

Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a Confirmed

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated
- Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

Policy information about [availability of computer code](#)

Data collection

No primary data collection was carried out for this analysis.

Data analysis

WorldClim v1.03 (<http://www.worldclim.org>) is derived from historic rainfall and temperature data (spanning the period 1961-2005, inclusive) collected from worldwide weather stations. Data from these weather stations were then interpolated to 30 arc seconds using a thin plate smoothing algorithm in the ANUSPLIN-SPLINA software. We calculated the average regression coefficients for each of the 17 Global Climate Models and downscaled to 2.5 minute pixels using a bi-cubic convolution algorithm from the MarkSim50 system as implemented in <http://gisweb.ciat.cgiar.org/MarkSimGCM/docs/doc.html>. Data were then projected to three time point in the future 2020, 2050 and 2080. The models were all fit using R version 3.5.1.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Data used were previously archived as described in Kraemer, M. U. G. et al. The global compendium of *Aedes aegypti* and *Ae . albopictus* occurrence. *Sci. Data* 2, 150035 (2015). Other data were accessed from other published sources as described in the methods sections 1.1-1.4 on data availability. We accessed human mobility data from the freely available dataset at <http://www.census.gov/hhes/commuting/>.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

- Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	The dengue occurrence database was first created as described in Messina et al (citation 2), with published literature, case report, and informal online searches last updated on 27th July, 2015. Usable location information was ultimately extracted from 2,229 published references and 1,648 informal online sources. This resulted in 35,467 entries which then underwent temporal standardization as described in detail in Messina et al. The final occurrence database contained 13,604 unique occurrences.
Data exclusions	After data cleaning described in Messina et al. no data were excluded.
Replication	This is an observational study using many years of survey data and could be replicated.
Randomization	As an observational mapping project, there were no experimental groups.
Blinding	Blinding was not relevant to this study, as it was an observational study using survey data.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Unique biological materials
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants

Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging