Supplemental Appendix: Cause-specific mortality by county, race, and ethnicity in the USA, 2000–2019: a systematic analysis of health disparities

Contents

1 GATHER Checklist

Item #	Checklist item	Description of Compliance
Objectives and funding		
1	Define the indicator(s), populations (including age, sex, and geographic entities), and time period(s) for which estimates were made.	Abstract, Introduction, Methods sections
2	List the funding sources for the work.	Article Information
Data Inputs		
For all data inputs from multiple sources that are synthesized as part of the study:		
3	Describe how the data were identified and how the data were accessed.	Methods section
4	Specify the inclusion and exclusion criteria. Identify all ad-hoc exclusions.	Methods section
5	Provide information on all included data sources and their main characteristics. For each data source used, report reference information or contact name/institution, population represented, data collection method, year(s) of data collection, sex and age range, diagnostic criteria or measurement method, and sample size, as relevant.	Methods section, Supplemental Methods, Appendix sections 3.2 and 3.4
6	Identify and describe any categories of input data that have potentially important biases (eg, based on characteristics listed in item 5).	Methods section
For data inputs that contribute to the analysis but were not synthesized as part of the study:		
7	Describe and give sources for any other data inputs.	N/A
For all data inputs:		
8	Provide all data inputs in a file format from which data can be efficiently extracted (eg, a spreadsheet rather than a PDF), including all relevant meta-data listed in item 5. For any data inputs that cannot be shared because of ethical or legal reasons, such as third-party ownership, provide a contact name or the name of the institution that retains the right to the data.	GHDx link (upon publication)
Data analysis		
9	Provide a conceptual overview of the data analysis method. A diagram may be helpful.	Methods section, appendix section 4.1
10	Provide a detailed description of all steps of the analysis, including mathematical formulae. This description should cover, as relevant, data cleaning, data pre-processing, data adjustments and weighting of data sources, and mathematical or statistical model(s).	Methods section, Appendix section 2
11	Describe how candidate models were evaluated and how the final model(s) were selected.	Appendix section 2
12	Provide the results of an evaluation of model performance, if done, as well as the results of any relevant sensitivity analysis.	Appendix section 2
13	Describe methods for calculating uncertainty of the estimates. State which sources of uncertainty were, and were not, accounted for in the uncertainty analysis.	Methods section, Appendix section 2
14	State how analytic or statistical source code used to generate estimates can be accessed.	GHDx link (upon publication)
Results and Discussion		
15	Provide published estimates in a file format from which data can be efficiently extracted.	GHDx link (upon publication)
16	Report a quantitative measure of the uncertainty of the estimates (eg uncertainty intervals).	Results section, GHDx link (upon publication)
17	Interpret results in light of existing evidence. If updating a previous set of estimates, describe the reasons for changes in estimates.	Introduction, Discussion sections
18	Discuss limitations of the estimates. Include a discussion of any modelling assumptions or data limitations that affect interpretation of the estimates.	Discussion section

Checklist template obtained from: http://gather-statement.org/

2 Supplemental Methods

The methods used for this analysis and described below are an extension of methods previously developed for estimating all-cause mortality and life expectancy by county and racial–ethnic group in the US.[1]

2.1 Deaths and population data processing

We used de-identified death records from the National Vital Statistics System (NVSS) and population estimates from the National Center for Health Statistics (NCHS) for the years 2000–2019 for this analysis (section 3.2). Deaths were tabulated by county, age group (0, 1–4, 5–9, …, 80–84, 85+ years of age), sex, racial–ethnic group, year, and cause. In cases where age was missing (0.0177% of deaths), we calculated the proportion of deaths within each age group by state, year, sex, and racial–ethnic group among those entries with age information and then reapportioned deaths without age information by using these proportions. This approach effectively assumes that age is missing at random. We are unable to verify this assumption; however, we believe it's unlikely that violations of this assumption would substantively impact the results of our analysis, given the rarity of missing age in the deaths data. In cases where death records were missing information on race or where race was coded as "other" (0.63%), NCHS imputed a value. In cases where multiple race information was collected and decedents were identified as two or more races (0.29%), NVSS included an imputed or "bridged" race value that corresponds to the predicted "primary" race for each decedent.[2] We used these imputed and bridged values for the present analysis. NCHS does not impute missing Latino ethnicity (0.29%); for the purposes of this analysis, deaths among individuals with unknown Latino ethnicity were redistributed in proportion to the size of the Latino and non-Latino populations in the same county, race, age, sex, and time period. To ensure stable ratios for this redistribution, we pooled data over time as needed to achieve a minimum population of 50. This threshold of 50 is somewhat arbitrary, but was selected in an attempt to balance the need for stable ratios with the desire to have ratios that reflect the distribution of the population within as specific a time-range as possible.

2.2 Cause list, misdiagnosis correction, and garbage code redistribution

We used the cause list developed for the Global Burden of Diseases, Injuries, and Risk Factors (GBD) 2021 study for this analysis. The GBD cause list is arranged hierarchically in four levels; within each level, the cause list is designed such that each death is assigned to exactly one cause. Level 1 includes three broad groups of causes (communicable, maternal, neonatal, and nutritional diseases; non-communicable diseases; and injuries), Level 2 includes 21 more detailed cause groupings, Level 3 includes 139 specific causes, and Level 4 is the most detailed with 226 causes (including 102 Level 3 causes that are not further disaggregated at Level 4). We utilised the map developed by the GBD study to translate ICD-10 codes into GBD causes (section 3.3).

Previous studies have identified two issues that require adjustments to the underlying cause of death codes recorded in death certificate data. First, trends in mortality due to Alzheimer's disease and other dementias, Parkinson's disease, and atrial fibrillation and flutter based on death certificate data are often inconsistent with trends in prevalence and case-fatality from other data sources. This inconsistency is thought be the result of changes over time and differences by location in coding practices related to these causes. Second, many deaths are observed to have been assigned an underlying cause of death code that instead refers to an intermediate or immediate cause of death (eg, cardiopulmonary arrest) or that is insufficiently specific (eg, malignant neoplasm of other and ill-defined sites); these codes are referred to as "garbage codes."[3] Failure to address garbage codes may result in erroneous geographic and temporal patterns as the prevalence of garbage codes varies over time and by location, and may also lead to incorrect relative rankings among causes as the likelihood that a death is assigned a garbage code varies by true underlying cause of death.

We used an existing suite of methods developed by the GBD to address these two issues.[4] In the first case, this suite of methods operates by reassigning some proportion of deaths originally assigned to other causes to Alzheimer's disease and other dementias, Parkinson's disease, or atrial fibrillation and flutter to address under-coding; or by reassigning some proportion of deaths originally assigned to Alzheimer's disease and other dementias to other causes to address over-coding (Parkinson's disease and atrial fibrillation and flutter are assumed to only ever be under-coded). In the second case, this suite of methods operates by reassigning deaths originally assigned to garbage codes to likely true underlying causes of death. In both cases, the key details are determining the "target" causes for any deaths being reassigned and determining the proportion of these deaths to be reassigned to each specific target cause. A variety of methods are used to determine the target causes and the redistribution proportions, which are described elsewhere.[4] For the purposes of this analysis, the same pairings of source and target codes and the associated redistribution proportions derived for the GBD at the national or state level in the USA were applied to deaths recorded for each racial–ethnic group and for each county within a given state.

This process ensures consistency in the data used for this analysis and for the GBD, and does not alter the total number of deaths observed in any county, racial–ethnic group, age, sex, or year combination, but only effects the allocation of these deaths among different causes.

2.3 Covariate imputation and smoothing

The small area estimation models used in the present study to estimate mortality rates leverages observed relationships between the level of mortality and sociodemographic and socioeconomic factors (covariates) to improve estimates where populations are small and the observed number of deaths is an imprecise indicator of the underlying mortality rate. Among the five covariates used in this analysis, educational attainment (bachelor's degree or higher), poverty rate, and proportion foreign-born were stratified by both county and race–ethnicity, whereas median household income and population density were stratified only by county and represent estimates for the total population in that county (section 3.4). The underlying data for the covariates stratified by both county and racial–ethnic group contained missing values and displayed instability and low precision for some strata with small populations. As covariate estimates are required for all location, year, and racial–ethnic group combinations to derive mortality predictions, small area imputation models were developed to derive smoothed covariate estimates in all years, counties, and racial–ethnic groups prior to including these covariates in the mortality models. Covariates that were not stratified by racial–ethnic group in addition to county were incorporated in the mortality models in their original (non-imputed) forms due to their larger sample sizes and complete spatial and temporal coverage.

Covariate data were derived primarily from the American Community Survey (ACS) and decennial population census. Racial classifications in the tabulated ACS and census data include separate groups for Asian and for Native Hawaiians and other Pacific Islander (NHPI) populations; covariate data for these groups were combined into a single group for consistency with the mortality models. Covariate data were also combined for merged counties to derive a stable location set matching that used in the mortality models (section 3.1). The ACS provides estimates of uncertainty as Margins of Error (MOE) at a confidence level of 90%, rather than providing variance estimates themselves. Per guidance from the Census Bureau,[5] variance was calculated as:

$$\mathrm{Var}(X_i) = \left(\frac{\mathrm{MOE}(X_i)}{1.645}\right)^2$$

where X_i is the reported estimate for group i. Also following Census guidance, variances for merged geographic and demographic entities were calculated as the sum of the variances over component groups, assuming independence:

$$\mathrm{Var}(X_1 + X_2) = \mathrm{Var}(X_1) + \mathrm{Var}(X_2)$$

As the ACS and decennial census data were derived from population samples but are reported as values scaled to total population sizes, their effective sample sizes were estimated to appropriately scale sampling variance in the imputation models, using a three-pronged strategy. The long-form decennial census questionnaires in 1990 and 2000, from which the education, poverty, and foreign-born data were derived for those years, were collected from a 20% and 17% population sample, respectively.[6] Effective sample sizes were therefore assumed to be 20% or 17% of the total population for each county, year, and racial–ethnic group combination in 1990 and 2000, respectively.

Effective sample sizes for ACS data, for which variances were calculated as above, were estimated by the relationship between effective sample size, $\hat{n}_{eff}$, estimates of the population proportion, $\hat{p}$, and its variance, $\mathrm{Var}(\hat{p})$:[7]

$$\hat{n}_{eff} = \frac{\hat{p}(1-\hat{p})}{\mathrm{Var}(\hat{p})}$$

As observations with observed proportions of 0·0 or 1·0 yield effective sample sizes of 0·0, the reported population fractions ($\hat{p}$) for these county, year, and race–ethnicity combinations were transformed via an empirical logit transformation[8] and then inverse-transformed by use of the standard inverse logit function before calculating the corresponding effective sample sizes:

$$\hat{p}_{emp} = \mathrm{logit}^{-1}\left(\log\left(\frac{\hat{p} + \frac{\varepsilon}{2}}{1 - \hat{p} + \frac{\varepsilon}{2}}\right)\right)$$

where logit^{-1} is the standard inverse logit function and ε is defined as the smallest non-zero proportion in the data set. Effective sample sizes were calculated by use of these transformed proportions and the original reported $\mathrm{Var}(\hat{p})$. Counts of individuals with the modelled outcome (attainment of a bachelor's degree or higher, living below the poverty line, or foreign-born) were then calculated for each row by multiplying their original reported proportions and estimated effective sample sizes.

Bayesian imputation models were fit in R-INLA[9] v.20.09.25 in R v3.5.1[10] by use of binomial likelihood models, and explicitly borrow strength over space, time, and racial–ethnic group in an approach analogous to the small area mortality models:

$$Y_{j,t,r} \sim \text{Binomial}(p_{j,t,r}, \hat{n}_{eff,j,t,r})$$
$$\text{logit}(p_{j,t,r}) = \beta_0 + \gamma_{1,j} + \gamma_{2,j,t,r} + \gamma_{3,j,t} + \gamma_{4,r}$$

where $Y_{j,t,r}$ is the estimated count of individuals in county *j*, year *t*, and racial–ethnic group *r* with the modelled outcome, among an effective sample size of $\hat{n}_{eff,j,t,r}$ with proportion $p_{i,t,r}$. Model terms consist of:

- β_0 is a global intercept with a Normal(0, 10) prior;
- $\gamma_{1,j}$ is a random intercept for county with a Besag-York-Mollie-type prior (BYM2) combining a conditional autoregressive distribution for spatial autocorrelation, based on county adjacency, with independent-and-identically-distributed (IID) Gaussian distribution;
- $\gamma_{2,j,t,r}$ is a random intercept for county, racial–ethnic group, and year combinations with a first-order autoregressive (AR1) temporal prior, grouped by county and racial–ethnic group;
- $\gamma_{3,j,t}$ is a random intercept for county and year combinations with an AR1 temporal prior grouped by county;
- and $\gamma_{4,r}$ is a random intercept for racial–ethnic group with an IID Gaussian prior.

Default INLA hyperpriors were used. The BYM2 parameterisation includes a parameter, φ, which indicates the contribution of the structured spatial effect to the marginal variance; $\text{logit}(\varphi)$ had a penalised complexity (PC) prior[11] corresponding to $\Pr(\varphi < 0.5) = 0.5$, and the log precision of the BYM2 model had a PC prior corresponding to $\Pr(\sigma > 1.0) = 0.1$. The AR1 models had Gamma(shape = 1·0, inverse-scale = $5 \cdot 10^{-5}$) priors on the precision and Normal(mean = 0·0, precision = 0·15) priors on the logit of the 1-year lagged correlation (ρ). The race–ethnicity IID term had a Gamma(shape = 1·0, inverse-scale = $5 \cdot 10^{-5}$) prior on the precision. These default priors were used as we considered them suitably vague, in the absence of a priori information with which to establish more informative priors. In

INLA, a Gaussian approximation strategy, an empirical Bayes integration strategy, and a step-length for hyperparameter gradient calculations of $1 \cdot 10^{-3}$ were utilised for model fitting. Due to numerical instability in the model for foreign-born proportion, a series of model fits were performed with iteratively decreasing values added to the diagonal of the joint precision matrix (100, 10, and 1, respectively) to derive starting parameter values for the final model run. Mean posterior predictions from the small area covariate models were used as covariate estimates in the small area mortality models.

2.4 Small area model specification

Although the focus of this study is on 19 causes of death, almost all causes of death in the GBD cause list were analysed concurrently. This is discussed in Section 2.7 (Calibration). Because of this, the following section includes descriptions of models that are not limited to the 19 causes included in this analysis.

County and racial–ethnic group model

Separate models were fitted for each cause of death at each level in the GBD hierarchy. The two exceptions to this were Level 1 cause "injuries" and Level 2 cause "maternal and neonatal disorders." In both cases, instead of modelling these causes directly, the estimates for each cause were constructed by summing the estimates from the separate models for component models. For Level 1 "injuries," this approach was taken because of the effect of large shocks in the mortality trends due to large scale disasters, such as Hurricane Katrina (included in Level 2 "unintentional injuries") and the September 11, 2001 terrorist attacks (included in Level 2 "Self-harm and interpersonal violence"). These shocks—which vary especially drastically by county, age, and racial-ethnic group—were not well modelled using a higher level "injuries" model, and aggregating these child causes proved to be better at fitting these shocks. The estimates for Level 2 "maternal and neonatal disorders" were formed by aggregating the component Level 3 causes "maternal disorders" and "neonatal disorders." This was done because the age groups for these two component causes are entirely distinct. For most causes, the following model was estimated separately for males and females:

$$
\begin{aligned}
D_{j,t,a,r} &\sim \text{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right) \\
\log\left(m_{j,t,a,r}\right) &= \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \left(\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}\right) \cdot \boldsymbol{X_{2,j,t,r}} \\
&\quad + \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right)
\end{aligned}
$$

Priors:

$$\boldsymbol{\gamma_1} \sim \text{IID}(\boldsymbol{\sigma_1})$$
$$\boldsymbol{\gamma_2} \sim \text{LCAR}(\rho_2, \sigma_2)$$
$$\boldsymbol{\gamma_3} \sim \text{LCAR: LCAR: IID}(\rho_{3,t}, \rho_{3,a}, \sigma_3)$$
$$\boldsymbol{\gamma_4} \sim \text{LCAR: LCAR: LCAR: IID}(\rho_{4,a'}, \rho_{4,t'}, \rho_{4,j}, \sigma_4)$$

Hyperpriors:

$$\sigma^{-2} \sim \text{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$$
$$\text{logit}(\rho) \sim \text{Normal}(0, 1.5)$$

where

- j, t, a, and r are indices for the county, calendar year (2000–2019, recoded sequentially from 0 to 19), age group (0, 1–4, 5–9, …, 80–84, and 85+ years old [or a subset, for causes that do not affect all age groups], recoded sequentially from 0 to 18), and racial–ethnic group (Latino, Black, White, AIAN, and Asian, recoded in that order from 0 to 4), respectively;
- $D_{j,t,a,r}$ and $P_{j,t,a,r}$ are the observed number of deaths and the population count, respectively, in county j, year t, age group a, and racial–ethnic group r;
- $m_{j,t,a,r}$ is the underlying mortality rate in county j, year t, age group a, and racial–ethnic group r;
- $\boldsymbol{X_{1,j,t}}$ is a vector of covariates for county j and year t, and $\boldsymbol{\beta_1}$ is the associated vector of regression coefficients;
- $\boldsymbol{X_{2,j,t,r}}$ is a vector of covariates for county j, year t, and racial–ethnic group r, and $\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}$ is the associated vector of regression coefficients, made up of a fixed component ($\boldsymbol{\beta_2}$) shared by all racial–ethnic groups, and a random slope component ($\boldsymbol{\gamma_{1,r}}$) that varies by racial–ethnic group;
- $\gamma_{2,j}$ is a random intercept for county;
- $\gamma_{3,a,t,r}$ is a random intercept for age group, year, and racial–ethnic group combinations;
- $\gamma_{4,j,t',a',r}$ is a random intercept for county, racial–ethnic group, year spline basis, and age spline basis combinations;
- k_t is the number of time knots (four knots, evenly spaced from 2000–2019) and t' is the corresponding index;
- k_a is the number of age knots, which varies by cause due to age restrictions (for causes with all age groups included, there are five knots at age groups 0, 25–29, 45–49, 65–69, and 85+ years old, but if the minimum age is less than 25 or maximum age is less than 85+, the initial and final

knots are adjusted to start and end at these values, although adjacent knots such as 40–44 and 45–49 are avoided by choosing a different second knot, for example 55–59; an exception is given for neonatal disorders, which has knots at ages 0 and 1; maternal disorders has only two age knots at 10 and 50 due to challenges modelling small numbers) and a' is the corresponding index;

- $S_{t'}(t)$ is the value of spline basis t' for a linear spline on year, evaluated at year t;
- and $S_{a'}(a)$ is the value of spline basis a' for a linear spline on age, evaluated at age group a.

