Supplemental Online Content

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This supplemental material has been provided by the authors to give readers additional information about their work.

eAppendix

In this technical appendix, we provide further description of the model structure, assumptions, data, and analysis in this study.

Model overview

This discrete-time stochastic SEIR model was applied to all four infectious diseases and incorporates age structure, heterogeneous mixing between age groups, and vaccination effects. In the case of rubella and measles, MMR vaccination is assumed to generate all-or-nothing protection against infection, where vaccine-derived immunity is modeled in the R compartment. The model accounts for vaccine-mediated reduction in transmission (only relevant for poliovirus and diphtheria model), which are not assumed to generate protection against infection. The model calculates transitions between compartments for each age group at each time step.

Model Notation

Let there be 18 age groups, indexed by $a \in \{1,2,\ldots,18\}$. Each US state is modeled independently. For each age group a at time t:

- $S_a(t), E_a(t), I_a(t), R_a(t)$: Counts in SEIR compartments
- $N_a(t) = S_a(t) + E_a(t) + I_a(t) + R_a(t)$: Total population in group a
- $v_a(t)$: Vaccination coverage in group a at time t (relevant to polio and diphtheria only)
- ϵ: Vaccine-derived reduction to transmission (relevant to polio and diphtheria only)
- β: Transmission coefficient
- C_{ab}: Age-specific social contact matrix (contacts from group a to b)
- σ: Rate of progression from exposed to infectious (1 / latent period)
- γ: Recovery rate (1 / duration of infectiousness)

Force of Infection Term

The force of infection $\lambda_a(t)$ for age group a is given by:

$$\lambda_a(t) = \beta \cdot \sum_{b=1}^{18} C_{ab} \cdot \left(\frac{I_b(t)}{N_b(t)}\right) \cdot \left(1 - \epsilon \cdot v_b(t)\right)$$

Note: The term $\left(1 - \epsilon \cdot v_b(t)\right)$ is only relevant for polio and diphtheria. For rubella and measles, vaccination provides protection against infection and individuals are placed directly into the recovered compartment.

Stochastic Transition Events

To reflect stochastic dynamics, transitions between compartments are modeled as binomial processes:

$$\Delta_{S\to E,a}(t) \sim \text{Binomial}\left(S_a(t), \lambda_a(t)\right)$$

$$\Delta_{E\to I,a}(t) \sim \text{Binomial}(E_a(t), \sigma)$$

$$\Delta_{I\to R,a}(t) \sim \text{Binomial}(I_a(t), \gamma)$$

Model Equations with Stochastic Transitions

For each age group a and time step t, the SEIR compartments are updated as follows:

$$S_a(t+1) = S_a(t) - \Delta_{S\to E,a}(t)$$

$$E_a(t+1) = E_a(t) + \Delta_{S\to E,a}(t) - \Delta_{E\to I,a}(t)$$

$$I_a(t+1) = I_a(t) + \Delta_{E\to I,a}(t) - \Delta_{I\to R,a}(t)$$

$$R_a(t+1) = R_a(t) + \Delta_{I\to R,a}(t)$$

For the youngest age group (a=1), we add births. For all age groups, we include an aging process and deaths. These demographic processes are not shown in the equations for ease of visualization.

Review of modern epidemiologic case data for each infectious disease

For recent historical estimates on the number of cases for each infectious disease, we obtained reported case data from the US Centers for Disease Control and Prevention (CDC) disease surveillance program (National Notifiable Diseases Surveillance System) over the recent historical period and relevant literature. The following is a description of contemporary estimates on number of cases for each infectious disease and considerations in interpretation of this data:

Measles: We used data from a recent *MMWR* publication on measles cases reported in the US from 2020-2024 and additionally from the National Notifiable Diseases Surveillance System over the past 10 years.[1,2] Measles was the most commonly imported infectious disease included in our study, with 34 annual imported cases in the US in 2023.[1] We included both international importations and imported virus or imported-virus-linked cases in this number. Unlike the other infectious diseases included in the study, a high proportion of confirmed measles cases in the US are from subsequent transmission from the imported case. Measles had the highest number of annual cases of the infectious diseases included in this study (a high proportion of which were secondary cases associated with an index traveler case), with annual cases ranging from 13 (2020) to 1,274 (2019) over the past 10 years; the median estimate was 121 annual cases, and mean was 295 annual cases over this time period.

Rubella: We used data from the National Notifiable Diseases Surveillance System and associated US CDC documentation on rubella cases reported in the US from 2016-2022.[3,4] Rubella had 38 total reported cases of rubella (annual range: 1-7 cases) and 8 total reported cases of congenital rubella syndrome (annual range: 1-5 cases) from 2016-2022. The mean annual cases of rubella was 5 cases over this time period. Given that rubella commonly causes mild illness, the total number of imported rubella cases in the US may be higher due to imperfect case ascertainment due to not seeking medical attention, confirmatory diagnosis, and reporting. This broad estimation is also consistent with data from similar countries.

Diphtheria: We used data from a recent publication on respiratory diphtheria cases in the US, with attention to toxigenic respiratory diphtheria cases from 2000—2018 (longer time period chosen based on rarity of the disease).[5] Over this period, there were 2 confirmed and 4 probable

cases for toxigenic respiratory diphtheria cases (n=6 cases total); of the 4 probable cases, 2 were positive for C. *diphtheriae* toxin genes by polymerase chain reaction which is highly suggestive for being a toxigenic respiratory diphtheria case. The mean annual cases of toxigenic respiratory diphtheria was 0.2-0.3 cases over this time period.

Poliomyelitis: We used data from the National Notifiable Diseases Surveillance System on poliomyelitis cases reported in the US from 2000-2022 (longer time period chosen based on rarity of the disease) and from relevant publications.[6-11] Over this period, there have been at least five documented cases of poliomyelitis, likely related to importation. In two of these imported cases, there was subsequent transmission.[10,12] Most notably, in the case of the paralytic poliomyelitis case diagnosed in New York in 2022, based on wastewater surveillance, there was evidence of ongoing transmission over an extended time period and many locations, suggesting numerous sub-clinical (non-paralytic) cases.[6] Therefore, this recent example of a poliovirus case was likely an outbreak that included additional secondary cases meaning that the true number of poliovirus cases in recent history is likely much higher than the single reported clinical case. The mean annual cases of likely imported poliomyelitis cases was approximately 0.2 cases over this time period. The total number of cases (including secondary transmission) is under-estimated due to lower case ascertainment, but likely larger than this estimate.

Additional considerations: Finally, additional considerations are needed when interpreting these numbers from surveillance datasets. For each infectious disease, case ascertainment may not be perfect due to unrecognized illness (due to sub-clinical infection), lack of formal diagnosis, or lack of reporting to public health departments. Therefore, the number of true imported cases and/or secondary cases in the US for these diseases may be larger than reported.

Importation risk for each infectious disease

This study simulated four infectious diseases eliminated from the US – measles, rubella, diphtheria, and poliomyelitis. The definition of elimination refers to a lack of sustained local transmission. Therefore, most observed cases in the US for these diseases in recent history are related to travel ("imported" cases). Commonly, imported cases are from an under-immunized US traveler who acquires the infection while traveling internationally in an endemic country and then returns to the US, potentially spreading to others. Under elimination status, some sporadic importation-related cases are observed, but this should not be sustained.

For this model, we assumed the annual rate of imported cases for each of the four eliminated infectious diseases based on review of data described in 'Review of modern epidemiologic case data for each infectious disease'. This data is further described here:

Measles: For measles, we assumed 34 annual imported cases.[1] Measles was the most common imported infectious disease included in our study, with 34 annual imported cases in the US in 2023.[1] We used the 2023 estimate for the US given this is more recent and less affected by travel restrictions during the COVID-19 pandemic.[1] We included both international importations and imported virus or imported-virus-linked cases in this estimate. This assumed number of imported cases is compatible with prior years (not affected by the COVID-19 pandemic) and prior literature.[4,13]

Rubella: For rubella, we assumed 5 annual imported cases.[1] This is informed by the range of cases seen 2016-2022. As described above, the number of imported cases may be larger due to lower case ascertainment.

Diphtheria: For respiratory toxigenic diphtheria, we assumed 0.2 annual imported cases in the US (based on period since 2000).[4,5] Given how rare respiratory diphtheria cases have been observed, we also informed our importation estimate from surveillance cases on respiratory diphtheria from Canada and the United Kingdom.[14,15]

Poliomyelitis: For poliomyelitis, we assumed 0.2 annual imported cases in the US, informed from importation data in the US (based on period since 2000). We did not distinguish between wild-type and circulating vaccine-derived poliovirus or serotype, which is a simplifying assumption in this model.

In the case of all four diseases, case ascertainment is likely imperfect, in part due to sub-clinical illness, not seeking medical care, and potential lack of clinical recognition of these diseases; therefore, our estimates may be an under-estimate. The age assignment of the imported case was weighted based on the age distribution of the state's population and age-specific susceptibility.

In the main analysis, we assumed an annual US-wide rate of imported (travel-associated) cases for each infectious disease. The rate for each state was proportional to their population size relative to the total US population size given this may approximate overall travel. Furthermore, we assumed the importation rate increased as the proportion of susceptible people in the population increased for a given infection. We did this by proportionally scaling the importation rate with the proportion of susceptible persons in the population, relative to the baseline population susceptibility (year 2024, "t0"). Therefore, the assumed importation rate was set for the baseline population (year 2024) and increased over time as population susceptibility increased. For each time step ("t") and state, the importation rate was calculated as the following:

$$Import\_rate_{state,\ t} = Import\_rate_{USA} * \frac{Population_{state}}{Population_{USA}} * \frac{Prop\_susceptible_{state,\ t}}{Prop\_susceptible_{state,\ t0}}$$

We generate a sensitivity analysis where the importation rate was assumed to be static (i.e., not related to population-level susceptibility), which is a conservative assumption.

Population immunity

We generated age-specific population immunity profiles, in 5-year age bins (0-4, 5-9, …, 85+), for each US state. We initialized the model to be starting in 2024. For age groups 24 years and younger, we estimated state-specific population immunity based on the upper bound of the estimated vaccine coverage data from the National Immunization Surveys (NIS) to be conservative, using the 35 month estimate.[16] We defined coverage based on completion of at least 1 dose of MMR for measles and rubella, 4 doses of DTaP for diphtheria, and 3 doses of IPV for poliomyelitis by 35 months; we did not account for delayed vaccination received after 35 months or partial vaccination. For adults over 25 years of age, we assumed a general US-wide adult population immunity profile for each infectious disease based on literature for measles[17-19], rubella[18,20], diphtheria[21,22], and poliovirus[6,23,24]. In the case of seroprevalence data, the model assumed that seroconversion conferred complete protection against infection. We did not account

for imperfect seroconversion or seroreversion. Broadly, the adult population was assumed to have a high level of immunity across all pathogens. Notably, protection for poliovirus accounted for the change from oral poliovirus vaccine (OPV) to inactivated poliovirus vaccine (IPV) in 2000, which changed the protection to be against clinical severity and transmission rather than against infection. For MMR, the recommendation changed from a single dose to two-dose schedule in 1989; we relied on seroprevalence data to assign protection for this cohort. Similarly, we assumed the diphtheria vaccine yielded protection against clinical severity and transmission rather than against infection, assuming the population with seropositivity against diphtheria was generated from vaccination rather than infection.

Pathogen-specific features and vaccination

We applied a SEIR model structure for all pathogens (see "Model Overview"), although there is variation in natural history and epidemiologic features of each pathogen. We did not account for sub-clinical infections or carriage and assumed perfect case ascertainment in our estimates, which is sensible given the goals of the study to predict total infections (rather than observed cases). In many scenarios, inclusion of sub-clinical infections explicitly into the model structure would not change the results. The model structure and parametrization for pathogens were parsimonious and informed by the best available data, and was supported by an evaluation of model validity, which showed model predicted cases were similar to current levels of observed cases under current and high vaccine coverage. We accounted for age-specific heterogenous social mixing using a published contact matrix[25]; R_0 was based on the dominant eigenvalue of the next-generation matrix.[26] Maternal immunity is assumed to generate approximately 6 months of protection to infants who are not vaccinated in the simulation. For children who are assigned to be vaccinated with the primary series in the simulation, we simulated onset of vaccine-derived protection at birth; this protection therefore represents a combination of maternal and vaccine-derived protection. We assumed that vaccine-derived protection was lifelong and did not wane, which is a conservative assumption; assuming waning of protection would lead to larger number of total cases. Additional pathogen-specific features relevant to the model structure and/or parameterization are discussed here:

Poliovirus: Poliovirus is the most distinct pathogen in the model given both wild type and vaccine-derived types and different serotypes. While there is substantial complexity, we designed a parsimonious model that assumes circulation of a single poliovirus in the US, although this is a simplification. As described above, our model assumed IPV did not block infection, but did reduce clinical severity and transmission. We assumed that vaccination during time period of using OPV did generate protection against infection. We conservatively assumed no paralytic poliomyelitis cases occurred in vaccinated persons. We assumed that infection led to protection against future infection. There are less certain aspects of poliovirus' natural history and parameter inputs; therefore, our estimates are more uncertain for poliovirus than for the other infectious diseases. This model structure was supported by an evaluation of model validity, which showed model predicted cases were similar to current levels of observed cases under current and high vaccine coverage; elimination of transmission was demonstrated in the model under current vaccination levels. Overall, this simple model is likely to adequately capture key aspects relevant to the scientific objective on epidemiologic predictions related to modeling declining vaccination.

Measles: Measles infection-acquired and vaccine-derived immunity against infection was assumed to be lifelong.[27] We did not account for breakthrough infections in vaccinated persons (who mounted an immune response to vaccination) or reinfections given their rarity.

Rubella: Rubella has distinct aspects of natural history and vaccine-induced protection.[27] We assumed vaccination yielded lifelong protection against infection. However, rubella infections in vaccinated persons and/or reinfection can occur with rubella (especially as protection wanes over time), although these are thought to be sub-clinical and far less infectious (including lack of viremia).[28,29] Therefore, for simplification in the model, we did not account for breakthrough infections in vaccinated persons (who mounted an immune response to vaccination) or reinfections given their likely minimal contribution to symptomatic cases and transmission.[28,29]

Diphtheria: The diphtheria model had unique aspects of vaccine-induced protection. Diphtheria toxoid vaccine-derived protection is thought to be primarily against clinical severity (5 doses yielding up to 97-99% protection against clinical disease; 3 doses yielding up to 87% protection against clinical disease).[4,30] While there is not strong evidence for vaccine-derived immunity blocking infection / colonization upon exposure, there is strong evidence that vaccination reduces subsequent transmission (60% reduction after 3 doses of vaccination) and likely duration of colonization.[30] This benefit is likely larger with the 5-dose DTaP regimen currently implemented in the US, which also includes additional TDaP doses every 10 years. It is also known that asymptomatic cases transmit far less than symptomatic cases (76% fewer secondary cases). Since 5-dose vaccine-derived protection yields up to 97-99% protection against clinical disease, this provides further evidence that vaccines reduce transmission, in part due to reduced symptomology (e.g., coughing), and also duration of carriage. The historic and dramatic reduction in diphtheria after introduction of vaccination in the US provides strong evidence of vaccine-derived indirect protection, given the rate of diphtheria decline, ongoing elimination of transmission, and evidence that both symptomatic and asymptomatic infection / colonization declined together (which would predominately be mediated by infection blocking protection and/or reducing subsequent transmission).[28] Therefore, our interpretation of the evidence is that vaccines have strong vaccine-derived reduction to transmission (and even potentially some degree of protection against infection). The aforementioned literature has some limitations in respect to use in the present modeling study: i) estimates rely on a 3-dose regimen, whereas the US uses 5-dose regimen with subsequent TDaP doses every 10 years (therefore protection may be higher than these historic estimates); ii) US is a lower transmission setting; and iii) key data for estimates of interest may be underpowered. To explain the elimination of diphtheria from the US and ongoing elimination status, vaccine-derived protection must yield strong protection against transmission (or infection). In the main analysis, we assumed that vaccine-derived protection yields 90% transmission reduction (for those with a complete DTaP series or ongoing serologic evidence of protection or history of vaccination in the older age groups). This higher estimate is based on a different vaccine schedule compared to historic literature, difference in transmission setting (likely lower risk compared to historic outbreak settings), and supported by our evaluation of model validity demonstrating elimination of transmission under these vaccine assumptions (to be consistent with recent epidemiologic case data). While we selected this version as the base case model, given uncertainty, we also performed additional sensitivity analyses. We ran a sensitivity analysis where we modeled diphtheria toxoid vaccines to block

infection as the mechanism of protection in the primary analysis. We assumed that infection led to protection against future infection.

