2.3741 [2.0905; 2.8674]
I^2 = 96.4% [96.0%; 96.8%]; H = 5.27 [4.98; 5.58]

Figure S3. Random-effects meta-analysis of human parainfluenza virus (HPIV) estimates (23 studies)

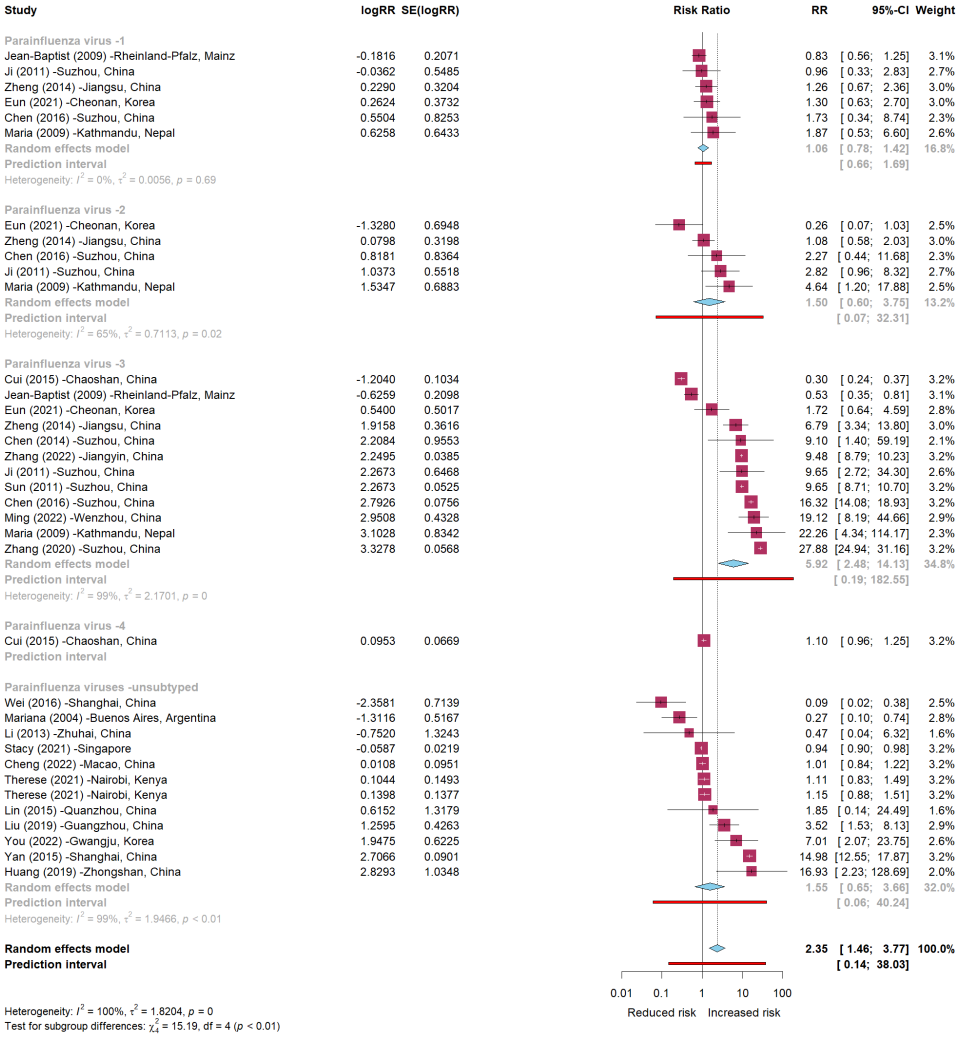


Figure S3-1. Subgroup analysis of human parainfluenza virus (HPIV) meta-analysis by Köppen-Geiger climate

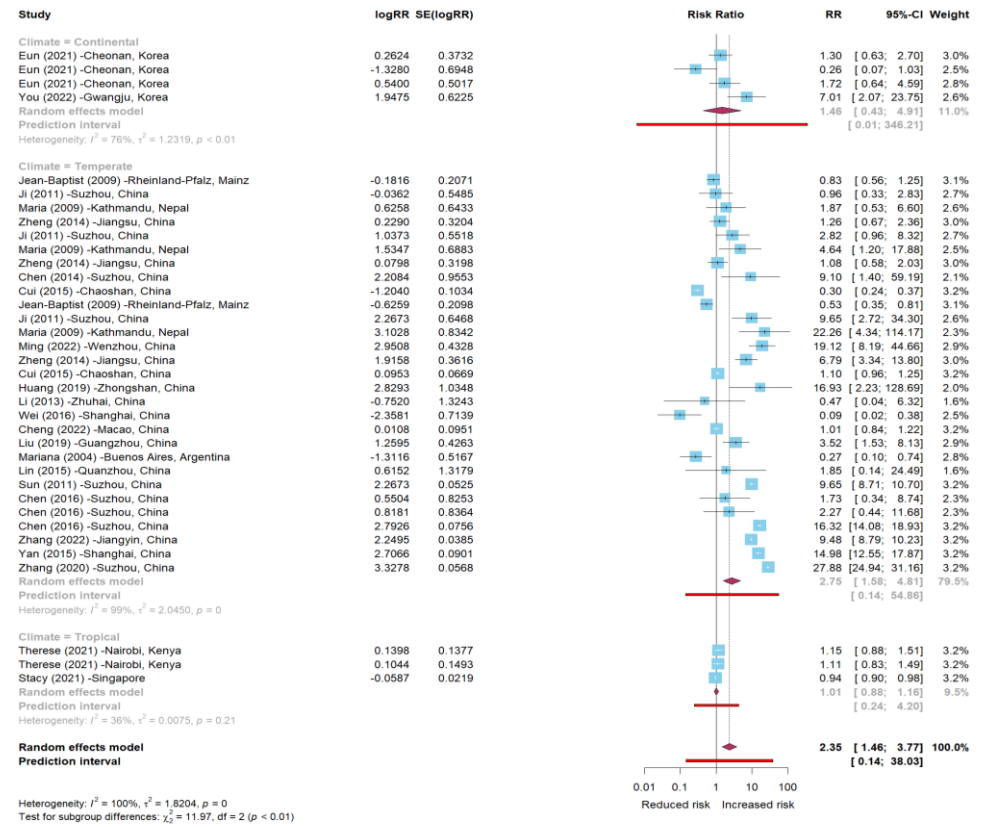


Figure S3-2. Subgroup analysis of human parainfluenza virus (HPIV) meta-analysis by World Bank income category

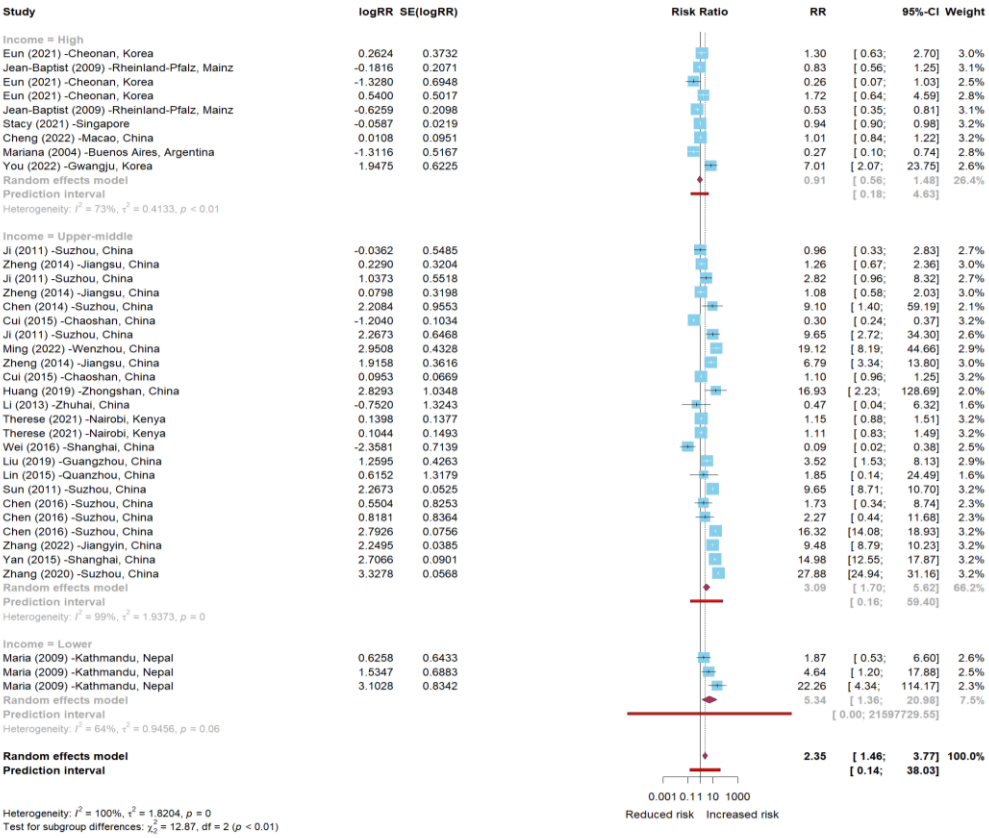


Figure S3-3. Subgroup analysis of human parainfluenza virus (HPIV) meta-analysis by temporal resolution

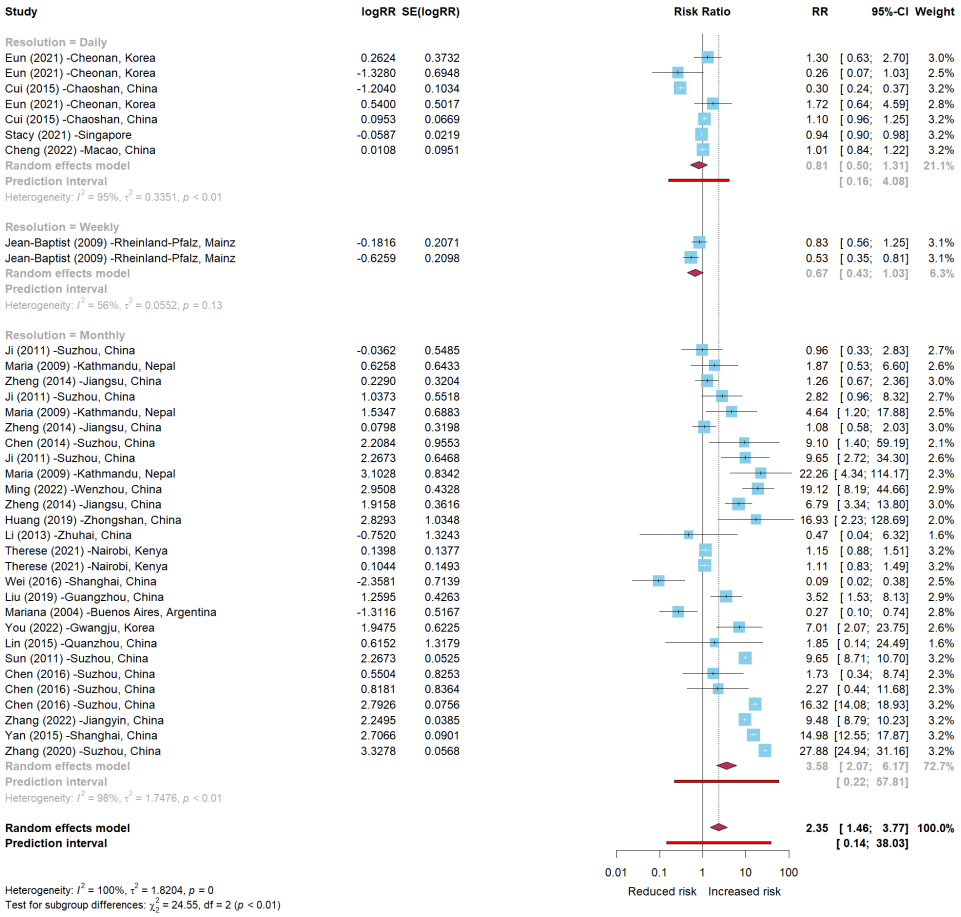


Figure S3-4. Subgroup analysis of human parainfluenza virus (HPIV) meta-analysis by exposure measure

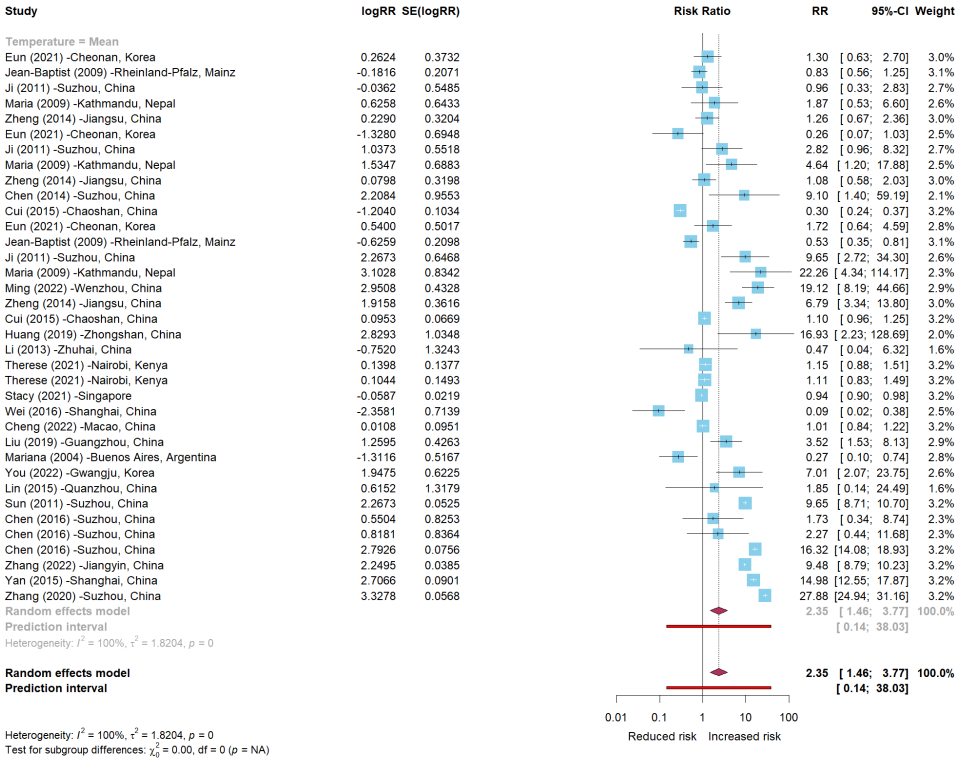


Figure S3-5. Subgroup analysis of human parainfluenza virus (HPIV) meta-analysis by modelling approach

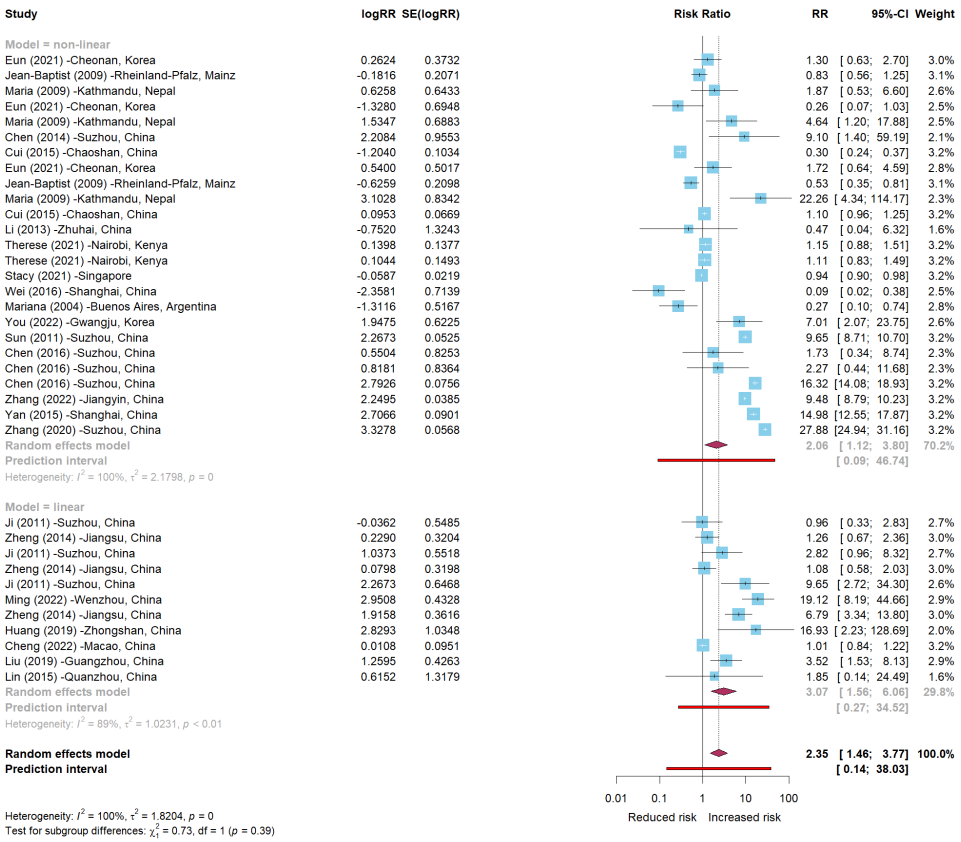


Figure S3-6. Subgroup analysis of human parainfluenza virus (HPIV) meta-analysis by lag type

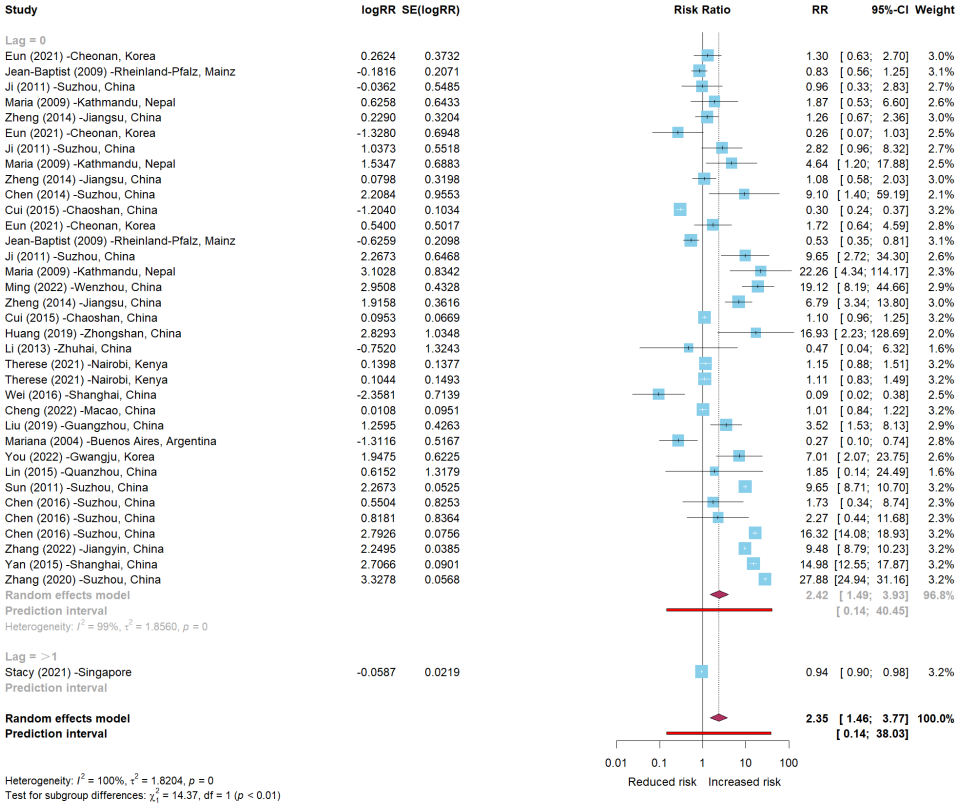


Figure S3-7. Leave-one-out analysis of human parainfluenza virus (HPIV) meta-analysis

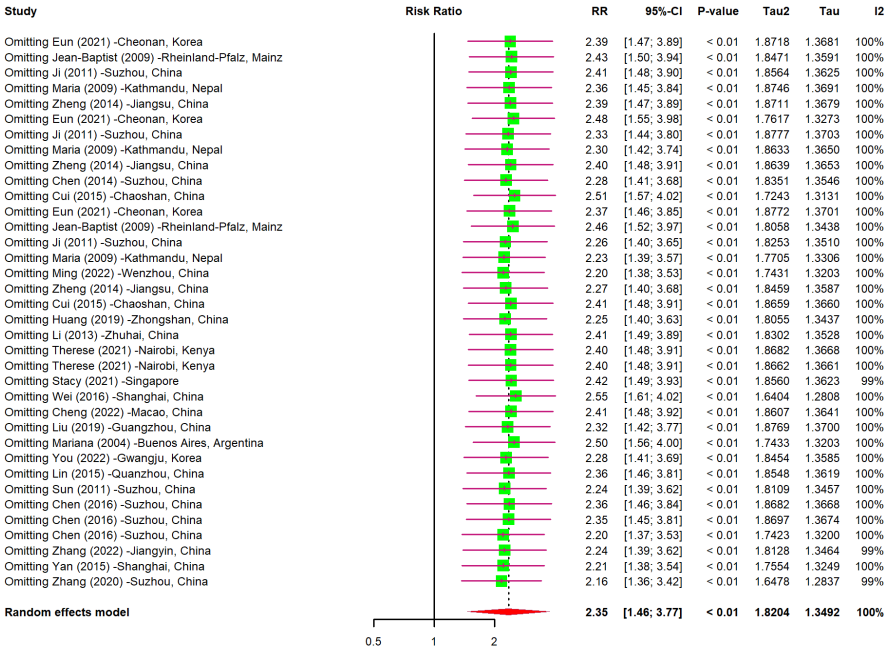
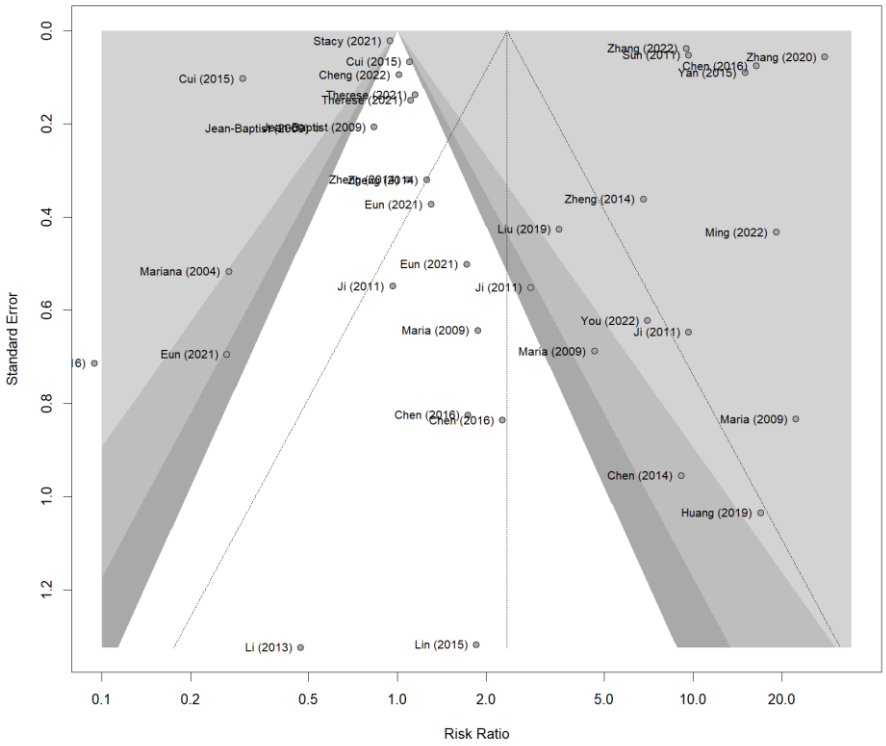


Figure S3-8. Funnel plot of human parainfluenza virus (HPIV) estimates



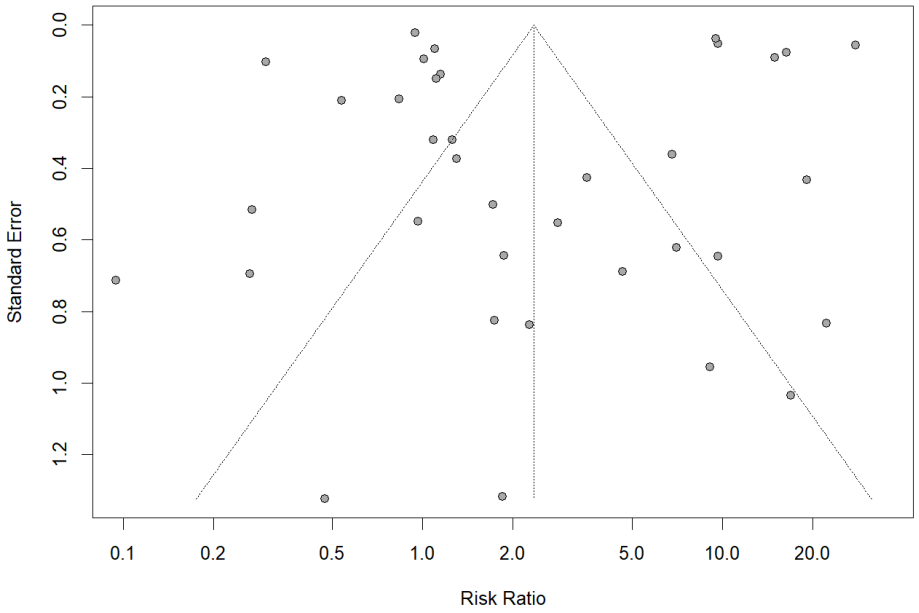
Linear regression test of funnel plot asymmetry