Prior distributions were assigned for each random component:

- Each element of $\boldsymbol{\gamma_1}$—corresponding to each covariate in $\boldsymbol{X_1}$—was assumed to follow an independent and identically distributed (IID) mean-0 Normal distribution. $\boldsymbol{\gamma_1}$ is associated with three hyperparameters ($\boldsymbol{\sigma_1^2}$), corresponding to the variance of this random intercept for each covariate.
- $\boldsymbol{\gamma_2}$ was assumed to follow a conditional autoregressive distribution of the form described by Leroux, Lei, and Breslow,[12] which corresponds to the following full conditional distribution for each individual element of $\boldsymbol{\gamma_2}$:

$$\gamma_j | \gamma_{k\sim j}, \sigma^2, \rho \sim \text{Normal}\left(\frac{\rho \cdot \sum_{k\sim j} \gamma_k}{n_j \cdot \rho + 1 - \rho}, \frac{\sigma^2}{n_j \cdot \rho + 1 - \rho}\right)$$

  where $k \sim j$ indicates the set of counties that are adjacent to county j and n_j is the number of counties in $k \sim j$. In this distribution, the σ^2 parameter controls the degree of spatial variation and the ρ parameter, which varies between 0 and 1, determines the degree of spatial smoothness.
- $\boldsymbol{\gamma_3}$ was assumed to follow a mean-0, multivariate Normal distribution with a separable covariance structure defined via the Kronecker product of the covariance matrix of three distributions:[13,14] a conditional autoregressive distribution as in γ_2 but defined for age groups rather than counties; a second conditional autoregressive distribution as in γ_2 but defined for years rather than counties; and a multivariate Normal distribution with a diagonal covariance matrix. This random intercept is associated with three hyperparameters: $\rho_{3,a}$ and $\rho_{3,t}$, which control the correlation across age groups and time, respectively; and σ_3^2 which controls the degree of variation.
- $\boldsymbol{\gamma_4}$ was also assumed to follow a mean-0, multivariate Normal distribution, in this case with a separable covariance structure defined via the Kronecker product of the covariance matrix of four

distributions: three conditional autoregressive distributions as described above, for county, age spline basis, and year spline basis; and an IID Normal distribution for racial–ethnic group. For this random intercept, there are two sets of hyperparameters: $\rho_{4,a'}$, $\rho_{4,t'}$, and $\rho_{4,j}$, which control the smoothness over the age spline, year spline, and county, respectively; and σ_4^2 which controls the degree of variation.

Finally, hyperpriors were defined for the standard deviation (σ) and, where applicable, autocorrelation (ρ) hyperparameters:

- Penalised complexity (PC) priors were specified for the inverse variance ($1/\sigma^2$) of each random effect.[11] PC priors shrink toward a base model, which in this case is where the marginal variance is 0. They are specified by setting the tail probability on each hyperparameter. We followed the recommendation by Fuglstad et al.,[11] selecting priors that satisfy $Pr(\sigma > \sigma_0) = 0.05$ where σ_0 is between 2.5 and 40 times the expected true marginal standard deviation. Specifically, we set $\sigma_0 = 5;\ Pr(\sigma > \sigma_0) = 0.05$.
- Normal(0, 1.5) priors were specified for the logit-transform of the correlation parameters (ρ).

Posterior means and standard errors for these hyperparameters are provided in section 3.6.

Descriptively, this model specifies the log of the underlying mortality rate ($m_{j,t,a,r}$) as a function of covariates and additional variation by county, year, age, and racial–ethnic group. The covariates we included in this model—educational attainment, poverty rate, proportion foreign-born, median household income, and population density—were selected based on data availability and previously observed relationships with all-cause mortality. The fixed effects ($\boldsymbol{\beta_1}, \boldsymbol{\beta_2}$) on covariates at the county level and covariates specific to county and racial–ethnic group combinations ($\boldsymbol{X_{1,j,t}}, \boldsymbol{X_{2,j,t,r}}$) capture the relationships between each covariate and mortality. For the covariates by racial–ethnic group, we additionally include random slopes, $\boldsymbol{\gamma_1}$, to allow for the relationship between these variables and mortality to vary by racial–ethnic group. The covariates do not explain all variation in mortality across time, age, geography, and racial–ethnic group, so further random intercepts are included in the model to capture additional variation. The random intercept $\boldsymbol{\gamma_2}$ allows for spatial (ie, between-county) variation in the level of mortality, shared across age, year, and racial–ethnic group. The random intercept $\boldsymbol{\gamma_3}$ allows for variation in mortality by age, time, and racial–ethnic group, shared across all counties. Finally, the random intercept $\boldsymbol{\gamma_4}$ was included to allow for county-specific deviations in the mortality patterns by age, time, and racial–ethnic group, compared with the general pattern captured by $\boldsymbol{\gamma_3}$. This random intercept incorporates a linear spline in the age and time dimensions to reduce computational complexity: the equivalent model for all age groups and years was found to be computationally infeasible. Although the splines in this random intercept are linear, we are not assuming that the time or age trends for $\log(m_{j,t,a,r})$ are linear, as both the contributions from the covariates as well as $\boldsymbol{\gamma_3}$ allow for non-linear variation. The number of age and year knots were chosen to maximise flexibility while maintaining a reasonable runtime.

We used the Template Model Builder (TMB) package[15] in R version 3.6.1[10] to fit these models using an empirical Bayes approach. TMB calculates analytic approximations to the posterior distribution based on Laplace approximations. We use TMB for fitting these models rather than INLA—another common alternative to classic Markov chain Monte Carlo (MCMC) methods and the tool that we used for the covariate imputation and smoothing models (section 2.3)—as TMB is substantially more flexible with respect to the model specification.[16] Of particular importance for this analysis: random effects in INLA are restricted to two-way interactions, whereas TMB allows us to incorporate higher-order interactions ($\boldsymbol{\gamma_3}$ and $\boldsymbol{\gamma_4}$) in our modelling approach.

In addition to the more formal model validation we describe below, we assessed model fit by inspecting plots comparing the estimated time and age trends in mortality to the observed data at the national, state, and (in selected counties) county level. Additionally, for the all-cause mortality model we used graphical posterior predictive checks[17] to assess if the observed data are over-dispersed or zero-inflated relative to our model; we found no evidence that this is the case. Finally, we examined plots of the binned residuals compared with each covariate to assess the assumption that the relationship between log mortality and each covariate is linear; we found no evidence of bias in our estimates as a result of non-linearity in these relationships.

Cause-specific model exceptions

The cause-specific models described above tend to smooth mortality over time and thus can perform poorly in cases where there are sudden substantial changes in mortality, particularly when those changes are short-term. In particular, we find that this model performed poorly when modelling intentional injuries, due to the pronounced increase in observed deaths as a consequence of the September 11, 2001 terrorists attacks, and when modelling unintentional injuries, due to the large increase in observed deaths as consequence of Hurricane Katrina in 2005.

In order to better reflect the impact of these events in our mortality estimates for intentional injuries and unintentional injuries, we added two additional random slopes (one by county, and one by age) to the models for these two causes, both of which are multiplied by an indicator variable I that is 1 for counties where there was at least one observed death due to the event in question, and 0 otherwise. For self-harm and interpersonal violence, ICD code U01.1 was used to identify deaths in 2001 that were due to 9/11. For unintentional injuries, ICD code X37.0 is used to identify deaths in 2005 that were likely due to Hurricane Katrina. With these additional random slopes, the model is specified as follows:

$$
\begin{aligned}
&D_{j,t,a,r} \sim \text{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right) \\
&\log\left(m_{j,t,a,r}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \left(\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}\right) \cdot \boldsymbol{X_{2,j,t,r}} \\
&\qquad + \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right) + \gamma_{5,j} \cdot I_{j,t} + \gamma_{6,a} \cdot I_{j,t}
\end{aligned}
$$

where:

$$
\begin{aligned}
&\boldsymbol{\gamma_5} \sim \text{IID}(\sigma_5) \\
&\sigma_5^{-2} \sim \text{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05 \\
&\boldsymbol{\gamma_6} \sim \text{IID}(\sigma_6) \\
&\sigma_6^{-2} \sim \text{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05
\end{aligned}
$$

Additionally, in order to better reflect these sharp increases in mortality throughout the cause hierarchy, we added random slopes for both of these events to the all-cause model, which was thus specified as follows:

$$
\begin{aligned}
&D_{j,t,a,r} \sim \text{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right) \\
&\log\left(m_{j,t,a,r}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \left(\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}\right) \cdot \boldsymbol{X_{2,j,t,r}} \\
&\qquad + \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right) + \gamma_{5,j} \cdot I_{j,t(2001)} + \gamma_{6,j} \\
&\qquad \cdot I_{j,t(2005)} + \gamma_{7,a} \cdot I_{j,t(2001)} + \gamma_{8,a} \cdot I_{j,t(2005)}
\end{aligned}
$$

where:

$$
\begin{aligned}
&\boldsymbol{\gamma_5} \sim \text{IID}(\sigma_5) \\
&\sigma_5^{-2} \sim \text{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05 \\
&\boldsymbol{\gamma_6} \sim \text{IID}(\sigma_6)
\end{aligned}
$$

$\sigma_6^{-2} \sim \mathrm{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$

$\boldsymbol{\gamma_7} \sim \mathrm{IID}(\sigma_7)$

$\sigma_7^{-2} \sim \mathrm{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$

$\boldsymbol{\gamma_8} \sim \mathrm{IID}(\sigma_8)$

$\sigma_8^{-2} \sim \mathrm{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$

County-level model

Similar models were estimated for each cause for all racial–ethnic groups combined. These models were specified as follows, with all terms defined as described above:

$$D_{j,t,a} \sim \mathrm{Poisson}\left(m_{j,t,a} \cdot P_{j,t,a}\right)$$

$$\log\left(m_{j,t,a}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \gamma_{2,j} + \gamma_{3,t,a} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a'} \cdot S_{t'}(t) \cdot S_{a'}(a)\right)$$

Priors:

$\boldsymbol{\gamma_2} \sim \mathrm{LCAR}(\rho_2, \sigma_2)$

$\boldsymbol{\gamma_3} \sim \mathrm{LCAR{:}\,LCAR}(\rho_{3,t}, \rho_{3,a}, \sigma_3)$

$\boldsymbol{\gamma_4} \sim \mathrm{LCAR{:}\,LCAR{:}\,LCAR}(\rho_{4,a'}, \rho_{4,t'}, \rho_{4,j}, \sigma_4)$

Hyperpriors:

$\sigma^{-2} \sim \mathrm{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$

$\mathrm{logit}(\rho) \sim \mathrm{Normal}(0, 1.5)$

Cause-specific model exceptions

Similar to the model specific to county and racial–ethnic group, an additional random slope was included for the models of unintentional injuries and self-harm and interpersonal violence. The indicators were created in the same way. Thus, the model is as follows:

$$D_{j,t,a,r} \sim \mathrm{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right)$$

$$\log\left(m_{j,t,a,r}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \left(\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}\right) \cdot \boldsymbol{X_{2,j,t,r}}$$

$$+ \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right) + \gamma_{5,j} \cdot I_{j,t} + \gamma_{6,a} \cdot I_{j,t}$$

where:

$$\boldsymbol{\gamma_5} \sim \mathrm{IID}(\sigma_5)$$
$$\sigma_5^{-2} \sim PC(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$$
$$\boldsymbol{\gamma_6} \sim \mathrm{IID}(\sigma_6)$$
$$\sigma_6^{-2} \sim \mathrm{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$$

Additionally, the all-cause model was constructed similarly:

$$D_{j,t,a,r} \sim \mathrm{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right)$$
$$\begin{aligned}\log\left(m_{j,t,a,r}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \left(\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}\right) \cdot \boldsymbol{X_{2,j,t,r}} \\ + \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right) + \gamma_{5,j} \cdot I_{j,t(2001)} + \gamma_{6,j} \\ \cdot I_{j,t(2005)} + \gamma_{7,a} \cdot I_{j,t(2001)} + \gamma_{8,a} \cdot I_{j,t(2005)}\end{aligned}$$

where:

$$\boldsymbol{\gamma_5} \sim \mathrm{IID}(\sigma_5)$$
$$\sigma_5^{-2} \sim \mathrm{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$$
$$\boldsymbol{\gamma_6} \sim \mathrm{IID}(\sigma_6)$$
$$\sigma_6^{-2} \sim \mathrm{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$$
$$\boldsymbol{\gamma_7} \sim \mathrm{IID}(\sigma_7)$$
$$\sigma_7^{-2} \sim \mathrm{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$$
$$\boldsymbol{\gamma_8} \sim \mathrm{IID}(\sigma_8)$$
$$\sigma_8^{-2} \sim \mathrm{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$$

Hyperprior sensitivity analysis

In previous work on all-cause mortality and life expectancy,[1] we tested a wide range of alternative hyperparameter specifications. Because testing all of these combinations across all causes would be computationally intractable, we chose a subset of both hyperparameter specifications and causes for the purposes of testing the effect of these by cause. Thus, a variety of penalised complexity (PC) specifications were chosen:

- $\sigma_0 = 1;\ \Pr(\sigma > \sigma_0) = 0.02, 0.05, 0.1$
- $\sigma_0 = 5;\ \Pr(\sigma > \sigma_0) = 0.1$

To test a range of models with varying burden, age restrictions, sex restrictions, and mortality patterns, the following Level 2 causes were modelled by use of each of the above hyperparameter combinations:

- Enteric infections
- HIV/AIDS & STIs
- Maternal disorders
- Neoplasms
- Substance use

The model results were very similar across parameterisations. The figure in section 4.2 shows the difference in the estimates derived from models using these alternate prior specifications compared with our main model. These differences are generally very small across all parameterisations and prior specifications.

2.5 Small area model validation

Approach

The framework used to evaluate the performance of the models in this analysis is an extension of a previously proposed[18] and extensively used framework designed specifically for county-level models in the USA. Previously,[1] this was modified to allow for evaluation of performance with respect to generating estimates of life expectancy by county and racial–ethnic group. Here, we use this framework to evaluate performance of the same model with respect to producing estimates of age-standardised mortality and to compare performance of two simplified versions of this model.

First, a "validation set" of county and racial–ethnic group pairs was identified. The validation set is a collection of county and racial–ethnic group pairs for which directly calculated mortality rates are a good representation of the underlying mortality rate—ie, where the population and corresponding number of deaths is sufficiently large to generate stable direct estimates. To increase the number of county and racial–ethnic group combinations that were retained in the validation set, deaths and population data were pooled across time by use of a moving window of three years for the purposes of defining the validation set. A series of criteria were used to remove county and racial–ethnic group combinations from the set of all county and racial–ethnic group combinations, with the remainder forming the validation set. First, any county and racial–ethnic group combination with zero pooled deaths in any age, sex, and year (window) combination were removed. Second, among the remaining county and racial–ethnic group combinations, those where the median (across all years, sexes, and age groups) coefficient of variation was greater than 20% for the age-specific mortality rates or greater than 5% for the age-standardised and crude mortality rates were removed. In order to calculate the coefficient of variation, 1000 draws of death counts were simulated for each age group, sex, and year, assuming a Poisson distribution with rate and size equal to the observed mortality rate and population size, respectively; age-specific, crude (all-ages), and age-standardised mortality rates were then calculated for each draw; and finally the coefficient of variation was calculated as the standard deviation of the draws divided by their mean. The validation set has 138 county and racial–ethnic group pairs, composed of 96 counties and four racial–ethnic groups (section 3.7). The AIAN group was not represented in the validation set. These pooled mortality rates were used as a "gold standard" against which to compare model predictions.

Next, "validation datasets" were constructed. A total of 40 validation sets were used: 5 iterations each of simulated datasets with reference population sizes of 10, 100, 1000, 3000, 5000, 10 000, 25 000, and 100 000. Additionally, a sixth iteration was prepared for each of these population sizes because, rarely, models for some iterations failed to converge; this sixth iteration was only used if a model failed to converge. The sizes 1000–100 000 were chosen because they correspond roughly to the 1st, 5th, 10th, 25th, 50th, and 80th percentiles for the total population (all racial–ethnic groups combined) across all counties and years. Sizes 10 and 100 were added because similar population sizes are common for specific racial–ethnic groups at the county level. To make these validation data sets, a population of the specified size was sampled for each county and racial–ethnic group in the validation set, with the probability of sampling an individual of a given age and sex proportional to the observed population structure for that county and racial–ethnic group. Then, for each age and sex within each county and racial–ethnic group, deaths were simulated from a Poisson distribution with mean equal to the observed mortality rate times the sampled population for that age group and sex. The data for all county and racial–ethnic group pairs that were not in the validation set were included without modification.

Finally, small area models were fit and predictions generated as described above to each of the 40 validation datasets. To evaluate the performance, the predictions based on each validation data set were compiled and compared against the gold standard mortality rates. First, errors were calculated as $m^{gs}_{j,t,r} - m^{pred}_{j,t,a,r}$ where $m^{gs}_{j,t,r}$ is the gold standard age-standardised mortality rate per 100 000, and $m^{pred}_{j,t,r}$ is the predicted age-standardised mortality rate per 100 000. The mean error and the mean absolute error—measures of bias and precision, respectively—were calculated across all county and racial–ethnic group combinations in the validation set and all iterations at each population level. Coverage (ie, the percentage of county, racial–ethnic group, and year combinations where the gold standard estimate was between the lower and upper uncertainty intervals for the modelled estimate) was also recorded.

This validation procedure was used to assess and compare model performance of three models:

1. The model for all-cause mortality used previously to estimate life expectancy:

$$D_{j,t,a,r} \sim \text{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right)$$
$$\log\left(m_{j,t,a,r}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \left(\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}\right) \cdot \boldsymbol{X_{2,j,t,r}} + \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right)$$

   where:

$$\boldsymbol{\gamma_4} \sim \text{LCAR: LCAR: LCAR: MVN}(\rho_{4,a'}, \rho_{4,t'}, \rho_{4,j}, \boldsymbol{\sigma_4}, \boldsymbol{\theta})$$

2. The model described above for most causes (except all-cause mortality, unintentional injuries, and self-harm and interpersonal violence, which have additional components to specifically model increases in mortality due to the 9/11 terrorist attacks and Hurricane Katrina):

$$D_{j,t,a,r} \sim \text{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right)$$
$$\log\left(m_{j,t,a,r}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \left(\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}\right) \cdot \boldsymbol{X_{2,j,t,r}} + \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right)$$

   Where:

$$\boldsymbol{\gamma_4} \sim \text{LCAR: LCAR: LCAR: IID}(\rho_{4,a'}, \rho_{4,t'}, \rho_{4,j}, \sigma_4)$$

3. The same model as (2), but with a $\boldsymbol{\sigma_4^2}$ (length = 5) term that controls the variation for each racial–ethnic group separately, thus allowing further variation across racial–ethnic groups.

$$D_{j,t,a,r} \sim \text{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right)$$
$$\log\left(m_{j,t,a,r}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \left(\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}\right) \cdot \boldsymbol{X_{2,j,t,r}} + \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right)$$

   Where:

$$\boldsymbol{\gamma_4} \sim \text{LCAR: LCAR: LCAR: IID}(\rho_{4,a'}, \rho_{4,t'}, \rho_{4,j}, \boldsymbol{\sigma_4})$$

$$\boldsymbol{\sigma}_{\boldsymbol{4i}}^{-\boldsymbol{2}} \sim \mathrm{PC}(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$$

The variant of the model that reduces the racial–ethnic group component of $\boldsymbol{\gamma}_{\boldsymbol{4}}$ to IID (model 2) was included to assess the performance of the model that was most computational feasible to run for all causes. The variant of the model with an identically (but not independent) distributed $\boldsymbol{\gamma}_{\boldsymbol{4}}$ racial–ethnic group intercept (model 3) was included to assess the importance of separate variance terms by racial–ethnic group.

Results

The mean relative error, mean absolute relative error, and coverage for each model are provided in sections 3.8 (table) and 4.2 (figure). The mean relative error is a measure of relative bias—ie, it indicates if the estimates from the models were systematically higher or lower than the gold standard values and is measured as a percent difference compared with the gold standard. As expected, mean relative error tended to improve (was closer to 0%) as the simulated population size increased for all models and all racial–ethnic groups. In model 1, there was evidence of bias for most racial–ethnic groups in populations < 10 000, although the mean relative errors were minimal at the two larger population sizes. At size 10, the model overestimated the age-standardised mortality rate for the Asian, Black, and Latino groups by 8.67%, 2.9%, and 2.57%, respectively. However, it underestimated for the White group by 1.07%. Both model 2 and 3 performed better than model 1 in terms of mean relative error at all population sizes except 100 000. However, the mean relative error was still quite large for the Asian group; at size 10, model 2 and model 3 overestimated by 7.77% and 6.98%, respectively. However, the Asian group only had four counties in the validation set, so it is difficult to draw general conclusions about bias for this racial–ethnic group. Across all racial–ethnic groups, the mean relative errors for model 2 were smaller in magnitude compared with the other models for about 70% of racial–ethnic groups and population sizes, but they were similar to those from model 3.

The mean absolute relative error is a measure of overall error—ie, how much the model estimates differ from true estimates irrespective of direction. It is also measured as a percent difference compared with the gold standard. As expected, mean absolute relative errors tended to improve as size increased for all models and all racial–ethnic groups. All three models performed similarly across population sizes, although model 1 performed slightly better for about 65% of the population sizes and racial–ethnic groups. Except for the estimates for the White population, model 1 did not perform as well at population sizes 10 and 100.

Coverage is a measure of the calibration of the uncertainty intervals. Ideally, coverage should be close to 95% because that means that the 95% uncertainty intervals were an appropriate reflection of an estimate's uncertainty. Coverage was similarly close to 95% in all models: across all racial–ethnic groups, model 1 had three coverage values within +/- 1 percentage point of 95, whereas models 2 and 3 had two values within this range. Across models, coverage varied similarly across racial–ethnic groups, resulting in a similar range of values. Coverage tended to be highest at the smallest population sizes, and then decreased as population size increased for most models and racial–ethnic groups. This is likely due to the wider uncertainty intervals at smaller population sizes, making it more likely for the gold standard to be included within the uncertainty interval.

2.6 Derivation of misclassification ratios by county, age, sex, and racial–ethnic group

Extraction

Overall misclassification ratios, as well as misclassification ratios by age and sex, census region, and co-ethnic density were extracted from Arias et al.[19] for five racial–ethnic groups: AIAN, Asian, Black, Latino and White. Specifically, data were extracted from the following numbered tables in Arias et al.:

- Overall misclassification ratios: Table 2, "Total" column for both sexes.
- Age-sex misclassification ratios: Table 2, age-specific columns for each sex separately.
- Census region misclassification ratios: Table 3, results by "Region"
- Co-ethnic density misclassification ratios: Table 3, results by "Coethnic concentration"; AIAN ratios extracted from the results shown for all AIAN because these were not available specifically for non-Latino AIAN.

The co-ethnic density misclassification ratios were assigned to a county by the same method outlined in Arias et al.[19] for the AIAN population, counties in Contract Health Service Delivery Areas (CHSDAs) were considered to have high co-ethnic density; for the Latino population, counties with high co-ethnic density were those within the first 50th percentile of ranked deaths by county between 1999 and 2011. This method assumes that the relative increase or decrease in misclassification for counties with low or high co-ethnic density compared with the total misclassification ratio for AIAN (including both Latino and non-Latino AIAN) is representative of that for non-Latino AIAN. We are not aware of any studies on this topic, but we make this assumption to include adjustment by co-ethnic density given the evidence that this form of misclassification is especially important with respect to the AIAN population.[20–22]

Combination

1000 draws of each misclassification ratio were generated assuming these ratios are log-Normally distributed. We selected a log-Normal distribution as it is restricted to positive numbers, which is appropriate for this ratio; however, we acknowledge that this selection is somewhat arbitrary and is at best an approximation of the true ratio distribution. The draws of misclassification were then combined (without ordering) by the following approach:

$$ratio_{final} = ratio_{overall} \cdot \frac{ratio_{age,sex}}{ratio_{overall}} \cdot \frac{ratio_{region}}{ratio_{overall}} \cdot \frac{ratio_{co-ethnic\ density}}{ratio_{overall}}$$

For the Asian, Black, and White populations, $ratio_{co-ethnic\ density}$ is equal to $ratio_{overall}$, so the last term is equal to 1 (ie, no adjustment by co-ethnic density). For the AIAN population, the $ratio_{overall}$ in the denominator of the final term was the overall misclassification ratio for both Latino and non-Latino AIAN populations combined, to match the numerator, which was available only for Latino and non-Latino AIAN populations combined; in all other terms, the values for the non-Latino AIAN population alone were used.

This approach assumes that the degree of misclassification is independent across each dimension. Thus, the degree of misclassification reported for a particular facet (eg, by age or sex) is the same across all other facets (eg, region and co-ethnic density). For example, the age or sex pattern of misclassification for a given racial–ethnic group will be the same regardless of region.

Mortality rate adjustment

The 1000 draws of misclassification ratios were merged onto the 1000 posterior draws of the mortality rate by age, sex, county (which reflected both region and co-ethnic density), and racial–ethnic group. The merge by age was conducted by aligning the age groups in the model (0, 1–4, 5–9, ..., 80–84, and 85+ years old) with the age bin to which each of the modelled ages belongs (ie, age groups 0, 1–4, 5–9, 10–14, 15–19, and 20–24 were merged onto the age bin 0–24). These draws were not ordered, thus assuming independence between the mortality rate and the misclassification ratio. Mortality rate draws were adjusted by multiplying by the corresponding misclassification ratio draw.

2.7 Calibration

After the modelling steps, results were calibrated to ensure consistency across three dimensions: cause hierarchy, racial–ethnic group, and geography. Adjustments by cause were needed for two reasons. First, SAE models were run independently for all-cause mortality and for each of the 20 modelled causes in the first and second level of the GBD cause hierarchy. Thus, the cause-specific model outputs do not necessarily nest as they should; that is, summing predicted deaths from the three Level 1 causes would not result in precisely the predicted all-cause mortality, although generally it would be close.

Second, adjustments were needed to ensure that the county and racial–ethnic group combination results were consistent with the directly modelled county-level estimates. This was important because the joint effect of modelling by racial–ethnic group and applying the misclassification ratios can lead to results that do not align precisely with the county-level model. Without this calibration step, the misclassification adjustment in particular could lead to inaccurate results given the assumption of independence between the various misclassification ratios (section 2.6). This is in addition to any differences that county-level estimates will have with county and racial–ethnic group estimates that have been population weighted to the county level.

To accomplish these goals, an algorithm known as raking (also called iterative proportional fitting) was utilised. This process has been described in detail previously.[23] Given an N-dimensional table whose internal entries denote uncertain values and whose marginal entries denote aggregated, more certain values, raking provides a means of fitting the internal entries to the margins while preserving the internal relationships of the table. This is accomplished simply by proportionately scaling the rows to add up to their marginal totals, then scaling the columns the same way, and repeating until the entries in the table stabilise (ie, converge).

Raking has been shown to converge if the sum of the margins are equal and there are no zeros or negative numbers in the margins.[24] Raking works on tables of arbitrary dimensionality and requires only a single iteration for a one-dimensional table. It should be noted that this algorithm was applied to mortality rates rather than death counts, and as such, an extra population-weighting step was required when raking to state estimates.

To rake county-level estimates across causes, one-dimensional raking was applied to fit county-level estimates of lower-level causes to higher-level cause estimates at each level of the cause hierarchy. Because we only model causes with more than 10 000 deaths in total and 1000 deaths each among males and females over 2000–2019, we must account for the non-modelled causes (Level 2 "Neglected tropical diseases and malaria" and "Mental disorders") before raking. Thus, we assume that any difference between mortality aggregated across child causes compared to the parent cause should be attributed to unmodelled causes in that branch of the cause hierarchy. Specifically, to make this adjustment by county, year, age, sex, and parent cause, we calculated the mean (ie, across draws) mortality rate aggregated across child causes and compared it to the mean mortality rate of the raked parent cause. If this aggregated value was larger than the parent cause value, we assumed that mortality attributed to the unmodelled causes was zero. Otherwise, we divided the aggregated mortality rate by the parent cause mortality rate to get the cause fraction of modelled causes. Finally, we multiplied the parent cause mortality rate (on a per draw basis) by 1 minus this cause fraction before raking the child causes.

To rake the county and racial–ethnic group estimates to the newly raked county-level estimates, first one-dimensional raking was applied to fit the county and racial–ethnic group all-cause mortality estimates to the raked county-level all-cause mortality estimates. Second, two-dimensional raking (across racial–ethnic group and cause) was applied at each level of the cause hierarchy.

Impact of misclassification adjustment and calibration

Both misclassification adjustment and model calibration play important roles in creating more accurate mortality estimates. First, misclassification adjustment accounts for under-reporting or over-reporting of certain racial–ethnic groups on death certificates. However, because this adjustment is done independently for each racial–ethnic group, it can change the overall level of mortality estimated for a given county. The primary purpose of our calibration procedure is to constrain the adjusted estimates such that the overall level of mortality implied by the racial–ethnic group-specific estimates is the same as when estimating at the county level. Because these two processes are linked, we show here the cumulative impact of both adjustment for misclassification and calibration for all-cause mortality.

The figure in section 4.4 demonstrates the impact of these calculations on mortality at the national level. The estimate of total mortality is not impacted by calibration, as all other estimates are raked to these mortality rates . The estimates for each racial–ethnic group are impacted by both adjustment for misclassification and the calibration procedure. The combined effect is small for the White and Black populations, as expected given the small size of the misclassification adjustments for these two groups. There are moderate increases in mortality for the Asian and Latino populations, as well as increases in the uncertainty of those estimates, reflecting the somewhat larger misclassification adjustments as well as increased uncertainty from these adjustments. These processes have the largest effect on mortality among the AIAN population: there are large increases in mortality once adjusted and calibrated in addition to a large increase in uncertainty.

The maps in section 4.5 show the corresponding impact at the county level. Again, for the total population, there are no changes due to calibration or adjustment. The more substantial changes in mortality are noted at the national level for the AIAN, Asian, and Latino populations are again noted here, with changes at the county level generally in the same direction (ie, increases in mortality). Perhaps counterintuitively, there are instances where for a particular county and racial–ethnic group, the change in mortality after misclassification adjustment and calibration is not in the same direction as at the national level. This is caused by the interaction between adjustment and calibration. For example, in Bethel Census Area, Alaska, misclassification adjustment alone caused an increase in mortality, but calibration caused mortality to decrease because, in this county, the unadjusted estimates aggregated across racial-ethnic groups were higher than the estimated mortality rates produced by the county-level model. Another example is Bennett County, South Dakota, where age-standardised mortality for the AIAN population is lower once adjusted and calibrated. In this case, this is not due to the unadjusted, aggregated racial-ethnic specific results being higher than the estimates modelled with the county-level model in this county. Instead, this is due to misclassification adjustment. This county—along with many of the other counties with unmasked estimates in South Dakota—is a Contract Health Service Delivery Area (CHSDA), and therefore has a lower misclassification adjustment. This adjustment is 1.17, and the denominator is 1.4 (the total AIAN misclassification ratio for both Latino and non-Latino AIAN). Thus, the ratios of ratios is less than 1. This is combined with the region misclassification ratio, which is 1.12 and has a denominator of 1.33 (the total non-Latino AIAN misclassification ratio). Thus, the contribution from the region misclassification ratio is also less than 1. This means that the combined misclassification ratios are less than 1 for most ages and sexes in this county, thus leading to lower mortality. In contrast, Brown

County, South Dakota exhibits increases in mortality due to raking and calibration. This is because Brown County is not a CHSDA, and thus its associated adjustment is larger than 1.

2.8 References

1 Dwyer-Lindgren L, Kendrick P, Kelly YO, *et al.* Life expectancy by county, race, and ethnicity in the USA, 2000–19: a systematic analysis of health disparities. *The Lancet* 2022; **400**: 25–38.

2 Kochanek KD, Murphy SL, Xu J, Arias E. Deaths: final data for 2017. *Natl Vital Stat Rep* 2019; **68**. https://www.cdc.gov/nchs/data/nvsr/nvsr68/nvsr68_09-508.pdf (accessed Dec 23, 2019).

3 Naghavi M, Makela S, Foreman K, O'Brien J, Pourmalek F, Lozano R. Algorithms for enhancing public health utility of national causes-of-death data. *Popul Health Metr* 2010; **8**: 9.

4 Vos T, Lim SS, Abbafati C, *et al.* Global burden of 369 diseases and injuries in 204 countries and territories, 1990–2019: a systematic analysis for the Global Burden of Disease Study 2019. *The Lancet* 2020; **396**: 1204–22.

5 US Census Bureau. Instructions for applying statistical testing to American Community Survey data. 2019. https://www2.census.gov/programs-surveys/acs/tech_docs/statistical_testing/2019_Instructions_for_Stat_Testing_ACS.pdf (accessed Dec 17, 2020).

6 US Census Bureau CHS. Overview - History - U.S. Census Bureau. https://www.census.gov/history/www/through_the_decades/overview/ (accessed July 1, 2022).

7 Comparative Study of Confidence Intervals for Proportions in Complex Sample Surveys - PubMed. https://pubmed-ncbi-nlm-nih-gov.offcampus.lib.washington.edu/31428658/ (accessed July 1, 2022).

8 The arcsine is asinine: the analysis of proportions in ecology - Warton - 2011 - Ecology - Wiley Online Library. https://esajournals.onlinelibrary.wiley.com/doi/10.1890/10-0340.1 (accessed July 1, 2022).

9 Rue H, Martino S, Chopin N. Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations. *J R Stat Soc Ser B Stat Methodol* 2009; **71**: 319–92.

10 R Core Team. R: A language and environment for statistical computing. 2019. https://www.R-project.org/.

11 Fuglstad G-A, Simpson D, Lindgren F, Rue H. Constructing Priors that Penalize the Complexity of Gaussian Random Fields. 2017; published online Nov 27. DOI:10.48550/arXiv.1503.00256.

12 Estimation of Disease Rates in Small Areas: A new Mixed Model for Spatial Dependence | SpringerLink. https://link.springer.com/chapter/10.1007/978-1-4612-1284-3_4 (accessed July 1, 2022).

13 Markov Chain Monte Carlo in Practice. Routledge CRC Press. https://www.routledge.com/Markov-Chain-Monte-Carlo-in-Practice/Gilks-Richardson-Spiegelhalter/p/book/9780412055515 (accessed July 1, 2022).

14 Knorr-Held L. Bayesian modelling of inseparable space-time variation in disease risk. *Stat Med* 2000; **19**: 2555–67.

15 Kristensen K, Nielsen A, Berg CW, Skaug H, Bell BM. TMB: Automatic Differentiation and Laplace Approximation. *J Stat Softw* 2016; **70**: 1–21.

16 Osgood-Zimmerman A, Wakefield J. A Statistical Introduction to Template Model Builder: A Flexible Tool for Spatial Modeling. 2021; published online March 17. DOI:10.48550/arXiv.2103.09929.

17 Bayesian Data Analysis. Routledge CRC Press. https://www.routledge.com/Bayesian-Data-Analysis/Gelman-Carlin-Stern-Dunson-Vehtari-Rubin/p/book/9781439840955 (accessed July 1, 2022).

18 Srebotnjak T, Mokdad AH, Murray CJ. A novel framework for validating and applying standardized small area measurement strategies. *Popul Health Metr* 2010; **8**: 26.

19 Arias E, Heron M, National Center for Health Statistics, Hakes J, US Census Bureau. The Validity of Race and Hispanic-origin Reporting on Death Certificates in the United States: An Update. *Vital Health Stat 2* 2016; : 1–21.

20 Dankovchik J, Hoopes MJ, Warren-Mears V, Knaster E. Disparities in Life Expectancy of Pacific Northwest American Indians and Alaska Natives: Analysis of Linkage-Corrected Life Tables. *Public Health Rep* 2015; **130**: 71–80.

21 Joshi S, Weiser T, Warren-Mears V. Drug, Opioid-Involved, and Heroin-Involved Overdose Deaths Among American Indians and Alaska Natives--Washington, 1999-2015. *Morb Mortal Wkly Rep* 2018; **67**: 1384–8.

22 Arias E, National Center for Health Statistics (U.S.), editors. The validity of race and Hispanic origin reporting on death certificates in the United States: data evaluation and methods research. Hyattsville, MD: U.S. Department of Health and Human Services/Centers for Disease Control and Prevention/National Center for Health Statistics, 2008.

23 Dwyer-Lindgren L, Bertozzi-Villa A, Stubbs RW, *et al.* US County-Level Trends in Mortality Rates for Major Causes of Death, 1980-2014. *JAMA* 2016; **316**: 2385–401.