Infection-related complications

For each simulation, we estimated the number of infection-related complications using binomial draws with probabilities based on previous literature (see Table 1, including relevant references). Specifically, for each measles simulation, each new infection had a 0.1% probability of resulting in post-measles neurological sequelae, 20% probability of resulting in hospitalization, and 0.3% probability of resulting in death. For measles, the post-measles neurological sequelae included a range of conditions including primary measles encephalitis with persistent complications, acute disseminated encephalomyelitis (ADEM), measles inclusion body encephalitis, and subacute sclerosing panencephalitis (SSPE; which is universally fatal and would be delayed 1-10 years after primary infection).[31] Measles case hospitalization fraction was based on recent CDC data on measles cases in the US over the last 10 years. Hospitalization for measles is often due to complications of pneumonia and/or dehydration, and more rarely, encephalitis. Case hospitalization fraction varies by age, although we assumed an overall average case hospitalization fraction in this analysis. For rubella, congenital rubella syndrome was modeled to occur in pregnant people during week 0-16 of pregnancy.[32,33] We assumed the risk of congenital rubella in such a case was 65% during week 0-16 as a simplified weighted average of declining risk over the duration of the pregnancy.[32,33] There are varying estimates on risk of congenital rubella, including documented risk into the second trimester; our estimate is generally aligned with the literature when considering integrated risk over the pregnancy duration and is based on prior literature.[32,33] Because the model does not have separate compartments by sex or pregnancy status, this probability was scaled by the probability a randomly selected person is female times the probability a randomly selected female was in their first 16 weeks of pregnancy, conditional on age group. These probabilities were obtained from the US Census Bureau and the National Family Growth Survey.[11,34] Death from congenital rubella is based on literature estimates.[35,36] For poliovirus and diphtheria, we assigned a case as vaccinated or unvaccinated based on the proportion of vaccinated individuals in the population relative to all susceptible individuals, since we did not assume vaccination blocked infection. For poliovirus, among those unvaccinated, there was a 0.5% probability of the case resulting in paralytic poliomyelitis; all of these cases resulted in hospitalization. All paralytic poliomyelitis cases are recommended for hospital admission for inpatient management, including monitoring for respiratory failure and other complications. Among those with paralytic poliomyelitis, there was a 10% probability of the case resulting in death. The case fatality rate of paralytic poliomyelitis varies with age, and our estimate was an overall average of estimates for children and adolescents and young adults (where case fatality is higher than children).[37] For respiratory diphtheria, among those unvaccinated, all cases resulted in hospitalization and 10% of cases resulted in death; we assumed all severe disease occurred in unvaccinated persons, which is a conservative assumption. All clinical diphtheria cases are recommended for hospital admission for inpatient management, including for antibiotics, antitoxin therapy, airway management, and supportive care. All estimates are chosen to reflect data considering current clinical management, supportive care, and disease-directed therapy for hospitalized cases, within the data constraints. Table 1 provides additional references for the described risk for infection-related complications.

Return to endemicity estimation

For each simulation, we estimated whether endemic transmission was re-established. We defined endemic transmission as sustained local transmission (>12 months). To estimate this, we estimated an approximate effective reproduction number averaged to a weekly scale over the simulation. This was based on the change in number of cases (growth rate) over subsequent periods on a national level, informed by the generation interval for a pathogen. This is a broad approximation of the effective reproduction number, and a value ≥ 1 suggests continued sustained transmission. We only included locally acquired and transmitted cases in this estimate (i.e., we excluded imported cases). We then determined whether endemic transmission was re-established by searching for whether the effective reproduction number was ≥1 for 12 months in the US. These findings were summarized over the simulations to determine probability for returning to endemicity over the simulation period and also associated timing for re-establishing endemicity. This definition is overall conservative and therefore may under-estimate the proportion of scenarios where endemic transmission is re-established, especially in settings with periodic patterns in cases; however, this concern is mitigated based on simultaneous independent simulation across all US states. Generally, endemicity is re-established once the population immunity drops below the critical threshold and an imported case is introduced, although there is stochastic variation in when this will lead to re-establishing endemic transmission due to these chance events. We generate plots to demonstrate the relationship between population immunity and timing of return to endemicity. We compared alternative definitions for return to endemicity, including when simulations met the following criteria: i) greater than 100,000 locally acquired cases over the simulation period; or ii) greater than 99% of cases are locally acquired infections. These definitions would not be affected by infectious diseases that establish endemicity with periodic behavior.

We include additional description about how population immunity relates to risk for outbreaks and eventually re-establishing endemicity. In a population with perfect immunity, an imported infectious disease will generate no secondary cases. In a population with very high population immunity (above the critical threshold to maintain elimination), there may be some secondary cases but no sustained ongoing transmission. As population immunity goes down further, the probability, size, and duration of outbreaks increase upon being challenged with an imported case of an infectious disease. And eventually, population immunity declines below the critical threshold to the point where endemicity may be re-established, defined as sustained local transmission. A crude estimation of the critical threshold to maintain elimination for measles, rubella, and diphtheria, and poliovirus based on their R_0, would be to achieve population immunity of 92%, 75%, 60%, and 75%, respectively. These targets for population immunity are based on immunity against infection, which therefore must account for imperfect vaccine efficacy against infection. Additionally, vaccination for poliovirus with IPV and diphtheria with DTaP predominately reduce transmission and do not generate strong protection against infection, therefore their interpretation is more complex in respect to these population immunity targets. Additionally, these estimates make assumptions including homogeneous social mixing and population immunity and an idealized population and conditions. However, these population immunity targets can provide a helpful guide on an estimated threshold to maintain.

Additional details on modeled population and analysis

To support interpretation of the model results, we include some demographic details about the simulated US population over 25 years. At the start of the simulation, the US population was

estimated at 328,329,053 people and at the end of the simulation was estimated at 327,203,220 people. Over the 25-year simulation, we estimate 94,624,178 births, which relate to the number of children eligible for vaccination. We estimate 134,962,197 person-years of women of reproductive age (15-44 years) who were susceptible to rubella infection in the absence of routine childhood vaccination.

For study estimates, we applied winsorization to the central 96% of base case estimates to mitigate the influence of extreme outliers. Specifically, values above the 98th percentile were assigned the value of the 98th percentile and values below the 2nd percentile were assigned the value of the 2nd percentile. No observations were dropped.

Evaluation of model validity

To evaluate model validity, we generated model-predicted estimates under two scenarios – 1) current state-level coverage for routine childhood vaccination ("current levels"); and 2) a high coverage level scenario with 95% coverage ("high uptake"). The model was run under these scenarios for 5 years for each infectious disease and then compared to recent historical estimates for number of cases of each disease to ensure the model was consistent with these observed case numbers, as a general test of model validity.

Based on recent case numbers (see above), over a 5-year period we would expect approximately 1,475 measles cases, 25 rubella cases, 1-2 respiratory diphtheria cases, and likely more than 1 poliomyelitis cases (since there was demonstrated secondary cases of poliovirus not detected by standard case surveillance suggesting many more non-paralytic poliomyelitis cases). The model assumes a number of imported cases (which are inputs to the model), which would lead to an average of 170 measles cases, 25 rubella cases, 1 diphtheria cases, and 1 poliovirus imported over the 5-year simulation period. Therefore, under the current levels scenarios, the majority of rubella and diphtheria cases are expected to be imported cases only. In the case of measles and to some extent, poliovirus, there is likely to be secondary transmission upon imported cases based on recent historical data. Since the simulation is stochastic, some simulations have more or less imported cases. Additionally, some simulations have some sporadic secondary cases after introduction.

The overall model-predicted estimates ("current levels" scenario) over a 5-year period were consistent with the number of observed cases over the recent historical period, and within the bounds of uncertainty in the estimate due to stochastic variation (eFigure 1). Further description of recent number of observed cases is described above, in the 'Review of modern epidemiologic case data for each infectious disease'. In the case of all four infectious diseases, the model predicted ongoing elimination status, with cases due to importation with some sporadic secondary transmission (but no sustained local transmission). Poliovirus had some secondary transmission in some simulations, which is likely consistent with a recent historical example (2022 New York poliomyelitis case, with undetected community transmission and non-paralytic poliovirus cases as evidenced by wastewater detection). Measles had the largest number of cases, including a majority being secondary cases; this was consistent with recent historical case numbers. In all cases, due to stochasticity and imperfect case detection, there is likely a wide range around these estimates and the model estimates fall within the bounds. Additional considerations for interpretation are discussed above for each disease. This supports that the

model is consistent with the current population immunity and transmission landscape for these infectious diseases. In an additional evaluation, we evaluated a high vaccine uptake scenario (95% uptake), and the model predicted minimal secondary cases for rubella, diphtheria, and poliomyelitis, with far fewer cases for measles (eFigure 1).

Probabilistic sensitivity analysis and uncertainty

We conducted a probabilistic sensitivity analysis, which is a multi-way sensitivity analysis that simultaneously varies multiple model inputs across a range of plausible values to generate an interval around the primary study estimate which accounts for this parameter uncertainty and stochastic uncertainty. In this analysis, we varied the basic reproduction number, population immunity profile, and importation rate for each pathogen, assuming a normal distribution for each parameter. eTable 1 includes the range of values and relevant references. We selected a normal distribution based on relevant literature on these model inputs, reasonable symmetry in uncertainty in the value, and for ease of interpretation. For the R_0, the range of values was largely informed by literature. For population immunity, the range was chosen to be broadly consistent with precision of measurement of state-level vaccine coverage from the National Immunization Survey. For importation rate, we varied this with a standard deviation of 25% of the mean to allow for variation in the importation rate from year to year based on available data for cases. For poliovirus and diphtheria, we also varied the vaccine-derived reduction in infectiousness. For this parameter, the chose of standard deviation of 2.5% is based on the range of values in literature, while still maintaining elimination status in the model validity exercise. To ensure adequate sampling of the multi-dimensional parameter space, we applied Latin Hypercube Sampling to obtain 1,000 random draws for each parameter of interest. For each set of sampled parameters, we ran the simulation 100 times and took the mean to reduce variation due to model stochasticity (isolating variation from the parameters of interest). Beyond this, there are many aspects of uncertainty – including model structure uncertainty and pathogen complexity – that were not captured in this analysis. To estimate the uncertainty bounds for infection-related complications under the main vaccine scenarios, we performed an additional analysis. We propagated the range of case estimates generated by the probabilistic sensitivity analysis to generate an optimistic and pessimistic estimate based on the using the lower and upper bound of values for infection-related complications (eTable 1).

eTable 1. Model inputs for probabilistic sensitivity analysis

Parameter description	Measles	Rubella	Diphtheria	Poliovirus	Ref
Model inputs					
Basic reproduction number (R_0)	$N(12, 0.5)$	$N(4, 0.5)$	$N(2.5, 0.5)$	$N(4, 0.5)$	30,38-40
Population immunity (absolute %)	$N(u_{immune}, 2.5)$	$N(u_{immune}, 2.5)$	$N(u_{immune}, 2.5)$	$N(u_{immune}, 2.5)$	16-24
Importation rate (cases per year)	$N(34, 8.5)$	$N(5, 1.25)$	$N(0.2, 0.05)$	$N(0.2, 0.05)$	Appendix
Relative infectiousness reduction from vaccination (%)			$N(0.9, 0.025)$	$N(0.9, 0.025)$	30,41
Inputs for infection-related complications					
Measles	Rubella		Diphtheria	Poliovirus	

Post-measles neurological sequelae: 0.1% Hospitalization: 10-30% Death: 0.1-0.3%	Congenital rubella syndrome (CRS): 65% of pregnancies 0-16 weeks Death: 20-35% of CRS cases	Hospitalization: 100% of unvaccinated cases Death: 5-10% of unvaccinated cases	Paralytic poliomyelitis: 0.05-0.5% unvaccinated cases Hospitalization: 100% of paralytic polio cases Death: 5-10% of paralytic polio cases

R_0, basic reproduction number; N, normal distribution; u, mean
See "Infection-related complications" in eAppendix for further description of relevant references and considerations and Table in article.

eTable 2. Baseline immunity against measles by state and age group.

	Age Group																	
State	**0-4**	**5-9**	**10-14**	**15-19**	**20-24**	**25-29**	**30-34**	**35-39**	**40-44**	**45-49**	**50-54**	**55-59**	**60-64**	**65-69**	**70-74**	**75-79**	**80-85**	**85+**
AK	91.3	92.3	92.8	93.1	93.5	95	93	93	91	88	88	88	88	94	98	99	98	98
AL	95.6	97.3	96.9	97.6	97.1	95	93	93	91	88	88	88	88	94	98	99	98	98
AR	95.8	95.5	95.3	94.2	95.2	95	93	93	91	88	88	88	88	94	98	99	98	98
AZ	94.4	96.2	93.3	94.1	93	95	93	93	91	88	88	88	88	94	98	99	98	98
CA	95.3	95.8	95.7	95.1	95	95	93	93	91	88	88	88	88	94	98	99	98	98
CO	94.5	96.3	94.3	94.2	94.9	95	93	93	91	88	88	88	88	94	98	99	98	98
CT	99.4	98.6	98	98	98.5	95	93	93	91	88	88	88	88	94	98	99	98	98
DC	94.7	95.7	97.1	96.6	96.3	95	93	93	91	88	88	88	88	94	98	99	98	98
DE	96.7	96.6	97.7	96.5	98.7	95	93	93	91	88	88	88	88	94	98	99	98	98
FL	96.2	96.3	96	95.7	96	95	93	93	91	88	88	88	88	94	98	99	98	98
GA	94.8	96.3	96.8	95.9	95.8	95	93	93	91	88	88	88	88	94	98	99	98	98
HI	94.3	93.7	96.8	96.3	95.5	95	93	93	91	88	88	88	88	94	98	99	98	98
IA	97.3	97.9	97.5	95.9	96.4	95	93	93	91	88	88	88	88	94	98	99	98	98
ID	94.4	96.3	95.2	92.4	93.3	95	93	93	91	88	88	88	88	94	98	99	98	98
IL	95.8	95.5	95.2	93.9	95.9	95	93	93	91	88	88	88	88	94	98	99	98	98
IN	96.8	93.4	95.8	93.6	95.4	95	93	93	91	88	88	88	88	94	98	99	98	98
KS	95.6	95.3	95.5	95.8	96.2	95	93	93	91	88	88	88	88	94	98	99	98	98
KY	95.2	96.3	94.9	94.6	96.1	95	93	93	91	88	88	88	88	94	98	99	98	98
LA	96.3	96.5	95.1	96.2	92.7	95	93	93	91	88	88	88	88	94	98	99	98	98
MA	99	99.3	98	97.6	98.9	95	93	93	91	88	88	88	88	94	98	99	98	98
MD	97.4	97.2	97.8	96.8	98.1	95	93	93	91	88	88	88	88	94	98	99	98	98
ME	98	97.1	96.9	95.1	96.1	95	93	93	91	88	88	88	88	94	98	99	98	98
MI	96.9	96.9	94.4	94.4	95.8	95	93	93	91	88	88	88	88	94	98	99	98	98
MN	96.3	97.7	96.7	97.1	96.3	95	93	93	91	88	88	88	88	94	98	99	98	98
MO	96.2	93.6	96	94	96.9	95	93	93	91	88	88	88	88	94	98	99	98	98
MS	95.4	95.3	97.1	94.5	95.6	95	93	93	91	88	88	88	88	94	98	99	98	98
MT	91.1	95.7	94.4	92.1	95.1	95	93	93	91	88	88	88	88	94	98	99	98	98
NC	97.9	97.2	97.3	97.2	99	95	93	93	91	88	88	88	88	94	98	99	98	98
ND	96.3	97.8	96.1	97	95.9	95	93	93	91	88	88	88	88	94	98	99	98	98
NE	98.1	97.7	97.1	97.2	96.6	95	93	93	91	88	88	88	88	94	98	99	98	98
NH	98.2	98.1	97.8	97.5	95.7	95	93	93	91	88	88	88	88	94	98	99	98	98
NJ	97.3	95.7	97.4	93.7	94.4	95	93	93	91	88	88	88	88	94	98	99	98	98
NM	95.7	96.7	94.9	94.3	94.4	95	93	93	91	88	88	88	88	94	98	99	98	98
NV	93.2	95.8	95.1	92.3	90.8	95	93	93	91	88	88	88	88	94	98	99	98	98
NY	94.8	95.7	95.7	94.1	97.1	95	93	93	91	88	88	88	88	94	98	99	98	98
OH	94.9	94.4	94.3	95.9	96.3	95	93	93	91	88	88	88	88	94	98	99	98	98
OK	95.4	95	95.6	96.3	95.4	95	93	93	91	88	88	88	88	94	98	99	98	98
OR	94.9	96.9	93.3	94.7	92.8	95	93	93	91	88	88	88	88	94	98	99	98	98
PA	94	97.6	94.9	95.2	97.4	95	93	93	91	88	88	88	88	94	98	99	98	98
RI	98.7	98.8	98.2	97.5	98.2	95	93	93	91	88	88	88	88	94	98	99	98	98
SC	95.2	95.8	95.5	94	95.6	95	93	93	91	88	88	88	88	94	98	99	98	98
SD	95.7	95.9	97.1	96.5	97.5	95	93	93	91	88	88	88	88	94	98	99	98	98
TN	97.2	96.5	95.6	97.4	95.1	95	93	93	91	88	88	88	88	94	98	99	98	98
TX	95.9	93	93.8	94.2	92.7	95	93	93	91	88	88	88	88	94	98	99	98	98
UT	96.7	95.8	93.8	93.9	94.9	95	93	93	91	88	88	88	88	94	98	99	98	98
VA	94.1	98.2	95.3	94.9	97.8	95	93	93	91	88	88	88	88	94	98	99	98	98
VT	98.4	97.4	96.7	96	97.2	95	93	93	91	88	88	88	88	94	98	99	98	98
WA	95.9	95.7	94.7	94	93.4	95	93	93	91	88	88	88	88	94	98	99	98	98
WI	95.9	96	96.3	97	96	95	93	93	91	88	88	88	88	94	98	99	98	98
WV	95.1	94.7	92.6	94.4	95	95	93	93	91	88	88	88	88	94	98	99	98	98
WY	95.9	95.1	95.1	94.1	94.2	95	93	93	91	88	88	88	88	94	98	99	98	98

eTable 3. Baseline immunity against rubella by state and age group.

	Age Group																	
State	**0-4**	**5-9**	**10-14**	**15-19**	**20-24**	**25-29**	**30-34**	**35-39**	**40-44**	**45-49**	**50-54**	**55-59**	**60-64**	**65-69**	**70-74**	**75-79**	**80-85**	**85+**
AK	91.3	92.3	92.8	93.1	93.5	98	96	95	95	93	93	94	95	95	95	95	95	95
AL	95.6	97.3	96.9	97.6	97.1	98	96	95	95	93	93	94	95	95	95	95	95	95
AR	95.8	95.5	95.3	94.2	95.2	98	96	95	95	93	93	94	95	95	95	95	95	95
AZ	94.4	96.2	93.3	94.1	93	98	96	95	95	93	93	94	95	95	95	95	95	95
CA	95.3	95.8	95.7	95.1	95	98	96	95	95	93	93	94	95	95	95	95	95	95
CO	94.5	96.3	94.3	94.2	94.9	98	96	95	95	93	93	94	95	95	95	95	95	95
CT	99.4	98.6	98	98	98.5	98	96	95	95	93	93	94	95	95	95	95	95	95
DC	94.7	95.7	97.1	96.6	96.3	98	96	95	95	93	93	94	95	95	95	95	95	95
DE	96.7	96.6	97.7	96.5	98.7	98	96	95	95	93	93	94	95	95	95	95	95	95
FL	96.2	96.3	96	95.7	96	98	96	95	95	93	93	94	95	95	95	95	95	95
GA	94.8	96.3	96.8	95.9	95.8	98	96	95	95	93	93	94	95	95	95	95	95	95
HI	94.3	93.7	96.8	96.3	95.5	98	96	95	95	93	93	94	95	95	95	95	95	95
IA	97.3	97.9	97.5	95.9	96.4	98	96	95	95	93	93	94	95	95	95	95	95	95
ID	94.4	96.3	95.2	92.4	93.3	98	96	95	95	93	93	94	95	95	95	95	95	95
IL	95.8	95.5	95.2	93.9	95.9	98	96	95	95	93	93	94	95	95	95	95	95	95
IN	96.8	93.4	95.8	93.6	95.4	98	96	95	95	93	93	94	95	95	95	95	95	95
KS	95.6	95.3	95.5	95.8	96.2	98	96	95	95	93	93	94	95	95	95	95	95	95
KY	95.2	96.3	94.9	94.6	96.1	98	96	95	95	93	93	94	95	95	95	95	95	95
LA	96.3	96.5	95.1	96.2	92.7	98	96	95	95	93	93	94	95	95	95	95	95	95
MA	99	99.3	98	97.6	98.9	98	96	95	95	93	93	94	95	95	95	95	95	95
MD	97.4	97.2	97.8	96.8	98.1	98	96	95	95	93	93	94	95	95	95	95	95	95
ME	98	97.1	96.9	95.1	96.1	98	96	95	95	93	93	94	95	95	95	95	95	95
MI	96.9	96.9	94.4	94.4	95.8	98	96	95	95	93	93	94	95	95	95	95	95	95
MN	96.3	97.7	96.7	97.1	96.3	98	96	95	95	93	93	94	95	95	95	95	95	95
MO	96.2	93.6	96	94	96.9	98	96	95	95	93	93	94	95	95	95	95	95	95
MS	95.4	95.3	97.1	94.5	95.6	98	96	95	95	93	93	94	95	95	95	95	95	95
MT	91.1	95.7	94.4	92.1	95.1	98	96	95	95	93	93	94	95	95	95	95	95	95
NC	97.9	97.2	97.3	97.2	99	98	96	95	95	93	93	94	95	95	95	95	95	95
ND	96.3	97.8	96.1	97	95.9	98	96	95	95	93	93	94	95	95	95	95	95	95
NE	98.1	97.7	97.1	97.2	96.6	98	96	95	95	93	93	94	95	95	95	95	95	95
NH	98.2	98.1	97.8	97.5	95.7	98	96	95	95	93	93	94	95	95	95	95	95	95
NJ	97.3	95.7	97.4	93.7	94.4	98	96	95	95	93	93	94	95	95	95	95	95	95
NM	95.7	96.7	94.9	94.3	94.4	98	96	95	95	93	93	94	95	95	95	95	95	95
NV	93.2	95.8	95.1	92.3	90.8	98	96	95	95	93	93	94	95	95	95	95	95	95
NY	94.8	95.7	95.7	94.1	97.1	98	96	95	95	93	93	94	95	95	95	95	95	95
OH	94.9	94.4	94.3	95.9	96.3	98	96	95	95	93	93	94	95	95	95	95	95	95
OK	95.4	95	95.6	96.3	95.4	98	96	95	95	93	93	94	95	95	95	95	95	95
OR	94.9	96.9	93.3	94.7	92.8	98	96	95	95	93	93	94	95	95	95	95	95	95
PA	94	97.6	94.9	95.2	97.4	98	96	95	95	93	93	94	95	95	95	95	95	95
RI	98.7	98.8	98.2	97.5	98.2	98	96	95	95	93	93	94	95	95	95	95	95	95
SC	95.2	95.8	95.5	94	95.6	98	96	95	95	93	93	94	95	95	95	95	95	95
SD	95.7	95.9	97.1	96.5	97.5	98	96	95	95	93	93	94	95	95	95	95	95	95
TN	97.2	96.5	95.6	97.4	95.1	98	96	95	95	93	93	94	95	95	95	95	95	95
TX	95.9	93	93.8	94.2	92.7	98	96	95	95	93	93	94	95	95	95	95	95	95
UT	96.7	95.8	93.8	93.9	94.9	98	96	95	95	93	93	94	95	95	95	95	95	95
VA	94.1	98.2	95.3	94.9	97.8	98	96	95	95	93	93	94	95	95	95	95	95	95
VT	98.4	97.4	96.7	96	97.2	98	96	95	95	93	93	94	95	95	95	95	95	95
WA	95.9	95.7	94.7	94	93.4	98	96	95	95	93	93	94	95	95	95	95	95	95
WI	95.9	96	96.3	97	96	98	96	95	95	93	93	94	95	95	95	95	95	95
WV	95.1	94.7	92.6	94.4	95	98	96	95	95	93	93	94	95	95	95	95	95	95
WY	95.9	95.1	95.1	94.1	94.2	98	96	95	95	93	93	94	95	95	95	95	95	95

eTable 4. Baseline immunity against diphtheria by state and age group.

	Age Group																	
State	0-4	5-9	10-14	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79	80-85	85+
AK	83.6	83	84.2	84.4	86.6	95	95	95	95	95	95	95	95	95	95	95	95	95
AL	90.4	89.9	90.3	91.3	92.4	95	95	95	95	95	95	95	95	95	95	95	95	95
AR	88	85.3	85.1	85.8	87	95	95	95	95	95	95	95	95	95	95	95	95	95
AZ	87.8	88.3	86.9	90.2	86.5	95	95	95	95	95	95	95	95	95	95	95	95	95
CA	86	90.2	89.5	88.8	88.3	95	95	95	95	95	95	95	95	95	95	95	95	95
CO	88.2	90.4	89.8	89.8	90.4	95	95	95	95	95	95	95	95	95	95	95	95	95
CT	96.2	94.5	93.6	93.9	95.7	95	95	95	95	95	95	95	95	95	95	95	95	95
DC	89.8	91.1	90.5	91	91.7	95	95	95	95	95	95	95	95	95	95	95	95	95
DE	91.8	91.8	93.4	91.1	94	95	95	95	95	95	95	95	95	95	95	95	95	95
FL	88.6	91.8	90.5	92.7	90.3	95	95	95	95	95	95	95	95	95	95	95	95	95
GA	88.3	86.8	91.5	89.5	92.5	95	95	95	95	95	95	95	95	95	95	95	95	95
HI	89.5	87.1	89.8	90.7	90.2	95	95	95	95	95	95	95	95	95	95	95	95	95
IA	90.5	92.4	92.5	90.6	93.4	95	95	95	95	95	95	95	95	95	95	95	95	95
ID	85.5	88.2	86.9	85.1	88.9	95	95	95	95	95	95	95	95	95	95	95	95	95
IL	88.2	89.2	89.1	87.7	91.7	95	95	95	95	95	95	95	95	95	95	95	95	95
IN	90.9	86.6	87.7	86.9	89.1	95	95	95	95	95	95	95	95	95	95	95	95	95
KS	87.2	86.7	89.3	92	91	95	95	95	95	95	95	95	95	95	95	95	95	95
KY	88.7	91.1	90.2	90.5	92	95	95	95	95	95	95	95	95	95	95	95	95	95
LA	88.8	85.5	87.1	88.6	83.8	95	95	95	95	95	95	95	95	95	95	95	95	95
MA	96	95.7	95	94.1	97.2	95	95	95	95	95	95	95	95	95	95	95	95	95
MD	92.9	90.5	91.6	93.5	92.3	95	95	95	95	95	95	95	95	95	95	95	95	95
ME	92.8	93.2	94.4	92.8	94.2	95	95	95	95	95	95	95	95	95	95	95	95	95
MI	88.2	90.2	87.8	92.1	90.4	95	95	95	95	95	95	95	95	95	95	95	95	95
MN	91.5	91.3	92.2	92.1	93.7	95	95	95	95	95	95	95	95	95	95	95	95	95
MO	88.5	85.3	88.3	86.1	91.5	95	95	95	95	95	95	95	95	95	95	95	95	95
MS	88.2	87.1	89.4	88.3	90.1	95	95	95	95	95	95	95	95	95	95	95	95	95
MT	81.3	86	86.9	83.1	87.4	95	95	95	95	95	95	95	95	95	95	95	95	95
NC	92.1	92.5	91.7	90.5	93.3	95	95	95	95	95	95	95	95	95	95	95	95	95
ND	89	90.4	88.7	90.5	91.2	95	95	95	95	95	95	95	95	95	95	95	95	95
NE	94	93.2	92.4	92	91.7	95	95	95	95	95	95	95	95	95	95	95	95	95
NH	94.7	93.9	94.8	94.3	93.5	95	95	95	95	95	95	95	95	95	95	95	95	95
NJ	92.2	89.3	91.8	88.5	90.5	95	95	95	95	95	95	95	95	95	95	95	95	95
NM	88.4	89.8	90	88.2	88.2	95	95	95	95	95	95	95	95	95	95	95	95	95
NV	82.7	87.3	87.6	81.7	79.6	95	95	95	95	95	95	95	95	95	95	95	95	95
NY	88.7	88.1	89.4	87.8	91.4	95	95	95	95	95	95	95	95	95	95	95	95	95
OH	88.8	88.2	87.2	90.9	90.7	95	95	95	95	95	95	95	95	95	95	95	95	95
OK	86.8	86.9	87.3	87.2	86	95	95	95	95	95	95	95	95	95	95	95	95	95
OR	85.8	87.2	88	86.4	87.7	95	95	95	95	95	95	95	95	95	95	95	95	95
PA	86.7	91	90.2	89.7	92.4	95	95	95	95	95	95	95	95	95	95	95	95	95
RI	94.5	94.3	94.5	90.8	93.6	95	95	95	95	95	95	95	95	95	95	95	95	95
SC	90.5	89.7	87.5	88.4	89.8	95	95	95	95	95	95	95	95	95	95	95	95	95
SD	85.5	86.9	89.3	88.3	93.2	95	95	95	95	95	95	95	95	95	95	95	95	95
TN	89.3	89.8	87.7	91.4	90.1	95	95	95	95	95	95	95	95	95	95	95	95	95
TX	87	85.2	84.1	86.6	84.6	95	95	95	95	95	95	95	95	95	95	95	95	95
UT	91.8	90.8	88.7	88.2	87.3	95	95	95	95	95	95	95	95	95	95	95	95	95
VA	87.9	94.3	90.2	89.3	92.1	95	95	95	95	95	95	95	95	95	95	95	95	95
VT	93.1	92.3	91.8	89.3	93.6	95	95	95	95	95	95	95	95	95	95	95	95	95
WA	89.8	89	89.4	87.6	89.6	95	95	95	95	95	95	95	95	95	95	95	95	95
WI	89.3	89.7	91.2	92.5	92.7	95	95	95	95	95	95	95	95	95	95	95	95	95
WV	87.2	87.8	86.3	87.4	90.3	95	95	95	95	95	95	95	95	95	95	95	95	95
WY	87.7	85.6	85.3	84.8	87.5	95	95	95	95	95	95	95	95	95	95	95	95	95

eTable 5. Baseline immunity against poliovirus by state and age group.

	Age Group																	
State	0-4	5-9	10-14	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79	80-85	85+
AK	93.2	93.5	94.9	95.8	93.8	98	98	98	98	98	98	98	98	98	98	98	98	98
AL	95.6	98.2	97.4	97.8	96.5	98	98	98	98	98	98	98	98	98	98	98	98	98
AR	95.1	95.6	96.6	95.7	95.2	98	98	98	98	98	98	98	98	98	98	98	98	98
AZ	95.1	96.7	95.4	96.1	92.9	98	98	98	98	98	98	98	98	98	98	98	98	98
CA	95.2	97.4	96.3	95.9	94.2	98	98	98	98	98	98	98	98	98	98	98	98	98
CO	96	97.7	96.4	96.3	95.9	98	98	98	98	98	98	98	98	98	98	98	98	98
CT	99.4	98.9	98.8	99.8	99	98	98	98	98	98	98	98	98	98	98	98	98	98
DC	95.8	97	96.7	95.7	97	98	98	98	98	98	98	98	98	98	98	98	98	98
DE	97.6	98.4	99.1	97	97.2	98	98	98	98	98	98	98	98	98	98	98	98	98
FL	95.1	96.8	97.7	97.2	94.8	98	98	98	98	98	98	98	98	98	98	98	98	98
GA	96.7	97.5	97.9	97.7	97	98	98	98	98	98	98	98	98	98	98	98	98	98
HI	94.8	95	97	96.8	94.5	98	98	98	98	98	98	98	98	98	98	98	98	98
IA	98.3	99.1	98.5	97.7	97.5	98	98	98	98	98	98	98	98	98	98	98	98	98
ID	94.3	96.6	95.9	95.5	95.6	98	98	98	98	98	98	98	98	98	98	98	98	98
IL	96.5	97.1	96.1	95.8	95.3	98	98	98	98	98	98	98	98	98	98	98	98	98
IN	98	96.4	97.1	96	95.8	98	98	98	98	98	98	98	98	98	98	98	98	98
KS	95.8	96.5	96	97.9	95.4	98	98	98	98	98	98	98	98	98	98	98	98	98
KY	97.3	98.6	96.7	97.6	98	98	98	98	98	98	98	98	98	98	98	98	98	98
LA	97	96.8	97.1	98.6	94.7	98	98	98	98	98	98	98	98	98	98	98	98	98
MA	99.3	99.8	98.9	98.8	98.6	98	98	98	98	98	98	98	98	98	98	98	98	98
MD	98	97.9	98.4	98.6	95.9	98	98	98	98	98	98	98	98	98	98	98	98	98
ME	98.9	97.6	97.6	96.7	97.1	98	98	98	98	98	98	98	98	98	98	98	98	98
MI	96.8	97.8	96.3	96.8	95.5	98	98	98	98	98	98	98	98	98	98	98	98	98
MN	96.8	98.4	98.5	98.2	98.5	98	98	98	98	98	98	98	98	98	98	98	98	98
MO	96.5	94.5	97.1	94.8	97.6	98	98	98	98	98	98	98	98	98	98	98	98	98
MS	96.6	96.5	98	97	97.4	98	98	98	98	98	98	98	98	98	98	98	98	98
MT	94.2	97.2	96.1	92.9	95.1	98	98	98	98	98	98	98	98	98	98	98	98	98
NC	98.7	98	98	97.8	97.9	98	98	98	98	98	98	98	98	98	98	98	98	98
ND	97.3	98.1	97.1	98.7	97	98	98	98	98	98	98	98	98	98	98	98	98	98
NE	97.7	98.3	98.7	97.9	97.3	98	98	98	98	98	98	98	98	98	98	98	98	98
NH	99.3	98.9	99.1	98.5	97.7	98	98	98	98	98	98	98	98	98	98	98	98	98
NJ	99	97.7	96.7	96.1	94.2	98	98	98	98	98	98	98	98	98	98	98	98	98
NM	96.5	97.2	96.2	95.3	94.6	98	98	98	98	98	98	98	98	98	98	98	98	98
NV	93.8	96.2	95.4	93.6	91.3	98	98	98	98	98	98	98	98	98	98	98	98	98
NY	95.8	95.6	96.9	95.6	95.5	98	98	98	98	98	98	98	98	98	98	98	98	98
OH	96.2	95	95.8	97.5	95.2	98	98	98	98	98	98	98	98	98	98	98	98	98
OK	97.1	96.3	96.7	95.7	95.1	98	98	98	98	98	98	98	98	98	98	98	98	98
OR	95.6	96.7	95	95.7	94	98	98	98	98	98	98	98	98	98	98	98	98	98
PA	94.9	97.8	96.5	96.6	96.4	98	98	98	98	98	98	98	98	98	98	98	98	98
RI	99.3	99.5	99.4	99.9	98.4	98	98	98	98	98	98	98	98	98	98	98	98	98
SC	96.9	97.7	97.7	97.4	96.4	98	98	98	98	98	98	98	98	98	98	98	98	98
SD	96.1	96.7	98	98.5	97.8	98	98	98	98	98	98	98	98	98	98	98	98	98
TN	98.4	97.5	97.2	98.1	96.3	98	98	98	98	98	98	98	98	98	98	98	98	98
TX	95.2	94.4	93.8	94.9	92.9	98	98	98	98	98	98	98	98	98	98	98	98	98
UT	97.3	97	96.4	95.3	93.1	98	98	98	98	98	98	98	98	98	98	98	98	98
VA	95.5	98.5	97.4	96.1	96.3	98	98	98	98	98	98	98	98	98	98	98	98	98
VT	99	97.2	97.7	97.5	98.4	98	98	98	98	98	98	98	98	98	98	98	98	98
WA	96.5	95.5	96.1	93.7	93.1	98	98	98	98	98	98	98	98	98	98	98	98	98
WI	96.1	96.1	96.3	97.4	97.8	98	98	98	98	98	98	98	98	98	98	98	98	98
WV	96.1	96.9	96.2	96.2	97.6	98	98	98	98	98	98	98	98	98	98	98	98	98
WY	96.4	96.3	96.6	96.3	94.9	98	98	98	98	98	98	98	98	98	98	98	98	98

eTable 6. State-specific demography: Birth and age-specific annual death rates.