Egger's test result: t = 0.43, df = 34, p = 0.6721

Sample estimates:

bias	se.bias	intercept	se.intercept
1.3038	3.0541	0.8533	0.2769

Figure S3-9 Trim and fill of human parainfluenza virus (HPIV) meta-analysis



Number of studies: k = 36 (with 0 added studies)

Random effects model: RR=2.3464 [1.4620-3.7656], z= 3.53, p=0.0004

Quantifying heterogeneity:

tau^2 = 1.8204 [1.0997; 3.2263]; tau = 1.3492 [1.0487; 1.7962]

I^2 = 99.5% [99.5%; 99.6%]; H = 14.72 [14.06; 15.41]

Figure S4. Random-effects meta-analysis of human metapneumoviruses (HMPV) estimates (14 studies)

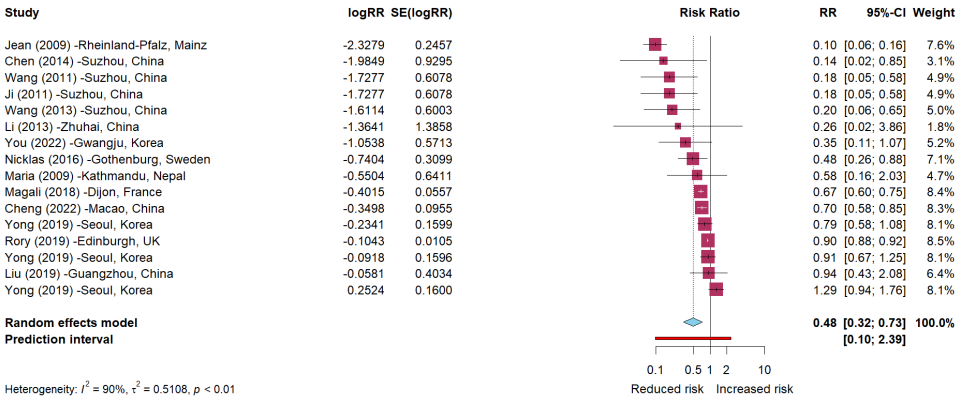


Figure S4-1. Subgroup analysis of human metapneumoviruses (HMPV) meta-analysis by Köppen-Geiger climate

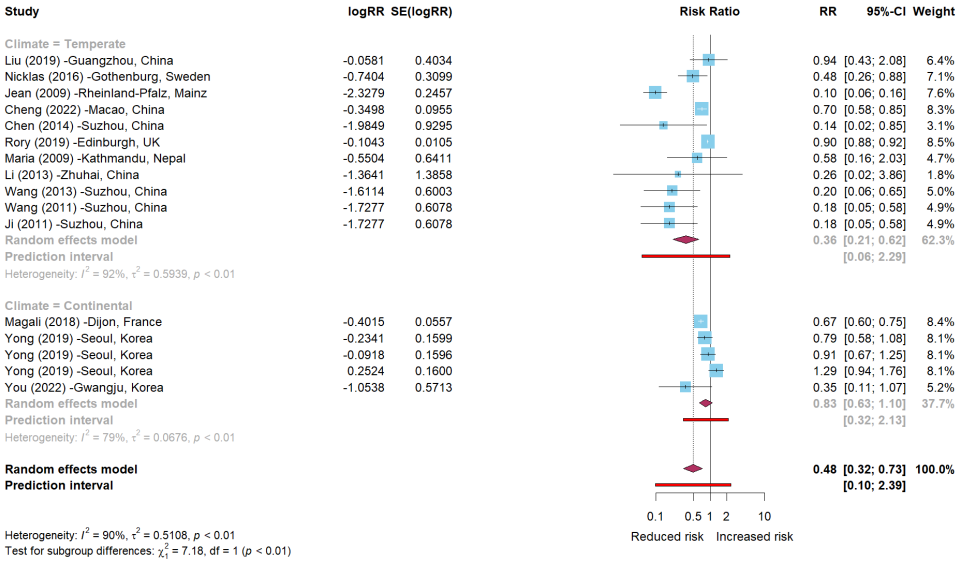


Figure S4-2. Subgroup analysis of human metapneumoviruses (HMPV) meta-analysis by World Bank income category

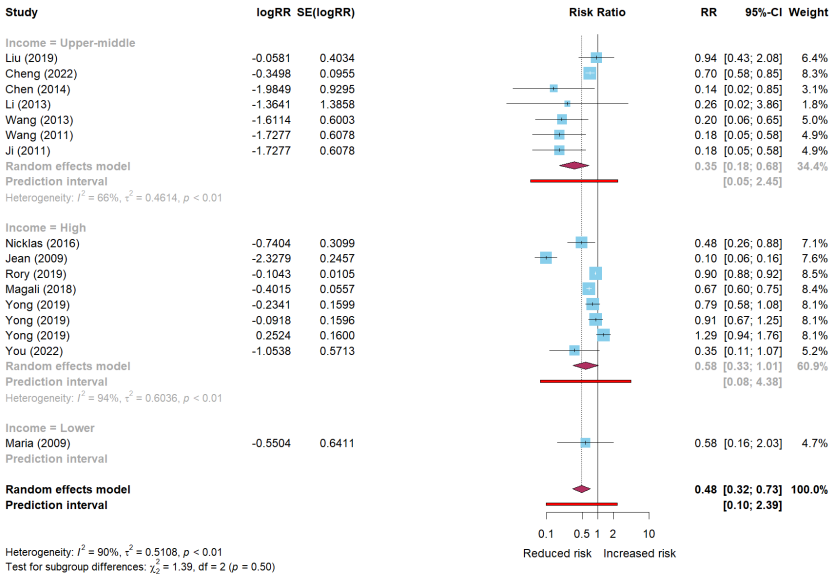


Figure S4-3. Subgroup analysis of human metapneumoviruses (HMPV) meta-analysis by temporal resolution

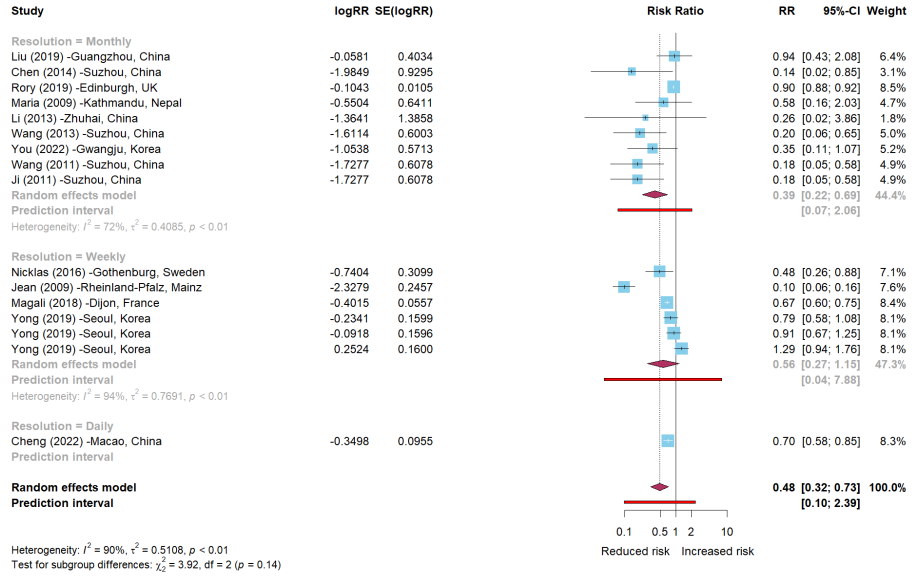


Figure S4-4. Subgroup analysis of human metapneumoviruses (HMPV) meta-analysis by exposure measure

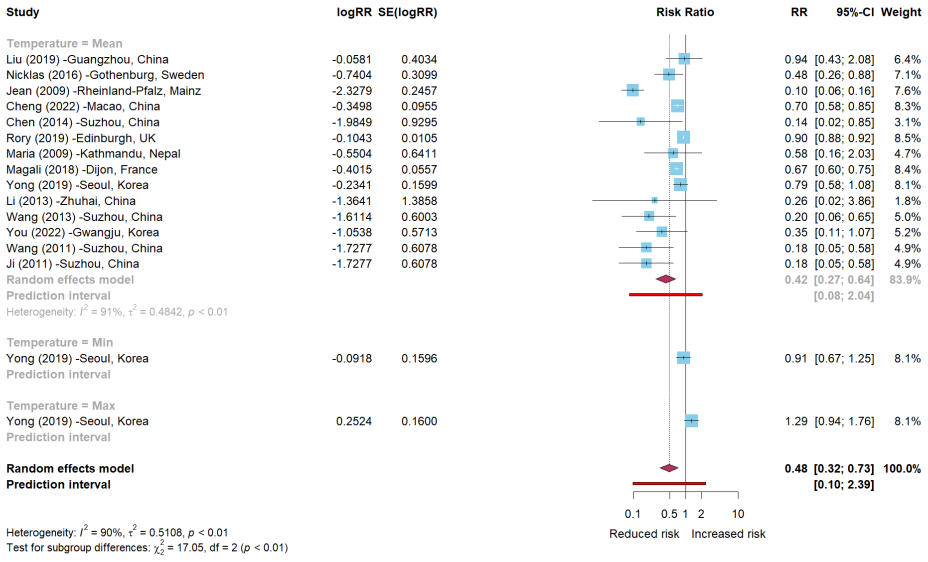


Figure S4-5. Subgroup analysis of human metapneumoviruses (HMPV) meta-analysis by modelling approach

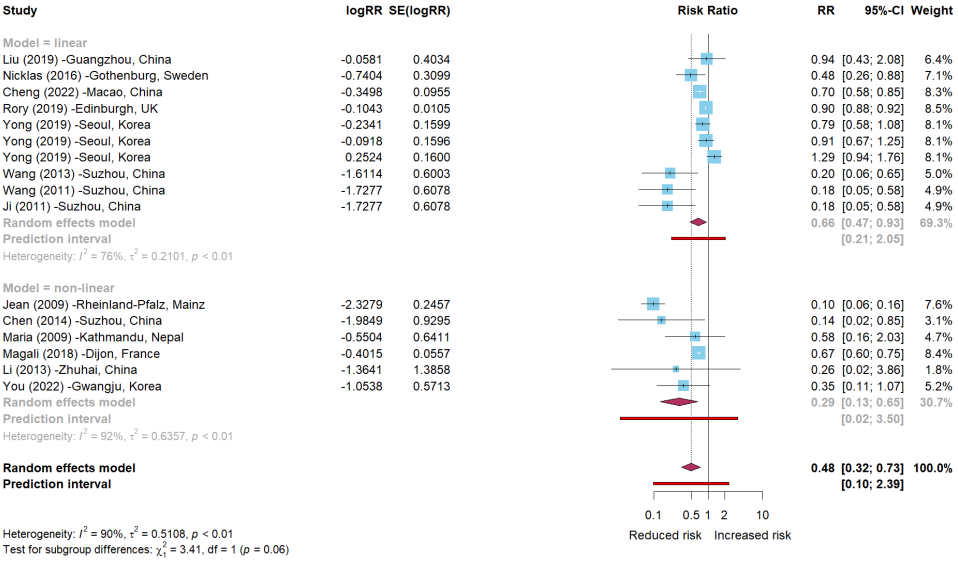


Figure S4-6. Leave-one-out analysis of human metapneumoviruses (HMPV) meta-analysis

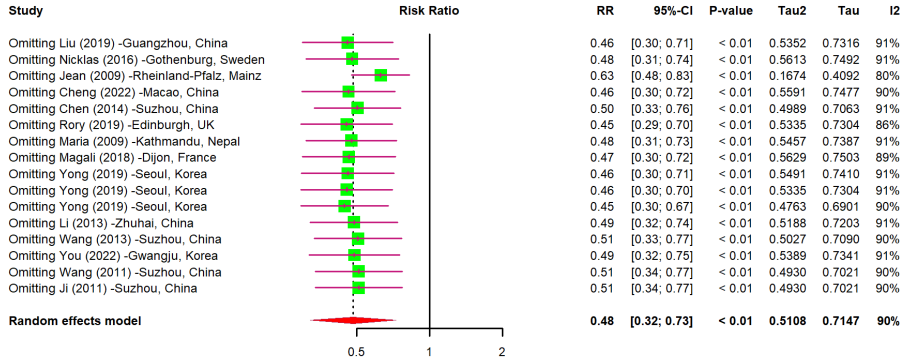
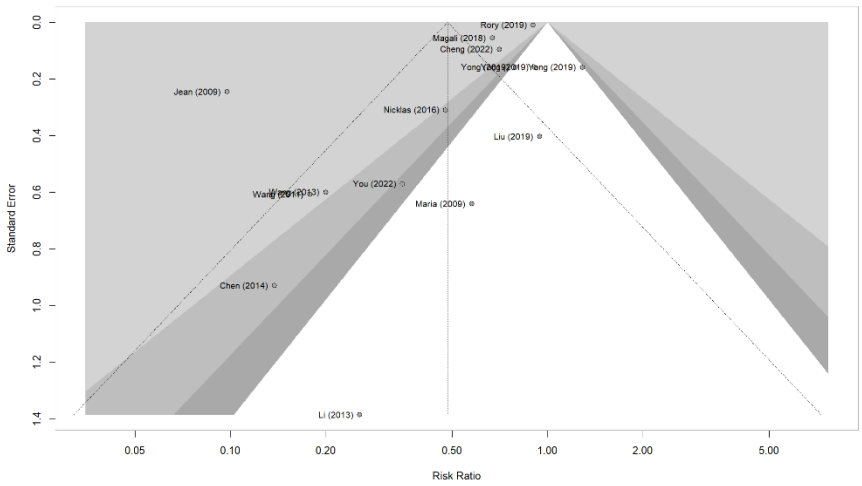


Figure S4-7. Funnel plot of human metapneumoviruses (HMPV) estimates



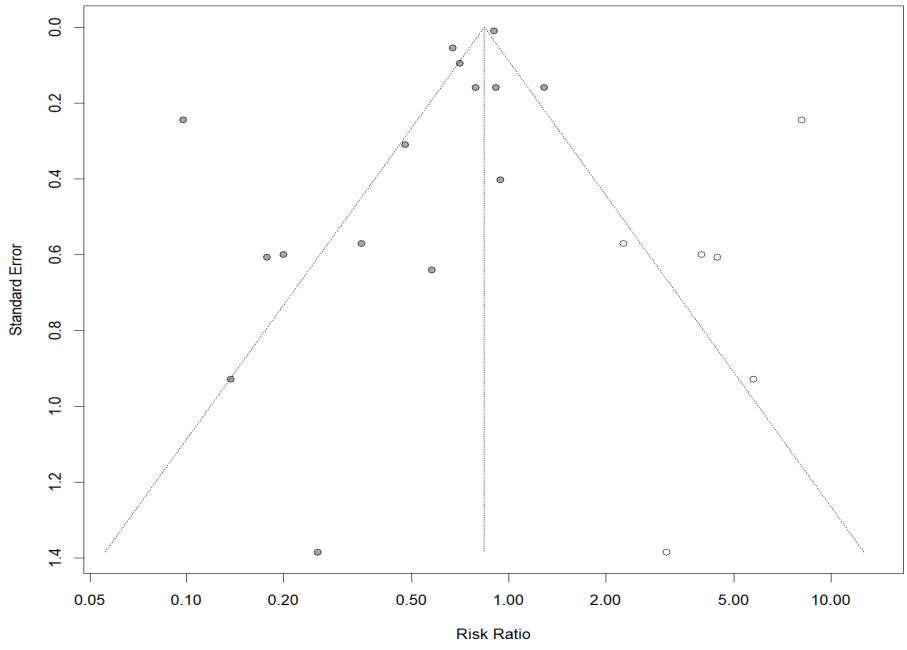
Linear regression test of funnel plot asymmetry

Egger's test result: t = -2.91, df = 14, p-value = 0.0115

Sample estimates:

bias	se.bias	intercept	se.intercept
-2.0778	0.7151	-0.0876	0.0290

Figure S4-8. Trim and fill of human metapneumoviruses (HMPV) meta-analysis



Number of studies: k = 23 (with 7 added studies)

Random effects model: RR= 0.8394 [0.5034; 1.3998] , Z =-0.67, *P*= 0.5023

Quantifying heterogeneity:

tau^2 = 1.2694 [0.6562, 2.9522]; tau = 1.1267 [0.8101, 1.7182]

I^2 = 91.6% [88.7%, 93.8%]; H = 3.45 [2.97, 4.00]

Figure S5. Random-effects meta-analysis of human rhinovirus (HRV) estimates (12 studies)

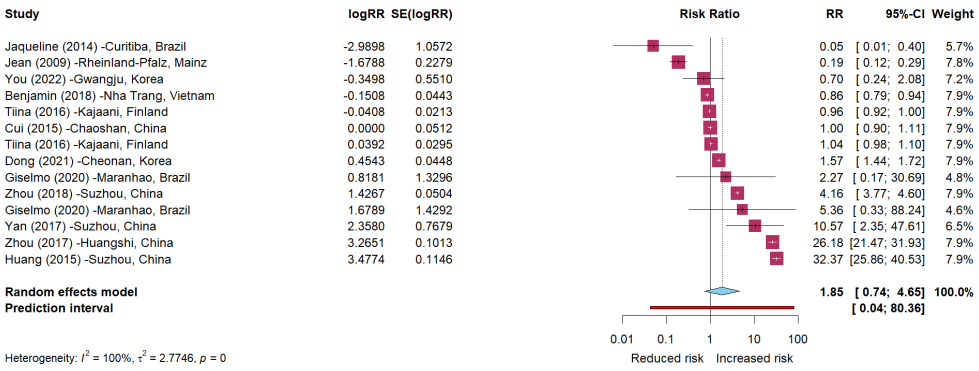


Figure S5-1. Subgroup analysis of human rhinovirus (HRV) meta-analysis by Köppen-Geiger climate

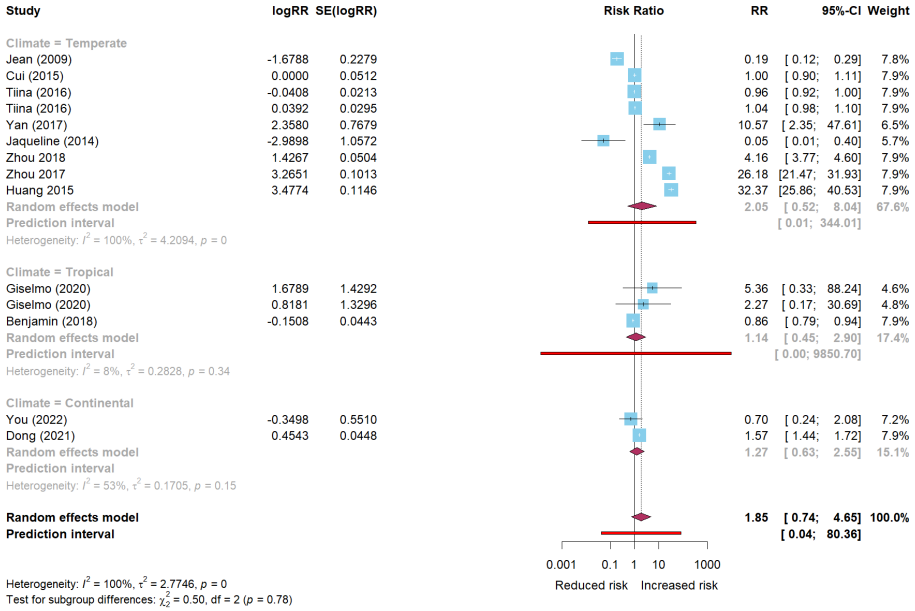


Figure S5-2. Subgroup analysis of human rhinovirus (HRV) meta-analysis by World Bank income category

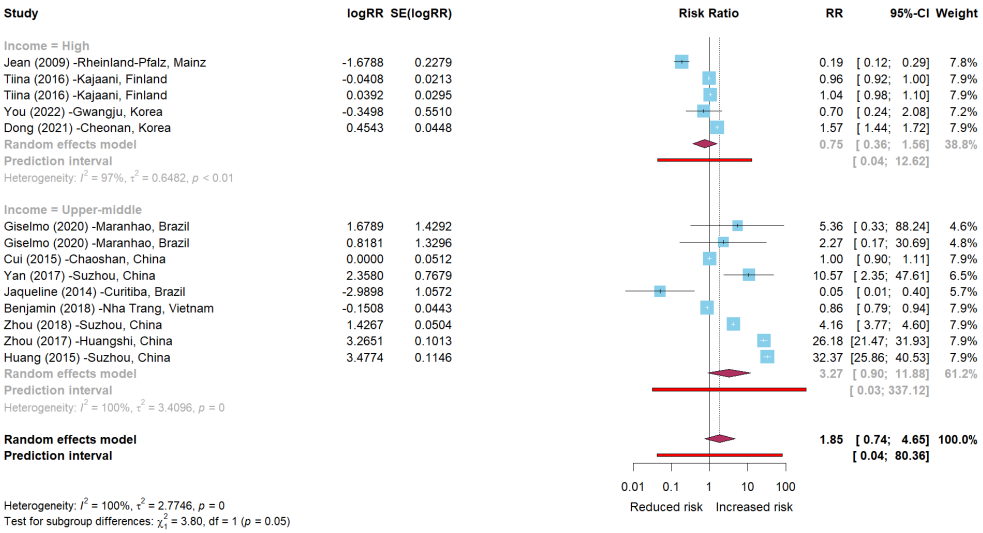


Figure S5-3. Subgroup analysis of human rhinovirus (HRV) meta-analysis by temporal resolution

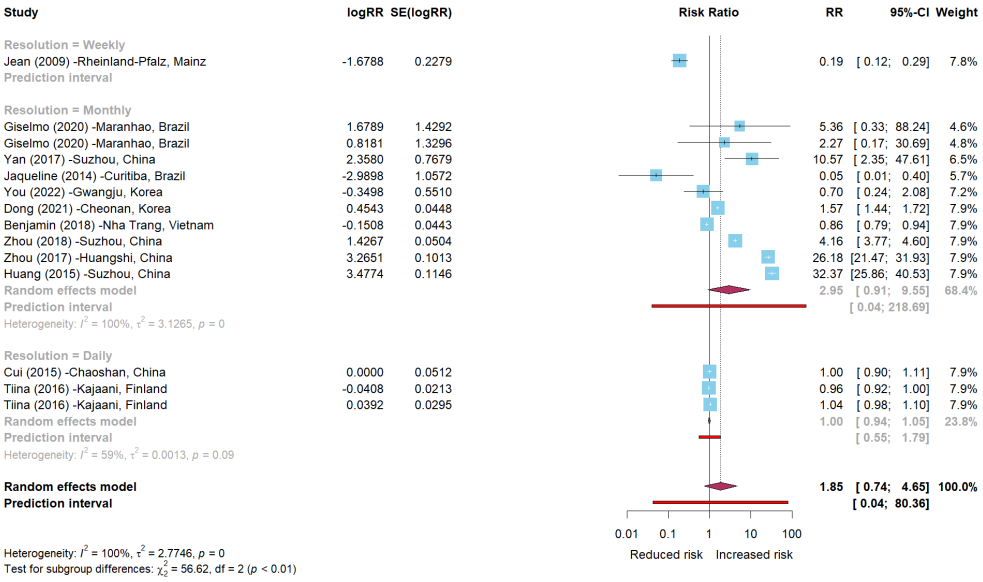


Figure S5-4. Subgroup analysis of human rhinovirus (HRV) meta-analysis by exposure measure

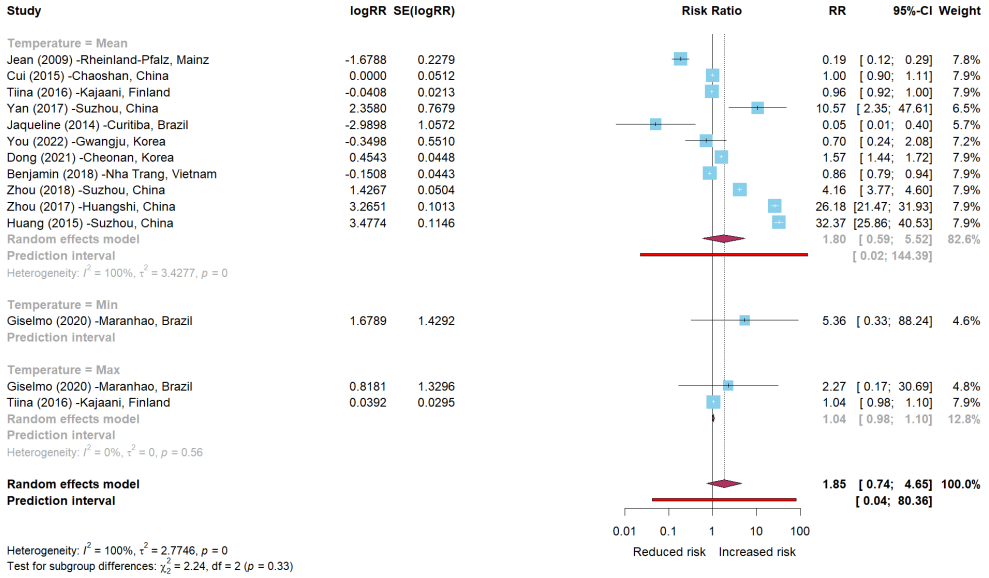


Figure S5-5. Subgroup analysis of human rhinovirus (HRV) meta-analysis by modelling approach