24 Fienberg SE. An Iterative Procedure for Estimation in Contingency Tables. *Ann Math Stat* 1970; **41**: 907–17.

3 Supplemental Tables

3.1 Counties combined to create historically stable units of analysis

State	Group	Counties (FIPS code)
Alaska	1	Chugach Census Area (2063), Copper River Census Area (2066), Valdez-Cordova Census Area (2261)*
	2	Kusilvak Census Area (2158), Wade Hampton Census Area (2270)*
	3	Kobuk Census Area (2140)*, Northwest Arctic Borough (2188)
	4	Aleutian Islands Census Area (2010)*, Aleutians East Borough (2013), Aleutians West Census Area (2016)
	5	Dillingham Census Area (2070), Lake and Peninsula Borough (2164)
	6	Denali Borough (2068), Yukon-Koyukuk Census Area (2290)
	7	Hoonah-Angoon Census Area (2105), Skagway Municipality (2230), Skagway-Yakutat-Angoon Census Area (2231)*, Skagway-Hoonah-Angoon Census Area (2232)*, Yakutat City and Borough (2282)
	8	Ketchikan Gateway Borough (2130), Petersburg Borough (2195), Prince of Wales-Hyder Census Area (2198), Prince of Wales-Outer Ketchikan Census Area (2201)*, Wrangell City and Borough (2275), Wrangell-Petersburg Census Area (2280)*
Arizona	1	La Paz County (4012), Yuma County (4027)
Colorado	1	Adams County (8001), Arapahoe County (8005), Boulder County (8013), Broomfield County (8014), Denver County (8031), Jefferson County (8059), Weld County (8123)
Florida	1	Dade County (12025)*, Miami-Dade County (12086)
Hawaii	1	Kalawao County (15005), Maui County (15009)
Maryland	1	Montgomery County (24031), Prince George's County (24033)
Montana	1	Park County (30067), Yellowstone National Park (30113)*
New Mexico	1	Cibola County (35006), Valencia County (35061)
South Dakota	1	Oglala Lakota County (46102), Shannon County (46113)*
	2	Jackson County (46071), Washabaugh County (46131)*
Virginia	1	Fairfax County (51059), Fairfax City (51600)
	2	Rockingham County (51165), Harrisonburg City (51660)
	3	James City County (51095), Williamsburg City (51830)
	4	Prince William County (51153), Manassas City (51683), Manassas Park City (51685)
	5	Rockbridge County (51163), Buena Vista City (51530)
	6	Spotsylvania County (51177), Fredericksburg City (51630)
	7	Augusta County (51015), Staunton City (51790), Waynesboro City (51820)
	8	Pittsylvania County (51143), Danville City (51590)
	9	Greensville County (51081), Emporia City (51595)
	10	Albemarle County (51003), Charlottesville City (51540)
	11	Bedford County (51019), Bedford City (51515)*
	12	Halifax County (51083), South Boston City (51780)*
	13	Southampton County (51175), Franklin City (51620)
	14	Alleghany County (51005), Clifton Forge City (51560)*
	15	York County (51199), Newport News City (51700)

*County no longer exists due to boundary or name change.

FIPS = Federal Information Processing Standards.

3.2 Deaths and population data sources

Data type	Data source and citation
Deaths	National Center for Health Statistics. National Vital Statistics System: Mortality Multiple Cause – All Counties Files, 2000-2019. Hyattsville, MD: National Center for Health Statistics, 2021. https://www.cdc.gov/nchs/nvss/nvss-restricted-data.htm
Population	National Center for Health Statistics, Centers for Disease Control and Prevention, US Census Bureau. United States Bridged-Race Intercensal Population Estimates 2000-2009. Hyattsville, United States: National Center for Health Statistics, Centers for Disease Control and Prevention, 2012. https://www.cdc.gov/nchs/nvss/bridged_race.htm. Accessed October 30, 2012. National Center for Health Statistics, Centers for Disease Control and Prevention, US Census Bureau. United States Vintage 2020 Bridged-Race Postcensal Population Estimates 2010-2020. Hyattsville, United States: National Center for Health Statistics, Centers for Disease Control and Prevention, 2020. https://www.cdc.gov/nchs/nvss/bridged_race.htm. Accessed February 17, 2022.

3.3 GBD cause list and associated ICD-10 codes

Cause Level	Cause	ICD-10 Codes
1	Communicable, maternal, neonatal, and nutritional diseases	A00–A00.9, A01.0–A14, A15–A28.9, A32–A39.9, A48.1–A48.2, A48.4–A48.5, A50–A58, A60–A60.9, A63–A63.8, A65–A65.0, A68–A70, A74, A74.8–A75.9, A77–A96.9, A98–A98.8, B00–B06.9, B10–B10.8, B15–B16.2, B17.0, B17.2, B19.1, B20–B27.9, B29.4, B33–B33.1, B33.3–B33.8, B34.2, B47–B48.8, B50–B53.8, B55.0, B56–B57.5, B60–B60.8, B63, B65–B67.9, B69–B72.0, B74.3–B75, B77–B77.9, B83–B83.8, B90–B91, B94.1, B95–B95.5, B97.2, B97.4–B97.6, C58–C58.0, D50.1–D50.8, D51–D52.0, D52.8–D53.9, D70.3, D89.3, E00–E02, E40–E46.9, E51–E61.9, E63–E64.0, E64.2–E64.9, F02.1, F02.4, F07.1, G00.0–G00.8, G03–G03.8, G04–G05.8, G14–G14.6, G21.3, H70–H70.9, I00, I02, I02.9, I98.0–I98.1, J00–J02.8, J03–J03.8, J04–J04.2, J05–J05.1, J06.0–J06.8, J09–J15.8, J16–J16.9, J20–J21.9, J36–J36.0, J91.0, K52.1–K52.3, K67.0–K67.8, K75.3, K76.3, K77.0, K93.0–K93.1, M03.1, M12.1, M49.0–M49.1, M73.0–M73.1, M89.6, N74.1, N96, N98–N98.9, O00–O07.9, O09–O16.9, O20–O26.9, O28–O36.9, O40–O48.1, O60–O77.9, O80–O92.7, O96–O98.6, O98.8–P04.2, P04.5–P05.9, P07–P15.9, P19–P22.9, P23.0–P23.4, P24–P29.9, P35–P37.2, P37.5–P39.9, P50–P61.9, P70–P70.1, P70.3–P72.9, P74–P78.9, P80–P81.9, P83–P84, P90–P92.9, P94–P94.9, P96, P96.3–P96.4, P96.8, R19.7, U04–U04.9, U06–U07.2, U82–U89, Z16–Z16.3
2	HIV/AIDS and sexually transmitted infections	A50–A58, A60–A60.9, A63–A63.8, B20–B24.9, B63, F02.4, I98.0, K67.0–K67.2, M03.1, M73.0–M73.1
3	HIV/AIDS	B20–B24.9, F02.4
4	HIV/AIDS–Drug-susceptible Tuberculosis	B20.0
4	HIV/AIDS resulting in other diseases	B20, B20.1–B24.9, F02.4
3	Sexually transmitted infections excluding HIV	A50–A58, A60–A60.9, A63–A63.8, B63, I98.0, K67.0–K67.2, M03.1, M73.0–M73.1
4	Syphilis	A50–A53.9, I98.0, K67.2, M03.1, M73.1
4	Chlamydial infection	A55–A56.8, K67.0
4	Gonorrhoea	A54–A54.9, K67.1, M73.0
4	Other sexually transmitted infections	A57–A58, A63–A63.8, B63
2	Respiratory infections and tuberculosis	A10–A14, A15–A19.9, A48.1, A70, B34.2, B90–B90.9, B97.2, B97.4–B97.6, H70–H70.9, J00–J02.8, J03–J03.8, J04–J04.2, J05–J05.1, J06.0–J06.8, J09–J15.8, J16–J16.9, J20–J21.9, J36–J36.0, J91.0, K67.3, K93.0, M49.0, N74.1, P23.0–P23.4, P37.0, U04–U04.9, U07–U07.2, U84.3

Cause Level	Cause	ICD-10 Codes
3	Tuberculosis	A10–A14, A15–A19.9, B90–B90.9, K67.3, K93.0, M49.0, N74.1, P37.0, U84.3
4	Drug-susceptible tuberculosis	A10–A14, A15–A19.9, B90–B90.9, K67.3, K93.0, M49.0, N74.1, P37.0
4	Multidrug-resistant tuberculosis without extensive drug resistance	U84.3
3	Lower respiratory infections	A48.1, A70, B34.2, B97.2, B97.4-B97.6, J09–J15.8, J16–J16.9, J20–J21.9, J91.0, P23.0–P23.4, U04–U04.9
4	Influenza	J09–J11.8, U04–U04.9
4	Pneumococcal pneumonia	J13–J13.9, J15.3–J15.4, J15.6
4	H influenzae type B pneumonia	J14–J14.0
4	Respiratory syncytial virus pneumonia	B97.4–B97.6, J12.1
4	Other lower respiratory infections	A48.1, A70, B34.2, B97.2, J12–J12.0, J12.2–J12.9, J15–J15.2, J15.5, J15.7–J15.8, J16–J16.9, J20–J21.9, J91.0, P23.0–P23.4
3	Upper respiratory infections	J00–J02.8, J03–J03.8, J04–J04.2, J05–J05.1, J06.0–J06.8, J36–J36.0
3	Otitis media	H70–H70.9
3	COVID-19	U07–U07.2
2	Enteric infections	A00–A00.9, A01.0–A09.9, A80–A80.9, K52.1–K52.3, R19.7
3	Diarrhoeal diseases	A00–A00.9, A02–A02.0, A02.8–A07, A07.2–A07.4, A08–A09.9, K52.1–K52.3, R19.7
3	Typhoid and paratyphoid	A01.0–A01.4
3	Leprosy	A30–A30.9
4	Typhoid fever	A01.0
4	Paratyphoid fever	A01.1–A01.4
3	Invasive Non-typhoidal Salmonella (iNTS)	A02.1–A02.2
3	Other intestinal infectious diseases	A07.0–A07.1, A07.8–A07.9, A80–A80.9
2	Neglected tropical diseases and malaria	A68–A68.9, A69.2–A69.9, A75–A75.9, A77–A79.9, A82–A82.9, A90–A96.9, A98–A98.8, B33.0–B33.1, B50–B53.8, B55.0, B56–B57.5, B60–B60.8, B65–B67.9, B69–B72.0, B74.3–B75, B77–B77.9, B83–B83.8, K93.1, P37.1, U06–U06.9
3	Malaria	B50–B53.8
3	Chagas disease	B57–B57.5, K93.1
3	Leishmaniasis	B55.0
4	Visceral leishmaniasis	B55.0

Cause Level	Cause	ICD-10 Codes
3	African trypanosomiasis	B56–B56.9
3	Schistosomiasis	B65–B65.9
3	Cysticercosis	B69–B69.9
3	Cystic echinococcosis	B67–B67.4, B67.8–B67.9
3	Dengue	A90–A91.9
3	Yellow fever	A95–A95.9
3	Rabies	A82–A82.9
3	Intestinal nematode infections	B77–B77.9
4	Ascariasis	B77–B77.9
3	Ebola	A98.4
3	Zika virus	U06–U06.9
3	Other neglected tropical diseases	A68–A68.9, A69.2–A69.9, A75–A75.9, A77–A79.9, A92–A94.0, A96–A96.9, A98–A98.3, A98.5–A98.8, B33.0–B33.1, B60–B60.8, B67.5–B67.7, B70–B71.9, B74.3–B75, B83–B83.8, P37.1
2	Other infectious diseases	A20–A28.9, A32–A39.9, A48.2, A48.4–A48.5, A65–A65.0, A69–A69.1, A74, A74.8–A74.9, A81–A81.9, A83–A89.9, B00–B06.9, B10–B10.8, B15–B16.2, B17.0, B17.2, B19.1, B25–B27.9, B29.4, B33, B33.3–B33.8, B47–B48.8, B91, B94.1, B95–B95.5, D70.3, D89.3, F02.1, F07.1, G00.0–G00.8, G03–G03.8, G04–G05.8, G14–G14.6, G21.3, I00, I02, I02.9, I98.1, K67.8, K75.3, K76.3, K77.0, M49.1, M89.6, P35–P35.9, P37, P37.2, P37.5–P37.9, U82–U84, U85–U89, Z16–Z16.3
3	Meningitis	A39–A39.9, A87–A87.9, G00.0–G00.8, G03–G03.8
3	Encephalitis	A83–A86.4, B94.1, F07.1, G04–G05.8, G21.3
3	Diphtheria	A36–A36.9
3	Pertussis	A37–A37.9
3	Tetanus	A33–A35.0
3	Measles	B05–B05.9
3	Varicella and herpes zoster	B01–B02.9, P35.8
3	Acute hepatitis	B15–B16.2, B17.0, B17.2, B19.1, P35.3
4	Acute hepatitis A	B15–B15.9
4	Acute hepatitis B	B16–B16.2, B17.0, B19.1, P35.3
4	Acute hepatitis E	B17.2
3	Other unspecified infectious diseases	A20–A28.9, A32–A32.9, A38–A38.9, A48.2, A48.4–A48.5, A65–A65.0, A69–A69.1, A74, A74.8–A74.9, A81–A81.9, A88–A89.9, B00–B00.9, B03–B04, B06–B06.9, B10–B10.8, B25–B27.9, B29.4, B33, B33.3–B33.8, B47–B48.8, B91, B95–B95.5, D70.3, D89.3, F02.1, G14–G14.6, I00, I02, I02.9, I98.1, K67.8, K75.3, K76.3, K77.0, M49.1, M89.6, P35–P35.2, P35.9, P37, P37.2, P37.5–P37.9, U82–U84, U85–U89, Z16–Z16.3

Cause Level	Cause	ICD-10 Codes
2	Maternal and neonatal disorders	C58–C58.0, N96, N98–N98.9, O00–O07.9, O09–O16.9, O20–O26.9, O28–O36.9, O40–O48.1, O60–O77.9, O80–O92.7, O96–O98.6, O98.8–P04.2, P04.5–P05.9, P07–P15.9, P19–P22.9, P24–P29.9, P36–P36.9, P38–P39.9, P50–P61.9, P70–P70.1, P70.3–P72.9, P74–P78.9, P80–P81.9, P83–P84, P90–P92.9, P94–P94.9, P96, P96.3–P96.4, P96.8
3	Maternal disorders	C58–C58.0, N96, N98–N98.9, O00–O07.9, O09–O16.9, O20–O26.9, O28–O36.9, O40–O48.1, O60–O77.9, O80–O92.7, O96–O98.6, O98.8–O99.9
4	Maternal haemorrhage	O20–O20.9, O43.2, O44–O46.9, O62–O62.9, O67–O67.9, O70, O72–O72.3
4	Maternal sepsis and other maternal infections	O23–O23.9, O85–O86.8, O91–O91.2
4	Maternal hypertensive disorders	O10–O16.9
4	Maternal obstructed labour and uterine rupture	O32–O33.9, O64–O66.9, O71–O71.9
4	Maternal abortion and miscarriage	N96, O01–O07.9
4	Ectopic pregnancy	O00–O00.9
4	Indirect maternal deaths	O24–O25.3, O98–O98.6, O98.8–O99.9
4	Late maternal deaths	O96–O97.9
4	Other direct maternal disorders	C58–C58.0, N98–N98.9, O09–O09.9, O21–O22.9, O26–O26.9, O28–O31.8, O34–O36.9, O40–O43.1, O43.8–O43.9, O47–O48.1, O60–O61.9, O63–O63.9, O68–O69.9, O70.0–O70.9, O73–O77.9, O80–O84.9, O87–O90.9, O92–O92.7
3	Neonatal disorders	P00–P04.2, P04.5–P05.9, P07–P15.9, P19–P22.9, P24–P29.9, P36–P36.9, P38–P39.9, P50–P61.9, P70–P70.1, P70.3–P72.9, P74–P78.9, P80–P81.9, P83–P84, P90–P92.9, P94–P94.9, P96, P96.3–P96.4, P96.8
4	Neonatal preterm birth	P01.0–P01.1, P05–P05.9, P07–P07.3, P22–P22.9, P25–P28.9, P52–P52.9, P61.2, P77–P77.9, P78.0–P78.9
4	Neonatal encephalopathy due to birth asphyxia and trauma	P01.7, P02–P03.9, P10–P15.9, P20–P21.9, P24–P24.9, P90–P91.9
4	Neonatal sepsis and other neonatal infections	P36–P36.9, P38–P39.9
4	Haemolytic disease and other neonatal jaundice	P55–P59.9

Cause Level	Cause	ICD-10 Codes
4	Other neonatal disorders	P00–P01, P01.2–P01.6, P01.8–P01.9, P04–P04.2, P04.5–P04.9, P08–P09, P19–P19.9, P29–P29.9, P50–P51.9, P53–P54.9, P60–P61.1, P61.3–P61.9, P70–P70.1, P70.3–P72.9, P74–P76.9, P78, P80–P81.9, P83–P84, P92–P92.9, P94–P94.9, P96, P96.3–P96.4, P96.8
2	Nutritional deficiencies	D50.1–D50.8, D51–D52.0, D52.8–D53.9, E00–E02, E40–E46.9, E51–E61.9, E63–E64.0, E64.2–E64.9, M12.1
3	Protein-energy malnutrition	E40–E46.9, E64.0
3	Other nutritional deficiencies	D51–D52.0, D52.8–D53.9, E00–E02, E51–E61.9, E63–E64, E64.2–E64.9, M12.1
1	Non-communicable diseases	A46–A46.0, A66–A67.9, B18–B18.9, B33.2, B86, C00–C13.9, C15–C22.8, C23–C25.9, C30–C34.9, C37–C38.8, C40–C41.9, C43–C45.9, C47–C54.9, C56–C57.8, C60–C63.8, C64–C67.9, C68.0–C68.8, C69.0–C69.8, C70–C73.9, C75–C75.8, C81–C82.9, C83.0–C83.8, C84–C85.0, C85.2–C85.8, C86–C86.6, C88–C91.0, C91.2–C91.3, C91.6, C92–C92.6, C93–C93.1, C93.3, C93.8, C94–C94.5, C94.7–C96.9, D00.1–D00.2, D01.0–D01.3, D02.0–D02.3, D03–D06.9, D07.0–D07.2, D07.4–D07.5, D09.0, D09.2–D09.3, D09.8, D10.0–D10.7, D11–D12.9, D13.0–D13.7, D14.0–D14.3, D15–D16.9, D22–D27.9, D28.0–D28.7, D29.0–D29.8, D30.0–D30.8, D31–D36, D36.1–D36.7, D37.1–D37.5, D38.0–D38.5, D39.1–D39.2, D39.8, D40.0–D40.8, D41.0–D41.8, D42–D43.9, D44.0–D44.8, D45–D47.9, D48.0–D48.6, D49.2–D49.4, D49.6, D55–D58.9, D59.1, D59.3, D59.5, D60–D61.9, D63.1, D64.0, D66–D67, D68.0–D69.4, D69.6–D69.8, D70–D70.0, D70.4–D75.8, D76–D77, D86–D86.9, D89–D89.2, E03–E03.1, E03.3–E06.3, E06.5–E07.1, E10–E11.9, E16.1–E16.9, E20–E23.0, E23.2–E24.1, E24.3–E27.2, E27.4–E34, E34.1–E34.8, E65–E66.0, E66.2–E68, E70–E85.2, E88–E88.2, E88.4–E88.9, F00–F02.0, F02.2–F02.3, F02.8–F03.9, F10–F16.9, F18–F18.9, F24, F50.0–F50.5, G10–G13.8, G20–G20.9, G23–G24, G24.1–G25.0, G25.2–G25.3, G25.5, G25.8–G26.0, G30–G31.9, G35–G37.9, G40–G41.9, G45–G46.8, G47.3, G61–G61.9, G62.1, G70–G72, G72.1–G73.7, G90–G90.9, G95–G95.9, H05.0–H05.1, I01–I01.9, I02.0, I05–I09.9, I11–I13.9, I20–I25.9, I27.0–I27.2, I28–I28.9, I30–I31.1, I31.8–I37.8, I38–I41.9, I42.1–I42.8, I43–I43.9, I47–I48.9, I51.0–I51.4, I60–I63.9, I65–I66.9, I67.0–I67.3, I67.5–I67.7, I68.0–I68.2, I69.0–I69.3, I70.2–I70.8, I71–I73.9, I77–I89.9, I98, I98.2, J30–J35.9, J37–J39.9, J41–J46.9, J60–J63.8, J66–J68.9, J70, J70.8–J70.9, J82, J84–J84.9, J91, J91.8–J92.9, K20–K20.9, K22–K22.6, K22.8–K29.9, K31–K31.8, K35–K38.9, K40–K42.9, K44–K46.9, K50–K52, K52.8–K52.9, K55–K62.6, K62.8–K62.9, K63.5, K64–K64.9, K66.8, K67, K68, K70–K70.3, K71.7, K73–K75, K75.1–K75.2, K75.4–K76.2, K76.4–K77, K77.8, K80–K83.9, K85–