	Birth rate	Age-specific death rate (deaths per 100,000 population)																	
State	(births per 1,000)	0-4	5-9	10-14	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79	80-85	85+
AK	13.4	129	7.7*	34.6	130.9	128.1	181.4	203.3	242.7	262.4	308.8	475.5	689.5	963.9	1417.7	2029.2	3255.9	6077.1	11536.3
AL	11.9	191	20.1	21.2	74.9	120.3	147.1	213	265.7	340.4	459.1	659	998.1	1426.8	2022.2	2798.1	4232.7	6781.9	14213.2
AR	12.1	161.6	14.5	20.9	68.4	126.8	114.5	174.5	225.2	317.5	416.4	664.2	990.3	1500.5	1939.8	2796.4	4196.3	6886.5	13768.1
AZ	10.9	118.9	11	19.4	62.6	109.7	137.7	162.5	200.2	231.5	317.3	481.4	719.2	980	1325	1878.2	2969.5	4931.8	11553.2
CA	11.3	92.5	8.9	10.7	36.7	74.9	85.8	104	129.5	166.4	240.2	370.7	580	861	1202.5	1779.2	2862.5	4882.2	12011.7
CO	10.9	103	11.5	17.9	59.9	96.4	110.7	129.6	159.1	188.6	263	388.3	607	852.4	1170	1750.3	2984.6	5423.9	13263
CT	9.6	94.6	6.2	10.7	31.1	68.7	114	154.6	170.3	198.8	252.5	384.5	564.1	837.4	1162.1	1842.8	2981.7	5213.3	13651.1
DC	12.8	100	13.1*	23.9*	82.3	128.1	86.8	88.6	154.3	232.7	376.5	681.1	1024.6	1452.4	1715.4	2172.6	3042.8	4912	10146.7
DE	10.8	155	3.5*	5.2*	54.6	95.8	169.1	223.2	279.1	276.4	371.6	490.2	742	999.1	1348.4	1872.2	3172.2	5538	13632.5
FL	10.2	136.1	12.1	13.5	49.6	100.5	127	164.8	195.9	235.8	315.1	478.6	734	1059.8	1358.2	1875	2850.1	4643.4	11237.2
GA	11.9	160.4	13.5	17.8	52.1	96.5	112.9	143.6	182.9	239.9	330.4	523.5	795.2	1235.2	1691.2	2410.5	3737.7	6085	13557.2
HI	11.9	120.6	2.3*	21.5	42.3	56.3	75.4	112	161.4	201.8	308.3	445.9	617.5	916.7	1141.4	1670.3	2518.4	4246.3	10270.7
IA	11.9	109.9	10.5	21.5	44.1	70.6	98	116.7	146.3	186.3	302.8	453.8	751.6	1023.8	1464.3	2218.8	3634.9	5943.3	14227.4
ID	12.3	102.4	26.7	19.7	46.3	92.2	89.4	101.6	143.7	184.9	265.3	396.5	616.8	893.4	1253.5	1974.2	3553.2	6262.1	15229.1
IL	11.1	123.6	9.4	12.1	48.3	85.7	111.7	131.8	163.9	209.7	304.2	444.5	703.3	993.4	1461.3	2135.5	3427.6	5660	13187.7
IN	12	147.9	12	18.1	58.2	102.7	138.6	181.1	204.2	265.8	373	553	829.1	1219.8	1703	2611.7	4037.4	6614.6	14544.1
KS	12.2	126.3	13.2	17.5	57.8	80.4	117.4	141.7	156.7	231.1	303	470	790.2	1136.7	1522.2	2445.2	3706	6405.1	14127.8
KY	11.9	118.4	13.4	21.1	54.1	98.7	134	207.9	264.5	334.3	454.4	720.8	1026.6	1472.1	1934.7	2857.1	4489.3	7116.8	14702
LA	12.7	180.5	14.3	22.8	75.7	126.5	144.4	196.2	263.5	327.4	429.7	657.2	1004.5	1372.6	1836	2623.8	4034.1	6394.9	13648.7
MA	10	82.6	8.7	8.9	24.4	57.6	105.1	129.7	153.2	195.8	252.2	386.3	560.8	837	1200.3	1829.3	3072.4	5480.6	14067.3
MD	11.6	132.8	7.3	13.2	49.1	111.4	143.6	185.8	204.3	220.7	303.8	464.7	707.7	998.5	1444.2	2069.5	3326.5	5500	12825.1
ME	8.7	109.3	14.8	1.4*	42.6	82.8	123	180.6	212.9	260.2	340.7	474.9	656.7	1039.1	1397.9	2110.4	3519.9	6550.3	14781.2
MI	10.8	142.3	13	18.7	41.3	82.6	132	171.6	189.6	242.1	321.1	492.6	764.4	1101.3	1574.9	2313.1	3676.8	6094.3	14742.1
MN	11.7	105.8	9.1	12.7	42.4	80.4	94.7	100.2	124.8	167.4	243.2	358.4	545.6	810.7	1198.6	1891.1	3160.4	5494.1	13784.3
MO	11.7	139	13.5	18.4	67.9	125.7	145.2	182	227.9	278.2	368	576.1	871.9	1216.9	1666.6	2502.6	3799.3	6264.6	13481.6
MS	12.3	206.9	24.3	25.2	80.8	135.7	164.6	205.6	283.2	368	515.2	695.8	1112.7	1610.5	2137.2	2915	4496.6	6996.5	14436.5
MT	10.3	109.9	18.7	18.3	82.5	98.5	102.5	170.1	177.1	287.2	321.7	516.1	650.2	986.6	1300.8	2144.3	3593.6	5933.7	14218.5
NC	11.3	154.5	13	12.9	54.8	101.9	139.4	163.5	198.4	235.6	332	502	795.6	1141.5	1560.1	2279.2	3680.4	6074.3	13944.4
ND	13.7	160.8	13.7*	22.6	56.8	62.1	94.6	170.7	186.5	224.8	340.6	418.2	714.2	944.9	1456.1	2079	3488.8	5526.5	13089
NE	12.8	111.5	12.8	17.9	46.8	70.2	94.7	105.8	144.6	173.4	309.4	469.1	694.3	929.4	1371.9	2117.2	3635.9	5925	14071.2
NH	8.7	73.8	5.8*	17.4	26.2	99.8	125.6	176.2	212.2	205.3	267.7	410.1	598.3	872.4	1224.2	2029.9	3358.5	6034.7	14082.1
NJ	11.2	94.8	8.6	11.8	32.2	69.2	121.2	143.8	162.2	185.7	264.1	394.9	596.4	850	1264.5	1922.5	3093.7	5313.9	13387.5
NM	10.9	129.6	15.8	16.4	78.3	139.5	206.6	258.1	314.9	370.6	487.4	635	809	1116.5	1411.5	2033.9	3241	5300.5	12565.2
NV	11.3	128	11.9	12	49.1	94.6	103.1	118.1	164.3	209.6	358.6	484.8	769.4	1143.8	1586.7	2374.1	3624.3	5900	13087.3
NY	11.4	98.2	11.6	12.2	28.2	66.3	84.2	106.7	133.1	176.5	243.6	391.6	577.2	864	1259.8	1854.8	2975.1	4929.5	12069.5
OH	11.5	154.9	9.7	19.5	49.8	101.4	154.4	187.9	238.5	284	377.7	550.7	858.1	1211.8	1689.2	2494	3987.5	6470.9	14686.7
OK	12.4	158.5	15.3	22.2	62	93.6	121.2	167	221.8	312.5	438.7	671.2	1032.3	1450.5	1988.1	2853.3	4219.2	6938.6	13897.3
OR	9.9	102.2	8.2	11.6	44.3	77.6	85.9	109.9	139.2	175.2	270.4	424.8	708.4	995.8	1324.7	2064.9	3349.2	5731.7	14289.1
PA	10.5	130.3	12.5	14.7	40.4	95.7	139.3	168.5	208.3	231.1	324.1	486.2	729.1	1039.5	1421.3	2218.9	3588.3	5995	14172.4
RI	9.6	128.5	16.4*	13.9*	21.2	58.6	84.5	138	176.6	225.4	294.7	434.9	605.5	873.4	1338.9	2058.5	3450.2	5908.1	14549.4
SC	11.1	160.5	11.7	18.5	66.1	127.8	148.8	181.5	242.4	298.7	419.8	584.6	882.2	1271.2	1613.5	2268.7	3717.9	6206.5	13760.3
SD	12.9	156.8	11.4*	1.6*	94.5	100.8	125	160.4	198	250.6	383.6	443.8	717.1	951.5	1303.5	2054.3	3729.7	5973.8	13840.8
TN	11.8	158.5	16.7	17.4	66.9	124	148.5	202.9	242.6	316.9	468.5	662.3	1010.6	1423.8	1882.2	2675	4193.4	6781.3	14433.5
TX	13	125.2	11.6	16	53.2	88.8	96	116.4	151.9	200	298.5	458.7	723	1095	1547	2255.2	3593.9	5885.5	13146.4
UT	14.6	120.9	11.2	15.6	54.7	68	92.3	126.5	157.4	189.2	218.3	403.3	565.8	831.2	1175.7	1851.3	3280.6	5974.3	15089.9
VA	11.4	128.4	10.8	11.6	45.6	80.1	107	120.7	158.9	183	273.2	421.4	686.3	1010.5	1428.9	2105.3	3438.2	5785.2	13617.4
VT	8.6	65.9	19.2*	3*	31.5	55.1	118	188.8	167.3	212.7	251.9	440.3	628.4	898.4	1281.3	2023.8	3098	5461	14155.8
WA	11.1	94.3	8.1	14.6	43.3	73.9	84.2	102.6	124.4	172.7	260.3	403.4	618.9	917.4	1287	1992.8	3220.4	5650.1	13729.5
WI	10.9	133.7	11.5	15.2	43.1	74.9	104.1	129.5	162.9	197.7	284.5	424	621.1	921.1	1336.7	2114.3	3497.8	6004.8	14986.9
WV	10.1	142.5	9.9	16.5	67.7	117.8	199.3	286.7	342.7	419.1	515.4	737.3	1093.3	1528.9	1923.8	2768.6	4313.9	7082.3	14704.9
WY	11.3	155.7	16.1*	10.1*	84.9	100	114.7	168.3	183.4	285.6	359.7	515.7	686.2	1012	1343.6	2185.7	3608.7	5769.8	13384

Note: * Cells with fewer than 10 deaths are suppressed in the NCHS data and were imputed by randomly sampling 1-9 deaths.

eTable 7. Current routine childhood vaccination rate by state and vaccine for 1+ doses MMR, 4+ doses of DTaP, and 3+ doses of IPV at 35 months.

	MMR	Polio	DTaP
Alabama	92.9%	93.3%	85.1%
Alaska	87.7%	89.7%	78.2%
Arizona	89.8%	91.1%	82.3%
Arkansas	90.7%	91.1%	79.8%
California	91.5%	92.2%	83.1%
Colorado	90.2%	92.3%	83.9%
Connecticut	95.4%	96.3%	90.0%
Delaware	93.4%	94.3%	87.1%
District of Columbia	92.0%	92.6%	85.3%
Florida	92.2%	92.5%	85.6%
Georgia	91.7%	93.8%	84.1%
Hawaii	91.2%	91.6%	84.0%
Idaho	89.7%	91.3%	80.9%
Illinois	92.2%	93.2%	85.0%
Indiana	90.7%	92.9%	82.6%
Iowa	92.9%	94.8%	86.4%
Kansas	91.6%	92.4%	83.7%
Kentucky	90.8%	94.0%	84.8%
Louisiana	91.5%	93.4%	81.0%
Maine	93.0%	94.3%	88.7%
Maryland	94.3%	94.6%	87.6%
Massachusetts	95.6%	96.7%	91.3%
Michigan	91.6%	92.8%	84.3%
Minnesota	92.7%	94.6%	86.8%
Mississippi	91.3%	93.2%	82.6%
Missouri	91.2%	92.3%	82.2%
Montana	89.0%	90.8%	78.5%
Nebraska	93.9%	95.0%	87.9%
Nevada	88.9%	89.7%	77.6%
New Hampshire	93.9%	95.6%	89.6%
New Jersey	91.6%	93.1%	85.0%
New Mexico	91.3%	92.4%	83.6%
New York	92.8%	93.1%	85.2%
North Carolina	94.3%	94.6%	86.8%
North Dakota	92.6%	94.0%	84.4%
Ohio	91.3%	92.3%	83.7%
Oklahoma	91.1%	92.1%	80.7%
Oregon	90.1%	91.0%	80.7%
Pennsylvania	92.5%	93.3%	85.7%
Rhode Island	95.4%	97.0%	89.0%
South Carolina	90.8%	93.4%	83.5%
South Dakota	92.6%	93.7%	82.7%
Tennessee	92.6%	94.1%	84.2%
Texas	91.1%	91.4%	81.5%
Utah	90.9%	91.8%	83.9%
Vermont	93.9%	94.8%	87.1%
Virginia	91.8%	92.7%	85.1%
Washington	91.0%	91.2%	84.2%
West Virginia	89.8%	92.7%	82.0%
Whole US	91.8%	92.8%	84.1%
Wisconsin	92.3%	93.0%	85.7%
Wyoming	90.4%	92.0%	80.0%

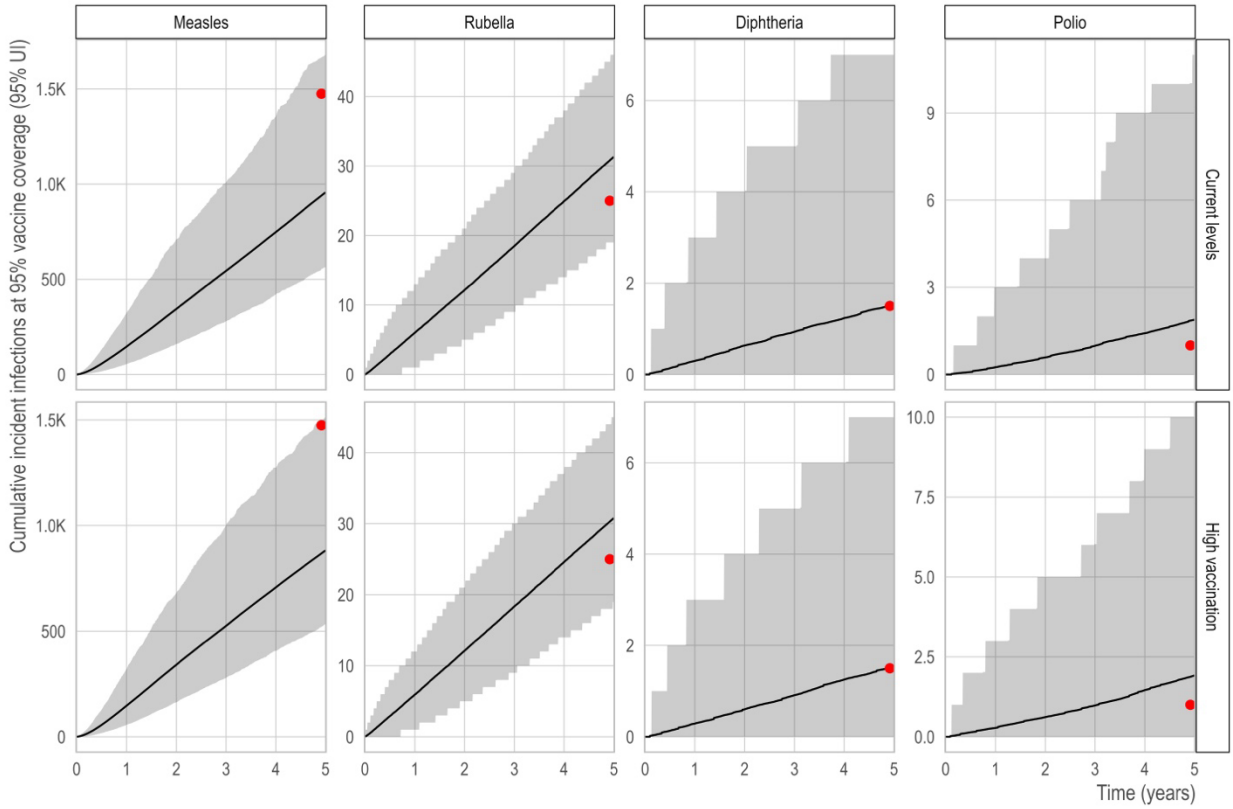
eTable 8. Infection-related complications under different vaccine scenarios.