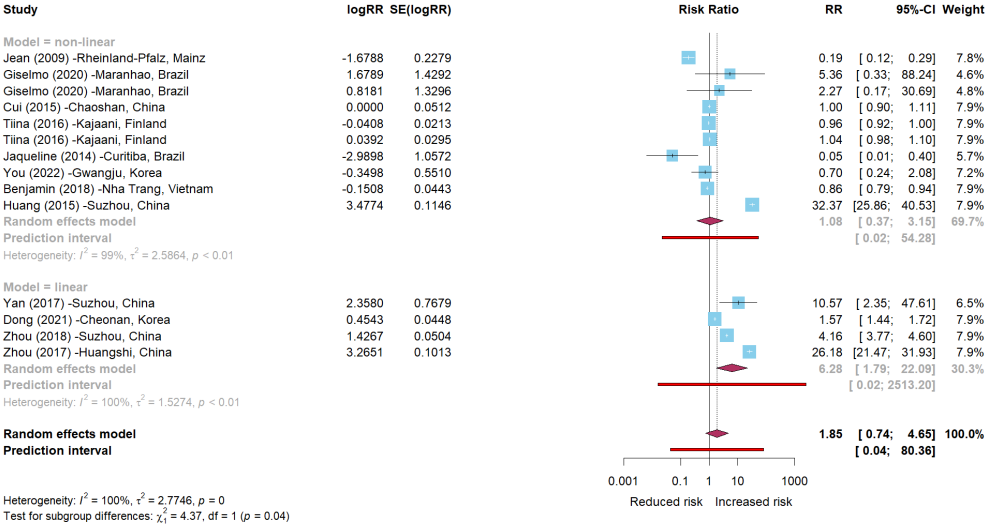


Figure S5-6. Leave-one-out analysis of human rhinovirus (HRV) meta-analysis

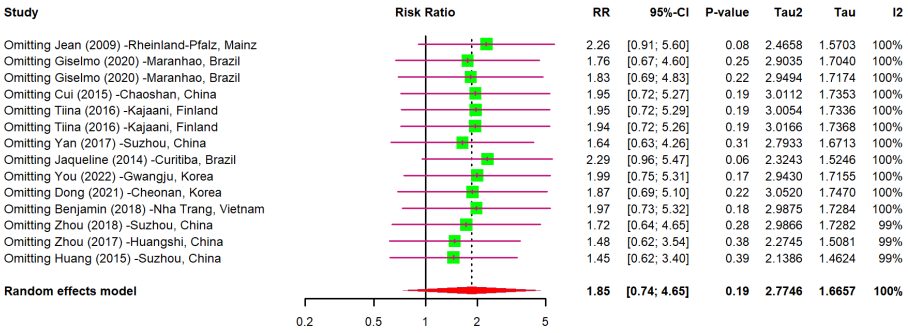
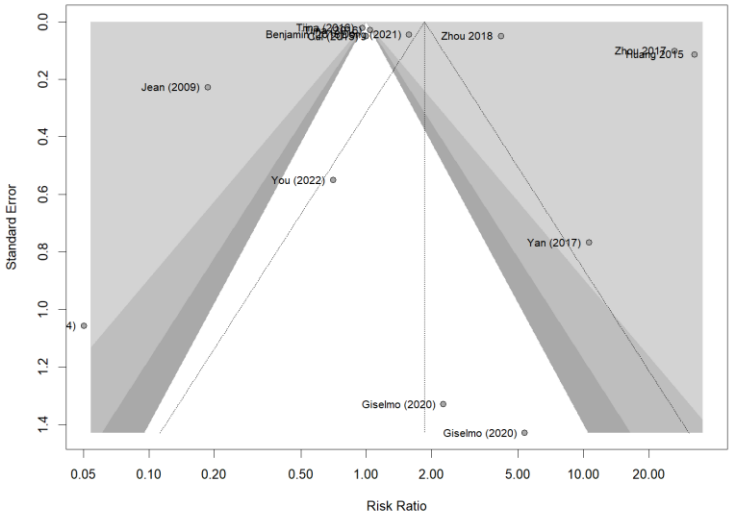


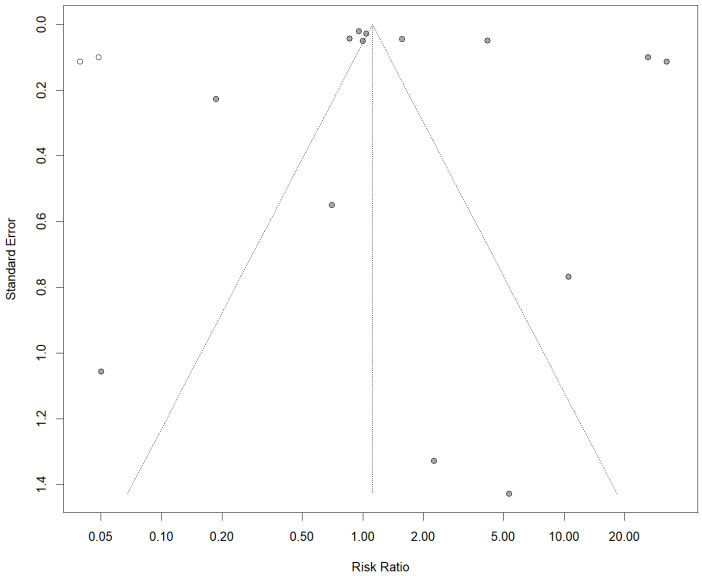
Figure S5-7. Funnel plot of human rhinovirus (HRV) estimates



Linear regression test of funnel plot asymmetry

Egger's test result: t = 1.32, df = 13, p-value = 0.2086

Figure S5-8. Trim and fill of human rhinovirus (HRV) meta-analysis



Number of studies: k = 16 (with 2 added studies)

Random effects model: RR 1.1163 [0.3960; 3.1466], Z=0.21, *P*= 0.8352

Quantifying heterogeneity: tau^2 = 4.1785 [2.1504; 10.1327]; tau = 2.0441 [1.4664; 3.1832]; I^2 = 99.7% [99.6%; 99.7%]; H = 17.43 [16.37; 18.54]

Figure S6. Random-effects meta-analysis of human adenoviruses (HAdVs) estimates (16 studies)

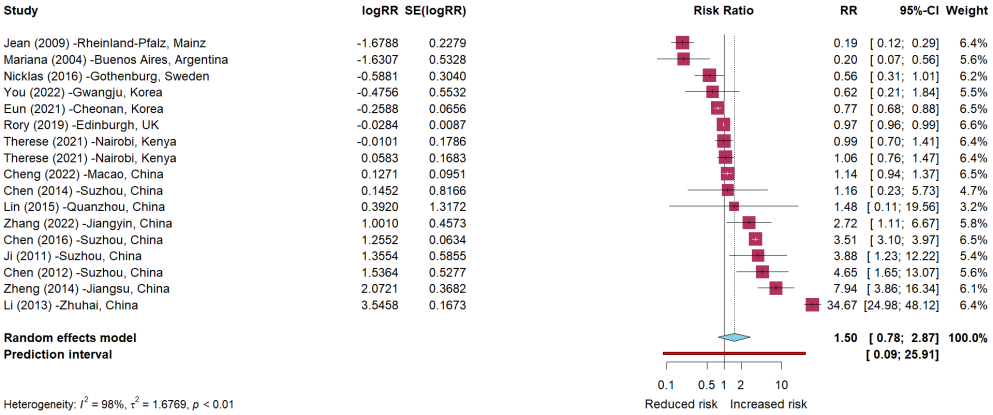


Figure S6-1. Subgroup analysis of human adenoviruses (HAdVs) meta-analysis by Köppen-Geiger climate

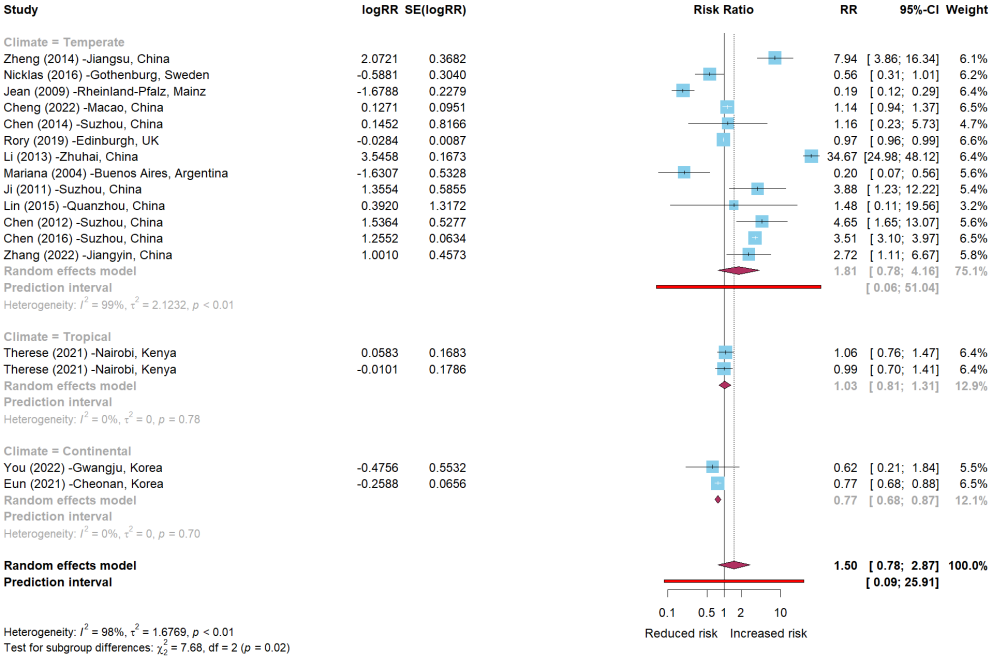


Figure S6-2. Subgroup analysis of human adenoviruses (HAdVs) meta-analysis by World Bank income category

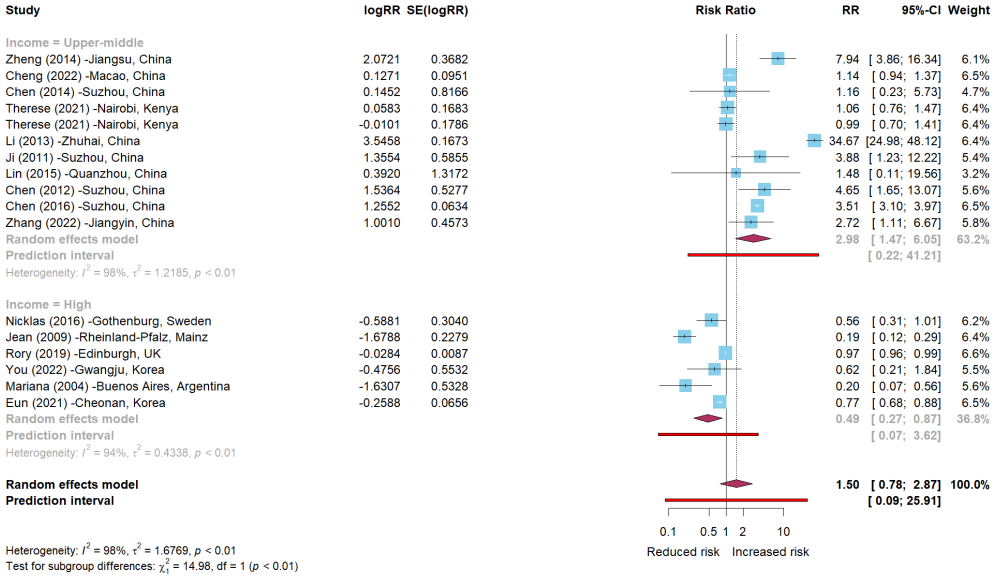


Figure S6-3. Subgroup analysis of human adenoviruses (HAdVs) meta-analysis by temporal resolution

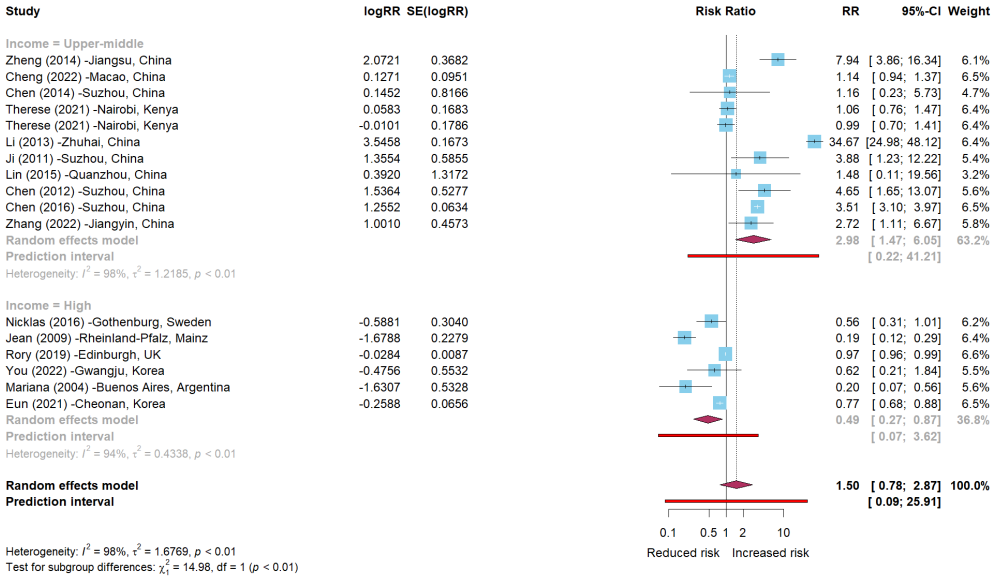


Figure S6-4. Subgroup analysis of human adenoviruses (HAdVs) meta-analysis by exposure measure

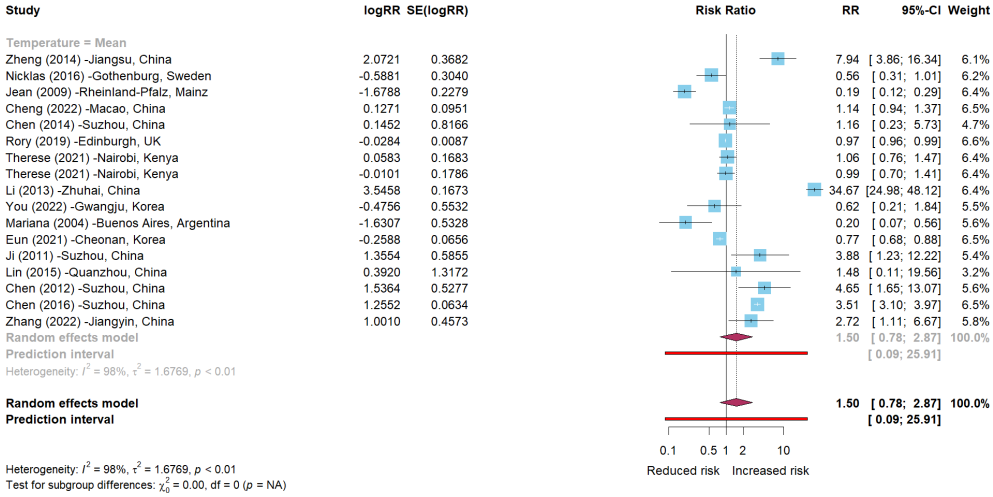


Figure S6-5. Subgroup analysis of human adenoviruses (HAdVs) meta-analysis by modelling approach

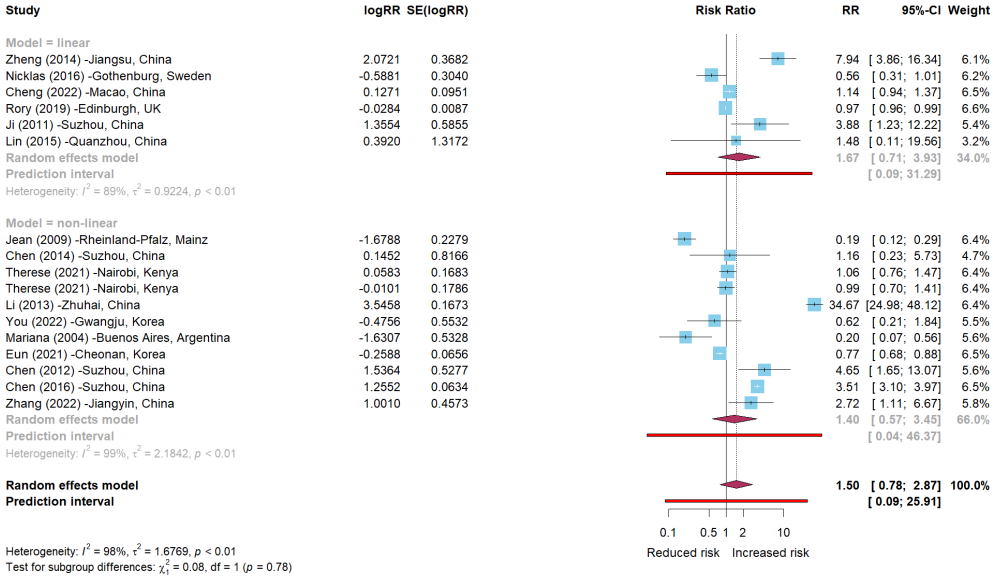


Figure S6-6. Leave-one-out analysis of human adenoviruses (HAdVs) meta-analysis

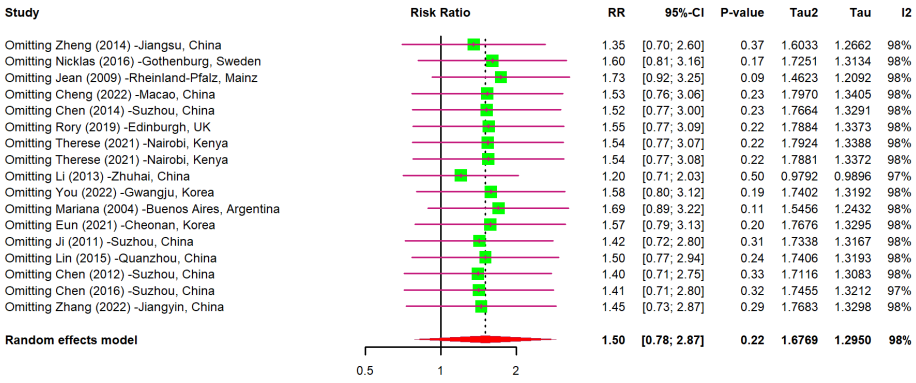
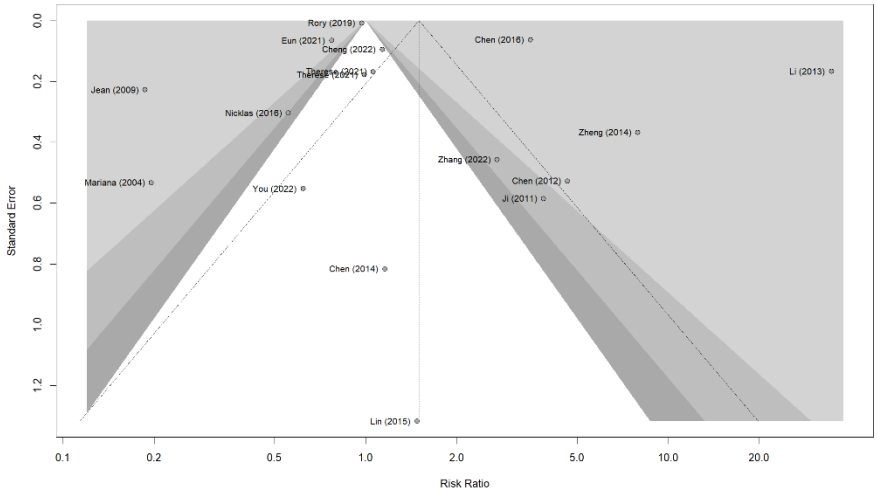


Figure S6-7. Funnel plot of human adenoviruses (HAdVs) estimates



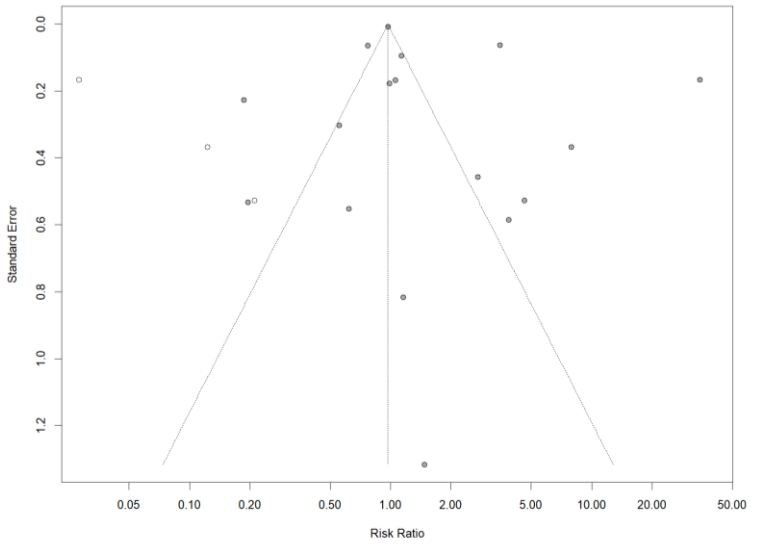
Linear regression test of funnel plot asymmetry

Egger's test result: t = 1.22, df = 15, p-value = 0.2409

Sample estimates:

bias	se.bias	intercept	se.intercept
2.5030	2.0500	-0.0349	0.0713

Figure S6-8. Trim and fill of human adenoviruses (HAdVs) meta-analysis



Number of studies: k = 20 (with 3 added studies)

Random effects model : RR=0.9707 [0.4667; 2.0189] , Z= -0.08 , P=0.9365

Quantifying heterogeneity:

tau^2 = 2.5968 [1.4069; 5.4493]; tau = 1.6114 [1.1861; 2.3344]

I^2 = 98.7% [98.5%; 98.9%]; H = 8.83 [8.09; 9.65]

Figure S7. Random-effects meta-analysis of human bocavirus (HBoV) estimates (nine studies)

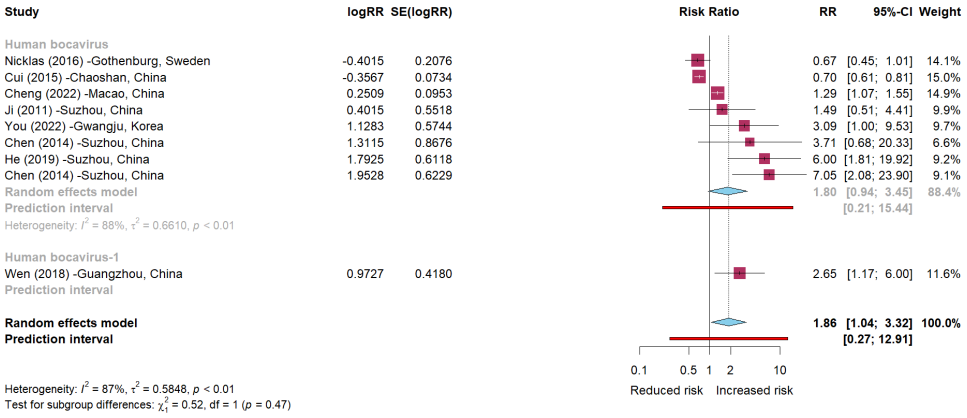


Figure S7-1. Subgroup analysis of human bocavirus (HBoV) meta-analysis by Köppen-Geiger climate

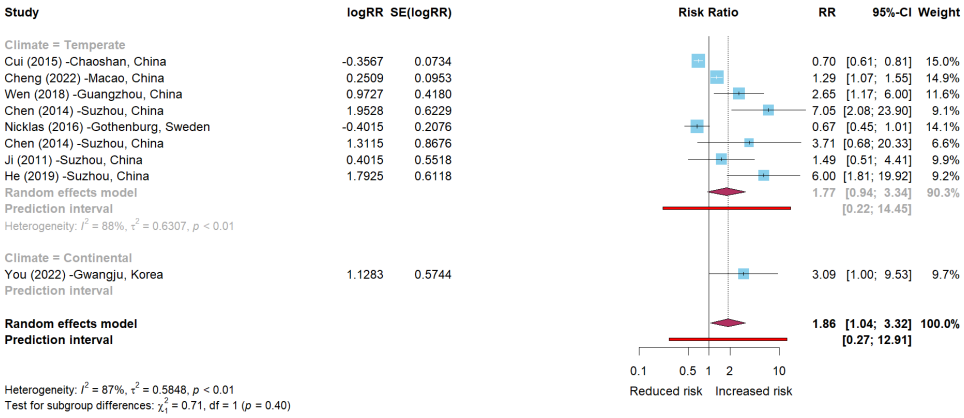


Figure S7-2. Subgroup analysis of human bocavirus (HBoV) meta-analysis by World Bank income category