Cause Level	Cause	ICD-10 Codes
		K86.9, K90–K90.9, K92.8, K93.8, L00–L05.9, L08–L08.9, L10–L14.0, L51–L51.9, L88–L89.9, L93–L93.2, L97–L98.4, M00–M03.0, M03.2–M03.6, M05–M09.8, M30–M36.8, M40–M43.1, M65–M65.0, M71.0–M71.1, M72.5–M72.6, M80–M82.8, M86.3–M86.4, M87–M87.0, M88–M89.0, M89.5, M89.7–M89.9, N00–N08.8, N10–N12.9, N13.6, N15–N16.8, N18–N18.9, N20–N23.0, N25–N28.1, N29–N30.3, N30.8–N32.0, N32.3–N32.4, N34–N34.3, N36–N36.9, N39–N39.2, N41–N41.9, N44–N44.0, N45–N45.9, N49–N49.9, N60–N60.9, N72–N72.0, N75–N77.8, N80–N81.9, N83–N83.9, N84.0–N84.1, N87–N87.9, P04.3–P04.4, P70.2, P96.0–P96.1, Q00–Q07.9, Q10.4–Q18.9, Q20–Q28.9, Q30–Q36, Q37–Q45.9, Q50–Q87.8, Q89–Q89.8, Q90–Q93.9, Q95–Q99.8, R78.0–R78.5, R95–R95.9, X45–X45.9, X65–X65.9, Y15–Y15.9
2	Neoplasms	C00–C13.9, C15–C22.8, C23–C25.9, C30–C34.9, C37–C38.8, C40–C41.9, C43–C45.9, C47–C54.9, C56–C57.8, C60–C63.8, C64–C67.9, C68.0–C68.8, C69.0–C69.8, C70–C73.9, C75–C75.8, C81–C82.9, C83.0–C83.8, C84–C85.0, C85.2–C85.8, C86–C86.6, C88–C91.0, C91.2–C91.3, C91.6, C92–C92.6, C93–C93.1, C93.3, C93.8, C94–C94.5, C94.7–C96.9, D00.1–D00.2, D01.0–D01.3, D02.0–D02.3, D03–D06.9, D07.0–D07.2, D07.4–D07.5, D09.0, D09.2–D09.3, D09.8, D10.0–D10.7, D11–D12.9, D13.0–D13.7, D14.0–D14.3, D15–D16.9, D22–D24.9, D26.0–D27.9, D28.0–D28.1, D28.7, D29.0–D29.8, D30.0–D30.8, D31–D36, D36.1–D36.7, D37.1–D37.5, D38.0–D38.5, D39.1–D39.2, D39.8, D40.0–D40.8, D41.0–D41.8, D42–D43.9, D44.0–D44.8, D45–D47.9, D48.0–D48.6, D49.2–D49.4, D49.6, K62.0–K62.1, K63.5, N60–N60.9, N84.0–N84.1, N87–N87.9
3	Lip and oral cavity cancer	C00–C08.9, D10.0–D10.5, D11–D11.9
3	Nasopharynx cancer	C11–C11.9, D10.6
3	Other pharynx cancer	C09–C10.9, C12–C13.9, D10.7
3	Oesophageal cancer	C15–C15.9, D00.1, D13.0
3	Stomach cancer	C16–C16.9, D00.2, D13.1, D37.1
3	Colon and rectum cancer	C18–C21.9, D01.0–D01.3, D12–D12.9, D37.3–D37.5
3	Liver cancer	C22–C22.8, D13.4
4	Hepatoblastoma	C22.2
3	Gallbladder and biliary tract cancer	C23–C24.9, D13.5
3	Pancreatic cancer	C25–C25.9, D13.6–D13.7
3	Larynx cancer	C32–C32.9, D02.0, D14.1, D38.0
3	Tracheal, bronchus, and lung cancer	C33–C34.9, D02.1–D02.3, D14.2–D14.3, D38.1

Cause Level	Cause	ICD-10 Codes
3	Malignant skin melanoma	C43–C43.9, D03–D03.9, D22–D23.9, D48.5
3	Non-melanoma skin cancer	C44–C44.9, D04–D04.9, D49.2
4	Non-melanoma skin cancer (squamous-cell carcinoma)	C44–C44.9, D04–D04.9, D49.2
3	Soft tissue and other extraosseous sarcomas	C49–C49.9
3	Malignant neoplasm of bone and articular cartilage	C40–C41.9
3	Breast cancer	C50–C50.9, D05–D05.9, D24–D24.9, D48.6, D49.3
3	Cervical cancer	C53–C53.9, D06–D06.9, D26.0
3	Uterine cancer	C54–C54.9, D07.0–D07.2, D26.1–D26.9
3	Ovarian cancer	C56–C56.9, D27–D27.9, D39.1
3	Prostate cancer	C61–C61.9, D07.5, D29.1, D40.0
3	Testicular cancer	C62–C62.9, D29.2–D29.8, D40.1–D40.8
3	Kidney cancer	C64–C65.9, D30.0–D30.1, D41.0–D41.1
3	Bladder cancer	C67–C67.9, D09.0, D30.3, D41.4–D41.8, D49.4
3	Brain and central nervous system cancer	C70–C72.9, C75.1–C75.3
3	Eye cancer	C69.0–C69.8
4	Retinoblastoma	C69.2
4	Other eye cancers	C69.0–C69.1, C69.3–C69.8
3	Neuroblastoma and other peripheral nervous cell tumours	C47–C47.9
3	Thyroid cancer	C73–C73.9, D09.3, D09.8, D34–D34.9, D44.0
3	Mesothelioma	C45–C45.9
3	Hodgkin lymphoma	C81–C81.9
3	Non-Hodgkin lymphoma	C82–C82.9, C83.0–C83.8, C84–C85.0, C85.2–C85.8, C86–C86.6, C96–C96.9
4	Burkitt lymphoma	C83.7
4	Other non-Hodgkin lymphoma	C82–C82.9, C83.0–C83.6, C83.8, C84–C85.0, C85.2–C85.8, C86–C86.6, C96–C96.9
3	Multiple myeloma	C88–C90.9
3	Leukaemia	C91–C91.0, C91.2–C91.3, C91.6, C92–C92.6, C93–C93.1, C93.3, C93.8, C94–C94.5, C94.7–C95.9
4	Acute lymphoid leukaemia	C91.0, C91.2–C91.3, C91.6

Cause Level	Cause	ICD-10 Codes
4	Acute myeloid leukaemia	C92.0, C92.3–C92.6, C93.0, C94.0, C94.2, C94.4–C94.5
4	Chronic myeloid leukaemia	C92.1–C92.2
4	Other leukaemia	C93.1, C93.3, C93.8, C94.1, C94.3, C94.7–C94.8
3	Other malignant neoplasms	C17–C17.9, C30–C31.9, C37–C38.8, C48–C48.9, C4A, C51–C52.9, C57–C57.8, C60–C60.9, C63–C63.8, C66–C66.9, C68.0–C68.8, C75–C75.0, C75.4–C75.8, D07.4, D09.2, D13.2–D13.3, D14.0, D15–D16.9, D28.0–D28.1, D28.7, D29.0, D30.2, D30.4–D30.8, D31–D31.9, D35–D35.2, D35.5–D36, D36.1–D36.7, D37.2, D38.2–D38.5, D39.2, D39.8, D41.2–D41.3, D44.1–D44.8, D48.0–D48.4
3	Other neoplasms	D32–D33.9, D35.3–D35.4, D42–D43.9, D45–D47.9, D49.6, K62.0–K62.1, K63.5, N60–N60.9, N84.0–N84.1, N87–N87.9
4	Myelodysplastic, myeloproliferative, and other haematopoietic neoplasms	D45–D47.9
4	Other benign and in situ neoplasms	N60–N60.9
2	Cardiovascular diseases	B33.2, G45–G46.8, I01–I01.9, I02.0, I05–I09.9, I11–I11.9, I20–I25.9, I27.0, I27.2, I28–I28.9, I30–I31.1, I31.8–I37.8, I38–I41.9, I42.1–I42.8, I43–I43.9, I47–I48.9, I51.0–I51.4, I60–I63.9, I65–I66.9, I67.0–I67.3, I67.5–I67.6, I68.0–I68.2, I69.0–I69.3, I70.2–I70.8, I71–I73.9, I77–I83.9, I86–I89.0, I89.9, I98, K75.1
3	Rheumatic heart disease	I01–I01.9, I02.0, I05–I09.9
3	Ischaemic heart disease	I20–I25.9
3	Stroke	G45–G46.8, I60–I63.9, I65–I66.9, I67.0–I67.3, I67.5–I67.6, I68.1–I68.2, I69.0–I69.3
4	Ischaemic stroke	G45–G46.8, I63–I63.9, I65–I66.9, I67.2–I67.3, I67.5–I67.6, I69.3
4	Intracerebral haemorrhage	I61–I62, I62.1–I62.9, I68.1–I68.2, I69.1–I69.2
4	Subarachnoid haemorrhage	I60–I60.9, I62.0, I67.0–I67.1, I69.0
3	Hypertensive heart disease	I11–I11.9
3	Non-rheumatic valvular heart disease	I34–I37.8
4	Non-rheumatic calcific aortic valve disease	I35–I35.9

Cause Level	Cause	ICD-10 Codes
4	Non-rheumatic degenerative mitral valve disease	I34–I34.9
4	Other non-rheumatic valve diseases	I36–I37.8
3	Cardiomyopathy and myocarditis	B33.2, I40–I41.9, I42.1–I42.8, I43–I43.9, I51.4
4	Myocarditis	B33.2, I40–I41.9, I51.4
4	Alcoholic cardiomyopathy	I42.6
4	Other cardiomyopathy	I42.1–I42.5, I42.7–I42.8, I43–I43.9
3	Pulmonary Arterial Hypertension	I27.0
3	Atrial fibrillation and flutter	I48–I48.9
3	Aortic aneurysm	I71–I71.9
3	Lower extremity peripheral arterial disease	I70.2–I70.8, I73–I73.9
3	Endocarditis	I33–I33.9, I38–I39.9
3	Other cardiovascular and circulatory diseases	I27.2, I28–I28.9, I30–I31.1, I31.8–I32.8, I47–I47.9, I51.0–I51.3, I68.0, I72–I72.9, I77–I83.9, I86–I89.0, I89.9, I98, K75.1
2	Chronic respiratory diseases	D86–D86.2, D86.9, G47.3, J30–J35.9, J37–J39.9, J41–J46.9, J60–J63.8, J66–J68.9, J70, J70.8–J70.9, J82, J84–J84.9, J91, J91.8–J92.9
3	Chronic obstructive pulmonary disease	J41–J44.9
3	Pneumoconiosis	J60–J63.8, J92.0
4	Silicosis	J62–J62.9
4	Asbestosis	J61–J61.0, J92.0
4	Coal workers pneumoconiosis	J60–J60.0
4	Other pneumoconiosis	J63–J63.8
3	Asthma	J45–J46.9
3	Interstitial lung disease and pulmonary sarcoidosis	D86–D86.2, D86.9, J84–J84.9
3	Other chronic respiratory diseases	G47.3, J30–J35.9, J37–J39.9, J66–J68.9, J70, J70.8–J70.9, J82, J91, J91.8–J92, J92.9
2	Digestive diseases	B18–B18.9, I84–I85.9, I98.2, K20–K20.9, K22–K22.6, K22.8–K29.9, K31–K31.8, K35–K38.9, K40–K42.9, K44–K46.9, K50–K52, K52.8–K52.9, K55–K62, K62.2–K62.6, K62.8–K62.9, K64–K64.9, K66.8, K67, K68, K70–K70.3, K71.7, K73–K75, K75.2,

Cause Level	Cause	ICD-10 Codes
		K75.4–K76.2, K76.4–K77, K77.8, K80–K83.9, K85–K86.9, K90–K90.9, K92.8, K93.8, M09.1
3	Cirrhosis and other chronic liver diseases	B18–B18.9, I85–I85.9, I98.2, K70–K70.3, K71.7, K73–K75, K75.2, K75.4–K76.2, K76.4–K76.9, K77.8
3	Upper digestive system diseases	K25–K29.9
4	Peptic ulcer disease	K25–K28.9
4	Gastritis and duodenitis	K29–K29.9
3	Appendicitis	K35–K37.9, K38.3–K38.9
3	Paralytic ileus and intestinal obstruction	K56–K56.9
3	Inguinal, femoral, and abdominal hernia	K40–K42.9, K44–K46.9
3	Inflammatory bowel disease	K50–K52, K52.8–K52.9, M09.1
4	Ulcerative colitis	K51–K52, K52.8–K52.9
4	Crohn's disease	K50–K50.9, M09.1
3	Vascular intestinal disorders	K55–K55.9
3	Gallbladder and biliary diseases	K80–K83.9
3	Pancreatitis	K85–K86.9
3	Other digestive diseases	I84–I84.9, K20–K20.9, K22–K22.6, K22.8–K24, K31–K31.8, K38–K38.2, K57–K62, K62.2–K62.6, K62.8–K62.9, K64–K64.9, K66.8, K67, K68, K77, K90–K90.9, K92.8, K93.8
2	Neurological disorders	F00–F02.0, F02.2–F02.3, F02.8–F03.9, G10–G13.8, G20–G20.9, G23–G24, G24.1–G25.0, G25.2–G25.3, G25.5, G25.8–G26.0, G30–G31.1, G31.8–G31.9, G35–G37.9, G40–G41.9, G61–G61.9, G70–G71.1, G71.3–G72, G72.2–G73.7, G90–G90.9, G95–G95.9, M33–M33.9
3	Alzheimer's disease and other dementias	F00–F02.0, F02.8–F03.9, G30–G31.1, G31.8–G31.9
3	Parkinson's disease	F02.3, G20–G20.9
3	Idiopathic epilepsy	G40–G41.9
3	Multiple sclerosis	G35–G35.9
3	Motor neuron disease	G12.2–G12.9
3	Other neurological disorders	F02.2, G10–G12.1, G13–G13.8, G23–G24, G24.1–G25.0, G25.2–G25.3, G25.5, G25.8–G26.0, G36–G37.9, G61–G61.9, G70–G71.1, G71.3–G72, G72.2–G73.7, G90–G90.9, G95–G95.9, M33–M33.9
2	Mental disorders	F24, F50.0–F50.5
3	Eating disorders	F50.0–F50.5
4	Anorexia nervosa	F50.0–F50.5

Cause Level	Cause	ICD-10 Codes
2	Substance use disorders	E24.4, F10–F16.9, F18–F18.9, G31.2, G62.1, G72.1, P04.3–P04.4, P96.1, Q86.0, R78.0–R78.5, X45–X45.9, X65–X65.9, Y15–Y15.9
3	Alcohol use disorders	E24.4, F10–F10.9, G31.2, G62.1, G72.1, P04.3, Q86.0, R78.0, X45–X45.9, X65–X65.9, Y15–Y15.9
3	Drug use disorders	F11–F16.9, F18–F18.9, P04.4, P96.1, R78.1–R78.5
4	Opioid use disorders	F11–F11.9, P96.1, R78.1
4	Cocaine use disorders	F14–F14.9, R78.2
4	Amphetamine use disorders	F15–F15.9
4	Other drug use disorders	F13–F13.9, F16–F16.9, F18–F18.9, P04.4, R78.3–R78.5
2	Diabetes and kidney diseases	D63.1, E10–E11.9, I12–I13.9, N00–N08.8, N15.0, N18–N18.9, P70.2, Q61–Q62.8
3	Diabetes mellitus	E10–E10.1, E10.3–E11.1, E11.3–E11.9, P70.2
4	Diabetes mellitus type 1	E10–E10.1, E10.3–E10.9, P70.2
4	Diabetes mellitus type 2	E11–E11.1, E11.3–E11.9
3	Chronic kidney disease	D63.1, E10.2, E11.2, I12–I13.9, N02–N08.8, N15.0, N18–N18.9, Q61–Q62.8
4	Chronic kidney disease due to diabetes mellitus type 1	E10.2
4	Chronic kidney disease due to diabetes mellitus type 2	E11.2
4	Chronic kidney disease due to hypertension	I12–I13.9
4	Chronic kidney disease due to glomerulonephritis	N03–N06.9
4	Chronic kidney disease due to other and unspecified causes	N02–N02.9, N07–N08.8, N15.0, Q61–Q62.8
3	Acute glomerulonephritis	N00–N01.9
2	Skin and subcutaneous diseases	A46–A46.0, A66–A67.9, B86, D86.3, H05.0–H05.1, I89.1–I89.8, L00–L05.9, L08–L08.9, L10–L14.0, L51–L51.9, L88–L89.9, L97–L98.4, M72.5–M72.6
3	Bacterial skin diseases	A46–A46.0, A66–A67.9, H05.0–H05.1, I89.1–I89.8, L00–L05.9, L08–L08.9, L88, L97–L98.4, M72.5–M72.6