Vaccine scenario	Complication	Mean (95% UI)
Current levels	Congenital rubella syndrome	0 (95% UI: 0 to 2)
Current levels	Death	2,553 (95% UI: 1,136 to 3,751)
Current levels	Hospitalization	170,227 (95% UI: 76,225 to 250,033)
Current levels	Paralytic polio	0 (95% UI: 0 to 0)
Current levels	Post-measles neurological sequelae	851 (95% UI: 372 to 1,266)
5% higher	Congenital rubella syndrome	0 (95% UI: 0 to 1)
5% higher	Death	18 (95% UI: 5 to 65)
5% higher	Hospitalization	1,176 (95% UI: 621 to 3,915)
5% higher	Paralytic polio	0 (95% UI: 0 to 0)
5% higher	Post-measles neurological sequelae	6 (95% UI: 1 to 21)
10% higher	Congenital rubella syndrome	0 (95% UI: 0 to 1)
10% higher	Death	9 (95% UI: 3 to 19)
10% higher	Hospitalization	553 (95% UI: 439 to 715)
10% higher	Paralytic polio	0 (95% UI: 0 to 0)
10% higher	Post-measles neurological sequelae	3 (95% UI: 0 to 6)
25% lower	Congenital rubella syndrome	1 (95% UI: 0 to 3)
25% lower	Death	80,660 (95% UI: 76,504 to 84,313)
25% lower	Hospitalization	5,375,998 (95% UI: 5,106,119 to 5,614,178)
25% lower	Paralytic polio	101 (95% UI: 0 to 1,330)
25% lower	Post-measles neurological sequelae	26,879 (95% UI: 25,456 to 28,142)
50% lower	Congenital rubella syndrome	10,667 (95% UI: 6,670 to 14,562)
50% lower	Death	159,181 (95% UI: 151,156 to 164,748)
50% lower	Hospitalization	10,261,536 (95% UI: 9,942,094 to 10,536,619)
50% lower	Paralytic polio	5,415 (95% UI: 0 to 26,261)
50% lower	Post-measles neurological sequelae	51,194 (95% UI: 49,641 to 52,636)

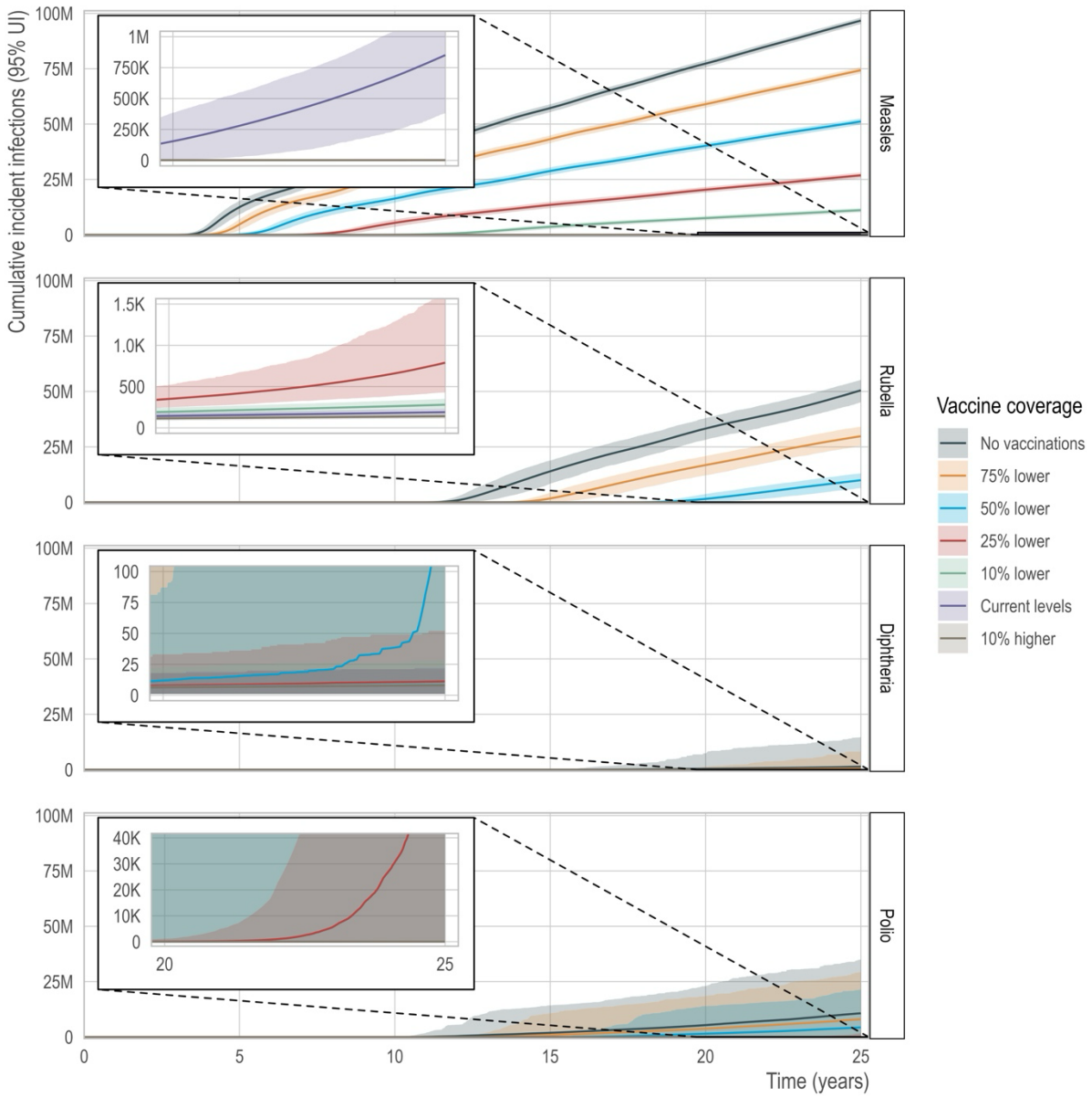
eTable 9. Infection-related complications under lower and upper bound assumptions.

Pathogen	Complication	Vaccine scenario	Mean (95% UI)
Measles	Death (lower bound)	Current levels	850 (95% UI: 377-1,249)
Measles	Hospitalization (lower bound)	Current levels	85,120 (95% UI: 38,228-125,362)
Measles	Hospitalization (upper bound)	Current levels	255,327 (95% UI: 114,567-375,041)
Measles	Death (lower bound)	10% lower	11,133 (95% UI: 10,100-12,107)
Measles	Hospitalization (lower bound)	10% lower	1,113,503 (95% UI: 1,012,808-1,206,928)
Measles	Hospitalization (upper bound)	10% lower	3,340,461 (95% UI: 3,039,653-3,618,230)
Measles	Death (lower bound)	20% lower	21,673 (95% UI: 20,424-22,855)
Measles	Hospitalization (lower bound)	20% lower	2,166,870 (95% UI: 2,043,611-2,284,240)
Measles	Hospitalization (upper bound)	20% lower	6,500,613 (95% UI: 6,129,587-6,851,763)
Measles	Death (lower bound)	50% lower	51,189 (95% UI: 49,620-52,592)
Measles	Hospitalization (lower bound)	50% lower	5,118,789 (95% UI: 4,970,526-5,254,484)
Measles	Hospitalization (upper bound)	50% lower	15,356,390 (95% UI: 14,914,843-15,760,089)
Rubella	Death (lower bound)	Current levels	0 (95% UI: 0-1)
Rubella	Death (upper bound)	Current levels	0 (95% UI: 0-1)
Rubella	Death (lower bound)	10% lower	0 (95% UI: 0-1)
Rubella	Death (upper bound)	10% lower	0 (95% UI: 0-1)
Rubella	Death (lower bound)	20% lower	0 (95% UI: 0-1)
Rubella	Death (upper bound)	20% lower	0 (95% UI: 0-1)
Rubella	Death (lower bound)	50% lower	2,132 (95% UI: 1,341-2,914)
Rubella	Death (upper bound)	50% lower	3,734 (95% UI: 2,321-5,111)
Polio	Death (lower bound)	10% lower	0 (95% UI: 0-0)
Polio	Paralytic polio (lower bound)	10% lower	0 (95% UI: 0-0)
Polio	Death (lower bound)	20% lower	0 (95% UI: 0-0)
Polio	Paralytic polio (lower bound)	20% lower	0 (95% UI: 0-1)
Polio	Death (lower bound)	50% lower	270 (95% UI: 0-1,290)
Polio	Paralytic polio (lower bound)	50% lower	543 (95% UI: 0-2,626)
Diphtheria	Death (lower bound)	Current levels	0 (95% UI: 0-2)
Diphtheria	Death (lower bound)	10% lower	0 (95% UI: 0-2)
Diphtheria	Death (lower bound)	20% lower	1 (95% UI: 0-3)
Diphtheria	Death (lower bound)	50% lower	928 (95% UI: 0-50)

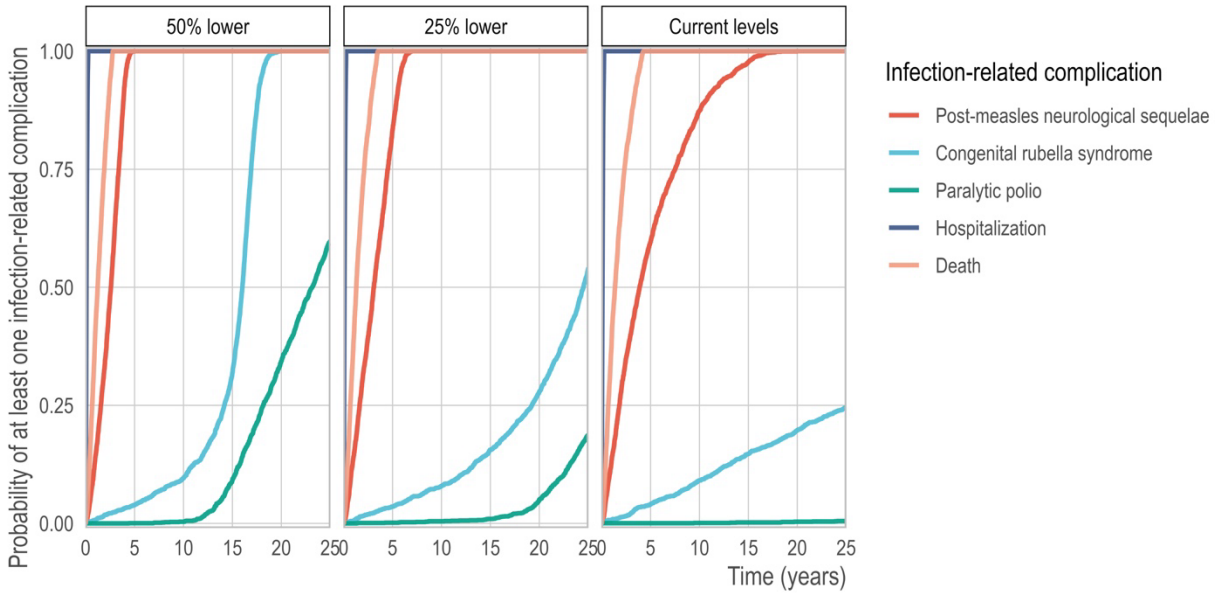
eTable 1 has range of values for infection-related complications. Table shows estimates that differ from base case.



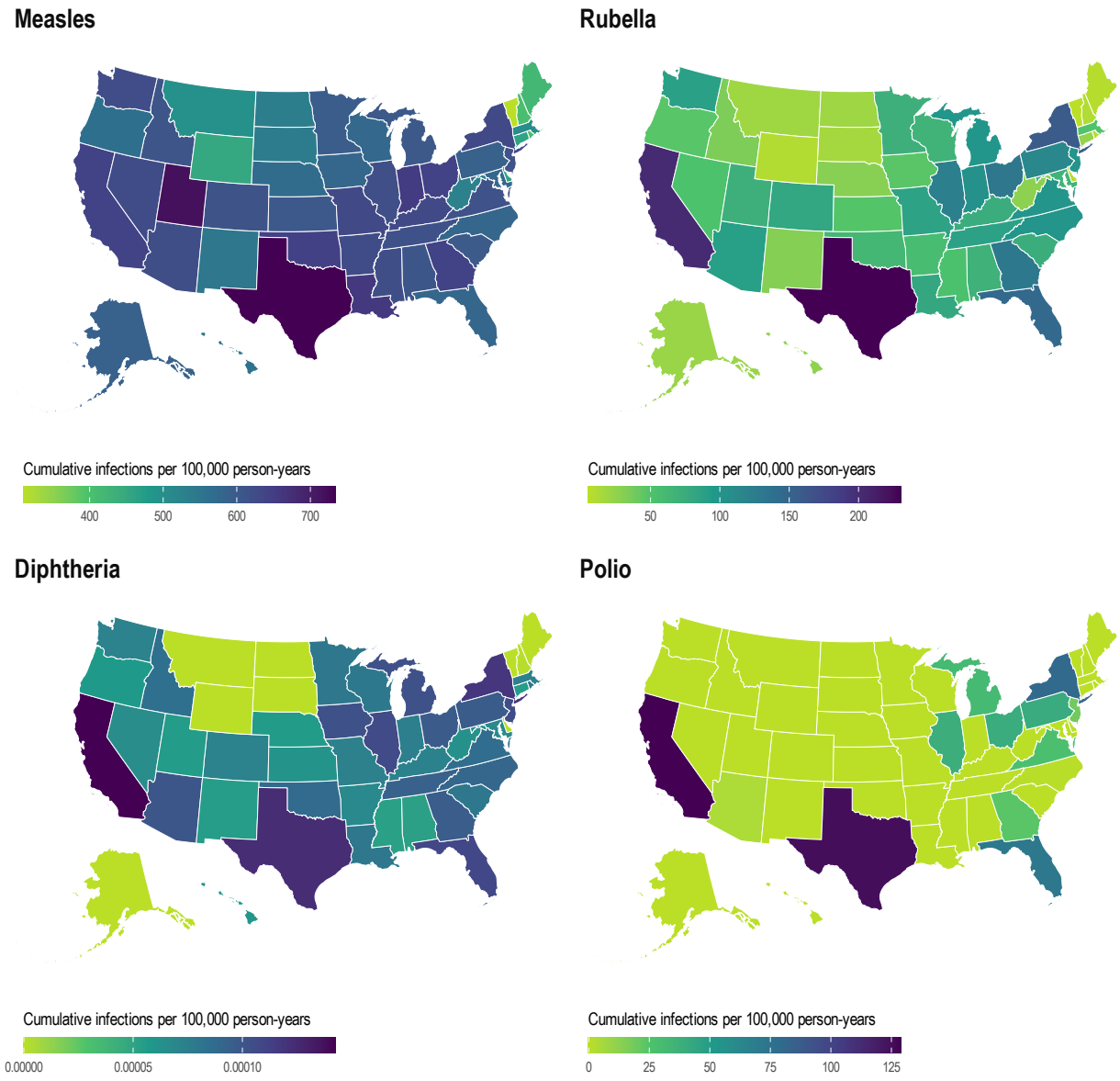
eFigure 1. Evaluation of model validity.
Cumulative incident infections under the current levels of vaccination over time (top row) and high vaccination scenario of 95% (bottom row) for each pathogen (columns) over 5 years. The black line is the mean model-based estimate with the associated uncertainty (gray shading), which can be compared against the red dots at year 5 that are the expected observed cumulative cases over a 5-year period based on recent historical case data. The model-based predictions and observed cases are shown to be similar, supporting model validity.