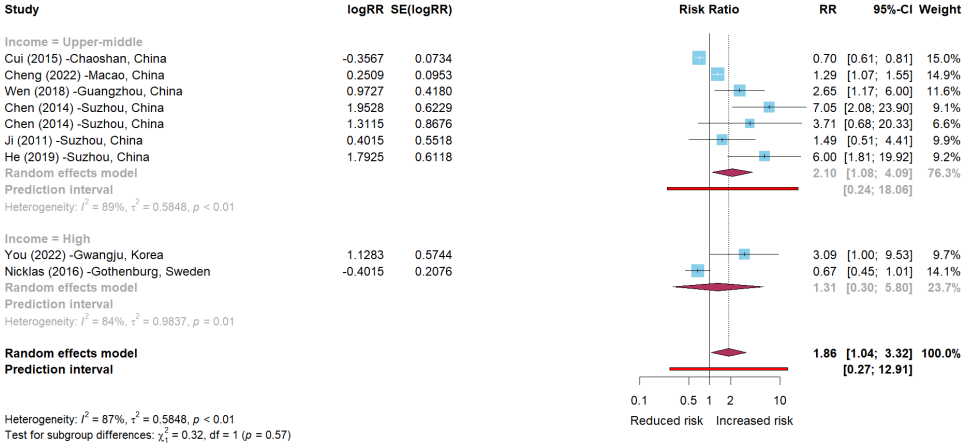


Figure S7-3. Subgroup analysis of human bocavirus (HBoV) meta-analysis by temporal resolution

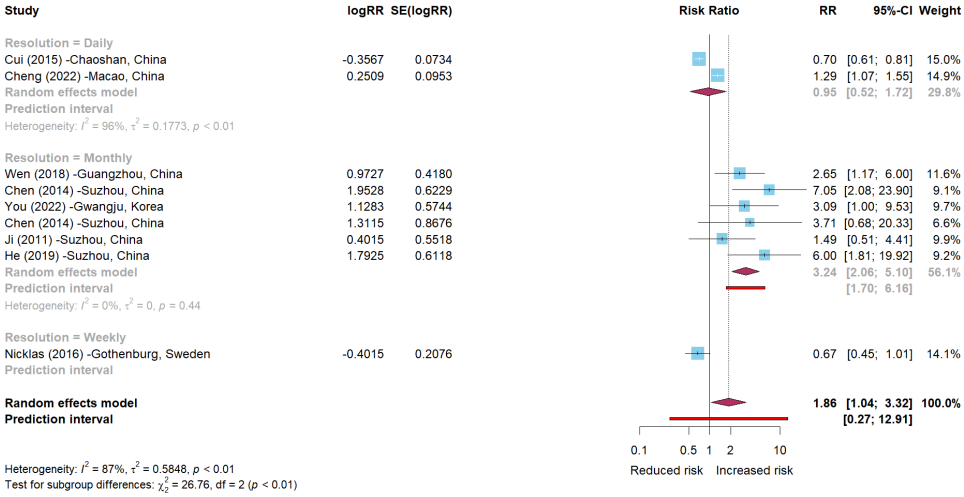


Figure S7-4. Subgroup analysis of human bocavirus (HBoV) meta-analysis by exposure measure

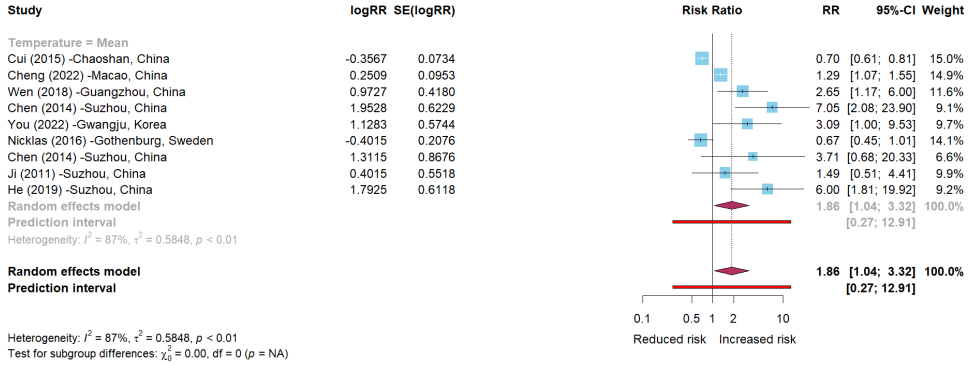


Figure S7-5. Subgroup analysis of human bocavirus (HBoV) meta-analysis by modelling approach

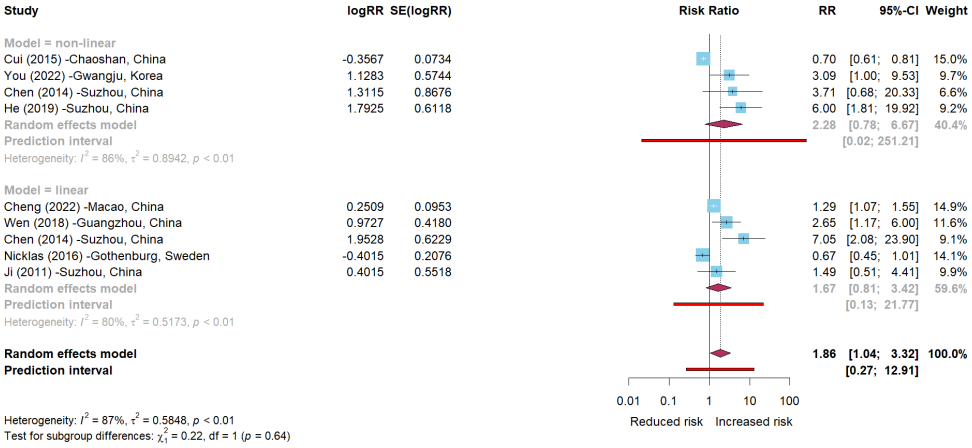


Figure S7-6. Leave-one-out analysis of human bocavirus (HBoV) meta-analysis

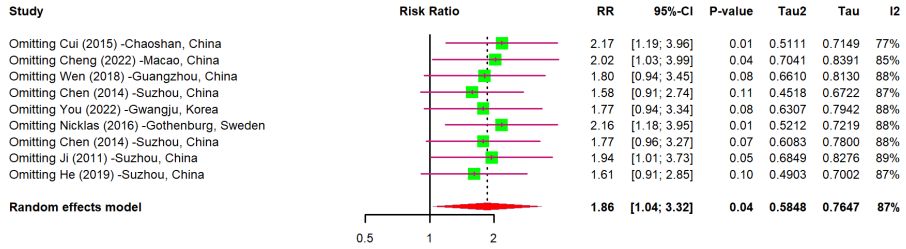


Figure S8. Random-effects meta-analysis of enterovirus(EV) estimates (four studies)

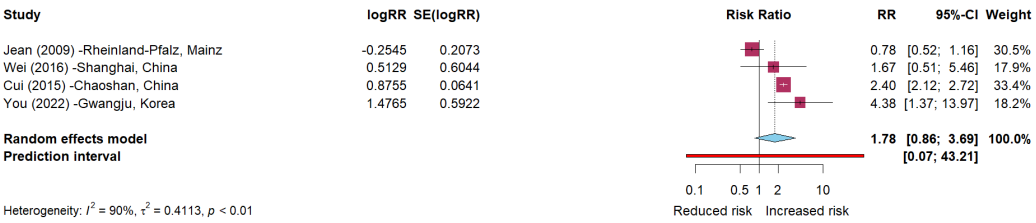


Figure S8-1. Subgroup analysis of enterovirus (EV) meta-analysis by Köppen-Geiger climate

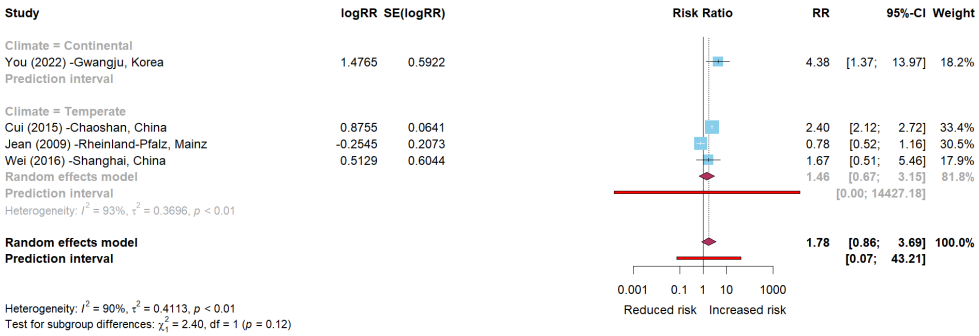


Figure S8-2. Subgroup analysis of enterovirus (EV) meta-analysis by World Bank income category

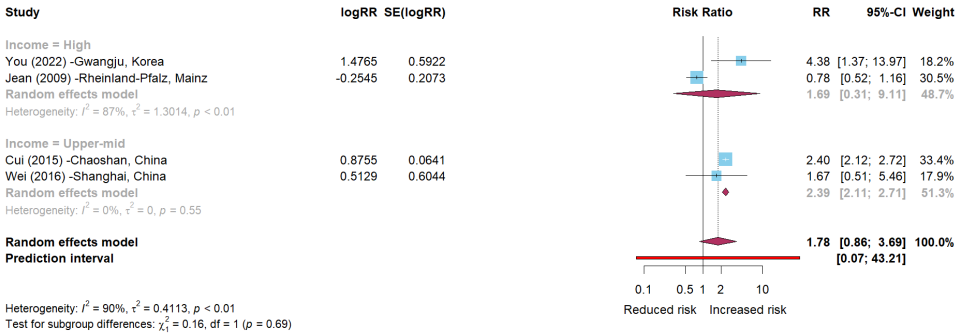


Figure S8-3. Subgroup analysis of enterovirus (EV) meta-analysis by temporal resolution

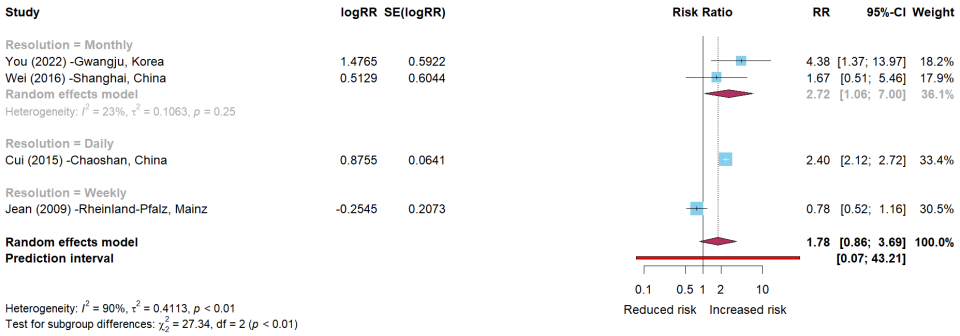


Figure S8-4. Subgroup analysis of enterovirus (EV) meta-analysis by exposure measure

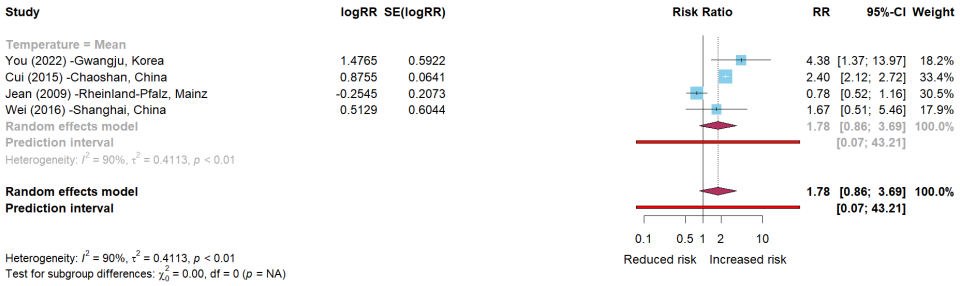


Figure S8-5. Subgroup analysis of enterovirus (EV) meta-analysis by modelling approach

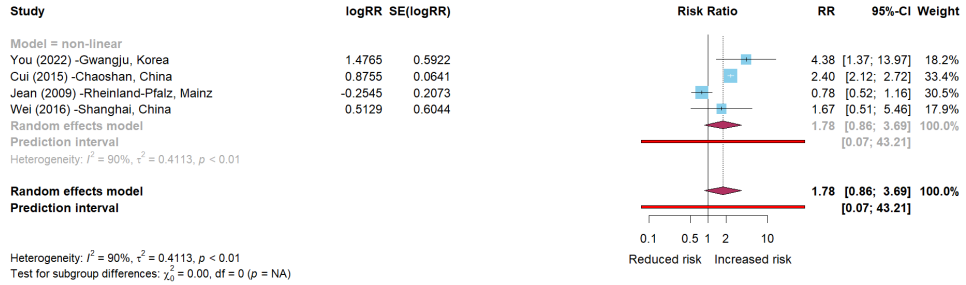


Figure S8-6. Leave-one-out analysis of enterovirus (EV) meta-analysis

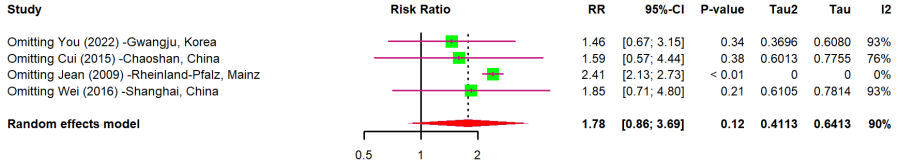


Figure S8-7. Sensitivity analysis by excluding study with high risk of bias for Jean et al 2009

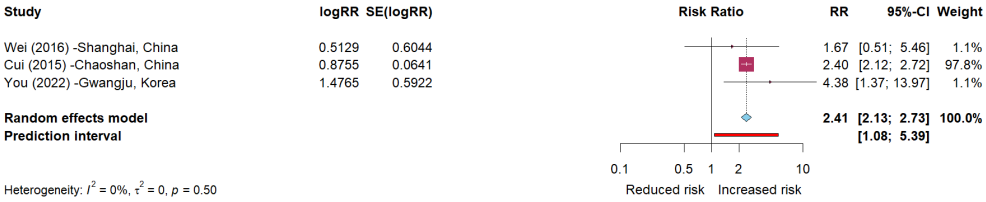


Figure S9. Random-effects meta-analysis of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) estimates (nine studies)

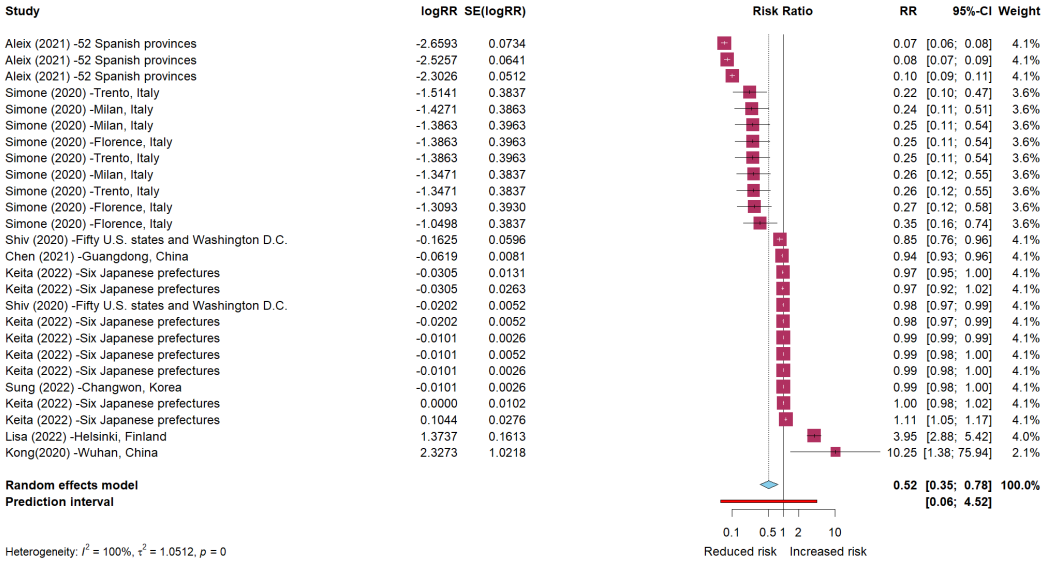


Figure S9-1. Subgroup analysis of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) meta-analysis by Köppen-Geiger climate

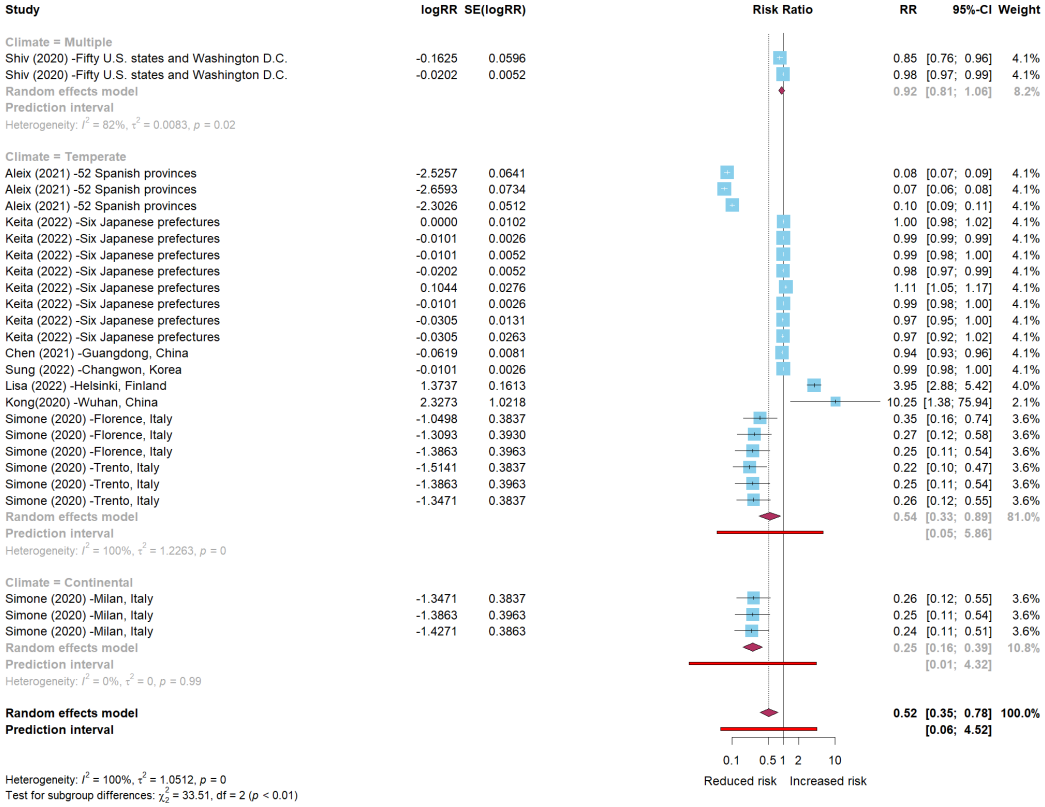


Figure S9-2. Subgroup analysis of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) meta-analysis by World Bank income category

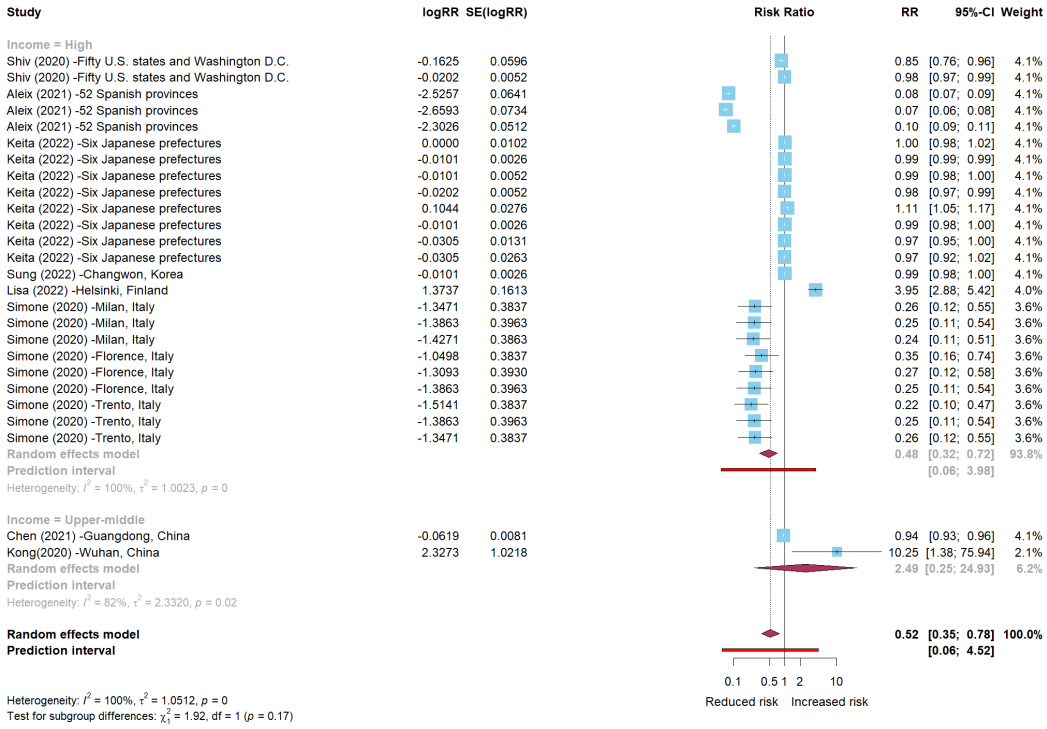


Figure S9-3. Subgroup analysis of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) meta-analysis by temporal resolution

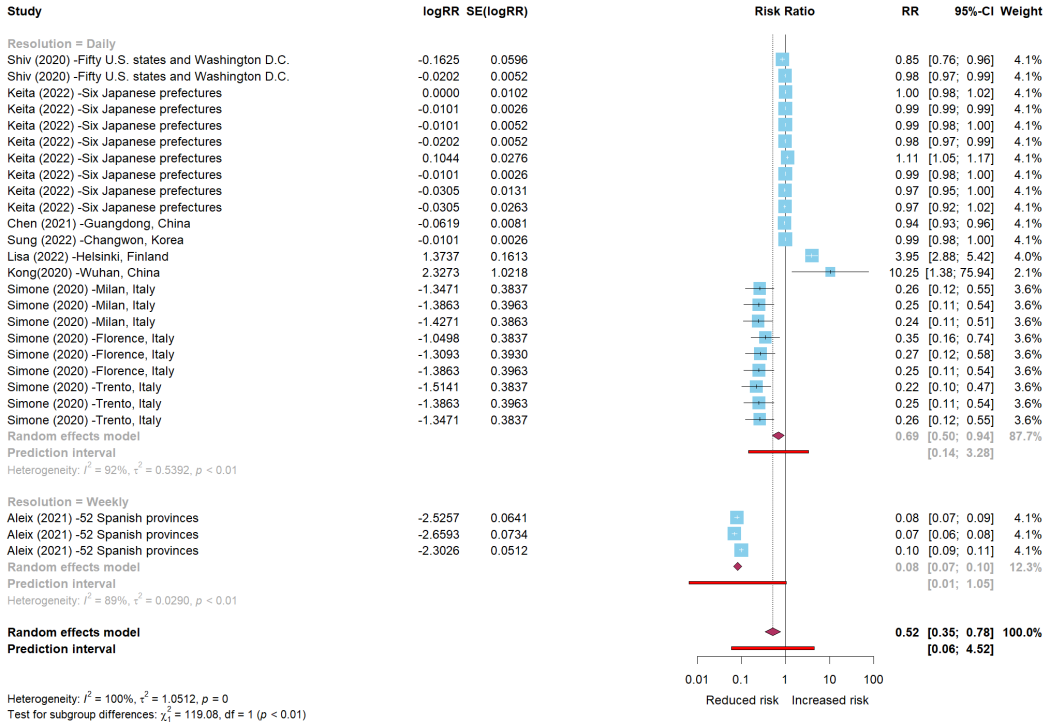


Figure S9-4. Subgroup analysis of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) meta-analysis by exposure measure

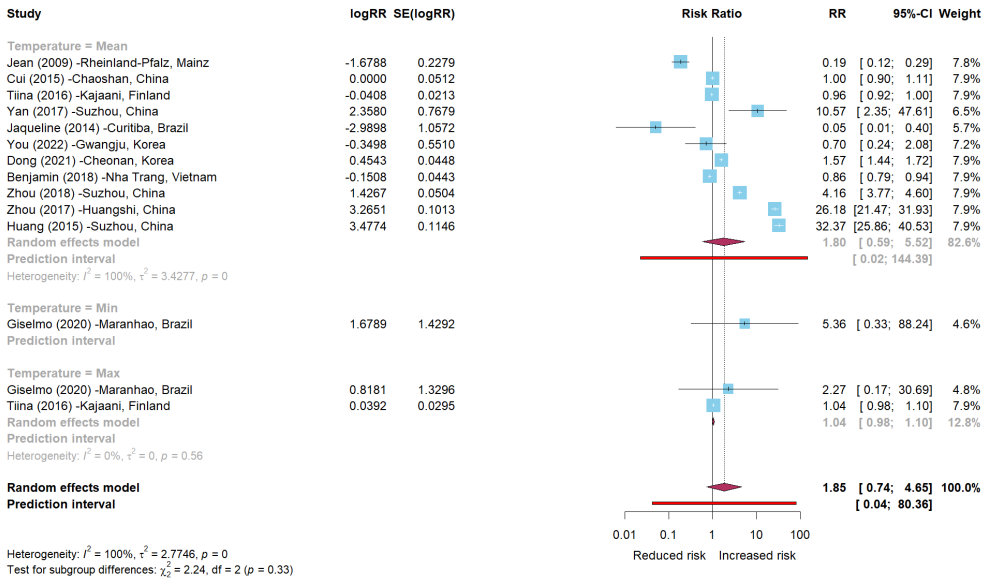


Figure S9-5. Subgroup analysis of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) meta-analysis by modelling approach