Cause Level	Cause	ICD-10 Codes
4	Cellulitis	H05.0, L03–L03.9, M72.5–M72.6
4	Pyoderma	A46–A46.0, A66–A67.9, H05.1, I89.1–I89.8, L00–L02.9, L04–L05.9, L08–L08.9, L88, L97–L98.4
3	Decubitus ulcer	L89–L89.9
3	Other skin and subcutaneous diseases	D86.3, L10–L14.0, L51–L51.9
2	Musculoskeletal disorders	I27.1, I67.7, L93–L93.2, M00–M03.0, M03.2–M03.6, M05–M09.0, M09.2–M09.8, M30–M32.9, M34–M36.8, M40–M43.1, M65–M65.0, M71.0–M71.1, M80–M82.8, M86.3–M86.4, M87–M87.0, M88–M89.0, M89.5, M89.7–M89.9
3	Rheumatoid arthritis	M05–M06.9, M08.0–M08.8
3	Other musculoskeletal disorders	I27.1, I67.7, L93–L93.2, M00–M03.0, M03.2–M03.6, M07–M08, M08.9–M09.0, M09.2–M09.8, M30–M32.9, M34–M36.8, M40–M43.1, M65–M65.0, M71.0–M71.1, M80–M82.8, M86.3–M86.4, M87–M87.0, M88–M89.0, M89.5, M89.7–M89.9
2	Other non-communicable diseases	D25–D26, D28.2, D55–D58.9, D59.1, D59.3, D59.5, D60–D61.9, D64.0, D66–D67, D68.0–D69.4, D69.6–D69.8, D70–D70.0, D70.4–D75.8, D76–D77, D86.8, D89–D89.2, E03–E03.1, E03.3–E06.3, E06.5–E07.1, E16.1–E16.9, E20–E23.0, E23.2–E24.1, E24.3, E24.8–E27.2, E27.4–E34, E34.1–E34.8, E65–E66.0, E66.2–E68, E70–E85.2, E88–E88.2, E88.4–E88.9, G71.2, N10–N12.9, N13.6, N15, N15.1–N16.8, N20–N23.0, N25–N28.1, N29–N30.3, N30.8–N32.0, N32.3–N32.4, N34–N34.3, N36–N36.9, N39–N39.2, N41–N41.9, N44–N44.0, N45–N45.9, N49–N49.9, N72–N72.0, N75–N77.8, N80–N81.9, N83–N83.9, P96.0, Q00–Q07.9, Q10.4–Q18.9, Q20–Q28.9, Q30–Q36, Q37–Q45.9, Q50–Q60.6, Q63–Q86, Q86.1–Q87.8, Q89–Q89.8, Q90–Q93.9, Q95–Q99.8, R95–R95.9
3	Congenital birth defects	G71.2, P96.0, Q00–Q07.9, Q10.4–Q18.9, Q20–Q28.9, Q30–Q36, Q37–Q45.9, Q50–Q60.6, Q63–Q86, Q86.1–Q87.8, Q89–Q89.8, Q90–Q93.9, Q95–Q99.8
4	Neural tube defects	Q00–Q01.9, Q05–Q05.9
4	Congenital heart anomalies	Q20–Q28.9
4	Orofacial clefts	Q35–Q36, Q37–Q37.9
4	Down syndrome	Q90–Q90.9
4	Other chromosomal abnormalities	Q87–Q87.8, Q91–Q93.9, Q95–Q95.9, Q97–Q97.9, Q99–Q99.8
4	Congenital musculoskeletal and limb anomalies	Q65–Q79, Q79.6–Q79.9
4	Urogenital congenital anomalies	P96.0, Q50–Q60.6, Q63–Q64.9

Cause Level	Cause	ICD-10 Codes
4	Digestive congenital anomalies	Q38–Q45.9, Q79.0–Q79.5
4	Other congenital birth defects	G71.2, Q02–Q04.9, Q06–Q07.9, Q10.4–Q18.9, Q30–Q34.9, Q80–Q86, Q86.1–Q86.8, Q89–Q89.8
3	Urinary diseases and male infertility	N10–N12.9, N13.6, N15, N15.1–N16.8, N20–N23.0, N25–N28.1, N29–N30.3, N30.8–N32.0, N32.3–N32.4, N34–N34.3, N36–N36.9, N39–N39.2, N41–N41.9, N44–N44.0, N45–N45.9, N49–N49.9
4	Urinary tract infections and interstitial nephritis	N10–N12.9, N13.6, N15, N15.1–N16.8, N30–N30.3, N30.8–N30.9, N34–N34.3, N39.0–N39.2
4	Urolithiasis	N20–N23.0
4	Other urinary diseases	N25–N28.1, N29–N29.8, N31–N32.0, N32.3–N32.4, N36–N36.9, N39, N41–N41.9, N44–N44.0, N45–N45.9, N49–N49.9
3	Gynaecological diseases	D25–D26, D28.2, E28.2, N72–N72.0, N75–N77.8, N80–N81.9, N83–N83.9
4	Uterine fibroids	D25–D26, D28.2
4	Endometriosis	N80–N80.9
4	Genital prolapse	N81–N81.9
4	Other gynaecological diseases	N72–N72.0, N75–N77.8, N83–N83.9
3	Haemoglobinopathies and haemolytic anaemias	D55–D58.9, D59.1, D59.3, D59.5, D60–D61.9, D64.0
4	Thalassaemias	D56–D56.9
4	Sickle cell disorders	D57–D57.8
4	G6PD deficiency	D55–D55.2
4	Other haemoglobinopathies and haemolytic anaemias	D55.3–D55.9, D58–D58.9, D59.1, D59.3, D59.5, D60–D61.9, D64.0
3	Endocrine, metabolic, blood, and immune disorders	D66–D67, D68.0–D69.4, D69.6–D69.8, D70–D70.0, D70.4–D75.8, D76–D77, D86.8, D89–D89.2, E03–E03.1, E03.3–E06.3, E06.5–E07.1, E16.1–E16.9, E20–E23.0, E23.2–E24.1, E24.3, E24.8–E27.2, E27.4–E28.1, E28.3–E34, E34.1–E34.8, E65–E66.0, E66.2–E68, E70–E85.2, E88–E88.2, E88.4–E88.9
4	Thyroid diseases	E03–E03.1, E03.3–E06.3, E06.5–E07, E07.1
4	Other endocrine, metabolic, blood, and immune disorders	D66–D67, D68.0–D69.4, D69.6–D69.8, D70–D70.0, D70.4–D75.8, D76–D77, D86.8, D89–D89.2, E07.0, E16.1–E16.9, E20–E23.0, E23.2–E24.1, E24.3, E24.8–E27.2, E27.4–E28.1, E28.3–E34, E34.1–E34.8, E67–E68, E70–E77.9, E79–E83.9, E85–E85.2, E88–E88.2, E88.4–E88.9
3	Sudden infant death syndrome	R95–R95.9

Cause Level	Cause	ICD-10 Codes
1	Injuries	D52.1, D59.0, D59.2, D59.6, D69.5, D70.1–D70.2, D78–D78.8, E03.2, E06.4, E09–E09.9, E16.0, E23.1, E24.2, E27.3, E36–E36.8, E66.1, E88.3, E89–E89.9, G21.0–G21.1, G24.0, G25.1, G25.4, G25.6–G25.7, G72.0, G93.7, G97–G97.9, I95.2–I95.3, I97–I97.9, I98.9, J70.0–J70.5, J95–J95.9, K43–K43.9, K52.0, K62.7, K91–K91.9, K94–K95.8, L55–L55.9, L56.3, L56.8–L56.9, L58–L58.9, M87.1, N14–N14.4, N30.4, N65–N65.1, N99–N99.9, P93–P93.8, P96.2, P96.5, R50.2, U00–U03, V00–V86.9, V87.2–V87.3, V88.2–V88.3, V90–V98.8, W00–W46.2, W49–W62.9, W64–W70.9, W73–W75.9, W77–W81.9, W83–W94.9, W97.9, W99–X06.9, X08–X39.9, X47–X48.9, X50–X54.9, X57–X58.9, X60–X64.9, X66–X83.9, X85–Y08.9, Y35–Y84.9, Y87.0–Y87.1, Y88–Y88.3, Y89.0–Y89.1
2	Transport injuries	V00–V86.9, V87.2–V87.3, V88.2–V88.3, V90–V98.8
3	Road injuries	V01–V04.9, V06–V80.9, V82–V82.9, V87.2–V87.3
4	Pedestrian road injuries	V01–V04.9, V06–V09.9
4	Cyclist road injuries	V10–V19.9
4	Motorcyclist road injuries	V20–V29.9
4	Motor vehicle road injuries	V30–V79.9, V87.2–V87.3
4	Other road injuries	V80–V80.9, V82–V82.9
3	Other transport injuries	V00–V00.8, V05–V05.9, V81–V81.9, V83–V86.9, V88.2–V88.3, V90–V98.8
2	Unintentional injuries	D52.1, D59.0, D59.2, D59.6, D69.5, D70.1–D70.2, D78–D78.8, E03.2, E06.4, E09–E09.9, E16.0, E23.1, E24.2, E27.3, E36–E36.8, E66.1, E88.3, E89–E89.9, G21.0–G21.1, G24.0, G25.1, G25.4, G25.6–G25.7, G72.0, G93.7, G97–G97.9, I95.2–I95.3, I97–I97.9, I98.9, J70.0–J70.5, J95–J95.9, K43–K43.9, K52.0, K62.7, K91–K91.9, K94–K95.8, L55–L55.9, L56.3, L56.8–L56.9, L58–L58.9, M87.1, N14–N14.4, N30.4, N65–N65.1, N99–N99.9, P93–P93.8, P96.2, P96.5, R50.2, W00–W46.2, W49–W62.9, W64–W70.9, W73–W75.9, W77–W81.9, W83–W94.9, W97.9, W99–X06.9, X08–X39.9, X47–X48.9, X50–X54.9, X57–X58.9, Y40–Y84.9, Y88–Y88.3
3	Falls	W00–W19.9
3	Drowning	W65–W70.9, W73–W74.9
3	Fire, heat, and hot substances	X00–X06.9, X08–X19.9
3	Poisonings	X47–X48.9
4	Poisoning by carbon monoxide	X47–X47.9
4	Poisoning by other means	X48–X48.9

Cause Level	Cause	ICD-10 Codes
3	Exposure to mechanical forces	W20–W38.9, W40–W43.9, W45.0–W45.2, W46–W46.2, W49–W52
4	Unintentional firearm injuries	W32–W34.9
4	Other exposure to mechanical forces	W20–W31.9, W35–W38.9, W40–W43.9, W45.0–W45.2, W46–W46.2, W49–W52
3	Adverse effects of medical treatment	D52.1, D59.0, D59.2, D59.6, D69.5, D70.1–D70.2, D78–D78.8, E03.2, E06.4, E09–E09.9, E16.0, E23.1, E24.2, E27.3, E36–E36.8, E66.1, E88.3, E89–E89.9, G21.0–G21.1, G24.0, G25.1, G25.4, G25.6–G25.7, G72.0, G93.7, G97–G97.9, I95.2–I95.3, I97–I97.9, I98.9, J70.0–J70.5, J95–J95.9, K43–K43.9, K52.0, K62.7, K91–K91.9, K94–K95.8, M87.1, N14–N14.4, N30.4, N65–N65.1, N99–N99.9, P93–P93.8, P96.2, P96.5, R50.2, Y40–Y84.9, Y88–Y88.3
3	Animal contact	W52.0–W62.9, W64–W64.9, X20–X29.9
4	Venomous animal contact	X20–X29.9
4	Non-venomous animal contact	W52.0–W62.9, W64–W64.9
3	Foreign body	W44–W45, W45.3–W45.9, W75–W75.9, W78–W80.9, W83–W84.9
4	Pulmonary aspiration and foreign body in airway	W75–W75.9, W78–W80.9, W83–W84.9
4	Foreign body in other body part	W44–W45, W45.3–W45.9
3	Environmental heat and cold exposure	L55–L55.9, L56.3, L56.8–L56.9, L58–L58.9, W88–W94.9, W97.9, W99–W99.9, X30–X32.9, X39–X39.9
3	Exposure to forces of nature	X33–X38.9
3	Other unintentional injuries	W39–W39.9, W77–W77.9, W81–W81.9, W85–W87.9, X50–X54.9, X57–X58.9
2	Self-harm and interpersonal violence	U00–U03, X60–X64.9, X66–X83.9, X85–Y08.9, Y35–Y38.9, Y87.0–Y87.1, Y89.0–Y89.1
3	Self-harm	X60–X64.9, X66–X83.9, Y87.0
4	Self-harm by firearm	X72–X74.9
4	Self-harm by other specified means	X60–X64.9, X66–X71.9, X75–X83.9, Y87.0
3	Interpersonal violence	X85–Y08.9, Y87.1
4	Physical violence by firearm	X93–X95.9
4	Physical violence by sharp object	X99–X99.9
4	Physical violence by other means	X85–X92.9, X96–X98.9, Y00–Y04.9, Y06–Y08.9, Y87.1

Cause Level	Cause	ICD-10 Codes
3	Conflict and terrorism	U00–U03, Y36–Y38.9, Y89.1
3	Police conflict and executions	Y35–Y35.9, Y89.0

3.4 Covariate data sources

Covariate	Data sources	Data processing	Citations
Household median income	2000-2019 Small Area Income and Poverty Estimates [1]; 2000-2019 Bureau of Labor Statistics, Consumer Price Index [2]	Data were adjusted for inflation using the consumer price index.	[1] US Census Bureau. Small Area Income and Poverty Estimates. https://www.census.gov/programs-surveys/saipe/data/datasets.html. Accessed October 6, 2022. [2] US Bureau of Labor Statistics. Consumer Price Index: All Urban Consumers History, All Items 1913-2021. https://www.bls.gov/data/. Accessed October 6, 2022.
Population density	2000-2019 NCHS bridged race files [3-4]; 2020 cartographic boundary file, state-county for United States [5] accessed using the tigris package [6]	The area of each county was calculated using an Albers Equal Area Conic projection. The total population of each county was divided by the total area of the county and was then log-transformed.	[3] National Center for Health Statistics, Centers for Disease Control and Prevention, US Census Bureau. United States Bridged-Race Intercensal Population Estimates 2000-2009. Hyattsville, United States: National Center for Health Statistics, Centers for Disease Control and Prevention, 2012. https://www.cdc.gov/nchs/nvss/bridged_race.htm. Accessed October 30, 2012. [4] National Center for Health Statistics, Centers for Disease Control and Prevention, US Census Bureau. United States Vintage 2020 Bridged-Race Postcensal Population Estimates 2010-2020. Hyattsville, United States: National Center for Health Statistics, Centers for Disease Control and Prevention, 2020. https://www.cdc.gov/nchs/nvss/bridged_race.htm. Accessed February 17, 2022. [5] US Census Bureau. TIGER/Line Shapefile, 2020 Cartographic Boundary File, State-County for United States, 1:20,000,000. https://www.census.gov/geographies/mapping-files/time-series/geo/tiger-line-file.2020.html#list-tab-790442341. Accessed October 12, 2022. [6] Walker K (2022). *tigris: Load Census TIGER/Line Shapefiles*. R package version 2.0, <https://github.com/walkerke/tigris>.

Covariate	Data sources	Data processing	Citations
Percent of the population age 25 and older who have completed a bachelor’s degree by race and ethnicity	1990 census [6]; 2000 census [7]; 2010-2020 ACS [8]	ACS estimates for the AIAN, Asian, Black, and NHPI populations were not available stratified by Latino ethnicity and were used as proxies for non-Latino AIAN, non-Latino Asian, non-Latino Black, and non-Latino NHPI estimates, respectively. Imputation via a small area estimation model was used to generate and smooth missing values.	[6] Minnesota Population Center. 1990 Census Summary Tape File 4, Table NPB44. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed August 25, 2020. [7] Minnesota Population Center. 2000 Census Summary File 4, Table NPCT064C. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed August 25, 2020. [8] US Census Bureau. American Community Survey, 2010-2020 American Community Survey 5-Year Estimates, Tables C15002A-C15002I; using Census data portal; https://data.census.gov/cedsci/. Accessed October 5, 2022.
Percent of the population below the poverty line by race and ethnicity	1990 census [9]; 2000 census [10]; 2010-2020 ACS [11]	ACS estimates for the AIAN, Asian, Black, and NHPI populations were not available stratified by Latino ethnicity and were used as proxies for non-Latino AIAN, non-Latino Asian, non-Latino Black, and non-Latino NHPI estimates, respectively. Imputation via a small area estimation model was used to generate and smooth missing values.	[9] Minnesota Population Center. 1990 Census Summary Tape File 4, Table NPB100. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed August 30, 2020. [10] Minnesota Population Center. 2000 Census Summary File 4, Table NPCT142A. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed August 30, 2020. [11] US Census Bureau. American Community Survey, 2010-2020 American Community Survey 5-Year Estimates, Tables B17001A-B17001I; using Census data portal; https://data.census.gov/cedsci/. Accessed October 5, 2022.

Covariate	Data sources	Data processing	Citations
Percent of the population that is foreign-born by race and ethnicity	1990 census [12]; 2000 census [13]; 2010-2020 ACS [14]	ACS estimates for the AIAN, Asian, Black, and NHPI populations were not available stratified by Latino ethnicity and were used as proxies for non-Latino AIAN, non-Latino Asian, non-Latino Black, and non-Latino NHPI estimates, respectively. Imputation via a small area estimation model was used to generate and smooth missing values.	[12] Minnesota Population Center. 1990 Census Summary Tape File 4, Table NPB28. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed October 8, 2020. [13] Minnesota Population Center. 2000 Census Summary File 4, Table NPCT043A. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed October 8, 2020. [14] US Census Bureau. American Community Survey, 2010-2020 American Community Survey 5-Year Estimates, Tables B05003A-B05003I; using Census data portal; https://data.census.gov/cedsci/. Accessed October 5, 2022.