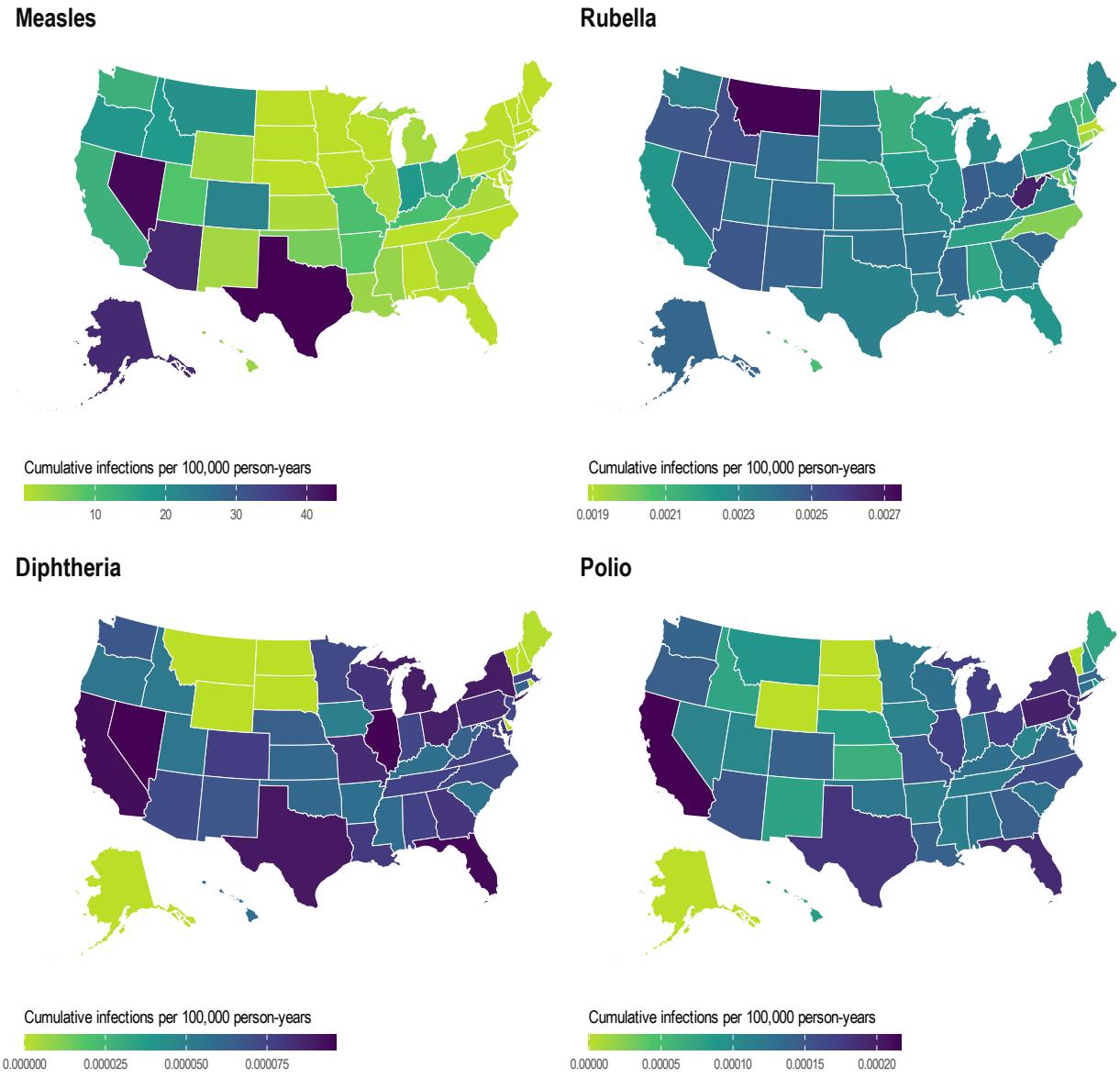
eFigure 2. Predicted cumulative cases of measles, rubella, diphtheria, and poliomyelitis over 25 years under different scenarios of childhood vaccination.
The model estimated mean number of cumulative cases of each disease (rows) under different routine childhood vaccination scenarios (colors), including current state-specific levels of vaccination. Each vaccination scenario is a relative reduced percentage of the current state-specific level of vaccination. The line represents the mean over 2,000 simulations and the shaded region represents the 95th percentile of stochastic uncertainty around the estimate.



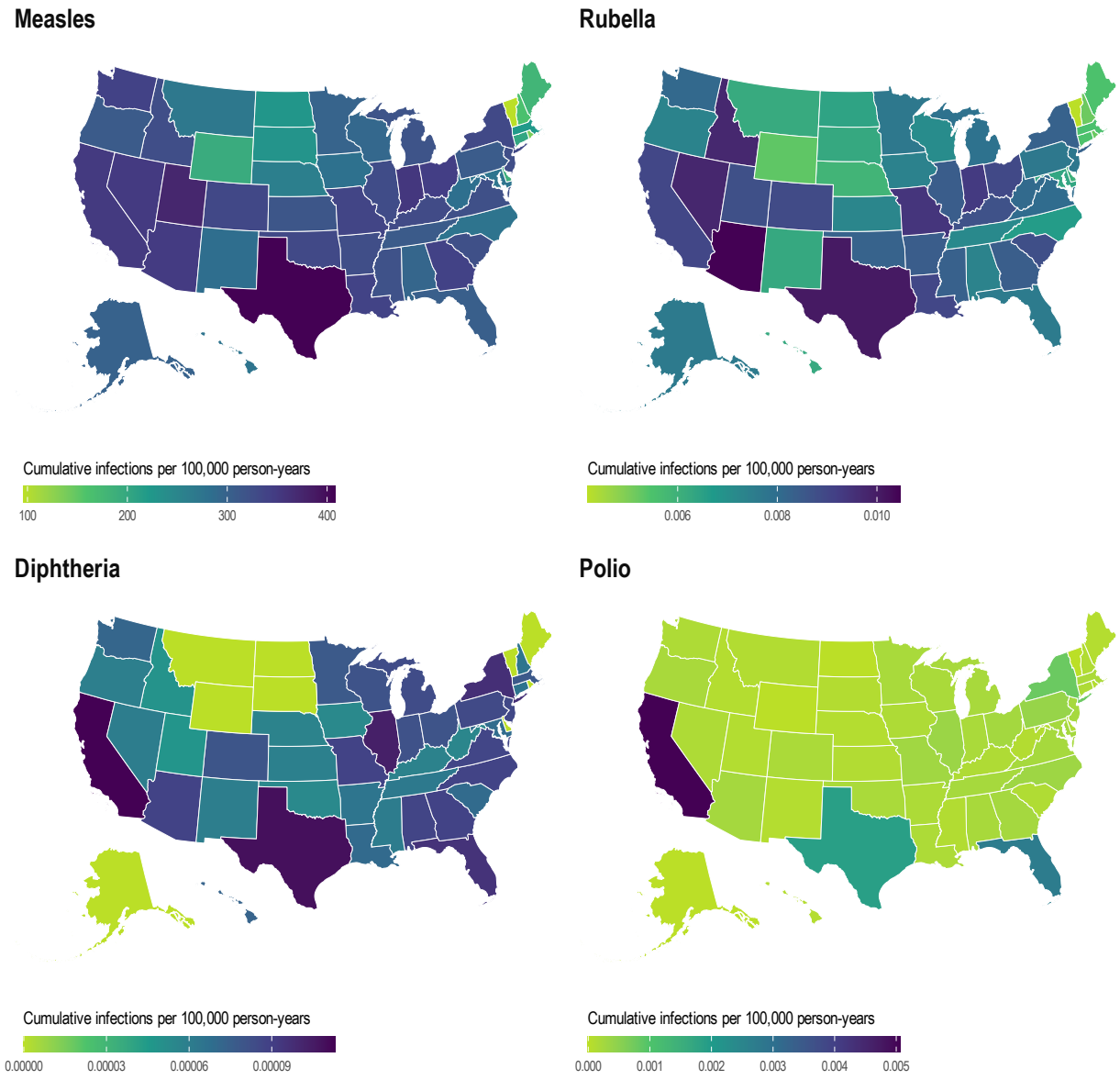
eFigure 3. Probability and timing of at least one infection-related complication under different scenarios of childhood vaccination.
The probability of at least one infection-related complication (y-axis) occurring was calculated as the proportion of simulations (out of 2,000) in which at least one complication occurred by that time (x-axis).



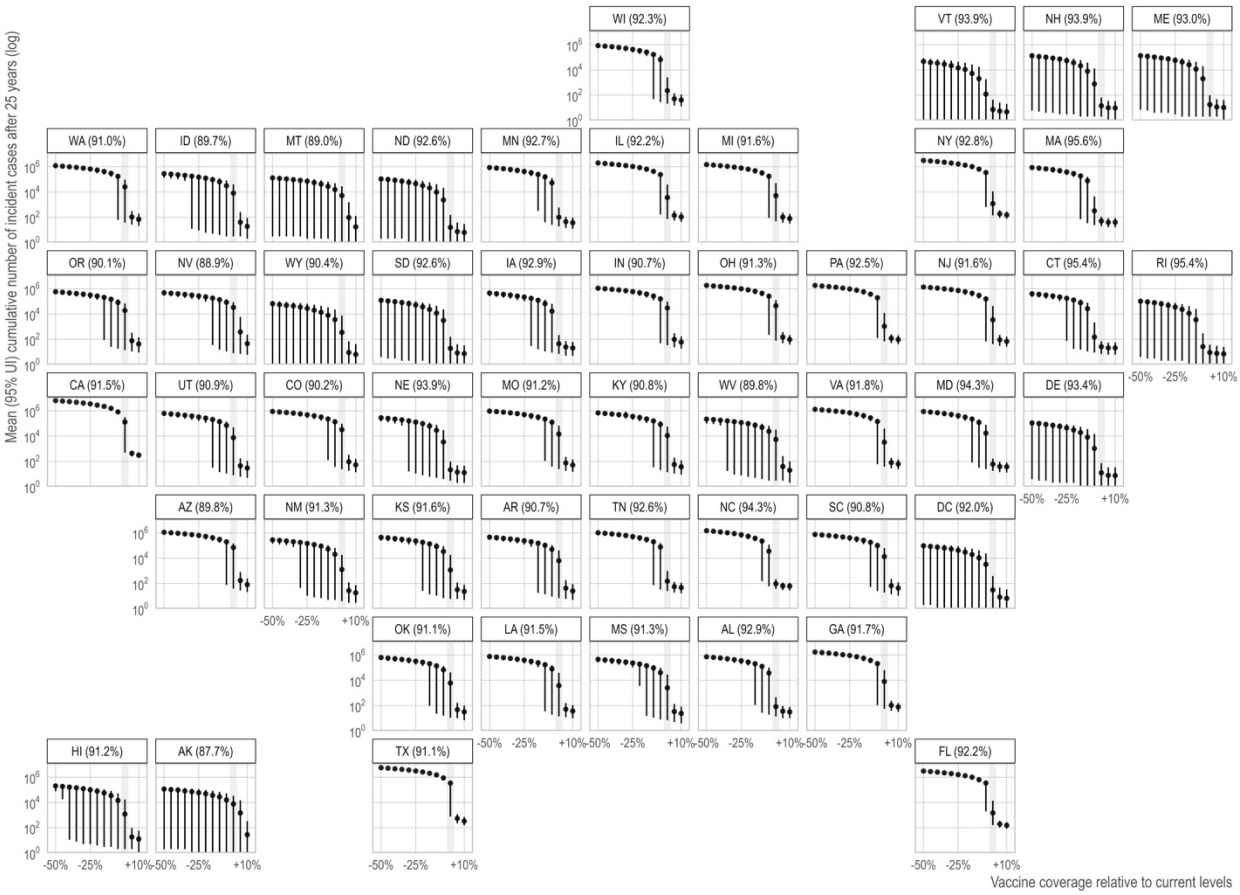
eFigure 4. State-level heterogeneity in cumulative incidence of measles, rubella, diphtheria, and poliomyelitis under 50% lower levels of routine childhood vaccination in the United States over 25 years.
The model generated estimates of cumulative incidence for each infectious disease (panels) under a scenario of 50% decline in childhood vaccination by state over the simulation period. The rate is averaged over the entire simulation period



eFigure 5. State-level heterogeneity in cumulative incidence of measles, rubella, diphtheria, and poliomyelitis under current levels of routine childhood vaccination in the United States over 25 years.
The model generated estimates of cumulative incidence for each infectious disease (panels) under current levels of childhood vaccination by state over the simulation period. The rate is averaged over the entire simulation period.

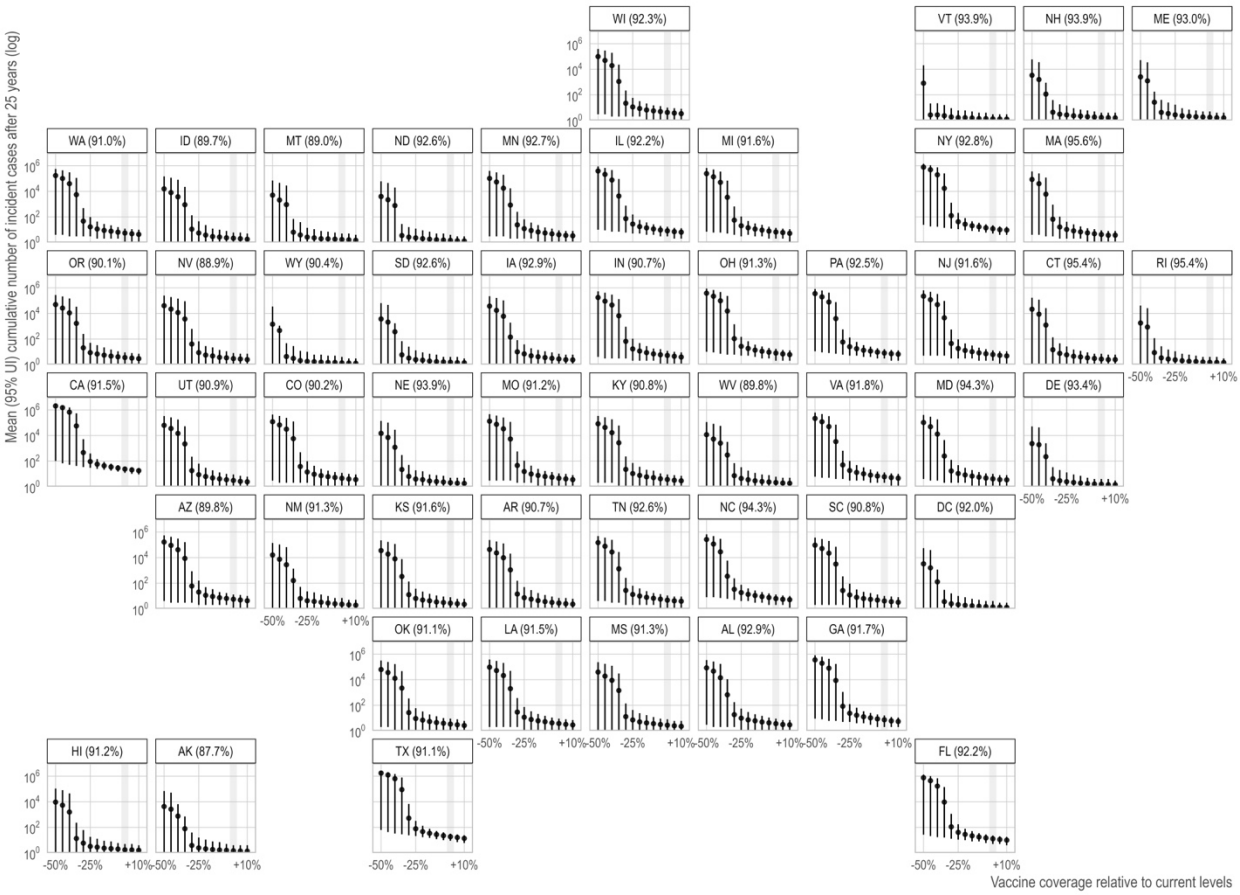


eFigure 6. State-level heterogeneity in cumulative incidence of measles, rubella, diphtheria, and poliomyelitis under 25% lower levels of routine childhood vaccination in the United States over 25 years.
The model generated estimates of cumulative incidence for each infectious disease (panels) under 25% lower levels of childhood vaccination by state over the simulation period. The rate (reported as continuous) is averaged over the entire simulation period, whereas Figure 4 reports discretized rates.