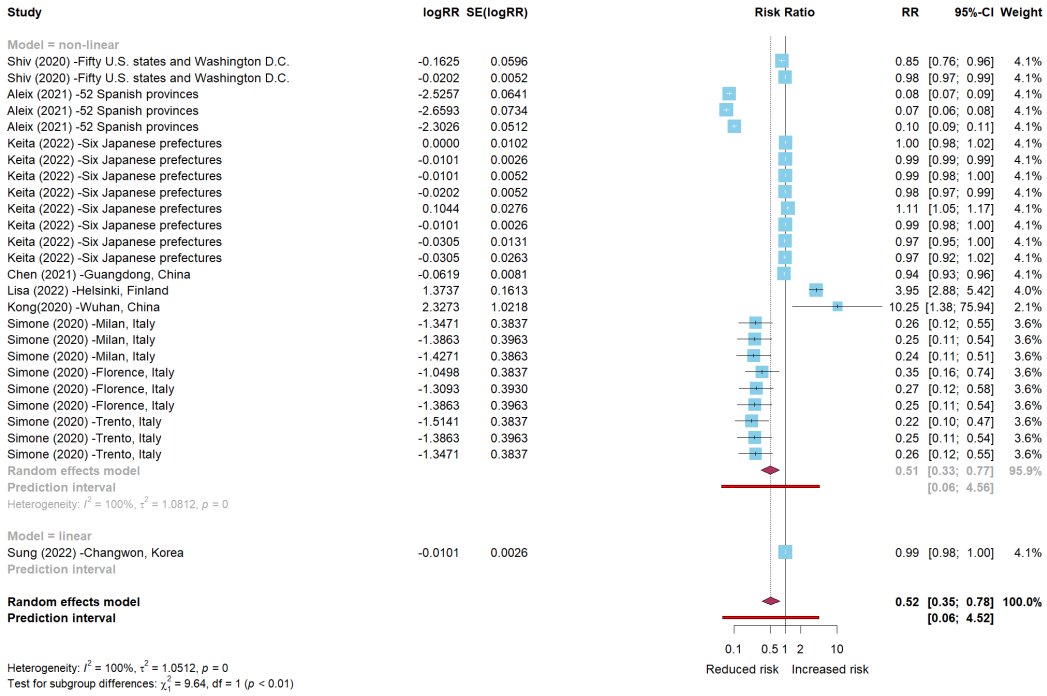


Figure S9-6. Subgroup analysis of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) meta-analysis by lag type

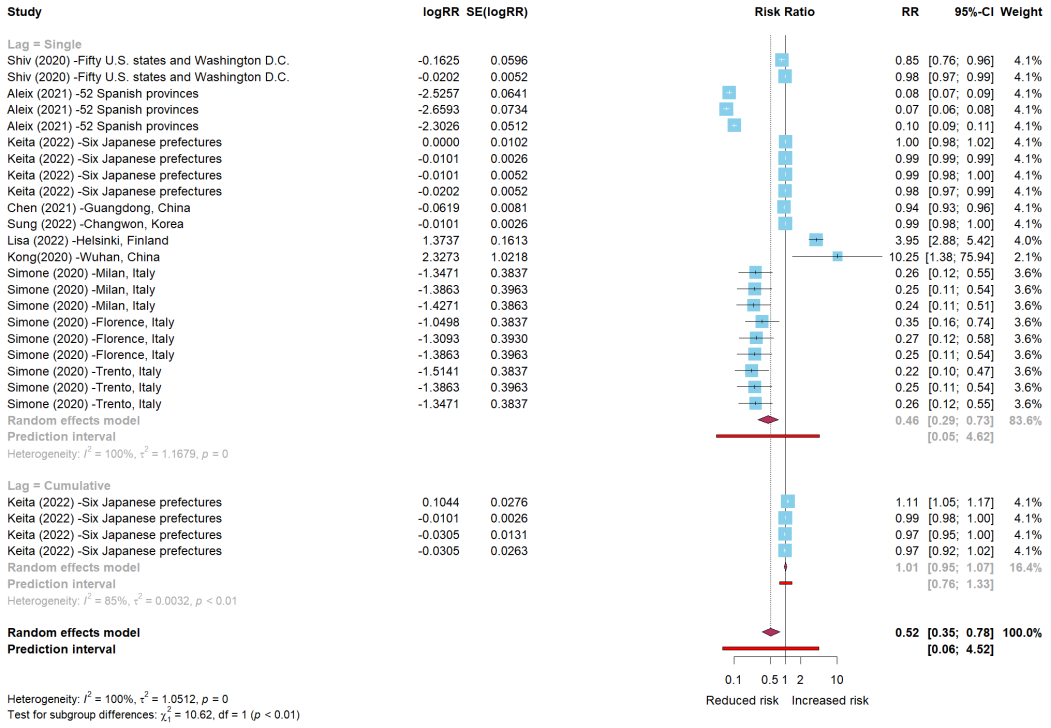


Figure S9-7. Leave-one-out analysis of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) meta-analysis

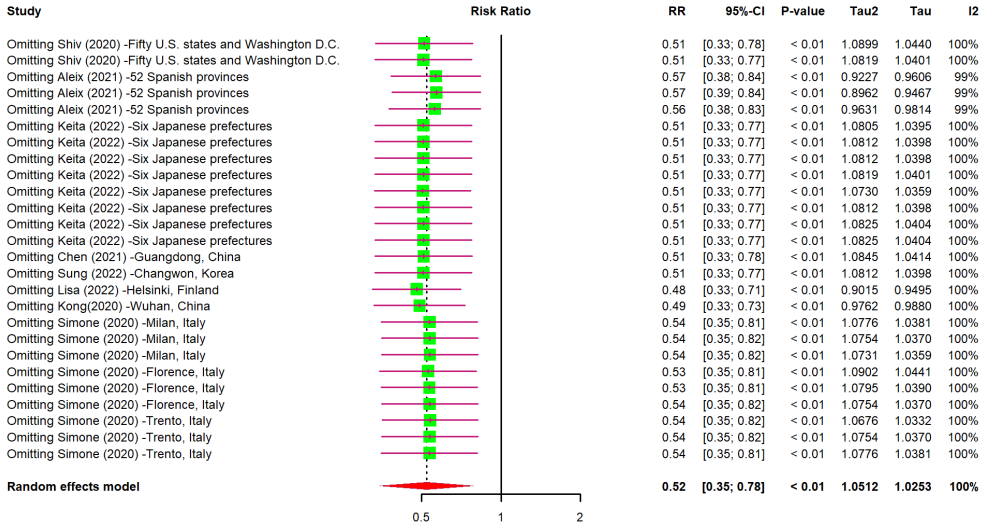


Figure S10. Random-effects meta-analysis of severe acute respiratory syndrome coronavirus (SARS-CoV) estimates (four studies)

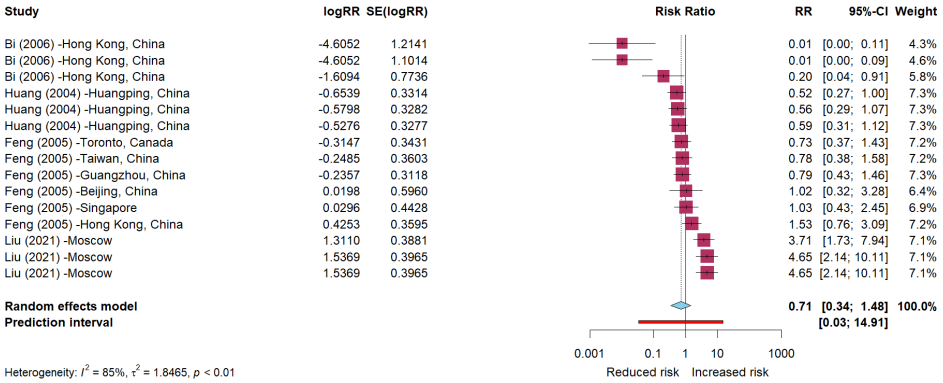


Figure S10-1. Subgroup analysis of severe acute respiratory syndrome (SARS) meta-analysis by Köppen-Geiger climate

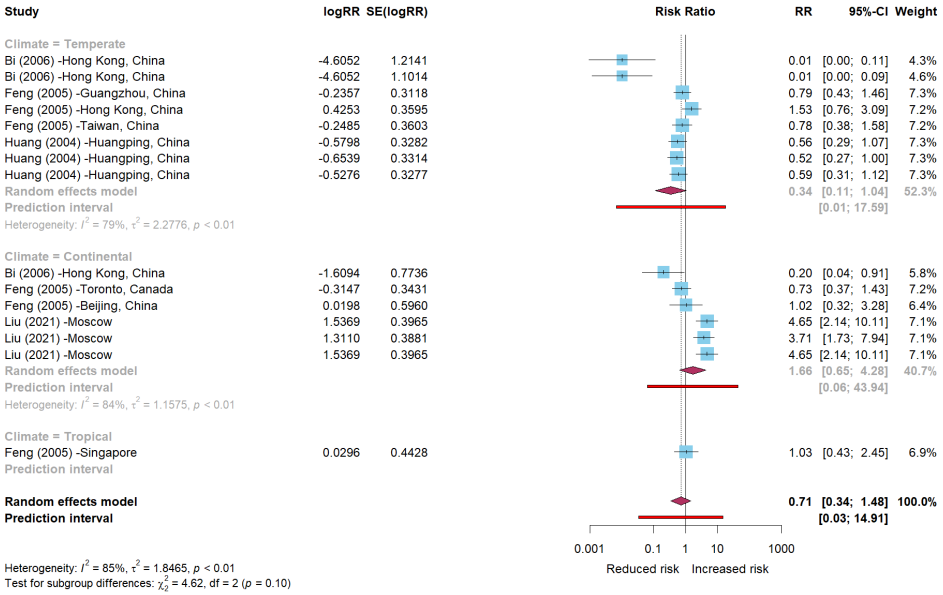


Figure S10-2. Subgroup analysis of severe acute respiratory syndrome coronavirus (SARS-CoV) meta-analysis by World Bank income category

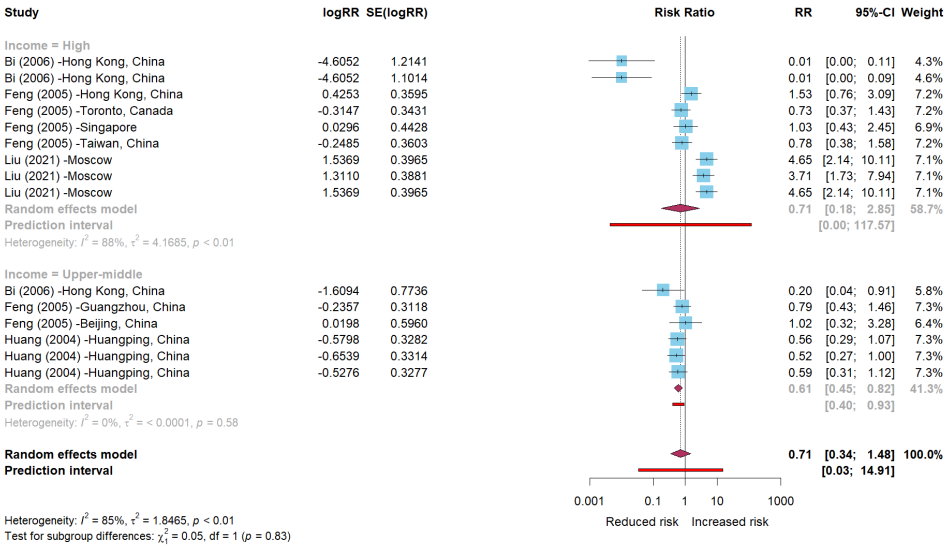


Figure S10-3. Subgroup analysis of severe acute respiratory syndrome coronavirus (SARS-CoV) meta-analysis by temporal resolution

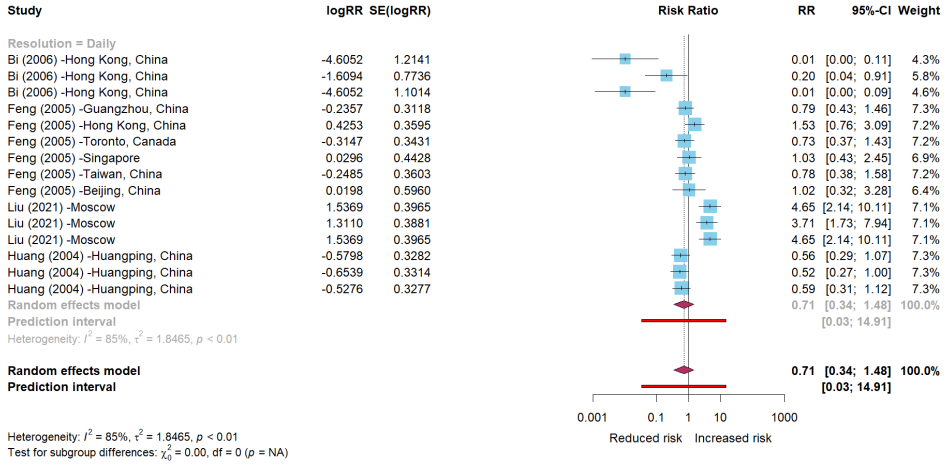


Figure S10-4. Subgroup analysis of severe acute respiratory syndrome coronavirus (SARS-CoV) meta-analysis by exposure measure

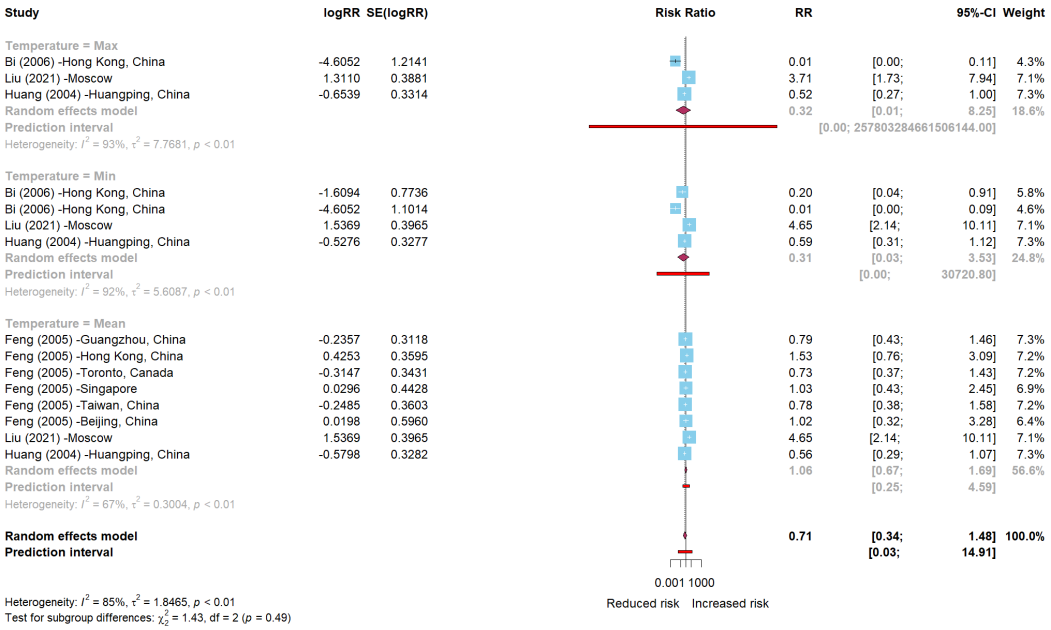


Figure S10-5. Subgroup analysis of severe acute respiratory syndrome coronavirus (SARS-CoV) meta-analysis by modelling approach

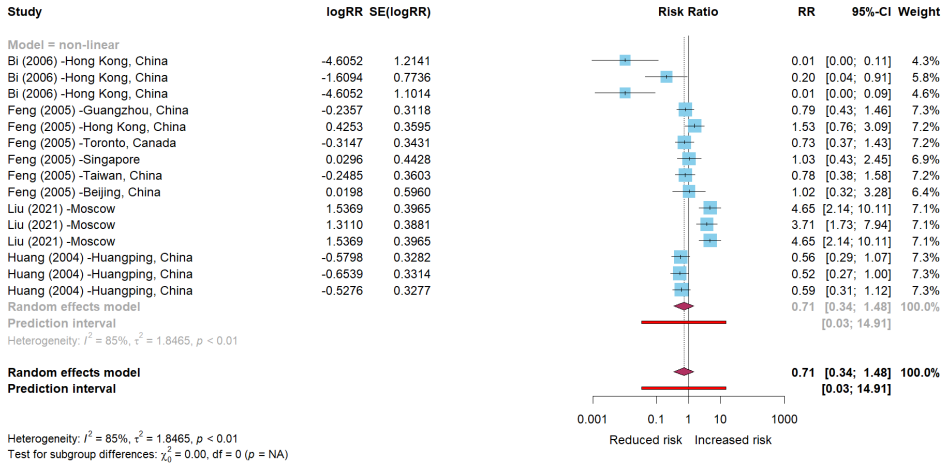


Figure S10-6. Leave-one-out analysis of severe acute respiratory syndrome coronavirus (SARS-CoV) meta-analysis

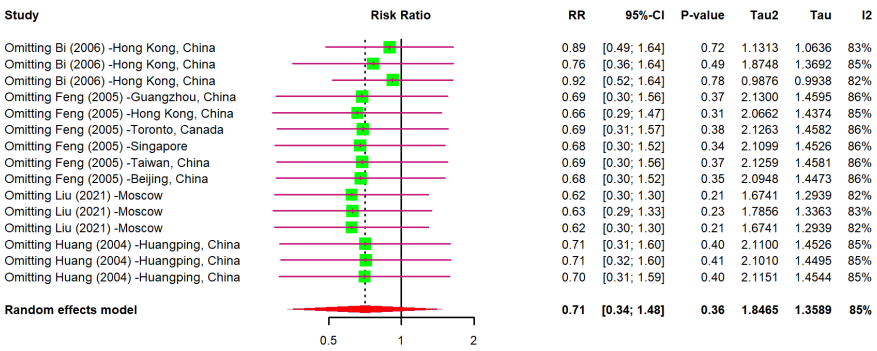


Figure S11. Random-effects meta-analysis of human coronavirus (HCoV) estimates (five studies)

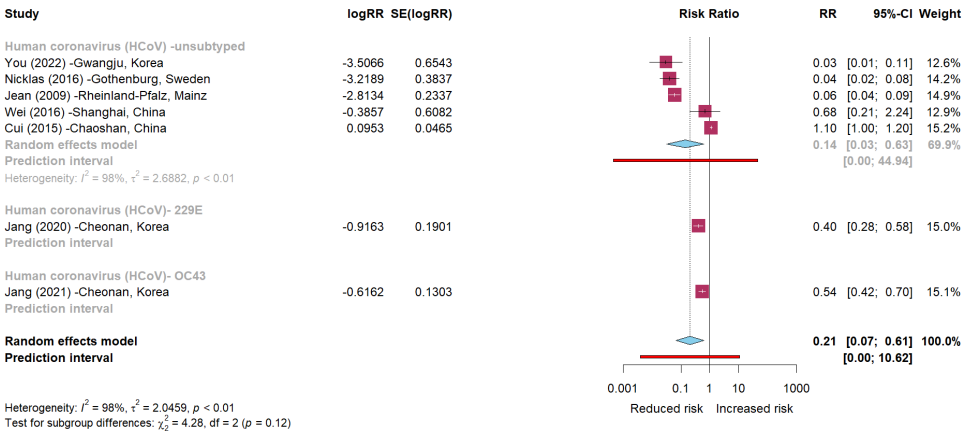


Figure S11-1. Subgroup analysis of human coronavirus (HCoV) meta-analysis by Köppen-Geiger climate

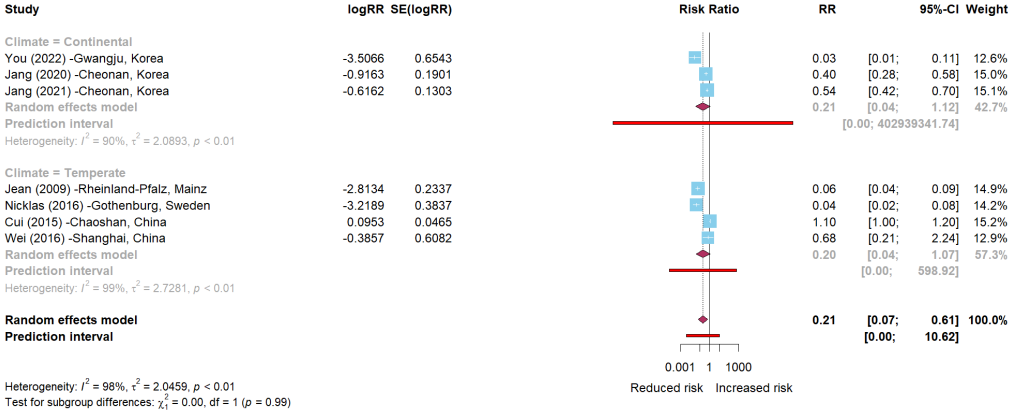


Figure S11-2. Subgroup analysis of human coronavirus (HCoV) meta-analysis by World Bank income category

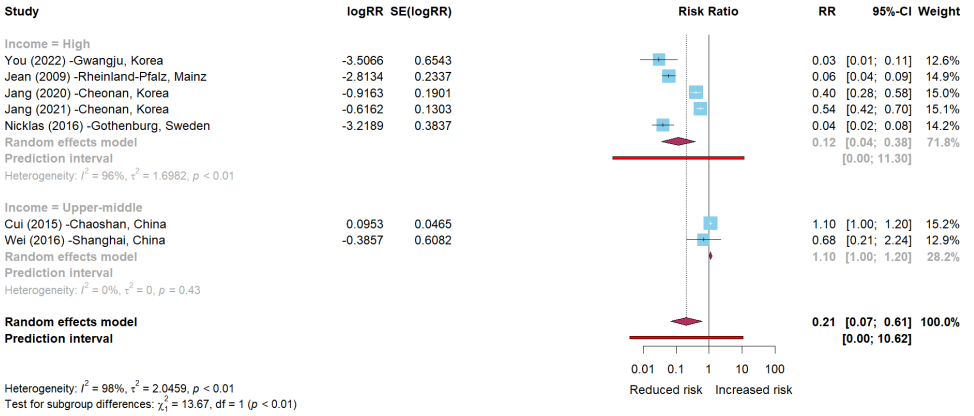


Figure S11-3. Subgroup analysis of human coronavirus (HCoV) meta-analysis by temporal resolution

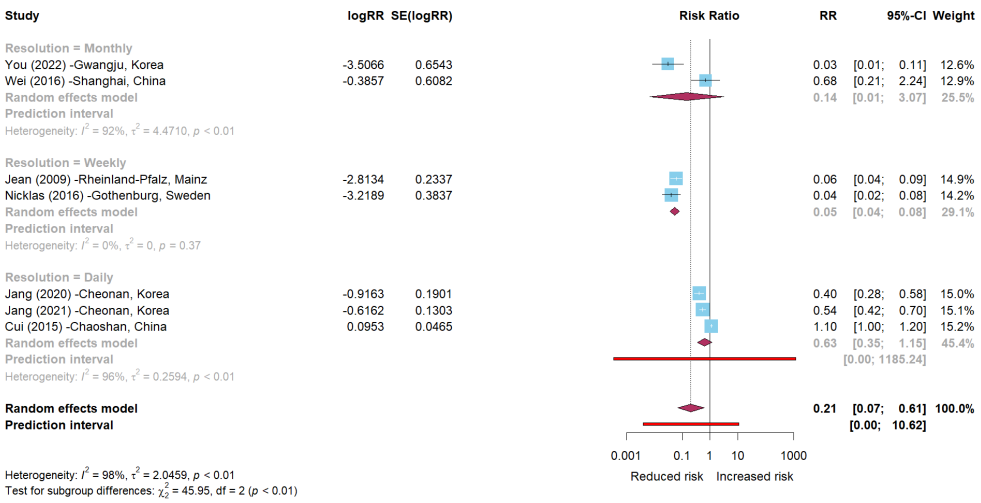


Figure S11-4. Subgroup analysis of human coronavirus (HCoV) meta-analysis by exposure measure