3.5 Population mask

	AIAN			Asian			Black			Latino			White			Total		
Strata	Counties masked	Person-years masked *	Percent person-years in strata	Counties masked	Person-years masked *	Percent person-years in strata	Counties masked	Person-years masked *	Percent person-years in strata	Counties masked	Person-years masked *	Percent person-years in strata	Counties masked	Person-years masked *	Percent person-years in strata	Counties masked	Person-years masked *	Percent person-years in strata
Total	2636 (84.8%)	9.1 (17.8%)		2443 (78.6%)	8.5 (2.6%)		1622 (52.2%)	7.5 (1.0%)		1632 (52.5%)	11.4 (1.2%)		59 (1.9%)	0.8 (0.0%)		31 (1.0%)	0.4 (0.0%)	
Urban or rural code																		
Large central metro	8 (10.1%)	0.1 (0.7%)	16.5%	0 (0.0%)	0.0 (0.0%)	51.8%	0 (0.0%)	0.0 (0.0%)	42.1%	0 (0.0%)	0.0 (0.0%)	49.5%	0 (0.0%)	0.0 (0.0%)	22.1%	0 (0.0%)	0.0 (0.0%)	30.6%
Large fringe metro	309 (78.0%)	1.5 (28.7%)	10.4%	184 (46.5%)	0.9 (1.1%)	24.7%	83 (21.0%)	0.5 (0.3%)	20.8%	103 (26.0%)	0.7 (0.4%)	17.2%	0 (0.0%)	0.0 (0.0%)	24.8%	0 (0.0%)	0.0 (0.0%)	23.0%
Medium metro	359 (73.6%)	1.5 (14.9%)	19.5%	239 (49.0%)	0.9 (1.7%)	15.9%	115 (23.6%)	0.5 (0.4%)	19.0%	121 (24.8%)	0.7 (0.4%)	19.8%	1 (0.2%)	0.0 (0.0%)	22.1%	0 (0.0%)	0.0 (0.0%)	21.0%
Small metro	356 (80.9%)	1.3 (22.0%)	11.6%	241 (54.8%)	1.0 (8.1%)	3.8%	125 (28.4%)	0.5 (0.9%)	6.9%	149 (33.9%)	0.8 (1.4%)	5.9%	2 (0.5%)	0.0 (0.0%)	10.4%	1 (0.2%)	0.0 (0.0%)	8.9%
Micropolitan	717 (87.5%)	2.1 (21.4%)	19.5%	693 (84.6%)	3.5 (37.0%)	2.9%	384 (46.9%)	2.4 (4.9%)	6.1%	307 (37.5%)	2.3 (4.8%)	4.9%	9 (1.1%)	0.1 (0.0%)	11.2%	6 (0.7%)	0.0 (0.0%)	9.2%
Noncore	1694 (92.7%)	2.6 (22.5%)	22.4%	1805 (98.8%)	2.2 (83.2%)	0.8%	1340 (73.3%)	3.6 (9.1%)	5.1%	1399 (76.6%)	6.8 (25.7%)	2.7%	59 (3.2%)	0.7 (0.2%)	9.4%	31 (1.7%)	0.4 (0.1%)	7.4%
Census region																		
South	1246 (88.6%)	3.9 (23.5%)	32.0%	1137 (80.8%)	4.0 (5.7%)	21.6%	451 (32.1%)	2.8 (0.6%)	56.1%	686 (48.8%)	5.4 (1.5%)	35.9%	19 (1.4%)	0.2 (0.0%)	34.8%	8 (0.6%)	0.1 (0.0%)	37.0%
West	269 (62.4%)	1.3 (5.6%)	44.3%	309 (71.7%)	1.2 (0.8%)	46.5%	319 (74.0%)	1.2 (1.6%)	9.2%	152 (35.3%)	0.9 (0.2%)	40.7%	18 (4.2%)	0.3 (0.0%)	19.5%	9 (2.1%)	0.1 (0.0%)	23.2%
Northeast	172 (79.3%)	0.9 (30.6%)	6.0%	110 (50.7%)	0.8 (1.3%)	20.0%	69 (31.8%)	0.6 (0.4%)	16.4%	67 (30.9%)	0.7 (0.5%)	14.1%	0 (0.0%)	0.0 (0.0%)	19.3%	0 (0.0%)	0.0 (0.0%)	18.0%
Midwest	949 (90.0%)	3.0 (33.5%)	17.7%	887 (84.1%)	2.5 (6.5%)	11.9%	783 (74.2%)	3.0 (2.1%)	18.4%	727 (68.9%)	4.4 (4.9%)	9.2%	22 (2.1%)	0.3 (0.0%)	26.4%	14 (1.3%)	0.2 (0.0%)	21.8%

*Person-years are given in millions.

Modelled age-standardised mortality estimates were masked (not displayed) in all years for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. The number of unique counties masked (and corresponding percentage of all counties), the person-years in millions represented by these county-years (and corresponding percentage of all person-years), and the percentage of the person-years masked in each strata are listed in this table. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

3.6 Hyperparameter posterior means and standard errors

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	All causes (Level 0)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.045 (SE = 0.02)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_1	Standard deviation, Proportion in poverty	0.038 (SE = 0.016)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_1	Standard deviation, Proportion foreign born	0.202 (SE = 0.081)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_2	Standard deviation	0.12 (SE = 0.004)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_2	Correlation parameter, County	0.992 (SE = 0.006)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_3	Standard deviation	0.017 (SE = 0.001)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_3	Correlation parameter, Age	0.944 (SE = 0.01)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_4	Standard deviation	0.151 (SE = 0.002)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_4	Correlation parameter, County	0.995 (SE = 0.001)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_4	Correlation parameter, Year spline	0.945 (SE = 0.002)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_4	Correlation parameter, Age spline	0.496 (SE = 0.012)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_5	Standard deviation, County (2001)	0.007 (SE = 0.003)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_6	Standard deviation, County (2005)	0.036 (SE = 0.009)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_7	Standard deviation, Age (2001)	0.025 (SE = 0.008)
By racial–ethnic group and county	All causes (Level 0)	Females	γ_8	Standard deviation, Age (2005)	0.008 (SE = 0.006)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.066 (SE = 0.027)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_1	Standard deviation, Proportion in poverty	0.034 (SE = 0.014)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_1	Standard deviation, Proportion foreign born	0.225 (SE = 0.09)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_2	Standard deviation	0.196 (SE = 0.005)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_2	Correlation parameter, County	0.969 (SE = 0.023)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_3	Standard deviation	0.02 (SE = 0.001)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_3	Correlation parameter, Age	0.947 (SE = 0.009)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	All causes (Level 0)	Males	γ_4	Standard deviation	0.148 (SE = 0.002)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_4	Correlation parameter, County	0.992 (SE = 0.001)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_4	Correlation parameter, Year spline	0.967 (SE = 0.001)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_4	Correlation parameter, Age spline	0.569 (SE = 0.01)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_5	Standard deviation, County (2001)	0.015 (SE = 0.003)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_6	Standard deviation, County (2005)	0.036 (SE = 0.009)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_7	Standard deviation, Age (2001)	0.033 (SE = 0.008)
By racial–ethnic group and county	All causes (Level 0)	Males	γ_8	Standard deviation, Age (2005)	0.016 (SE = 0.006)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.061 (SE = 0.034)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_1	Standard deviation, Proportion in poverty	0.07 (SE = 0.03)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_1	Standard deviation, Proportion foreign born	0.328 (SE = 0.135)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_2	Standard deviation	0.174 (SE = 0.008)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_2	Correlation parameter, County	0.969 (SE = 0.023)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_3	Standard deviation	0.034 (SE = 0.002)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_3	Correlation parameter, Age	0.967 (SE = 0.007)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_4	Standard deviation	0.324 (SE = 0.006)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_4	Correlation parameter, County	0.987 (SE = 0.002)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_4	Correlation parameter, Year spline	0.815 (SE = 0.008)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_4	Correlation parameter, Age spline	0.367 (SE = 0.021)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.047 (SE = 0.022)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_1	Standard deviation, Proportion in poverty	0.091 (SE = 0.038)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_1	Standard deviation, Proportion foreign born	0.364 (SE = 0.148)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_2	Standard deviation	0.2 (SE = 0.007)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_2	Correlation parameter, County	0.974 (SE = 0.017)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_3	Standard deviation	0.043 (SE = 0.002)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_3	Correlation parameter, Age	0.935 (SE = 0.012)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_4	Standard deviation	0.304 (SE = 0.006)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_4	Correlation parameter, County	0.989 (SE = 0.002)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_4	Correlation parameter, Year spline	0.864 (SE = 0.006)
By racial–ethnic group and county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_4	Correlation parameter, Age spline	0.33 (SE = 0.02)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.04 (SE = 0.029)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.063 (SE = 0.054)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.281 (SE = 0.129)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_2	Standard deviation	0.407 (SE = 0.021)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_2	Correlation parameter, County	0.973 (SE = 0.018)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_3	Standard deviation	0.058 (SE = 0.005)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_3	Correlation parameter, Age	0.956 (SE = 0.012)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_4	Standard deviation	0.369 (SE = 0.02)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_4	Correlation parameter, County	0.997 (SE = 0.001)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.866 (SE = 0.016)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.47 (SE = 0.055)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.092 (SE = 0.048)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.109 (SE = 0.054)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.205 (SE = 0.113)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_2	Standard deviation	0.451 (SE = 0.016)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_2	Correlation parameter, County	0.974 (SE = 0.016)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_3	Standard deviation	0.072 (SE = 0.004)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_3	Correlation parameter, Age	0.941 (SE = 0.012)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_4	Standard deviation	0.308 (SE = 0.014)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_4	Correlation parameter, County	0.996 (SE = 0.001)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.894 (SE = 0.01)
By racial–ethnic group and county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.62 (SE = 0.034)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.039 (SE = 0.032)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.081 (SE = 0.036)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.399 (SE = 0.164)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_2	Standard deviation	0.266 (SE = 0.011)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_2	Correlation parameter, County	0.964 (SE = 0.021)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_3	Standard deviation	0.041 (SE = 0.002)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_3	Correlation parameter, Age	0.992 (SE = 0.002)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_4	Standard deviation	0.34 (SE = 0.008)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_4	Correlation parameter, County	0.973 (SE = 0.004)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.762 (SE = 0.014)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.524 (SE = 0.026)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.042 (SE = 0.033)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.09 (SE = 0.039)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.416 (SE = 0.171)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_2	Standard deviation	0.249 (SE = 0.01)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_2	Correlation parameter, County	0.96 (SE = 0.026)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_3	Standard deviation	0.039 (SE = 0.002)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_3	Correlation parameter, Age	0.99 (SE = 0.002)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_4	Standard deviation	0.288 (SE = 0.008)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_4	Correlation parameter, County	0.985 (SE = 0.003)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.819 (SE = 0.011)
By racial–ethnic group and county	Respiratory infections and tuberculosis (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.571 (SE = 0.025)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.036 (SE = 0.03)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.106 (SE = 0.053)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.421 (SE = 0.202)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_2	Standard deviation	0.288 (SE = 0.014)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_2	Correlation parameter, County	0.967 (SE = 0.02)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_3	Standard deviation	0.068 (SE = 0.005)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_3	Correlation parameter, Age	0.973 (SE = 0.007)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_4	Standard deviation	0.305 (SE = 0.02)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_4	Correlation parameter, County	0.985 (SE = 0.005)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.139 (SE = 0.051)
By racial–ethnic group and county	Enteric infections (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.814 (SE = 0.034)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.031 (SE = 0.03)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.128 (SE = 0.062)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.587 (SE = 0.267)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_2	Standard deviation	0.293 (SE = 0.015)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_2	Correlation parameter, County	0.963 (SE = 0.024)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_3	Standard deviation	0.07 (SE = 0.005)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_3	Correlation parameter, Age	0.976 (SE = 0.006)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_4	Standard deviation	0.308 (SE = 0.021)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_4	Correlation parameter, County	0.991 (SE = 0.003)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.242 (SE = 0.074)
By racial–ethnic group and county	Enteric infections (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.753 (SE = 0.048)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.083 (SE = 0.05)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.143 (SE = 0.064)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.198 (SE = 0.191)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_2	Standard deviation	0.139 (SE = 0.014)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.974 (SE = 0.029)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_3	Standard deviation	0.028 (SE = 0.004)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.972 (SE = 0.011)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_4	Standard deviation	0.122 (SE = 0.017)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.996 (SE = 0.002)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.9 (SE = 0.029)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.427 (SE = 0.094)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.063 (SE = 0.042)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.073 (SE = 0.041)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.541 (SE = 0.248)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_2	Standard deviation	0.185 (SE = 0.012)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.98 (SE = 0.014)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_3	Standard deviation	0.033 (SE = 0.004)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.973 (SE = 0.01)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_4	Standard deviation	0.141 (SE = 0.017)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.996 (SE = 0.002)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.866 (SE = 0.034)
By racial–ethnic group and county	Other infectious diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.414 (SE = 0.09)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.061 (SE = 0.039)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_1	Standard deviation, Proportion in poverty	0.125 (SE = 0.063)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_1	Standard deviation, Proportion foreign born	0.218 (SE = 0.169)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_2	Standard deviation	0.248 (SE = 0.024)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_2	Correlation parameter, County	0.988 (SE = 0.008)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_3	Standard deviation	0.152 (SE = 0.013)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_3	Correlation parameter, Year	0.999 (SE < 0.001)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_3	Correlation parameter, Age	0.856 (SE = 0.034)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_4	Standard deviation	0.516 (SE = 0.033)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_4	Correlation parameter, County	0.994 (SE = 0.002)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_4	Correlation parameter, Year spline	0.062 (SE = 0.044)
By racial–ethnic group and county	Maternal disorders (Level 3)	Females	γ_4	Correlation parameter, Age spline	0.04 (SE = 0.029)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.088 (SE = 0.067)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_1	Standard deviation, Proportion in poverty	0.079 (SE = 0.037)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_1	Standard deviation, Proportion foreign born	0.417 (SE = 0.19)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_2	Standard deviation	0.257 (SE = 0.013)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_2	Correlation parameter, County	0.942 (SE = 0.029)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_3	Standard deviation	0.034 (SE = 0.005)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_3	Correlation parameter, Age	0.135 (SE = 0.105)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_4	Standard deviation	0.245 (SE = 0.041)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_4	Correlation parameter, County	0.953 (SE = 0.019)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_4	Correlation parameter, Year spline	0.485 (SE = 0.089)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Females	γ_4	Correlation parameter, Age spline	0.457 (SE = 0.269)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.041 (SE = 0.022)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_1	Standard deviation, Proportion in poverty	0.101 (SE = 0.043)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_1	Standard deviation, Proportion foreign born	0.405 (SE = 0.182)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_2	Standard deviation	0.248 (SE = 0.012)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_2	Correlation parameter, County	0.946 (SE = 0.028)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_3	Standard deviation	0.041 (SE = 0.006)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_3	Correlation parameter, Age	0.141 (SE = 0.108)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_4	Standard deviation	0.289 (SE = 0.019)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_4	Correlation parameter, County	0.956 (SE = 0.014)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_4	Correlation parameter, Year spline	0.548 (SE = 0.067)
By racial–ethnic group and county	Neonatal disorders (Level 3)	Males	γ_4	Correlation parameter, Age spline	0.216 (SE = 0.165)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.125 (SE = 0.069)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.102 (SE = 0.057)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.2 (SE = 0.201)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_2	Standard deviation	0.477 (SE = 0.019)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_2	Correlation parameter, County	0.987 (SE = 0.007)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_3	Standard deviation	0.037 (SE = 0.004)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_3	Correlation parameter, Age	0.989 (SE = 0.003)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_4	Standard deviation	0.57 (SE = 0.025)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_4	Correlation parameter, County	0.94 (SE = 0.017)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.345 (SE = 0.046)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.603 (SE = 0.052)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.06 (SE = 0.045)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.135 (SE = 0.068)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.706 (SE = 0.352)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_2	Standard deviation	0.465 (SE = 0.022)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_2	Correlation parameter, County	0.979 (SE = 0.012)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_3	Standard deviation	0.041 (SE = 0.005)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_3	Correlation parameter, Age	0.989 (SE = 0.003)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_4	Standard deviation	0.446 (SE = 0.033)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_4	Correlation parameter, County	0.961 (SE = 0.014)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.374 (SE = 0.064)
By racial–ethnic group and county	Nutritional deficiencies (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.72 (SE = 0.055)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.043 (SE = 0.019)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_1	Standard deviation, Proportion in poverty	0.039 (SE = 0.016)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_1	Standard deviation, Proportion foreign born	0.195 (SE = 0.079)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_2	Standard deviation	0.122 (SE = 0.004)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_2	Correlation parameter, County	0.99 (SE = 0.007)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_3	Standard deviation	0.016 (SE = 0.001)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_3	Correlation parameter, Age	0.949 (SE = 0.01)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_4	Standard deviation	0.149 (SE = 0.002)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_4	Correlation parameter, County	0.996 (SE = 0.001)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_4	Correlation parameter, Year spline	0.943 (SE = 0.002)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Females	γ_4	Correlation parameter, Age spline	0.471 (SE = 0.013)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.066 (SE = 0.027)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_1	Standard deviation, Proportion in poverty	0.034 (SE = 0.014)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_1	Standard deviation, Proportion foreign born	0.231 (SE = 0.092)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_2	Standard deviation	0.176 (SE = 0.005)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_2	Correlation parameter, County	0.968 (SE = 0.024)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_3	Standard deviation	0.021 (SE = 0.001)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_3	Correlation parameter, Age	0.945 (SE = 0.009)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_4	Standard deviation	0.147 (SE = 0.002)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_4	Correlation parameter, County	0.996 (SE = 0.001)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_4	Correlation parameter, Year spline	0.961 (SE = 0.001)
By racial–ethnic group and county	Non-communicable diseases (Level 1)	Males	γ_4	Correlation parameter, Age spline	0.506 (SE = 0.012)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.063 (SE = 0.028)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.042 (SE = 0.018)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.247 (SE = 0.1)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_2	Standard deviation	0.074 (SE = 0.004)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_2	Correlation parameter, County	0.99 (SE = 0.008)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_3	Standard deviation	0.012 (SE = 0.001)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_3	Correlation parameter, Age	0.977 (SE = 0.005)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_4	Standard deviation	0.099 (SE = 0.002)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_4	Correlation parameter, County	0.995 (SE = 0.001)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.94 (SE = 0.003)
By racial–ethnic group and county	Neoplasms (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.462 (SE = 0.022)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.071 (SE = 0.031)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.041 (SE = 0.017)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.275 (SE = 0.109)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_2	Standard deviation	0.118 (SE = 0.004)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_2	Correlation parameter, County	0.982 (SE = 0.013)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_3	Standard deviation	0.014 (SE = 0.001)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_3	Correlation parameter, Age	0.975 (SE = 0.005)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_4	Standard deviation	0.1 (SE = 0.002)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_4	Correlation parameter, County	0.995 (SE = 0.001)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.956 (SE = 0.002)
By racial–ethnic group and county	Neoplasms (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.437 (SE = 0.021)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.052 (SE = 0.024)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.039 (SE = 0.017)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.206 (SE = 0.085)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_2	Standard deviation	0.148 (SE = 0.005)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.983 (SE = 0.012)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_3	Standard deviation	0.015 (SE = 0.001)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.98 (SE = 0.004)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_4	Standard deviation	0.183 (SE = 0.003)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.992 (SE = 0.001)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.922 (SE = 0.003)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.383 (SE = 0.017)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.06 (SE = 0.026)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.039 (SE = 0.017)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.216 (SE = 0.088)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_2	Standard deviation	0.159 (SE = 0.005)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.981 (SE = 0.012)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_3	Standard deviation	0.015 (SE = 0.001)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.976 (SE = 0.005)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_4	Standard deviation	0.148 (SE = 0.003)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.993 (SE = 0.001)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.944 (SE = 0.002)
By racial–ethnic group and county	Cardiovascular diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.532 (SE = 0.016)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.038 (SE = 0.02)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.041 (SE = 0.02)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.235 (SE = 0.1)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_2	Standard deviation	0.163 (SE = 0.008)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.983 (SE = 0.012)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_3	Standard deviation	0.024 (SE = 0.001)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.972 (SE = 0.006)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_4	Standard deviation	0.209 (SE = 0.005)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.989 (SE = 0.002)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.929 (SE = 0.004)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.338 (SE = 0.023)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.043 (SE = 0.02)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.032 (SE = 0.015)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.32 (SE = 0.131)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_2	Standard deviation	0.183 (SE = 0.007)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.986 (SE = 0.009)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_3	Standard deviation	0.02 (SE = 0.001)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.973 (SE = 0.007)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_4	Standard deviation	0.185 (SE = 0.005)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.991 (SE = 0.002)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.928 (SE = 0.004)
By racial–ethnic group and county	Chronic respiratory diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.34 (SE = 0.025)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.048 (SE = 0.024)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.08 (SE = 0.033)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.291 (SE = 0.12)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_2	Standard deviation	0.14 (SE = 0.007)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.997 (SE = 0.002)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_3	Standard deviation	0.03 (SE = 0.002)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.946 (SE = 0.012)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_4	Standard deviation	0.137 (SE = 0.005)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.997 (SE = 0.001)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.951 (SE = 0.004)
By racial–ethnic group and county	Digestive diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.283 (SE = 0.029)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.076 (SE = 0.035)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.05 (SE = 0.022)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.391 (SE = 0.155)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_2	Standard deviation	0.192 (SE = 0.007)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.995 (SE = 0.003)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_3	Standard deviation	0.036 (SE = 0.002)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.926 (SE = 0.015)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_4	Standard deviation	0.159 (SE = 0.005)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.996 (SE = 0.001)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.948 (SE = 0.003)
By racial–ethnic group and county	Digestive diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.294 (SE = 0.027)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.042 (SE = 0.023)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.04 (SE = 0.019)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.262 (SE = 0.11)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_2	Standard deviation	0.252 (SE = 0.008)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_2	Correlation parameter, County	0.973 (SE = 0.015)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_3	Standard deviation	0.007 (SE = 0.001)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_3	Correlation parameter, Age	0.982 (SE = 0.006)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_4	Standard deviation	0.242 (SE = 0.005)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_4	Correlation parameter, County	0.956 (SE = 0.008)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.816 (SE = 0.01)
By racial–ethnic group and county	Neurological disorders (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.456 (SE = 0.027)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.027 (SE = 0.016)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.077 (SE = 0.033)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.263 (SE = 0.113)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_2	Standard deviation	0.111 (SE = 0.008)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_2	Correlation parameter, County	0.039 (SE = 0.028)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_3	Standard deviation	0.008 (SE = 0.001)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_3	Correlation parameter, Age	0.984 (SE = 0.005)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_4	Standard deviation	0.147 (SE = 0.005)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_4	Correlation parameter, County	0.988 (SE = 0.003)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.929 (SE = 0.005)
By racial–ethnic group and county	Neurological disorders (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.586 (SE = 0.026)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.069 (SE = 0.035)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.134 (SE = 0.06)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.238 (SE = 0.108)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_2	Standard deviation	0.403 (SE = 0.014)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_2	Correlation parameter, County	0.991 (SE = 0.005)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_3	Standard deviation	0.056 (SE = 0.003)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_3	Correlation parameter, Age	0.972 (SE = 0.006)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_4	Standard deviation	0.539 (SE = 0.012)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_4	Correlation parameter, County	0.993 (SE = 0.001)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.775 (SE = 0.013)
By racial–ethnic group and county	Substance use disorders (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.462 (SE = 0.026)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.121 (SE = 0.051)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.107 (SE = 0.046)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.349 (SE = 0.146)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_2	Standard deviation	0.411 (SE = 0.012)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_2	Correlation parameter, County	0.988 (SE = 0.008)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_3	Standard deviation	0.05 (SE = 0.002)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_3	Correlation parameter, Age	0.979 (SE = 0.004)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_4	Standard deviation	0.555 (SE = 0.009)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_4	Correlation parameter, County	0.995 (SE = 0.001)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.808 (SE = 0.008)
By racial–ethnic group and county	Substance use disorders (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.448 (SE = 0.019)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.139 (SE = 0.058)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.077 (SE = 0.032)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.281 (SE = 0.117)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_2	Standard deviation	0.226 (SE = 0.008)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.978 (SE = 0.016)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_3	Standard deviation	0.018 (SE = 0.001)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.973 (SE = 0.007)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_4	Standard deviation	0.188 (SE = 0.005)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.993 (SE = 0.001)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.925 (SE = 0.004)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.511 (SE = 0.023)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.128 (SE = 0.054)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.079 (SE = 0.033)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.413 (SE = 0.164)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_2	Standard deviation	0.229 (SE = 0.008)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.974 (SE = 0.019)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_3	Standard deviation	0.017 (SE = 0.001)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.983 (SE = 0.004)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_4	Standard deviation	0.178 (SE = 0.005)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.992 (SE = 0.002)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.926 (SE = 0.004)
By racial–ethnic group and county	Diabetes and kidney diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.589 (SE = 0.022)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.104 (SE = 0.054)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.105 (SE = 0.054)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.226 (SE = 0.17)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_2	Standard deviation	0.25 (SE = 0.014)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.964 (SE = 0.028)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_3	Standard deviation	0.025 (SE = 0.004)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.976 (SE = 0.008)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_4	Standard deviation	0.214 (SE = 0.015)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.997 (SE = 0.001)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.842 (SE = 0.026)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.378 (SE = 0.074)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.05 (SE = 0.039)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.075 (SE = 0.043)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.128 (SE = 0.1)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_2	Standard deviation	0.274 (SE = 0.015)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.974 (SE = 0.017)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_3	Standard deviation	0.026 (SE = 0.004)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.977 (SE = 0.008)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_4	Standard deviation	0.185 (SE = 0.019)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.998 (SE = 0.001)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.854 (SE = 0.031)
By racial–ethnic group and county	Skin and subcutaneous diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.525 (SE = 0.076)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.063 (SE = 0.035)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.11 (SE = 0.049)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.419 (SE = 0.187)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_2	Standard deviation	0.148 (SE = 0.015)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_2	Correlation parameter, County	0.995 (SE = 0.004)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_3	Standard deviation	0.015 (SE = 0.002)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_3	Correlation parameter, Age	0.994 (SE = 0.002)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_4	Standard deviation	0.169 (SE = 0.013)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_4	Correlation parameter, County	0.995 (SE = 0.002)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.933 (SE = 0.01)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.45 (SE = 0.047)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.149 (SE = 0.109)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.034 (SE = 0.027)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.369 (SE = 0.226)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_2	Standard deviation	0.077 (SE = 0.045)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_2	Correlation parameter, County	0.722 (SE = 0.396)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_3	Standard deviation	0.02 (SE = 0.003)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_3	Correlation parameter, Age	0.99 (SE = 0.003)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_4	Standard deviation	0.105 (SE = 0.019)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_4	Correlation parameter, County	0.996 (SE = 0.001)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.963 (SE = 0.013)
By racial–ethnic group and county	Musculoskeletal disorders (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.591 (SE = 0.073)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.043 (SE = 0.021)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.084 (SE = 0.036)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.395 (SE = 0.16)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_2	Standard deviation	0.148 (SE = 0.008)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.98 (SE = 0.013)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_3	Standard deviation	0.017 (SE = 0.001)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.965 (SE = 0.01)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_4	Standard deviation	0.221 (SE = 0.007)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.97 (SE = 0.005)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.866 (SE = 0.009)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.375 (SE = 0.03)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.062 (SE = 0.032)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.067 (SE = 0.03)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.316 (SE = 0.134)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_2	Standard deviation	0.101 (SE = 0.011)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.071 (SE = 0.054)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_3	Standard deviation	0.023 (SE = 0.002)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.951 (SE = 0.013)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_4	Standard deviation	0.222 (SE = 0.008)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.982 (SE = 0.003)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.868 (SE = 0.01)
By racial–ethnic group and county	Other non-communicable diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.449 (SE = 0.03)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.095 (SE = 0.047)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.078 (SE = 0.034)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.452 (SE = 0.185)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_2	Standard deviation	0.216 (SE = 0.01)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_2	Correlation parameter, County	0.99 (SE = 0.006)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_3	Standard deviation	0.033 (SE = 0.002)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_3	Correlation parameter, Age	0.978 (SE = 0.005)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_4	Standard deviation	0.205 (SE = 0.011)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_4	Correlation parameter, County	0.989 (SE = 0.002)
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.89 (SE = 0.012)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Transport injuries (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.646 (SE = 0.03)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.121 (SE = 0.052)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.084 (SE = 0.035)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.421 (SE = 0.169)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_2	Standard deviation	0.262 (SE = 0.008)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_2	Correlation parameter, County	0.987 (SE = 0.007)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_3	Standard deviation	0.029 (SE = 0.002)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_3	Correlation parameter, Age	0.98 (SE = 0.004)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_4	Standard deviation	0.203 (SE = 0.007)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_4	Correlation parameter, County	0.989 (SE = 0.002)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.924 (SE = 0.005)
By racial–ethnic group and county	Transport injuries (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.632 (SE = 0.023)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.017 (SE = 0.013)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.075 (SE = 0.033)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.352 (SE = 0.149)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_2	Standard deviation	0.148 (SE = 0.009)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_2	Correlation parameter, County	0.992 (SE = 0.005)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_3	Standard deviation	0.03 (SE = 0.002)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_3	Correlation parameter, Age	0.928 (SE = 0.017)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_4	Standard deviation	0.308 (SE = 0.008)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_4	Correlation parameter, County	0.976 (SE = 0.004)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.833 (SE = 0.01)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.452 (SE = 0.025)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_5	Standard deviation, County (2005)	0.613 (SE = 0.073)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Females	γ_6	Standard deviation, Age	0.062 (SE = 0.048)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.037 (SE = 0.019)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.07 (SE = 0.031)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.487 (SE = 0.193)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_2	Standard deviation	0.125 (SE = 0.009)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_2	Correlation parameter, County	0.994 (SE = 0.004)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_3	Standard deviation	0.034 (SE = 0.002)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_3	Correlation parameter, Age	0.931 (SE = 0.014)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_4	Standard deviation	0.23 (SE = 0.007)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_4	Correlation parameter, County	0.985 (SE = 0.002)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.921 (SE = 0.005)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.411 (SE = 0.022)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_5	Standard deviation, County (2005)	0.48 (SE = 0.06)
By racial–ethnic group and county	Unintentional injuries (Level 2)	Males	γ_6	Standard deviation, Age	0.119 (SE = 0.039)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_1	Standard deviation, Proportion with Bachelors Degree	0.022 (SE = 0.027)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_1	Standard deviation, Proportion in poverty	0.085 (SE = 0.037)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_1	Standard deviation, Proportion foreign born	0.342 (SE = 0.148)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_2	Standard deviation	0.237 (SE = 0.012)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_2	Correlation parameter, County	0.992 (SE = 0.005)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_3	Standard deviation	0.04 (SE = 0.003)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_3	Correlation parameter, Age	0.905 (SE = 0.025)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_4	Standard deviation	0.229 (SE = 0.011)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_4	Correlation parameter, County	0.99 (SE = 0.002)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.878 (SE = 0.012)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.646 (SE = 0.029)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_5	Standard deviation, County (2001)	0.337 (SE = 0.031)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Females	γ_6	Standard deviation, Age	0.055 (SE = 0.03)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_1	Standard deviation, Proportion with Bachelors Degree	0.121 (SE = 0.051)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_1	Standard deviation, Proportion in poverty	0.088 (SE = 0.037)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_1	Standard deviation, Proportion foreign born	0.308 (SE = 0.128)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_2	Standard deviation	0.28 (SE = 0.009)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_2	Correlation parameter, County	0.99 (SE = 0.006)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_3	Standard deviation	0.031 (SE = 0.002)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_3	Correlation parameter, Age	0.96 (SE = 0.009)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_4	Standard deviation	0.246 (SE = 0.007)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_4	Correlation parameter, County	0.971 (SE = 0.004)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.914 (SE = 0.005)