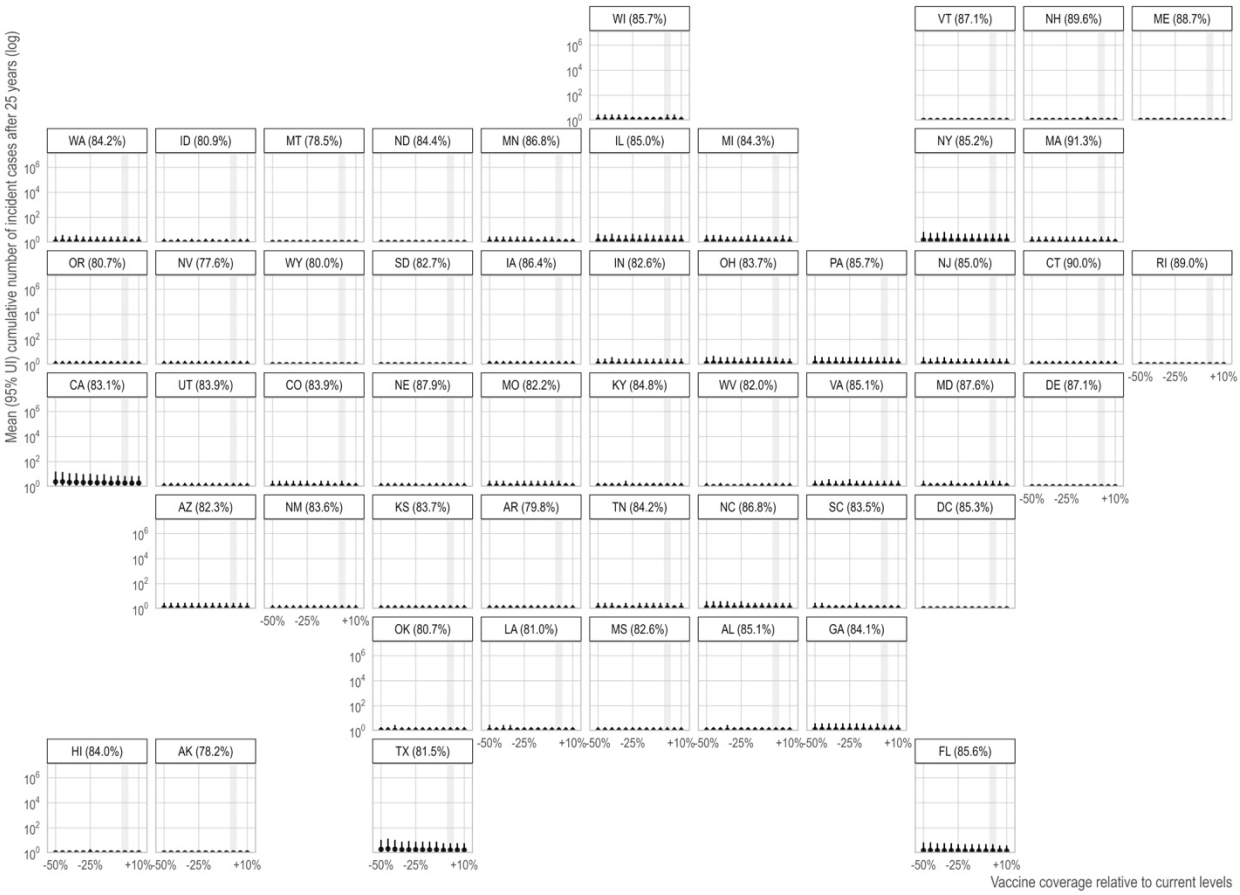


eFigure 7. State-level cumulative incidence of measles under various levels of routine childhood vaccination in the United States over 25 years

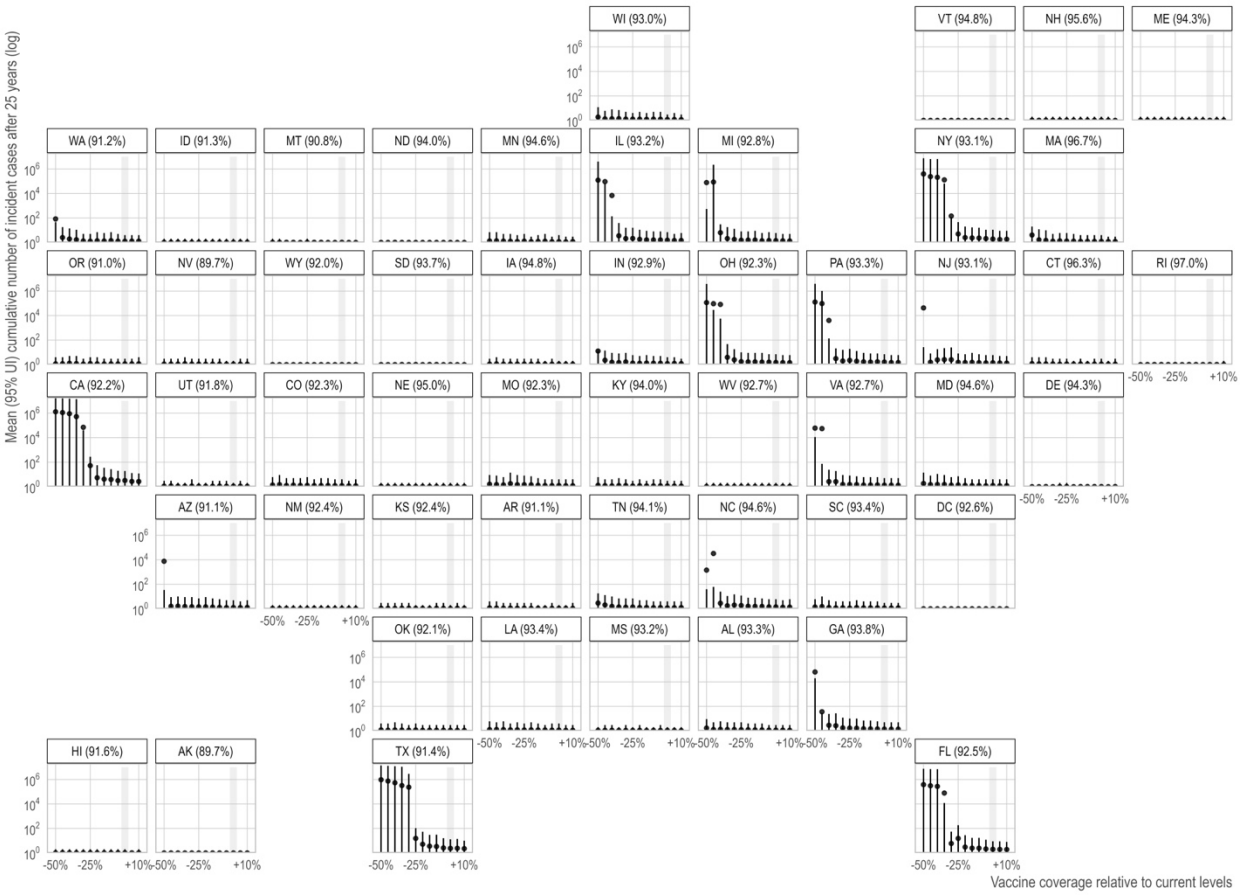
The model generated estimates of cumulative incidence for each state (facet) under different levels of childhood vaccination by state over the simulation period. The states are in approximate geographic location and the value shows the current vaccination level for that state. The rate is averaged over the entire simulation period.



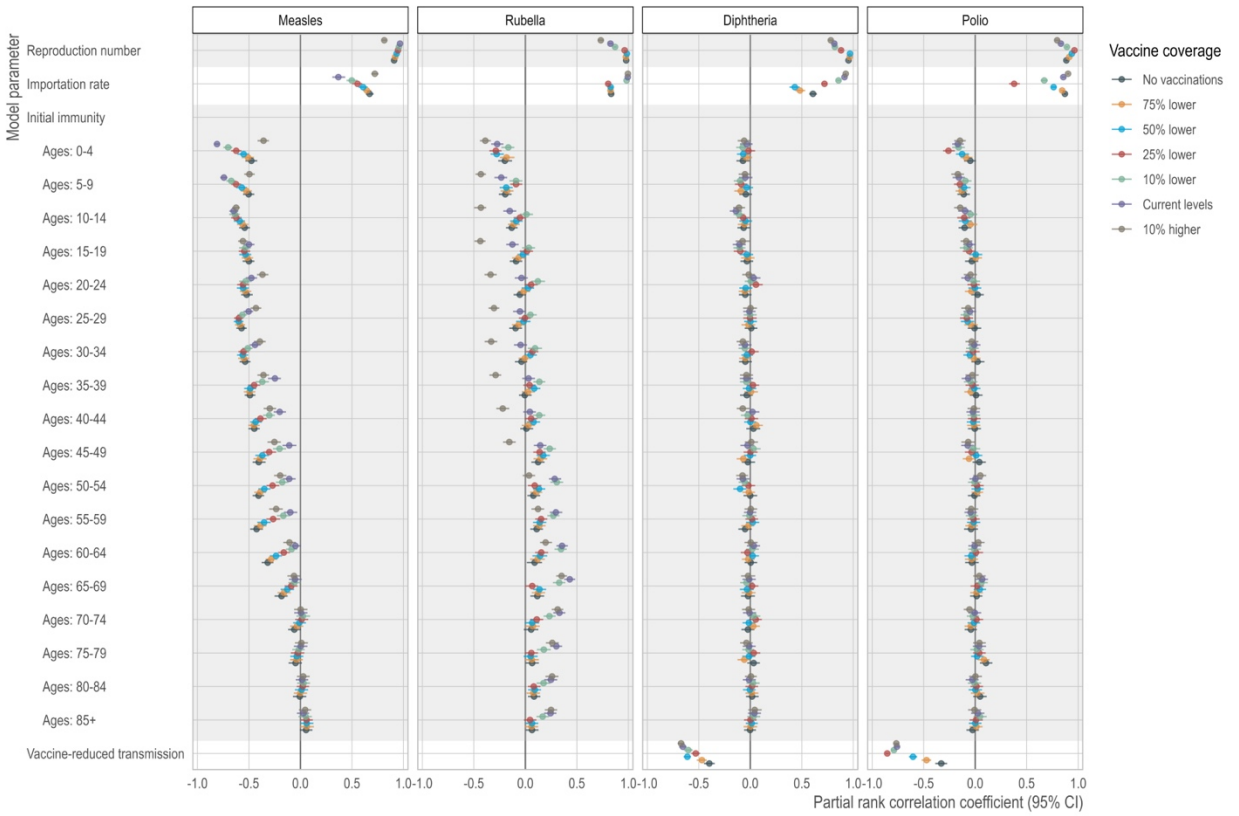
eFigure 8. State-level cumulative incidence of rubella under various levels of routine childhood vaccination in the United States over 25 years.
The model generated estimates of cumulative incidence for each state (facet) under different levels of childhood vaccination by state over the simulation period. The states are in approximate geographic location and the value shows the current vaccination level for that state. The rate is averaged over the entire simulation period.



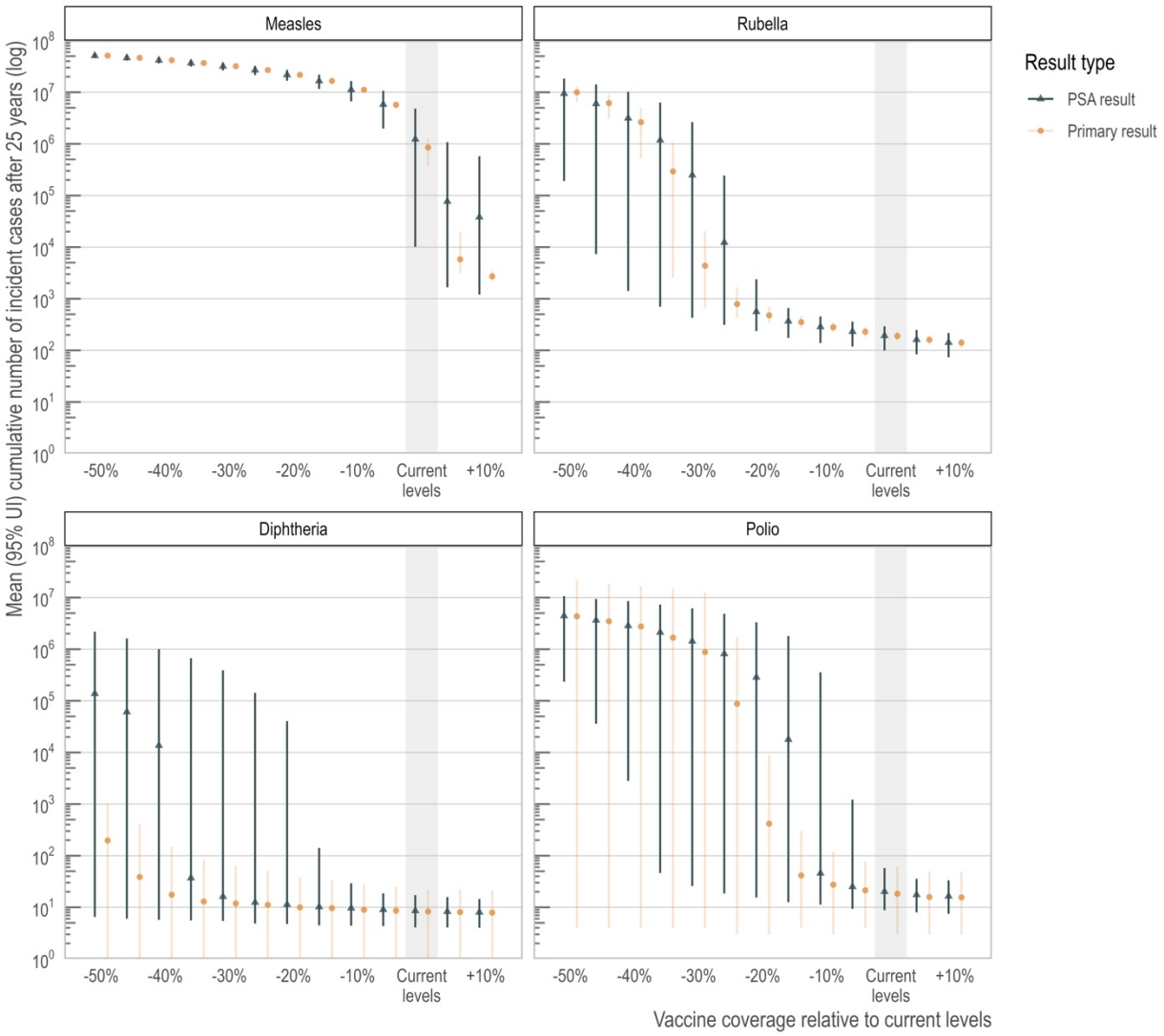
eFigure 9. State-level cumulative incidence of diphtheria under various levels of routine childhood vaccination in the United States over 25 years.
The model generated estimates of cumulative incidence for each state (facet) under different levels of childhood vaccination by state over the simulation period. The states are in approximate geographic location and the value shows the current vaccination level for that state. The rate is averaged over the entire simulation period.



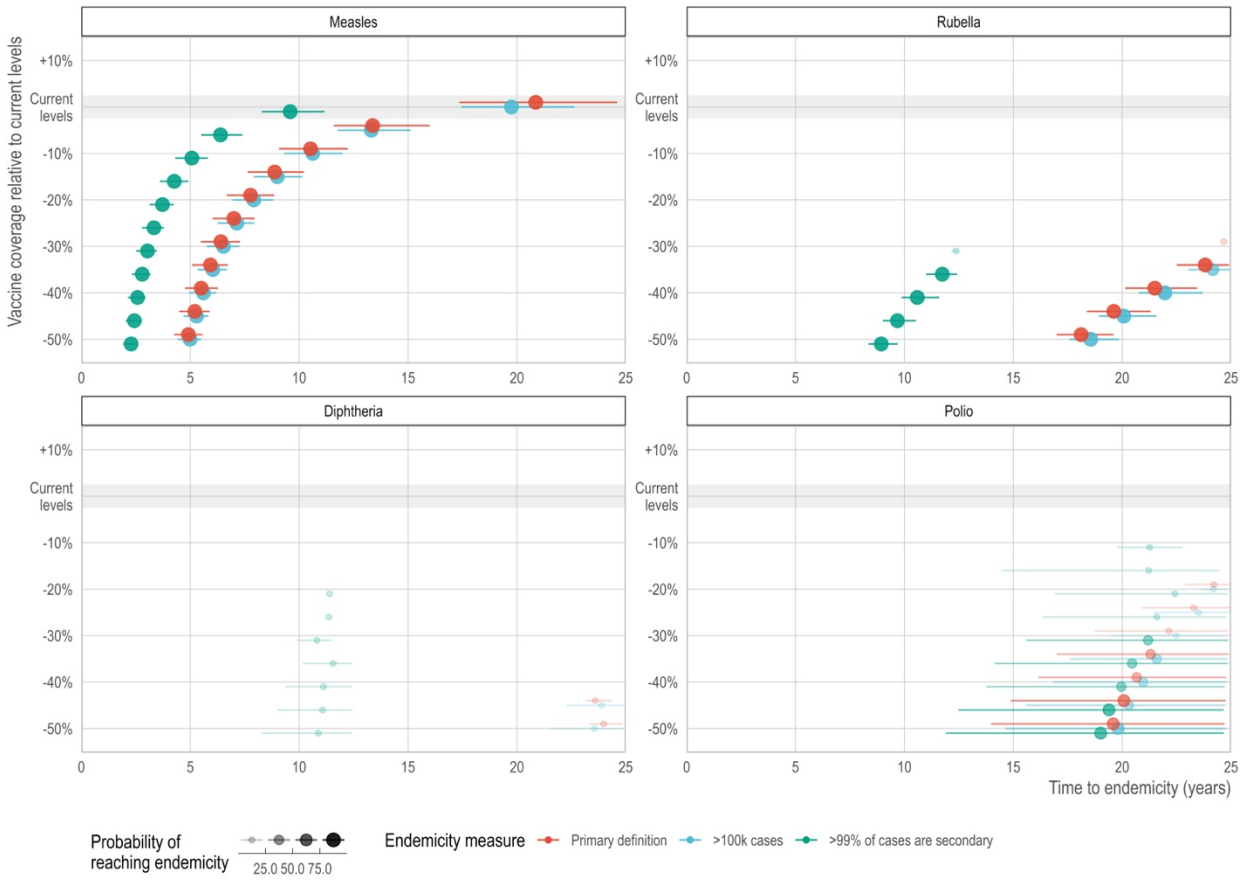
eFigure 10. State-level cumulative incidence of poliomyelitis under various levels of routine childhood vaccination in the United States over 25 years.
The model generated estimates of cumulative incidence for each state (facet) under different levels of childhood vaccination by state over the simulation period. The states are in approximate geographic location and the value shows the current vaccination level for that state. The rate is averaged over the entire simulation period.