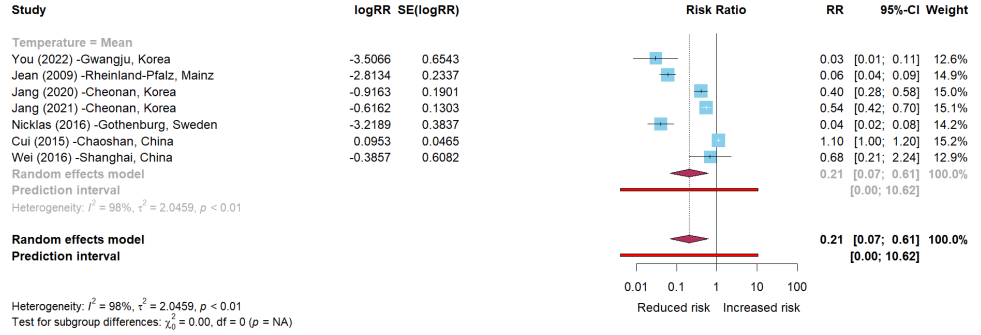


Figure S11-5. Subgroup analysis of human coronavirus (HCoV) meta-analysis by modelling approach

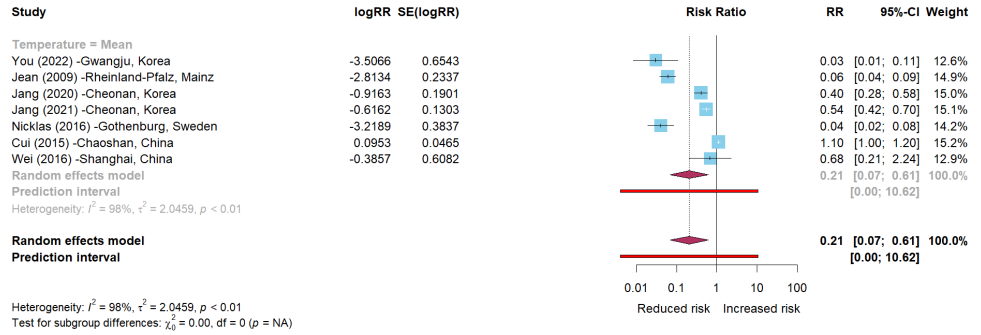


Figure S11-6. Leave-one-out analysis of human coronavirus (HCoV) meta-analysis

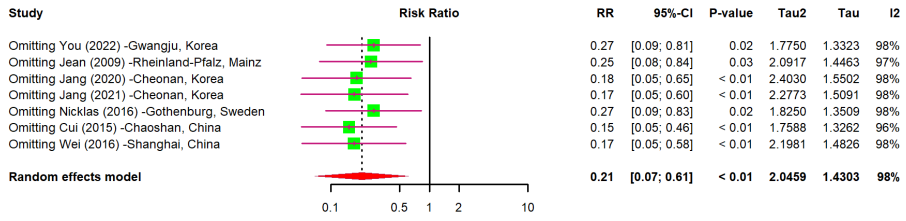


Figure S12. Random-effects meta-analysis of Human rhinoviruses/enteroviruses (HRVs/EVs) estimates (two studies)

Figure S12-1. Subgroup analysis of Human rhinoviruses/enteroviruses (HRVs/EVs) meta-analysis by Köppen-Geiger climate

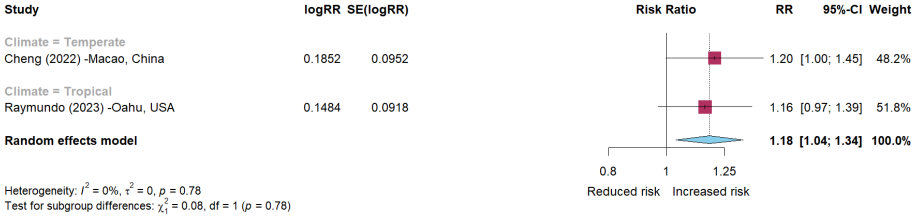


Figure S12-2. Subgroup analysis of Human rhinoviruses/enteroviruses (HRVs/EVs) meta-analysis by World Bank income category

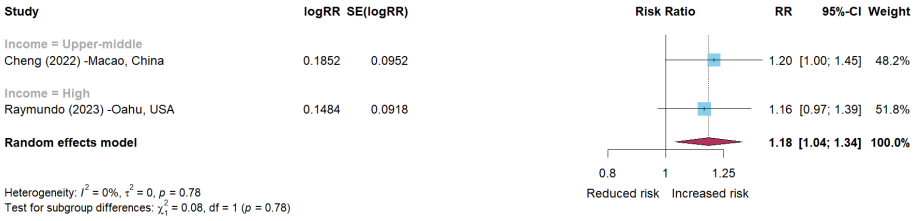


Figure S12-3. Subgroup analysis of Human rhinoviruses/enteroviruses (HRVs/EVs) meta-analysis by temporal resolution

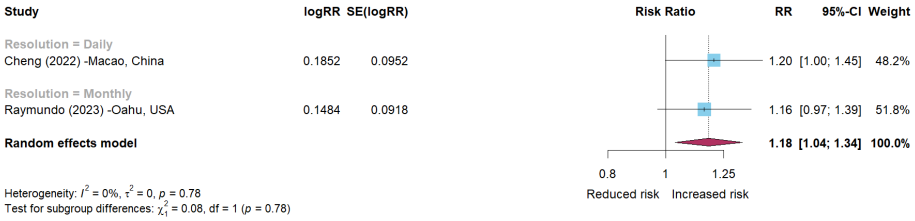


Figure S12-4. Subgroup analysis of Human rhinoviruses/enteroviruses (HRVs/EVs) meta-analysis by exposure measure

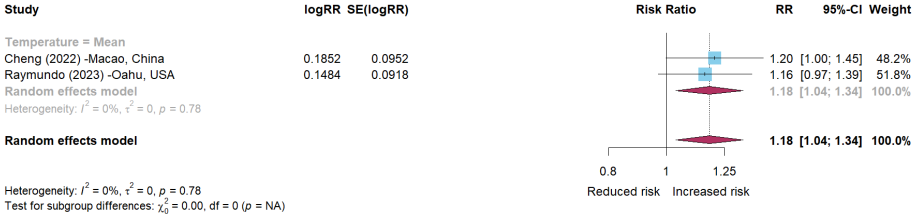


Figure S12-5. Subgroup analysis of Human rhinoviruses/enteroviruses (HRVs/EVs) meta-analysis by modelling approach

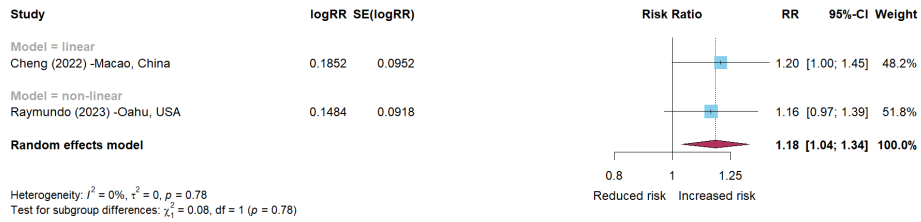


Figure S13. Subgroup analysis of bacterial respiratory infections meta-analysis by pathogen

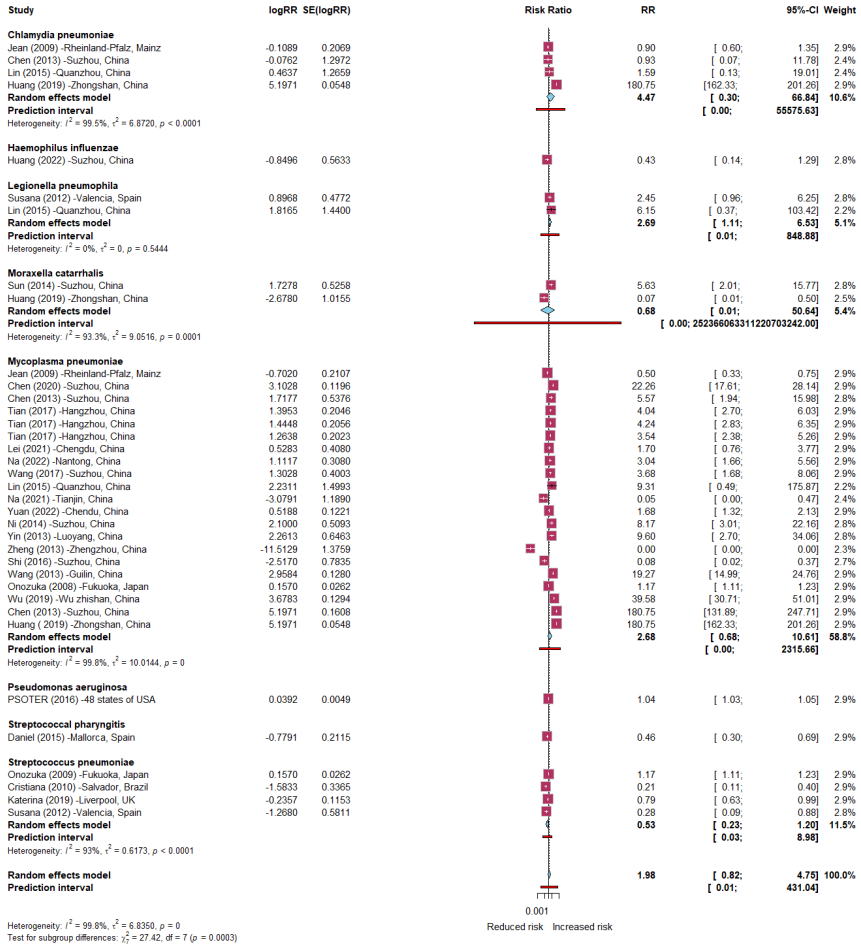


Figure S14. Random-effects meta-analysis of *Streptococcus pneumoniae* estimates (four studies)

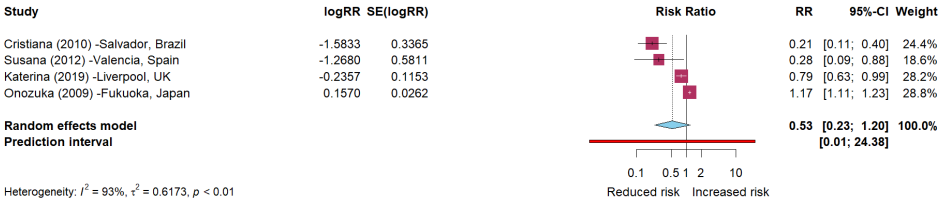


Figure S14-1. Subgroup analysis of *Streptococcus pneumoniae* meta-analysis by Köppen-Geiger climate

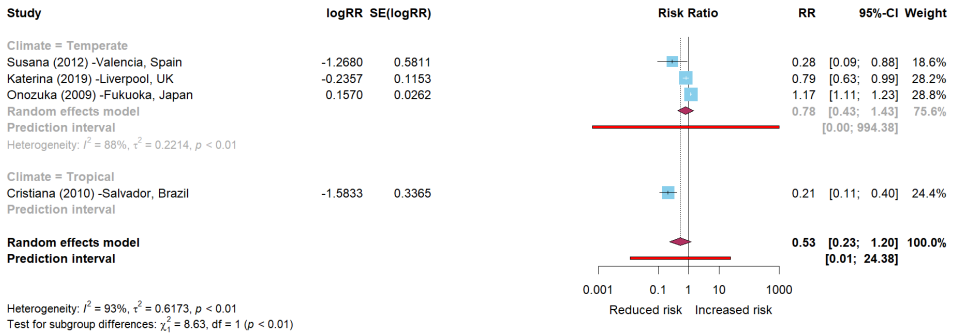


Figure S14-2. Subgroup analysis of *Streptococcus pneumoniae* meta-analysis by World Bank income category

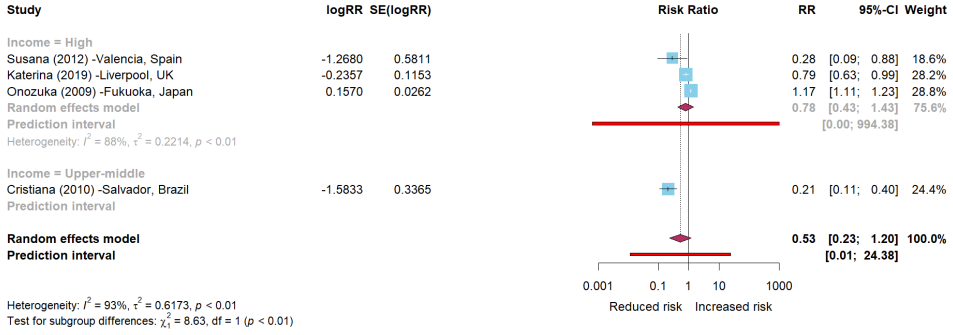


Figure S14-3. Subgroup analysis of *Streptococcus pneumoniae* meta-analysis by temporal resolution

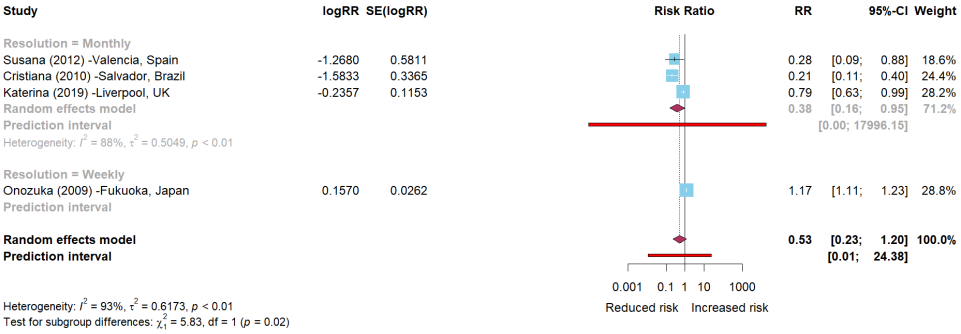


Figure S14-4. Subgroup analysis of *Streptococcus pneumoniae* meta-analysis by exposure measure

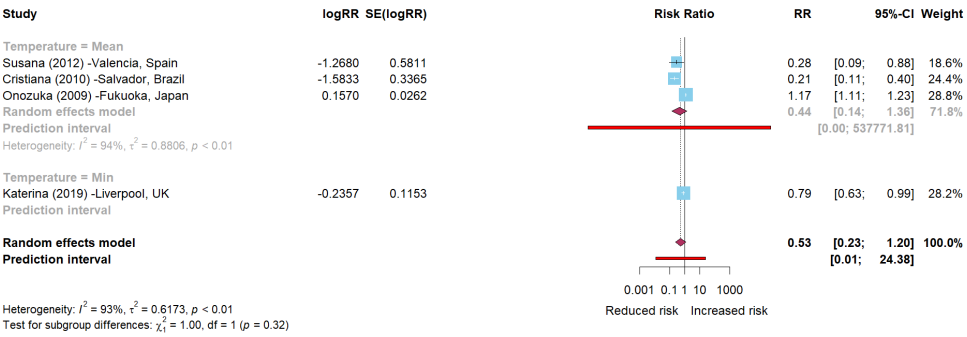


Figure S14-5. Subgroup analysis of *Streptococcus pneumoniae* meta-analysis by modelling approach

Figure S14-6. Leave-one-out analysis of *Streptococcus pneumoniae* meta-analysis

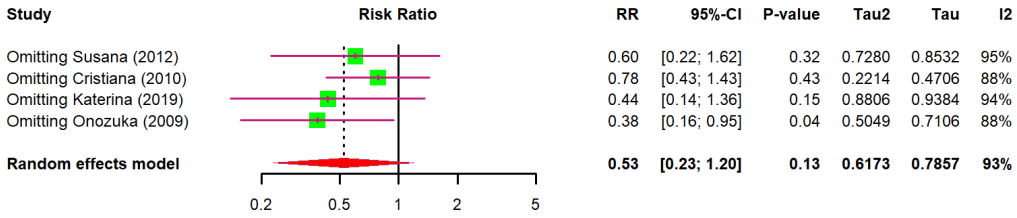


Figure S15. Random-effects meta-analysis of *Mycoplasma pneumoniae* estimates (19 studies)

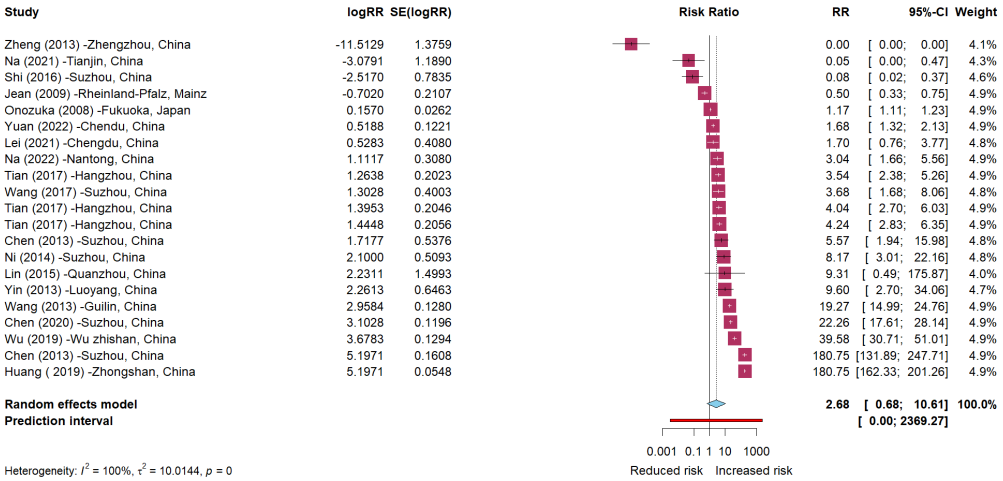


Figure S15-1. Subgroup analysis of *Mycoplasma pneumoniae* meta-analysis by Köppen-Geiger climate

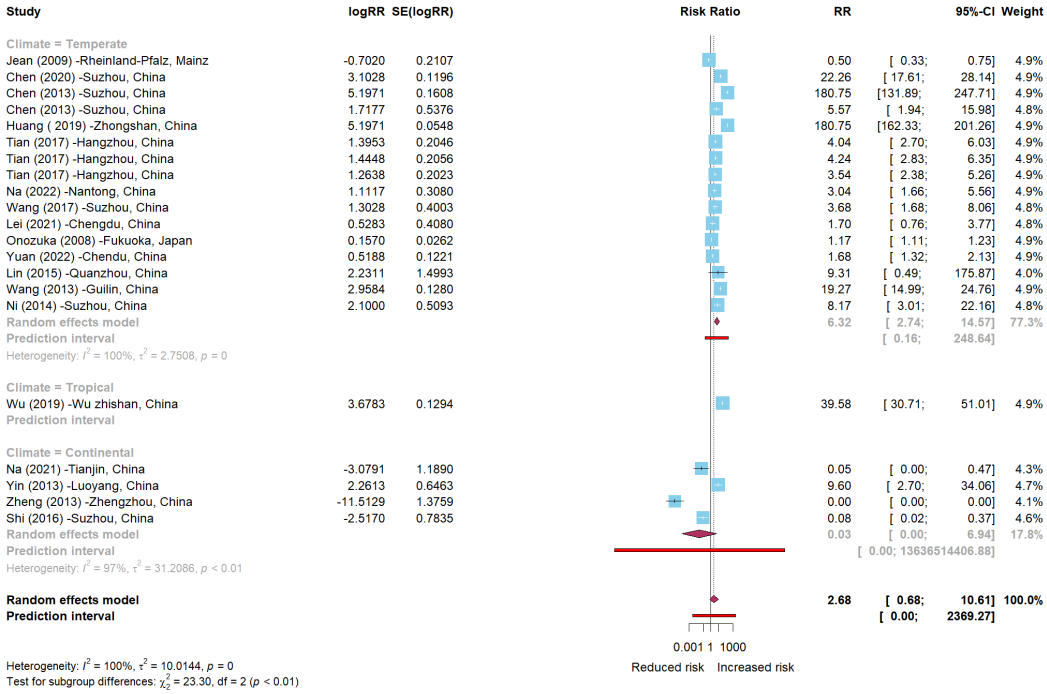


Figure S15-2. Subgroup analysis of *Mycoplasma pneumoniae* meta-analysis by World Bank income category

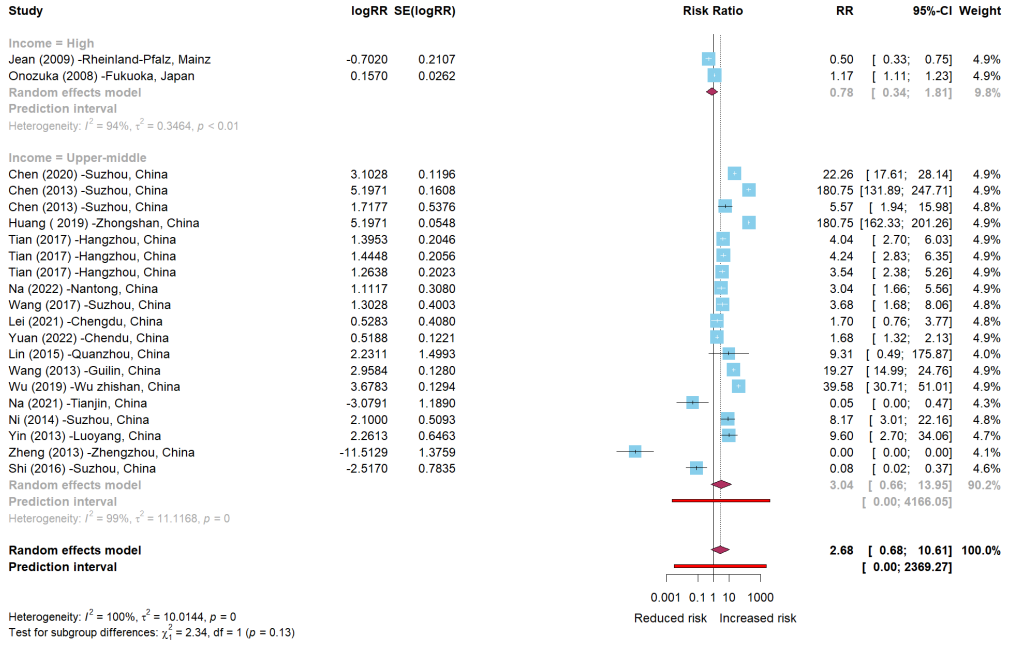


Figure S15-3. Subgroup analysis of *Mycoplasma pneumoniae* meta-analysis by temporal resolution

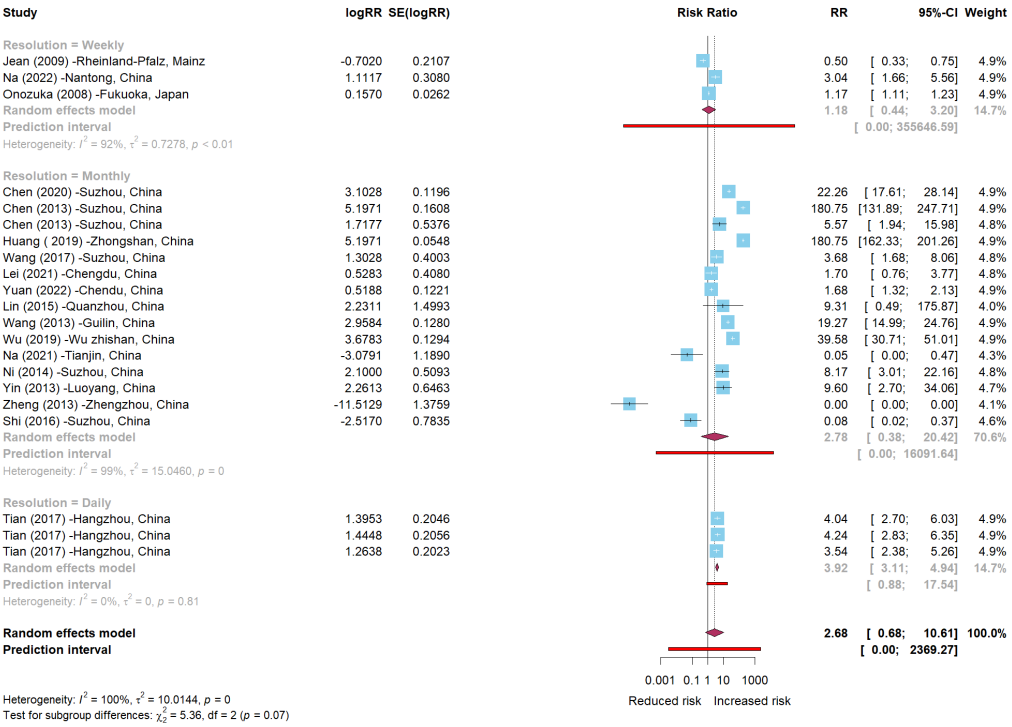


Figure S15-4. Subgroup analysis of *Mycoplasma pneumoniae* meta-analysis by exposure measure

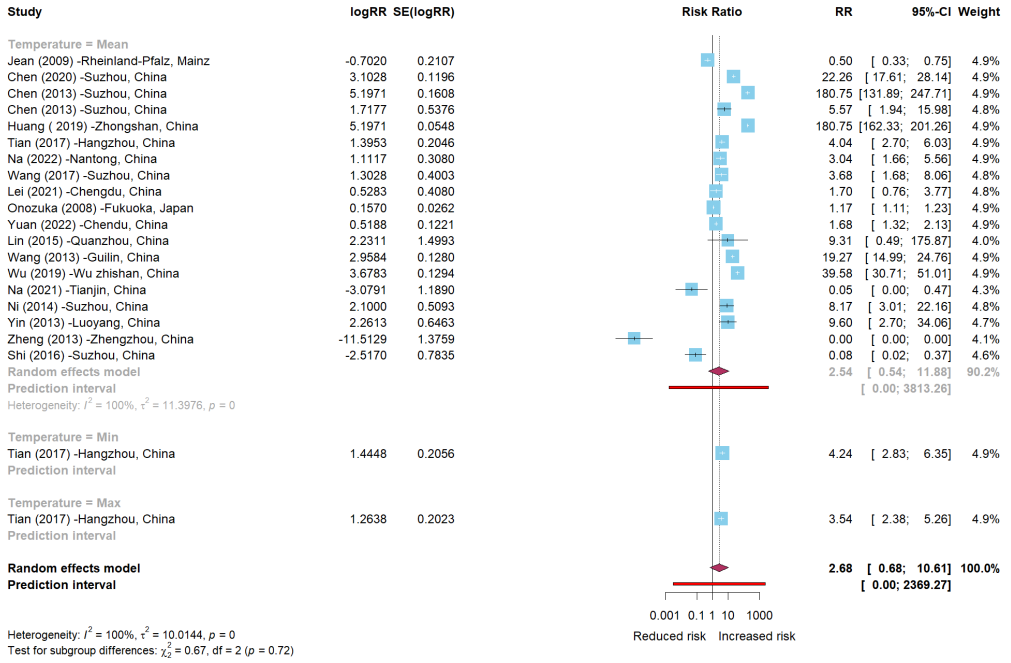


Figure S15-5. Subgroup analysis of *Mycoplasma pneumoniae* meta-analysis by modelling approach

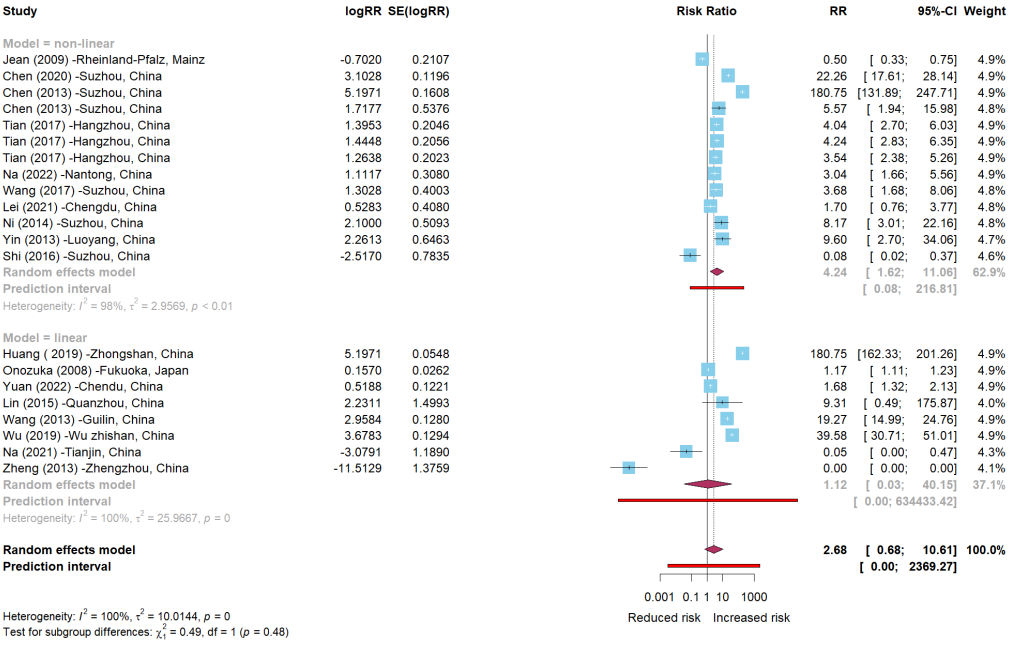


Figure S15-6. Leave-one-out analysis of *Mycoplasma pneumoniae* meta-analysis

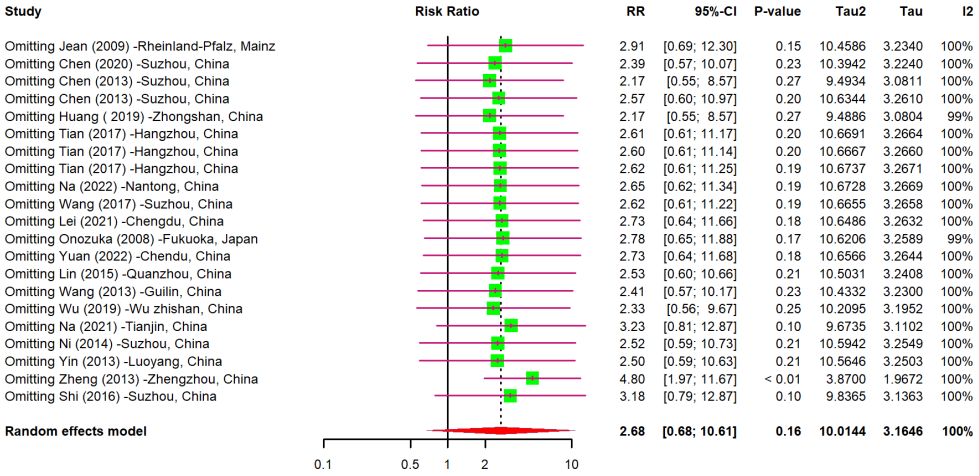
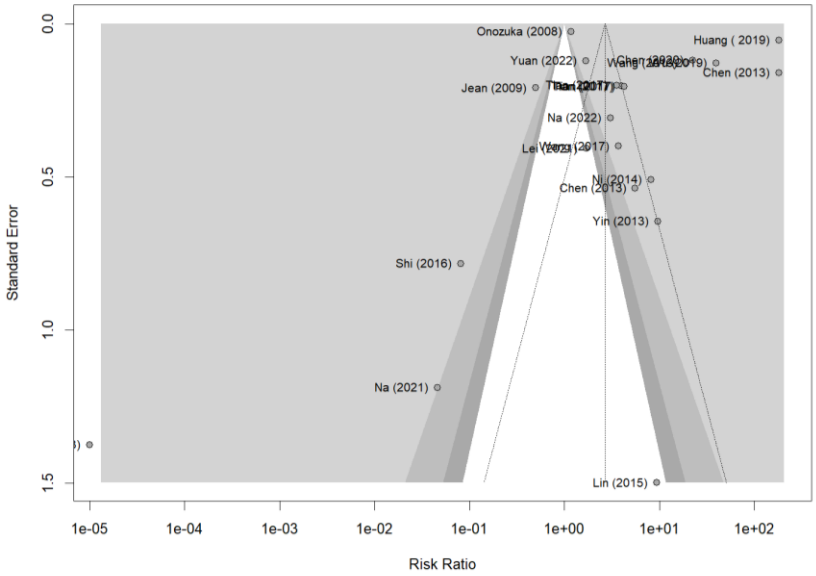


Figure S15-7. Funnel plot of *Mycoplasma pneumoniae* estimates



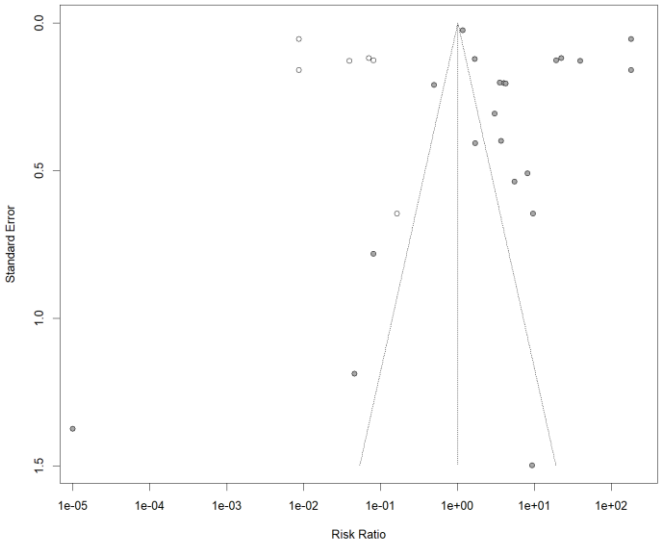
Linear regression test of funnel plot asymmetry

Test result: t = 0.86, df = 19, p-value = 0.4024

Sample estimates:

bias	se.bias	intercept	se.intercept
4.8989	5.7192	1.0285	0.5566

Figure S15-8. Trim and fill of *Mycoplasma pneumoniae* meta-analysis



Number of studies: k = 27 (with 6 added studies)

Random effects model: RR= 1.0086 [0.2755; 3.6929], Z=0.01, P=0.9896

Quantifying heterogeneity: tau^2 = 11.5561 [7.1899; 23.2580]; tau = 3.3994 [2.6814; 4.8227], I^2 = 99.9%; H = 29.17

Figure S16. Random-effects meta-analysis of *Chlamydia pneumoniae* estimates (four studies)

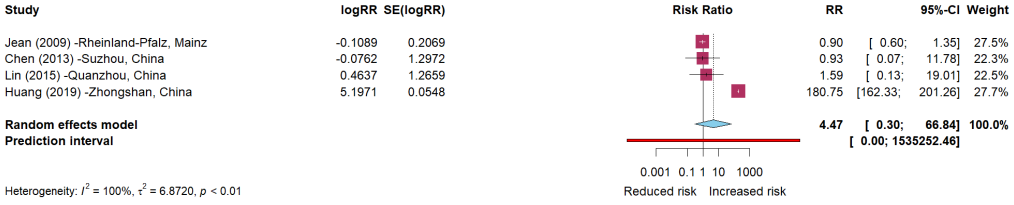


Figure S16-1. Subgroup analysis of *Chlamydia pneumoniae* meta-analysis by Köppen-Geiger climate

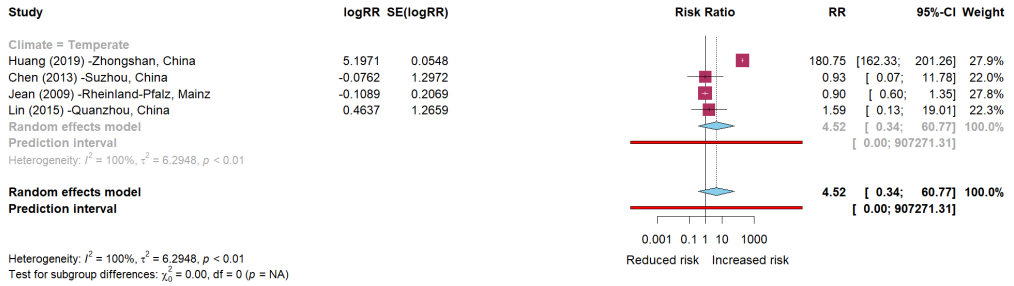


Figure S16-2. Subgroup analysis of *Chlamydia pneumonia* meta-analysis by World Bank income category

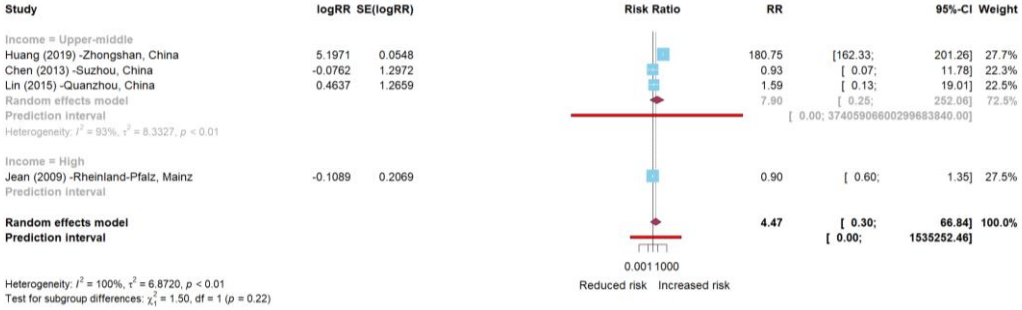


Figure S16-3. Subgroup analysis of *Chlamydia pneumoniae* meta-analysis by temporal resolution

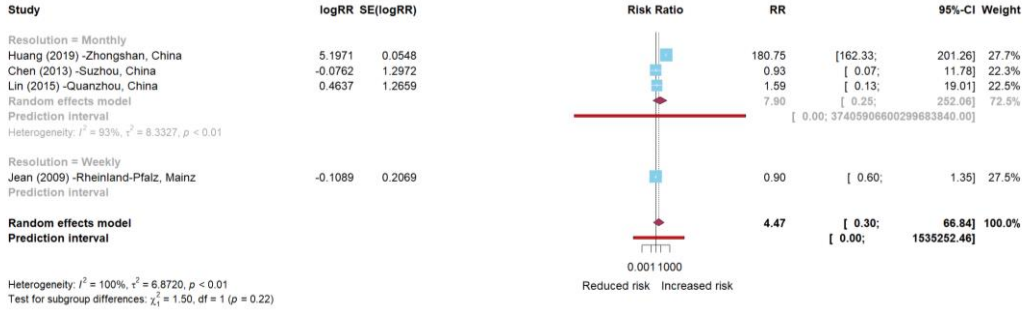


Figure S16-4. Subgroup analysis of *Chlamydia pneumoniae* meta-analysis by exposure measure

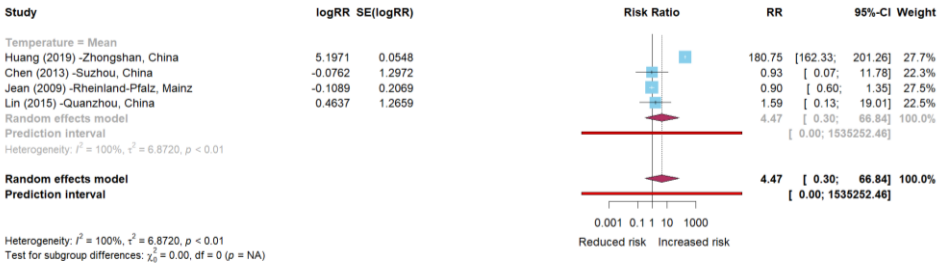


Figure S16-5. Subgroup analysis of *Chlamydia pneumoniae* meta-analysis by modelling approach

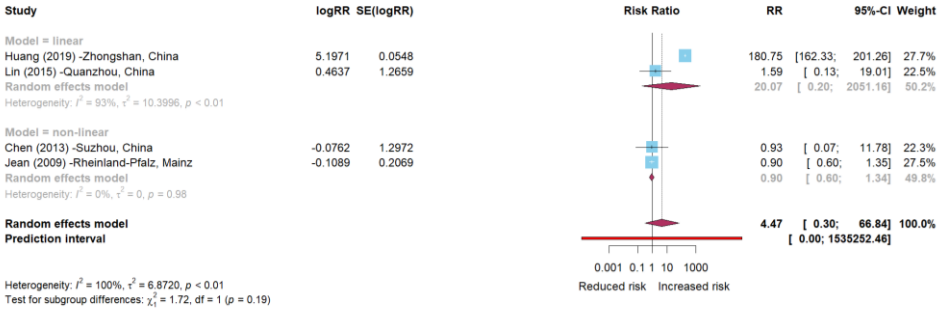


Figure S16-6. Leave-one-out analysis of *Chlamydia pneumoniae* meta-analysis

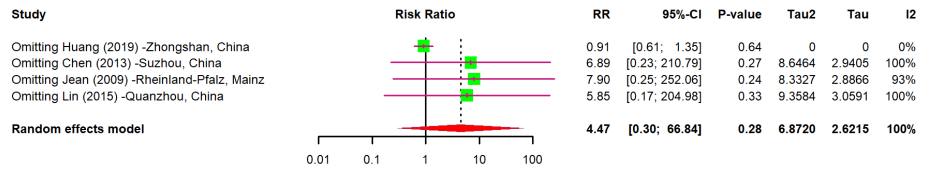


Figure S16-7. Sensitivity analysis by excluding study with high risk of bias for Huang et al 2019

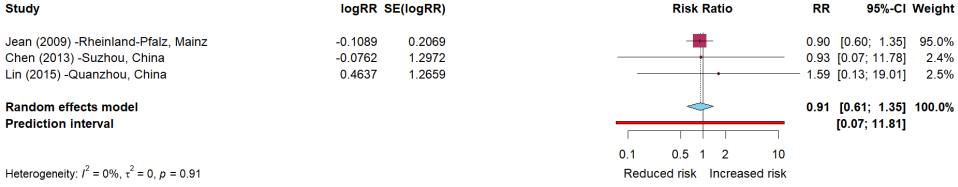


Table X1. Estimates of individual effects from 137 included studies

Study	Location	Cases	Pathogen	RR	lower	upper
Santiago (2004)	Leon, Spain	221	Respiratory syncytial virus -unsubtyped	0.4588	0.2859	0.7274
Santiago (2004)	Leon, Spain	221	Respiratory syncytial virus -unsubtyped	0.5767	0.362	0.9113
Santiago (2004)	Leon, Spain	221	Respiratory syncytial virus -unsubtyped	0.5149	0.3221	0.8159
Zhang (2013)	Suzhou, China	42664	Respiratory syncytial virus -unsubtyped	0.004	0.001	0.011
Liu (2019)	Guangzhou, China	11398	Respiratory syncytial virus -unsubtyped	14.16	5.66	39.99
Natalia (2016)	Athens, Greece	7516	Respiratory syncytial virus -unsubtyped	0.76	0.74	0.79
Natalia (2016)	Athens, Greece	7516	Respiratory syncytial virus -unsubtyped	0.72	0.68	0.8
Silvia (2013)	Bologna, Italy	327	Respiratory syncytial virus -unsubtyped	0.3196	0.1958	0.5348
Omer (2008)	Lombok, Indonesia	2878	Respiratory syncytial virus -unsubtyped	1.44	1.24	1.66
Omer (2008)	Lombok, Indonesia	2878	Respiratory syncytial virus -unsubtyped	1.39	1.22	1.5
Virginia (2015)	Nine states, United States	Not reported	Respiratory syncytial virus -unsubtyped	0.0078	0.0036	0.0159
Patrick (2015)	Kuala Lumpur, Malaysia	5691	Respiratory syncytial virus -unsubtyped	0.2253	0.127	0.3878
Patrick (2015)	Kuala Lumpur, Malaysia	2561	Respiratory syncytial virus -unsubtyped	0.2937	0.1682	0.5002
Patrick (2015)	Kuala Lumpur, Malaysia	2959	Respiratory syncytial virus -unsubtyped	0.2151	0.1209	0.3711
Hailin (2019)	Wenzhou, China	89898	Respiratory syncytial virus -unsubtyped	0.0327	0.0125	0.0764
Zheng (2014)	Jiangsu, China	42104	Respiratory syncytial virus -unsubtyped	0.0039	0.0011	0.0113
Ilada (2020)	Bangkok, Thailand	8209	Respiratory syncytial virus -unsubtyped	0.6215	0.2767	1.3652
Nicklas (2016)	Gothenburg, Sweden	20062	Respiratory syncytial virus -unsubtyped	0.0012	0.0003	0.0039
Jean-Baptist (2009)	Rheinland-Pfalz, Mainz	3044	Respiratory syncytial virus -unsubtyped	0.0144	0.0075	0.0261
Noyola (2009)	San Luis Potosi, Mexico	1393	Respiratory syncytial virus -unsubtyped	0.32	0.04	1.3
Noyola (2009)	San Luis Potosi, Mexico	1393	Respiratory syncytial virus -unsubtyped	2.55	1.34	5.63
Rodriguez (2015)	Bogota, Colombia	3931	Respiratory syncytial virus -unsubtyped	3.14	1.56	6.31
Zhi (2021)	Suzhou, China	1157	Respiratory syncytial virus -A	0.0726	0.0131	0.2951
Zhi (2021)	Suzhou, China	1157	Respiratory syncytial virus -B	0.0792	0.0146	0.318
Gamba (2016)	Bogota, Colombia	3931	Respiratory syncytial virus -unsubtyped	2.25	1.11	4.53
Cheng (2022)	Macao, China	4880	Respiratory syncytial virus -A	0.7982	0.6621	0.9618

Cheng (2022)	Macao, China	4880	Respiratory syncytial virus -B	1.2346	1.0247	1.4884
Chee (2023)	Kuala Lumpur, Malaysia	2950	Respiratory syncytial virus -unsubtyped	1.1605	1.022	3.0255
Chen (2014)	Suzhou, China	998	Respiratory syncytial virus -unsubtyped	0.0002	0.0001	0.0054
Liu (2021)	Chongqing, China	3107	Respiratory syncytial virus -unsubtyped	1.93	1.08	3.46
Liu (2021)	Chongqing, China	3107	Respiratory syncytial virus -unsubtyped	0.87	0.77	0.98
Liu (2021)	Chongqing, China	3107	Respiratory syncytial virus -unsubtyped	1.14	1.03	1.26
Liu (2021)	Chongqing, China	3107	Respiratory syncytial virus -unsubtyped	1.06	1.02	1.09
Liu (2021)	Chongqing, China	3107	Respiratory syncytial virus -unsubtyped	0.93	0.87	0.98
Liu (2021)	Chongqing, China	3107	Respiratory syncytial virus -unsubtyped	0.4395	0.3896	0.4955
Liu (2021)	Chongqing, China	3107	Respiratory syncytial virus -unsubtyped	0.4413	0.3911	0.4974
Liu (2021)	Chongqing, China	3107	Respiratory syncytial virus -unsubtyped	0.4395	0.3896	0.4955
Giselmo (2020)	Maranhao, Brazil	151	Respiratory syncytial virus -unsubtyped	0.5348	0.0353	6.145
Giselmo (2020)	Maranhao, Brazil	151	Respiratory syncytial virus -unsubtyped	0.0109	0.0001	0.2325
Rory (2019)	Edinburgh, UK	52060	Respiratory syncytial virus -unsubtyped	0.827	0.808	0.847
Tian (2017)	Hangzhou, China	36500	Respiratory syncytial virus -unsubtyped	0.0074	0.0038	0.0136
Tian (2017)	Hangzhou, China	36500	Respiratory syncytial virus -unsubtyped	0.0122	0.0066	0.0215
Tian (2017)	Hangzhou, China	36500	Respiratory syncytial virus -unsubtyped	0.0288	0.0168	0.0478
Cui (2015)	Chaoshan, China	1074	Respiratory syncytial virus -unsubtyped	0.51	0.5	0.6
Lu (2015)	Suzhou, China	1803	Respiratory syncytial virus -unsubtyped	0.0054	0.0009	0.0241
Cristiana (2010)	Salvador, Brazil	184	Respiratory syncytial virus -unsubtyped	0.2053	0.1042	0.3873
Maria (2009)	Kathmandu, Nepal	887	Respiratory syncytial virus -unsubtyped	0.81	0.2305	2.7781
Magali (2018)	Dijon, France	4300	Respiratory syncytial virus -unsubtyped	0.5987	0.5365	0.6679
Magali (2018)	Dijon, France	4300	Respiratory syncytial virus -unsubtyped	0.7205	0.646	0.8033
Therese (2021)	Nairobi, Kenya	17261	Respiratory syncytial virus -unsubtyped	1.68	1.03	2.76
Therese (2021)	Nairobi, Kenya	17261	Respiratory syncytial virus -unsubtyped	1.61	0.95	2.73
Li (2013)	Zhuhai, China	924	Respiratory syncytial virus -unsubtyped	0.0288	0.0004	0.4608
Daniel (2012)	Mallorca, Spain	2384	Respiratory syncytial virus -unsubtyped	0.0109	0.0039	0.0266
Daniel (2012)	Mallorca, Spain	2384	Respiratory syncytial virus -unsubtyped	0.0126	0.0046	0.0302