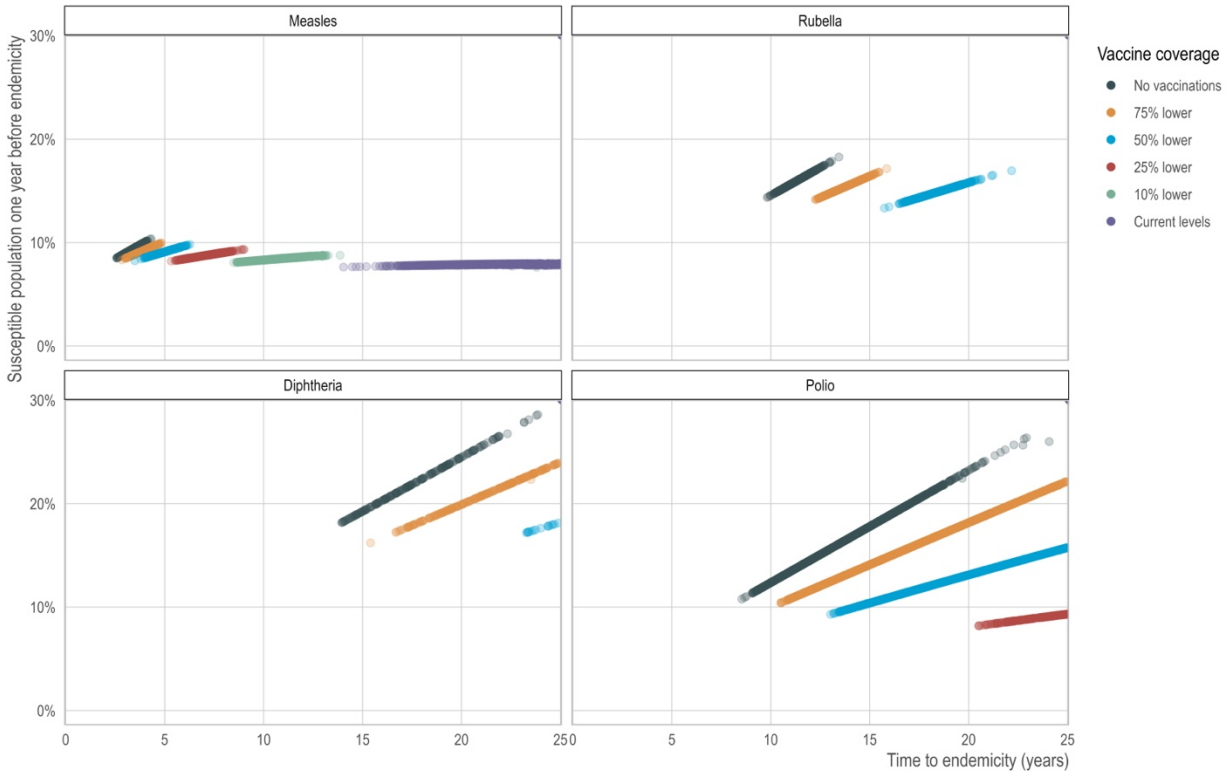
eFigure 11. Partial rank correlation coefficients of the probabilistic sensitivity analysis. Each point indicates the association between the parameter of interest and the cumulative number of incident infections after 25 years after accounting for the correlation of other parameters. For all pathogens, the basic reproduction number and importation rate are most highly associated with cumulative infections with varying degrees of association for initial immunity. For poliovirus and diphtheria, lower levels of vaccine-related transmission reduction were associated with higher cumulative infections. See eTable 1 for range of parameter values.



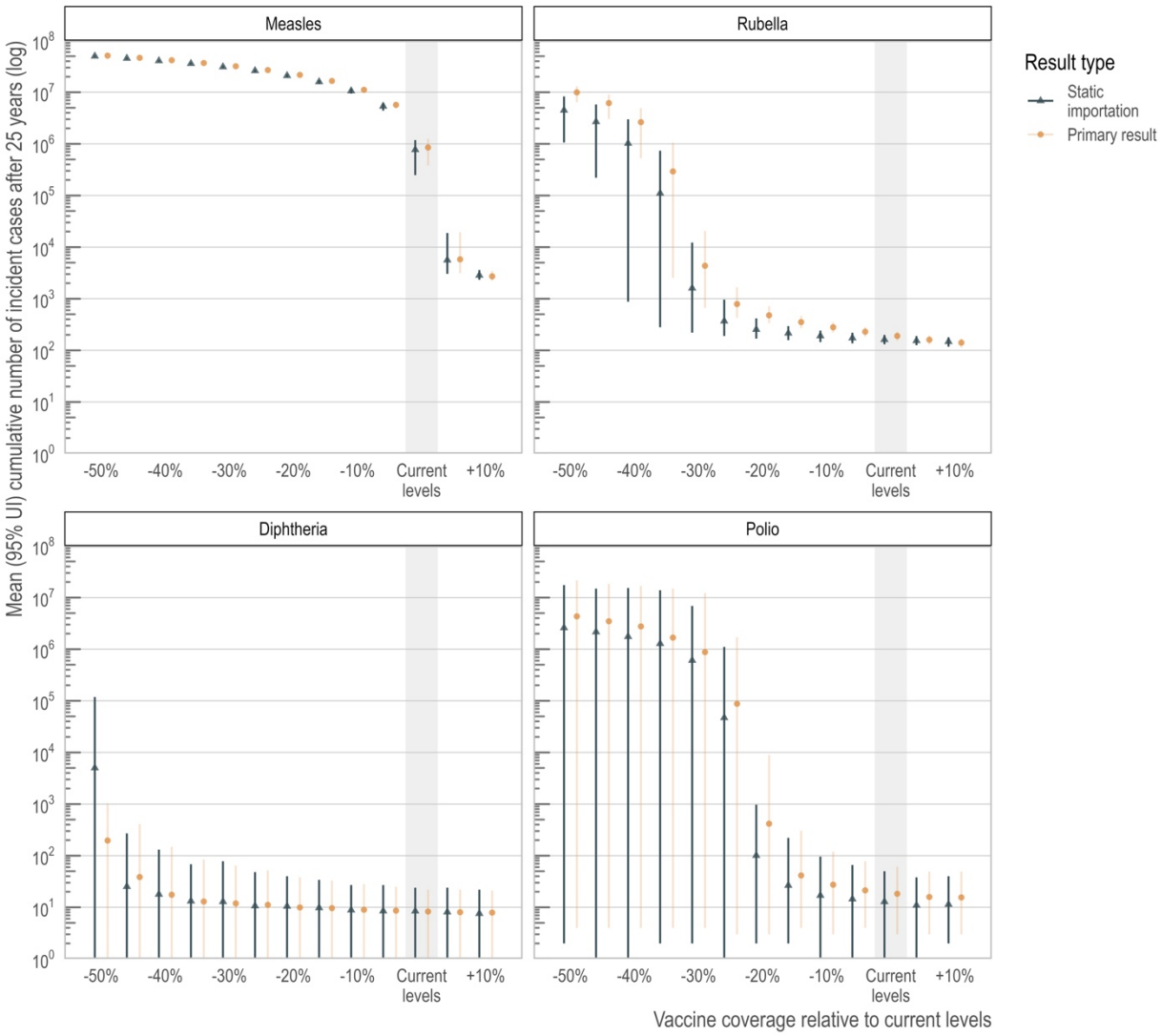
eFigure 12. Results from probabilistic sensitivity analysis for cumulative cases compared to primary results.
See eTable 1 for range of parameter values.



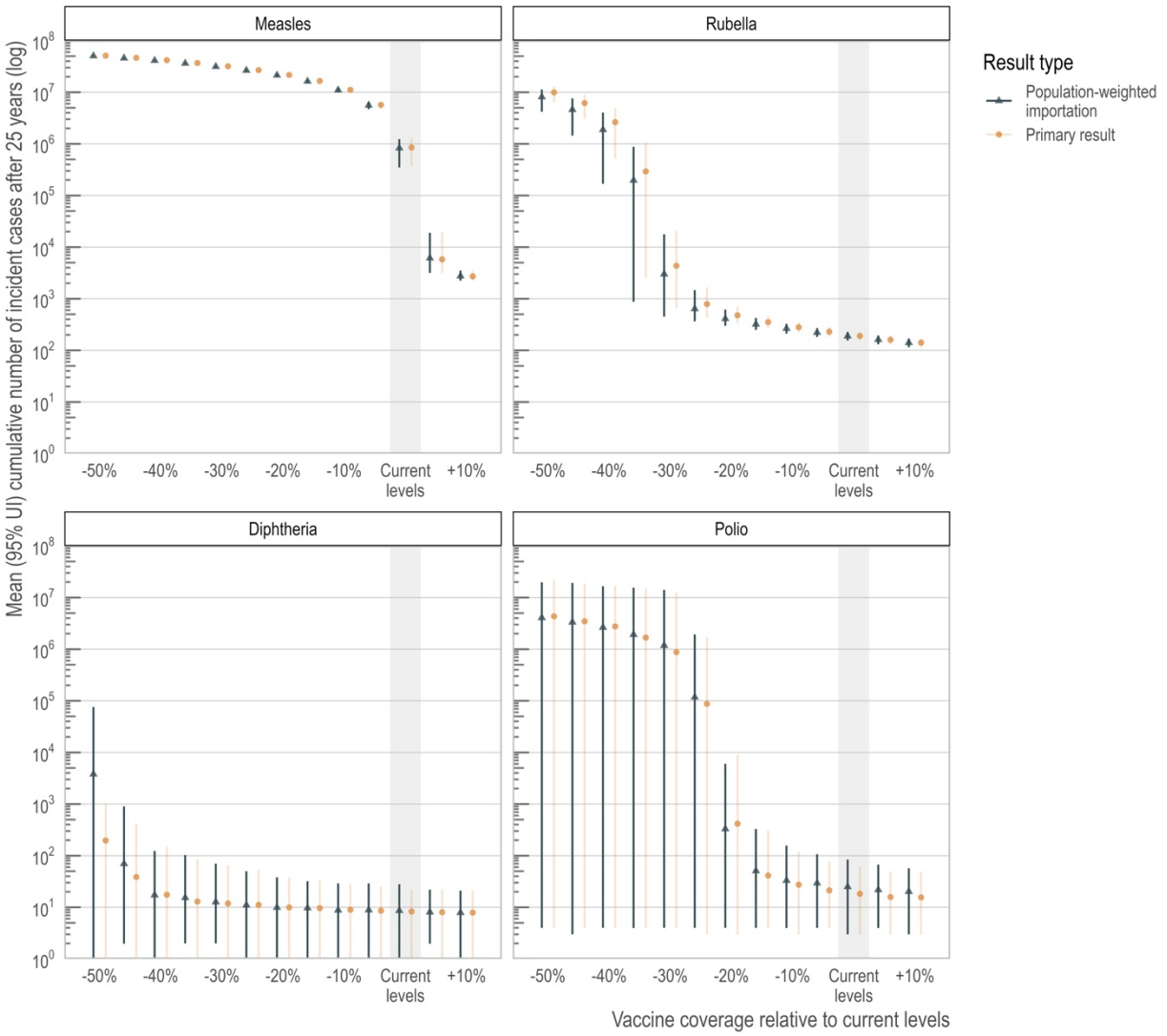
eFigure 13. Comparison of alternative definitions of endemicity for predicting probability and timing for return to endemicity for measles, rubella, diphtheria, and poliomyelitis. We compare the primary definition for endemicity ($R_e \geq 1$ for a year) to alternative definitions, including when >100,000 locally transmitted cases have occurred and when >99% of cases are locally acquired over the simulation period.



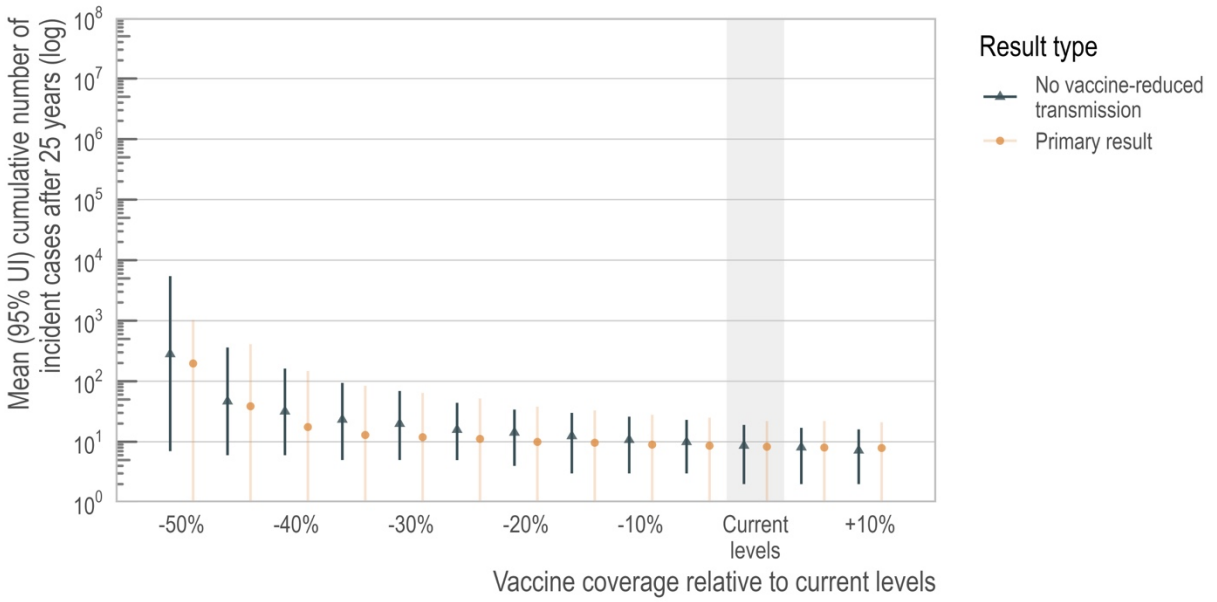
eFigure 14. Mean US population immunity and timing for return to endemicity in simulations with endemicity for measles, rubella, diphtheria, and poliomyelitis.
We estimated the population-weighted mean of population immunity over the entire US population at the time point when a pathogen re-establishes endemic transmission for a given scenario. Therefore, many states (including those with endemic transmission) have lower population immunity at the time of a pathogen re-establishing endemic transmission than the plotted US population average of immunity.



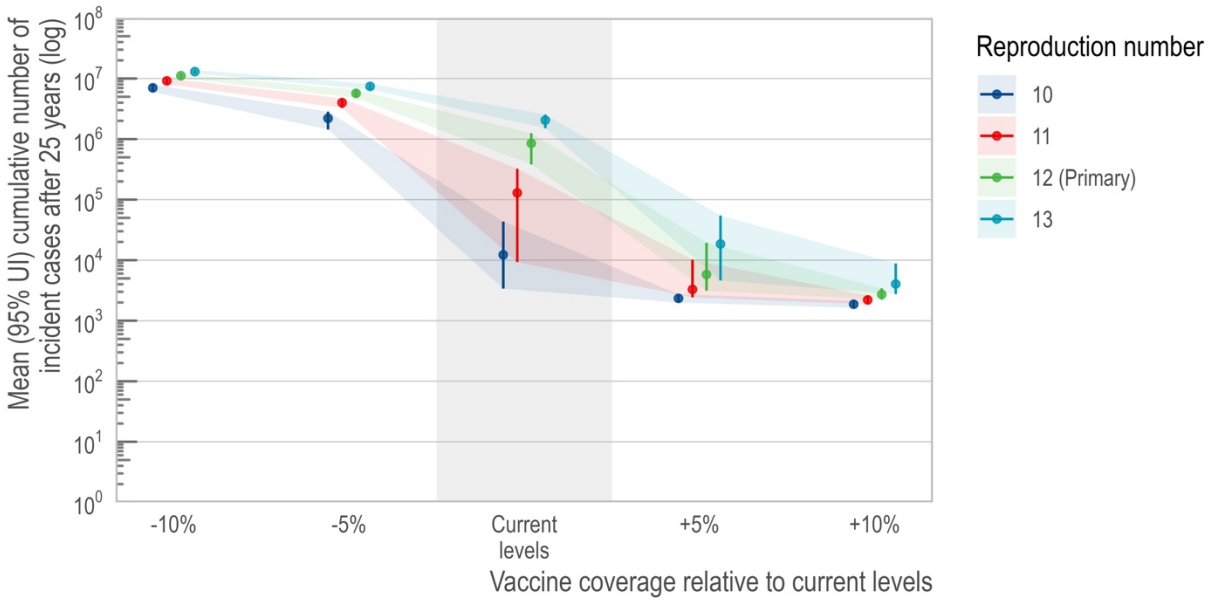
eFigure 15. Sensitivity analysis with static infection importation rate.
This sensitivity analysis conservatively modeled a fixed (static) importation risk for each infectious disease, which did not vary with the proportion of susceptible people in the US population. The static importation rates are shown in Table 1. This is compared against the primary analysis with dynamic importation risk, which did increase with population susceptibility.



eFigure 16. Sensitivity analysis using population-weighted distribution of imported cases. This sensitivity analysis distributes the imported cases by population size (compared to the primary model, which distributes imported cases by susceptibility).



eFigure 17. Sensitivity analysis on mode of vaccine-derived protection for diphtheria. This sensitivity analysis models diphtheria vaccines providing 97% protection against infection (labeled as no vaccine-reduced transmission) compared to the primary analysis, where the diphtheria vaccine only reduces clinical severity and transmission.



eFigure 18. Sensitivity analysis on the basic reproduction number (R_0) for measles.
This sensitivity analysis models measles at different basic reproduction numbers under select levels of routine childhood vaccination. While we use a conservative R_0 of 12, we find similar results at R_0 of 11 and while measles is not endemic under current levels when R_0 is set to 10, it does have similar endemic behavior when vaccination is reduced by 5% (or more).

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