Daniel (2012)	Mallorca, Spain	2384	Respiratory syncytial virus -unsubtyped	0.0067	0.0023	0.0173
Daniel (2012)	Mallorca, Spain	2384	Respiratory syncytial virus -unsubtyped	0.0003	0.0002	0.0007
Daniel (2012)	Mallorca, Spain	2384	Respiratory syncytial virus -unsubtyped	0.0006	0.0003	0.0011
Daniel (2012)	Mallorca, Spain	2384	Respiratory syncytial virus -unsubtyped	0.0002	0.0001	0.0004
Asma (2008)	Doha, Qatar	3121	Respiratory syncytial virus -unsubtyped	0.0188	0.0045	0.0622
Raffaella (2017)	Rome, Italy	723	Respiratory syncytial virus -unsubtyped	0.1527	0.0733	0.3008
Sheikh (2020)	Bukit Timah, Singapore	9905	Respiratory syncytial virus -unsubtyped	1.12	1.16	1.24
Sheikh (2020)	Bukit Timah, Singapore	9905	Respiratory syncytial virus -unsubtyped	1.04	1.12	1.16
Sheikh (2020)	Bukit Timah, Singapore	9905	Respiratory syncytial virus -unsubtyped	1.24	1.19	1.44
Ines (2018)	Sousse, Northern Africa	5131	Respiratory syncytial virus -unsubtyped	0.0109	0.0041	0.0257
You (2022)	Gwangju, Korea	3922	Respiratory syncytial virus -unsubtyped	0.1691	0.0473	0.5186
Chee-Sieng (2012)	Kuala Lumpur, Malaysia	10269	Respiratory syncytial virus -unsubtyped	0.6546	0.4387	0.9721
Rosalie (2021)	Amsterdam, The Netherlands	2161	Respiratory syncytial virus -unsubtyped	0.1287	0.0111	0.2463
Rosalie (2021)	Amsterdam, The Netherlands	2161	Respiratory syncytial virus -unsubtyped	0.254	0.156	0.352
Rosalie (2021)	Amsterdam, The Netherlands	2161	Respiratory syncytial virus -unsubtyped	0.1427	0.0055	0.2799
Rosalie (2021)	Amsterdam, The Netherlands	2161	Respiratory syncytial virus -unsubtyped	0.3166	0.2186	0.4146
Rosalie (2021)	Amsterdam, The Netherlands	2161	Respiratory syncytial virus -unsubtyped	0.493	0.3754	0.6106
Rosalie (2021)	Amsterdam, The Netherlands	2161	Respiratory syncytial virus -unsubtyped	0.249	0.1706	0.3274
Wei (2016)	Shanghai, China	2819	Respiratory syncytial virus -unsubtyped	0.4678	0.1358	1.4916
Keita (2023)	47 prefectures, Japan	721709	Respiratory syncytial virus -unsubtyped	1.053	1.015	1.093
Keita (2023)	47 prefectures, Japan	721709	Respiratory syncytial virus -unsubtyped	0.936	0.91	0.964
Qing (2016)	Hangzhou, China	36500	Respiratory syncytial virus -unsubtyped	0.0074	0.0038	0.0136
Jang (2017)	Cheonan, Korea	6279	Respiratory syncytial virus -A	0.8159	0.6667	0.9978
Jang (2017)	Cheonan, Korea	6279	Respiratory syncytial virus -B	0.7781	0.6357	0.9517
Terezinha (2017)	Sao Paulo, Brazil	Not reported	Respiratory syncytial virus -unsubtyped	0.2694	0.1507	0.4684
Terezinha (2017)	Sao Paulo, Brazil	Not reported	Respiratory syncytial virus -unsubtyped	0.2053	0.1128	0.3612
You (2022)	13 European countries	30965	Respiratory syncytial virus -unsubtyped	0.06	0.05	0.07
Mariana (2004)	Buenos Aires, Argentina	18561	Respiratory syncytial virus -unsubtyped	0.0006	0.0001	0.0039

Ping-Ing (2023)	Taiwan, China	1740	Respiratory syncytial virus -unsubtyped	1.4241	0.8641	2.3629
Ping-Ing (2023)	Taipei City, China	1740	Respiratory syncytial virus -unsubtyped	2.0969	1.2669	3.5199
Ping-Ing (2023)	Tainan City, China	1740	Respiratory syncytial virus -unsubtyped	3.405	2.0309	5.8431
Chan (2021)	Hong Kong, China	9635	Respiratory syncytial virus -unsubtyped	15.5187	12.2083	19.8827
Onozuka (2014)	Fukuoka, Japan	30215	Respiratory syncytial virus -unsubtyped	0.51	0.39	0.68
Benjamin (2018)	Nha Trang, central Vietnam	2998	Respiratory syncytial virus -unsubtyped	1.14	0.98	1.33
Meng (2023)	Kent Hill, Singapore	15715	Respiratory syncytial virus -unsubtyped	1.168	1.068	1.277
Meng (2023)	Kent Hill, Singapore	15715	Respiratory syncytial virus -unsubtyped	0.92	0.863	0.981
TNS (2012)	Middle Anatolian, Turkey	3464	Respiratory syncytial virus -unsubtyped	0.0288	0.003	0.1632
TNS (2012)	Mediterranean, Aegean, Marmara, Turkey	3464	Respiratory syncytial virus -unsubtyped	0.005	0.0003	0.0423
TNS (2012)	Black Sea, Turkey	3464	Respiratory syncytial virus -unsubtyped	0.0499	0.0062	0.2546
TNS (2012)	Anatolian Eastern, Turkey	3464	Respiratory syncytial virus -unsubtyped	0.0895	0.0134	0.4156
Wang (2005)	Hangzhou, China	13642	Respiratory syncytial virus -unsubtyped	0.0045	0.0003	0.0316
Geng (2015)	Suzhou, China	42664	Respiratory syncytial virus -unsubtyped	0.0036	0.0011	0.0106
Jung (2018)	Seoul, Korea	9113	Respiratory syncytial virus -unsubtyped	0.0658	0.0247	0.1567
Lin (2015)	Quanzhou, China	6020	Respiratory syncytial virus -unsubtyped	0.19	0.01	2.26
Wu (2021)	Haikou, China	309	Respiratory syncytial virus -A	0.0696	0.0124	0.2849
Wu (2021)	Haikou, China	309	Respiratory syncytial virus -B	0.0751	0.0137	0.3038
Tang (2013)	Suzhou, China	1883	Respiratory syncytial virus -unsubtyped	0.001	0.0001	0.002
Wan (2013)	Suzhou, China	28871	Respiratory syncytial virus -unsubtyped	0.0081	0.002	0.026
Chen (2016)	Suzhou, China	3672	Respiratory syncytial virus -unsubtyped	0.0086	0.0004	0.0774
Zhang (2022)	Jiangyin, China	12294	Respiratory syncytial virus -unsubtyped	0.0112	0.0025	0.0391
Ji (2011)	Suzhou, China	6655	Respiratory syncytial virus -unsubtyped	0.0012	0.0001	0.0087
Chen (2016)	Suzhou, China	3672	Parainfluenza virus -1	1.7339	0.362	9.1988
Chen (2016)	Suzhou, China	3672	Parainfluenza virus -2	2.2662	0.4746	12.5981
Chen (2016)	Suzhou, China	3672	Parainfluenza virus -3	16.3229	14.0957	18.9573
Zhang (2022)	Jiangyin, China	12294	Parainfluenza virus -3	9.4827	8.7965	10.2296
Yan (2015)	Shanghai, China	2526	Parainfluenza viruses -unsubtyped	14.9778	12.5783	17.9086

Zhang (2020)	Suzhou, China	7525	Parainfluenza virus -3	27.8768	24.9627	31.1838
Liu (2019)	Guangzhou, China	11398	human metapneumovirus (HMPV)	0.9436	0.4276	2.079
Nicklas (2016)	Gothenburg, Sweden	20062	human metapneumovirus (HMPV)	0.4769	0.2572	0.8668
Jean (2009)	Rheinland-Pfalz, Mainz	3044	human metapneumovirus (HMPV)	0.0975	0.0594	0.1556
Cheng (2022)	Macao, China	4880	human metapneumovirus (HMPV)	0.7048	0.5842	0.8495
Chen (2014)	Suzhou, China	998	human metapneumovirus (HMPV)	0.1374	0.0185	0.7074
Rory (2019)	Edinburgh, UK	52060	human metapneumovirus (HMPV)	0.901	0.883	0.92
Maria (2009)	Kathmandu, Nepal	887	human metapneumovirus (HMPV)	0.5767	0.1591	1.9639
Magali (2018)	Dijon, France	4300	human metapneumovirus (HMPV)	0.6693	0.6	0.7464
Yong (2019)	Seoul, Korea	23694	human metapneumovirus (HMPV)	0.7913	0.5779	1.0816
Yong (2019)	Seoul, Korea	23694	human metapneumovirus (HMPV)	0.9123	0.667	1.247
Yong (2019)	Seoul, Korea	23694	human metapneumovirus (HMPV)	1.2871	0.9415	1.7627
Li (2013)	Zhuhai, China	924	human metapneumovirus (HMPV)	0.2556	0.0125	2.8583
Wang (2013)	Suzhou, China	6655	human metapneumovirus (HMPV)	0.1996	0.0574	0.6038
You (2022)	Gwangju, Korea	4195	human metapneumovirus (HMPV)	0.3486	0.1087	1.0205
Wang (2011)	Suzhou, China	6599	human metapneumovirus (HMPV)	0.1777	0.0501	0.5427
Ji (2011)	Suzhou, China	6655	human metapneumovirus (HMPV)	0.1777	0.0501	0.5427
You (2022)	Gwangju, Korea	4195	Human coronavirus (HCoV) -unsubtyped	0.03	0.01	0.13
Jean (2009)	Rheinland-Pfalz, Mainz	3044	Human coronavirus (HCoV) -unsubtyped	0.06	0.04	0.1
Jang (2020)	Cheonan, Korea	9010	Human coronavirus (HCoV)- 229E	0.4	0.28	0.59
Jang (2021)	Cheonan, Korea	9010	Human coronavirus (HCoV)- OC43	0.54	0.42	0.7
Nicklas (2016)	Gothenburg, Sweden	20062	Human coronavirus (HCoV) -unsubtyped	0.04	0.02	0.09
Cui (2015)	Chaoshan, China	1074	Human coronavirus (HCoV) -unsubtyped	1.1	1	1.2
Wei (2016)	Shanghai, China	2819	Human coronavirus (HCoV) -unsubtyped	0.68	0.2	2.17
Jean (2009)	Rheinland-Pfalz, Mainz	3044	Human rhinovirus	0.1866	0.1181	0.2886
Giselmo (2020)	Maranhao, Brazil	151	Human rhinovirus	5.3594	0.4718	127.9191
Giselmo (2020)	Maranhao, Brazil	151	Human rhinovirus	2.2662	0.2005	36.7868
Cui (2015)	Chaoshan, China	1074	Human rhinovirus	1	0.9	1.1

Tiina (2016)	Kajaani, Finland	386	Human rhinovirus	0.96	0.92	1
Tiina (2016)	Kajaani, Finland	386	Human rhinovirus	1.04	0.98	1.1
Yan (2017)	Suzhou, China	6194	Human rhinovirus	10.5699	2.6955	54.6864
Jaqueline (2016)	Curitiba, Brazil	755	Human rhinovirus	0.0503	0.0048	0.3027
You (2022)	Gwangju, Korea	4195	Human rhinovirus	0.7048	0.2358	2.0445
Dong (2021)	Cheonan, Korea	1920	Human rhinovirus	1.575	1.443	1.72
Benjamin (2018)	Nha Trang, Vietnam	2998	Human rhinovirus	0.86	0.79	0.94
Zhou 2018	Suzhou, China	5994	Human rhinovirus	4.1649	3.7751	4.5991
Zhou 2017	Huangshi, China	2326	Human rhinovirus	26.184	21.5272	32.0206
Huang 2015	Suzhou, China	1926	Human rhinovirus	32.3742	25.9496	40.6707
Zheng (2014)	Jiangsu, China	42104	human adenoviruses (HAdVs)	7.9418	3.9794	16.8532
Nicklas (2016)	Gothenburg, Sweden	20062	human adenoviruses (HAdVs)	0.5554	0.3016	0.993
Jean (2009)	Rheinland-Pfalz, Mainz	3044	human adenoviruses (HAdVs)	0.1866	0.1181	0.2886
Cheng (2022)	Macao, China	4880	human adenoviruses (HAdVs)	1.1355	0.9425	1.3684
Chen (2014)	Suzhou, China	998	human adenoviruses (HAdVs)	1.1563	0.2365	5.8082
Rory (2019)	Edinburgh, UK	52060	human adenoviruses (HAdVs)	0.972	0.955	0.988
Therese (2021)	Nairobi, Kenya	17261	human adenoviruses (HAdVs)	1.06	0.76	1.47
Therese (2021)	Nairobi, Kenya	17261	human adenoviruses (HAdVs)	0.99	0.7	1.41
Li (2013)	Zhuhai, China	924	human adenoviruses (HAdVs)	34.668	25.1629	48.4754
You (2022)	Gwangju, Korea	4195	human adenoviruses (HAdVs)	0.6215	0.2059	1.8007
Mariana (2004)	Buenos Aires, Argentina	18561	human adenoviruses (HAdVs)	0.1958	0.0652	0.5264
Eun (2021)	Cheonan, Korea	9010	human adenoviruses (HAdVs)	0.772	0.679	0.878
Ji (2011)	Suzhou, China	6655	human adenoviruses (HAdVs)	3.8783	1.3047	12.9526
Lin (2015)	Quanzhou, China	6020	human adenoviruses (HAdVs)	1.48	0.12	20.97
Chen (2012)	Suzhou, China	8197	human adenoviruses (HAdVs)	4.6479	1.7406	13.7737
Chen (2016)	Suzhou, China	3672	human adenoviruses (HAdVs)	3.5087	3.1008	3.9754
Zhang (2022)	Jiangyin, China	12294	human adenoviruses (HAdVs)	2.721	1.142	6.8566
You (2022)	Gwangju, Korea	4195	Enterovirus (EV)	4.3778	1.4613	14.8906

Cui (2015)	Chaoshan, China	1074	Enterovirus (EV)	2.4	2.1	2.7
Jean (2009)	Rheinland-Pfalz, Mainz	3044	Enterovirus (EV)	0.7753	0.5156	1.162
Wei (2016)	Shanghai, China	2819	Enterovirus (EV)	1.6702	0.5244	5.6051
Shiv (2020)	Fifty U.S. states and Washington D.C.	974	SARS-CoV-2	0.85	0.76	0.96
Shiv (2020)	Fifty U.S. states and Washington D.C.	974	SARS-CoV-2	0.98	0.97	0.99
Aleix (2021)	52 Spanish provinces	2418250	SARS-CoV-2	0.08	0.07	0.09
Aleix (2021)	52 Spanish provinces	2418250	SARS-CoV-2	0.07	0.06	0.08
Aleix (2021)	52 Spanish provinces	2418250	SARS-CoV-2	0.1	0.09	0.11
Keita (2022)	Six Japanese prefectures	2982262	SARS-CoV-2	1	0.98	1.02
Keita (2022)	Six Japanese prefectures	2982262	SARS-CoV-2	0.99	0.99	1
Keita (2022)	Six Japanese prefectures	2982262	SARS-CoV-2	0.99	0.98	1
Keita (2022)	Six Japanese prefectures	2982262	SARS-CoV-2	0.98	0.97	0.99
Keita (2022)	Six Japanese prefectures	2982262	SARS-CoV-2	1.11	1.05	1.17
Keita (2022)	Six Japanese prefectures	2982262	SARS-CoV-2	0.99	0.98	0.99
Keita (2022)	Six Japanese prefectures	2982262	SARS-CoV-2	0.97	0.95	1
Keita (2022)	Six Japanese prefectures	2982262	SARS-CoV-2	0.97	0.92	1.02
Chen (2021)	Guangdong, China	1347	SARS-CoV-2	0.94	0.93	0.96
Sung (2022)	Changwon, Korea	3234	SARS-CoV-2	0.99	0.98	0.99
Lisa (2022)	Helsinki, Finland	48013	SARS-CoV-2	3.95	2.88	5.42
Kong(2020)	Wuhan, China	Not reported	SARS-CoV-2	10.25	1.76	96.61
Simone (2020)	Milan, Italy	Not reported	SARS-CoV-2	0.26	0.12	0.54
Simone (2020)	Milan, Italy	Not reported	SARS-CoV-2	0.25	0.11	0.52
Simone (2020)	Milan, Italy	Not reported	SARS-CoV-2	0.24	0.11	0.5
Simone (2020)	Florence, Italy	Not reported	SARS-CoV-2	0.35	0.16	0.72
Simone (2020)	Florence, Italy	Not reported	SARS-CoV-2	0.27	0.12	0.56
Simone (2020)	Florence, Italy	Not reported	SARS-CoV-2	0.25	0.11	0.52
Simone (2020)	Trento, Italy	Not reported	SARS-CoV-2	0.22	0.1	0.45
Simone (2020)	Trento, Italy	Not reported	SARS-CoV-2	0.25	0.11	0.52

Simone (2020)	Trento, Italy	Not reported	SARS-CoV-2	0.26	0.12	0.54
Asmaa (2020)	Riyadh, Saudi Arabia	Not reported	MERS-CoV	1.054	1.043	1.065
Cheng (2022)	Macao, China	4880	Human rhinoviruses/enteroviruses (HRVs/EVs)	1.2035	0.9989	1.4508
Raymundo (2023)	Oahu, USA	7143	Human rhinoviruses/enteroviruses (HRVs/EVs)	1.16	0.97	1.39
Bi (2006)	Hong Kong, China	2142	SARS-CoV	0.01	0.0006	0.07
Bi (2006)	Beijing, China	2142	SARS-CoV	0.2	0.04	0.83
Bi (2006)	Hong Kong, China	2142	SARS-CoV	0.01	0.0012	0.09
Feng (2005)	Guangzhou, China	138	SARS-CoV	0.79	0.43	1.46
Feng (2005)	Hong Kong, China	108	SARS-CoV	1.53	0.76	3.11
Feng (2005)	Toronto, Canada	116	SARS-CoV	0.73	0.37	1.42
Feng (2005)	Singapore	72	SARS-CoV	1.03	0.43	2.44
Feng (2005)	Taiwan, China	106	SARS-CoV	0.78	0.38	1.56
Feng (2005)	Beijing, China	41	SARS-CoV	1.02	0.32	3.31
Liu (2021)	Moscow	Not reported	SARS-CoV	4.65	2.2	10.41
Liu (2021)	Moscow	Not reported	SARS-CoV	3.71	1.78	8.15
Liu (2021)	Moscow	Not reported	SARS-CoV	4.65	2.2	10.41
Huang (2004)	Huangping, China	1491	SARS-CoV	0.56	0.29	1.05
Huang (2004)	Huangping, China	1491	SARS-CoV	0.52	0.27	0.99
Huang (2004)	Huangping, China	1491	SARS-CoV	0.59	0.31	1.12
Susana (2012)	Valencia, Spain	243	Streptococcus pneumoniae	0.2814	0.0853	0.8321
Cristiana (2010)	Salvador, Brazil	184	Streptococcus pneumoniae	0.2053	0.1048	0.3919
Katerina (2019)	Liverpool, UK	374	Streptococcus pneumoniae	0.79	0.63	0.99
Onozuka (2009)	Fukuoka, Japan	13056	Streptococcus pneumoniae	1.17	1.11	1.23
Daniel (2015)	Mallorca, Spain	60659	Streptococcal pharyngitis	0.4588	0.3016	0.6911
Huang (2019)	Zhongshan, China	13705	Moraxella catarrhalis	0.0687	0.0073	0.3909
Sun (2014)	Suzhou, China	8143	Moraxella catarrhalis	5.628	2.0781	16.3229
PSOTER (2016)	48 states of USA	3463	Pseudomonas aeruginosa	1.04	1.03	1.05
Susana (2012)	Valencia, Spain	243	Legionella pneumophila	2.4518	1.1877	7.7123

Lin (2015)	Quanzhou, China	6020	Legionella pneumophila	6.15	0.53	149.9
Huang (2022)	Suzhou, China	7940	Haemophilus influenzae	0.4276	0.1367	1.2438
Jean (2009)	Rheinland-Pfalz, Mainz	3044	Mycoplasma pneumoniae	0.4956	0.3265	0.7456
Chen (2020)	Suzhou, China	998	Mycoplasma pneumoniae	22.2606	17.6757	28.2451
Chen (2013)	Suzhou, China	1598	Mycoplasma pneumoniae	180.7475	146.4838	275.1224
Chen (2013)	Suzhou, China	8157	Mycoplasma pneumoniae	5.5715	2.0588	16.9388
Huang (2019)	Zhongshan, China	13705	Mycoplasma pneumoniae	180.7475	179.2791	222.2747
Tian (2017)	Hangzhou, China	3769	Mycoplasma pneumoniae	4.0363	2.7227	6.0729
Tian (2017)	Hangzhou, China	3769	Mycoplasma pneumoniae	4.2408	2.8561	6.3941
Tian (2017)	Hangzhou, China	3769	Mycoplasma pneumoniae	3.539	2.3968	5.2961
Na (2022)	Nantong, China	51665	Mycoplasma pneumoniae	3.0394	1.6853	5.6372
Wang (2017)	Suzhou, China	15098	Mycoplasma pneumoniae	3.6796	1.7246	8.2816
Lei (2021)	Chengdu, China	22882	Mycoplasma pneumoniae	1.696	0.7718	3.8203
Onozuka (2008)	Fukuoka, Japan	13056	Mycoplasma pneumoniae	1.17	1.11	1.23
Yuan (2022)	Chendu, China	5127	Mycoplasma pneumoniae	1.68	1.32	2.13
Lin (2015)	Quanzhou, China	6020	Mycoplasma pneumoniae	9.31	0.77	274.79
Wang (2013)	Guilin, China	1342	Mycoplasma pneumoniae	19.2665	15.0558	24.8649
Wu (2019)	Wu zhishan, China	1597	Mycoplasma pneumoniae	39.5804	30.8471	51.2382
Na (2021)	Tianjin, China	63821	Mycoplasma pneumoniae	0.046	0.0098	1.0362
Ni (2014)	Suzhou, China	10596	Mycoplasma pneumoniae	8.1661	3.1915	23.4988
Yin (2013)	Luoyang, China	8368	Mycoplasma pneumoniae	9.5957	2.9793	37.5377
Zheng (2013)	Zhengzhou, China	256	Mycoplasma pneumoniae	0.00001	0.00001	0.0022
Shi (2016)	Suzhou, China	2323	Mycoplasma pneumoniae	0.0807	0.015	0.3235
Huang (2019)	Zhongshan, China	13705	Chlamydia pneumoniae	180.7475	179.2791	222.2747
Chen (2013)	Suzhou, China	1598	Chlamydia pneumoniae	0.9266	0.0717	11.5859
Jean (2009)	Rheinland-Pfalz, Mainz	3044	Chlamydia pneumoniae	0.8968	0.5975	1.3444
Lin (2015)	Quanzhou, China	6020	Chlamydia pneumoniae	1.59	0.16	22.87

The code is as follows:

```
setwd(dir="C:/Users/86183/Desktop/data.csv")
getwd()
bin.metagen <- read.csv("C:/Users/86183/Desktop/data.csv")
head(bin.metagen,150)
View(bin.metagen)
library("meta")
library(base)
bin.metagen$RR <- log(bin.metagen$RR)
bin.metagen$lower <- log(bin.metagen$lower)
bin.metagen$upper <- log(bin.metagen$upper)
bin.metagen$seTE <- (bin.metagen$upper - bin.metagen$lower)/3.92
fit<-metagen(TE=RR,
             seTE=seTE,
             studlab = paste(Study), method.tau="REML",
             sm = "RR", data = bin.metagen,byvar = Suboutcome,print.byvar = FALSE,
             comb.random = TRUE,
             comb.fixed = FALSE, prediction= TRUE, prediction.subgroup = TRUE,
             label.left ="Reduced risk",
             label.right ="Increased risk")
forest(fit,col.diamond ="skyblue",col.square="maroon",col.diamond.lines ="black", sortvar = TE,
       base_family = "Times New Roman", family="sans",fontsize=11,
       col.predict = "#FF0000",colgap.studlab = "4cm", colgap.forest.left = "5.0cm",
       leftlabs = c("Study"))
forest(fit,col.diamond = "maroon",col.square="skyblue",col.diamond.lines = "black",sortvar = TE,
       family="mono",fontsize=11,colgap.studlab = "4cm", colgap.forest.left = "5.0cm",
```

```
      base_family = "Times New Roman",col.predict = "#FF0000",
      leftlabs = c("Study"))

Subgroup analysis
fit<-metagen(TE=RR,
            seTE=seTE,
            studlab = paste(Study),
            method.tau="REML",
            sm = "RR",
            data = bin.metagen,byvar = Climate/Income/Resolution/Measurement/Model/Lag,
            comb.random = TRUE,
            comb.fixed = FALSE, prediction.subgroup = TRUE, prediction= TRUE,
            label.left ="Reduced risk",
            label.right ="Increased risk")
forest(fit,col.diamond ="skyblue",col.square="maroon",col.diamond.lines ="black",
      base_family = "Times New Roman",colgap.studlab = "4cm", colgap.forest.left = "5.0cm",
      family="sans",fontsize=11, col.predict = "#FF0000",
      leftlabs = c("Study"))
forest(fit,col.diamond ="maroon",col.square="skyblue",col.diamond.lines ="black",
      base_family = "Times New Roman",
      family="sans",fontsize=11, col.predict = "#FF0000",colgap.studlab = "4cm",colgap.forest.left = "5.0cm",
      leftlabs = c("Study"))

Sensitivity analysis
fit<-metagen(TE=RR,
```

```
        seTE=seTE,
        studlab = paste(Study),
        method.tau="REML",
        sm = "RR",
        data = bin.metagen,
        comb.random = TRUE,
        comb.fixed = FALSE,
        label.left ="Reduced risk",
        label.right ="Increased risk")
forest(metainf(fit,pooled="random"),
    comb.random=TRUE,family="sans",base_family = "Arial",refline_col = "#004CFFFF",
    fontsize=11,lwd=2,col.diamond.fixed="#4D9221",col.diamond.lines.fixed="#4D9221",
    col.diamond.random="#FF0000",col.diamond.lines.random="maroon",
    col.square="#00FF00",col.study="#C51B7D",lty.fixed=4,
    plotwidth="8cm",colgap.forest.left="1cm",
    colgap.forest.right="1cm",just.forest="right",colgap.left="0.5cm",
    colgap.right="0.5cm")

funnel(fit,
    contour.levels = c (0.9,0.95,0.99),studlab = TRUE,
    col.contour = c('darkgray', 'gray', 'lightgray'))
legend(1,0.02, c("0.1 > p > 0.05", "0.05 > p >0.01", "< 0.01"), fill=c("white", "gray", "darkgray"))
par(mfrow=c(2,2))
dev.off()
```

```
tf.publ<-trimfill(fit)
summary(tf.publ)
funnel (tf.publ)
dev.off()

metabias(fit,method="linreg")
```