Model	Cause	Sex	Parameter		Mean (SE)*
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.681 (SE = 0.017)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_5	Standard deviation, County (2001)	0.328 (SE = 0.024)
By racial–ethnic group and county	Self-harm and interpersonal violence (Level 2)	Males	γ_6	Standard deviation, Age	0.095 (SE = 0.024)
By county	All causes (Level 0)	Females	γ_2	Standard deviation	0.059 (SE = 0.012)
By county	All causes (Level 0)	Females	γ_2	Correlation parameter, County	0.089 (SE = 0.095)
By county	All causes (Level 0)	Females	γ_3	Standard deviation	0.016 (SE = 0.001)
By county	All causes (Level 0)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	All causes (Level 0)	Females	γ_3	Correlation parameter, Age	0.929 (SE = 0.02)
By county	All causes (Level 0)	Females	γ_4	Standard deviation	0.151 (SE = 0.002)
By county	All causes (Level 0)	Females	γ_4	Correlation parameter, County	0.977 (SE = 0.004)
By county	All causes (Level 0)	Females	γ_4	Correlation parameter, Year spline	0.939 (SE = 0.002)
By county	All causes (Level 0)	Females	γ_4	Correlation parameter, Age spline	0.334 (SE = 0.016)
By county	All causes (Level 0)	Females	γ_5	Standard deviation, County (2001)	0.008 (SE = 0.003)
By county	All causes (Level 0)	Females	γ_6	Standard deviation, County (2005)	0.038 (SE = 0.009)
By county	All causes (Level 0)	Females	γ_7	Standard deviation, Age (2001)	0.037 (SE = 0.01)
By county	All causes (Level 0)	Females	γ_8	Standard deviation, Age (2005)	0.009 (SE = 0.006)
By county	All causes (Level 0)	Males	γ_2	Standard deviation	0.077 (SE = 0.008)
By county	All causes (Level 0)	Males	γ_2	Correlation parameter, County	0.059 (SE = 0.042)
By county	All causes (Level 0)	Males	γ_3	Standard deviation	0.017 (SE = 0.001)
By county	All causes (Level 0)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	All causes (Level 0)	Males	γ_3	Correlation parameter, Age	0.939 (SE = 0.017)
By county	All causes (Level 0)	Males	γ_4	Standard deviation	0.145 (SE = 0.002)
By county	All causes (Level 0)	Males	γ_4	Correlation parameter, County	0.969 (SE = 0.005)
By county	All causes (Level 0)	Males	γ_4	Correlation parameter, Year spline	0.955 (SE = 0.001)
By county	All causes (Level 0)	Males	γ_4	Correlation parameter, Age spline	0.273 (SE = 0.015)
By county	All causes (Level 0)	Males	γ_5	Standard deviation, County (2001)	0.015 (SE = 0.003)
By county	All causes (Level 0)	Males	γ_6	Standard deviation, County (2005)	0.032 (SE = 0.01)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	All causes (Level 0)	Males	γ_7	Standard deviation, Age (2001)	0.032 (SE = 0.008)
By county	All causes (Level 0)	Males	γ_8	Standard deviation, Age (2005)	0.016 (SE = 0.006)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_2	Standard deviation	0.03 (SE = 0.02)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_2	Correlation parameter, County	0.516 (SE = 0.388)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_3	Standard deviation	0.036 (SE = 0.003)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_3	Correlation parameter, Age	0.97 (SE = 0.01)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_4	Standard deviation	0.339 (SE = 0.006)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_4	Correlation parameter, County	0.973 (SE = 0.004)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_4	Correlation parameter, Year spline	0.85 (SE = 0.006)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Females	γ_4	Correlation parameter, Age spline	0.505 (SE = 0.018)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_2	Standard deviation	0.056 (SE = 0.011)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_2	Correlation parameter, County	0.06 (SE = 0.065)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_3	Standard deviation	0.041 (SE = 0.003)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_3	Correlation parameter, Age	0.947 (SE = 0.016)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_4	Standard deviation	0.31 (SE = 0.006)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_4	Correlation parameter, County	0.972 (SE = 0.004)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_4	Correlation parameter, Year spline	0.892 (SE = 0.005)
By county	Communicable, maternal, neonatal, and nutritional diseases (Level 1)	Males	γ_4	Correlation parameter, Age spline	0.446 (SE = 0.021)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_2	Standard deviation	0.57 (SE = 0.034)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_2	Correlation parameter, County	0.98 (SE = 0.014)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_3	Standard deviation	0.056 (SE = 0.006)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_3	Correlation parameter, Age	0.937 (SE = 0.027)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_4	Standard deviation	0.41 (SE = 0.024)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_4	Correlation parameter, County	0.996 (SE = 0.002)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.872 (SE = 0.02)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.485 (SE = 0.075)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_2	Standard deviation	0.521 (SE = 0.04)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_2	Correlation parameter, County	0.989 (SE = 0.008)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_3	Standard deviation	0.067 (SE = 0.005)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_3	Correlation parameter, Age	0.941 (SE = 0.02)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_4	Standard deviation	0.3 (SE = 0.022)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_4	Correlation parameter, County	0.993 (SE = 0.003)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.898 (SE = 0.016)
By county	HIV/AIDS and sexually transmitted infections (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.729 (SE = 0.053)
By county	Respiratory infections and tuberculosis (Level 2)	Females	γ_2	Standard deviation	0.03 (SE = 0.021)
By county	Respiratory infections and tuberculosis (Level 2)	Females	γ_2	Correlation parameter, County	0.533 (SE = 0.369)
By county	Respiratory infections and tuberculosis (Level 2)	Females	γ_3	Standard deviation	0.044 (SE = 0.003)
By county	Respiratory infections and tuberculosis (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Respiratory infections and tuberculosis (Level 2)	Females	γ_3	Correlation parameter, Age	0.993 (SE = 0.002)
By county	Respiratory infections and tuberculosis (Level 2)	Females	γ_4	Standard deviation	0.324 (SE = 0.008)
By county	Respiratory infections and tuberculosis (Level 2)	Females	γ_4	Correlation parameter, County	0.959 (SE = 0.007)
By county	Respiratory infections and tuberculosis (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.836 (SE = 0.009)
By county	Respiratory infections and tuberculosis (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.689 (SE = 0.018)
By county	Respiratory infections and tuberculosis (Level 2)	Males	γ_2	Standard deviation	0.031 (SE = 0.022)
By county	Respiratory infections and tuberculosis (Level 2)	Males	γ_2	Correlation parameter, County	0.556 (SE = 0.354)
By county	Respiratory infections and tuberculosis (Level 2)	Males	γ_3	Standard deviation	0.041 (SE = 0.003)
By county	Respiratory infections and tuberculosis (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Respiratory infections and tuberculosis (Level 2)	Males	γ_3	Correlation parameter, Age	0.991 (SE = 0.003)
By county	Respiratory infections and tuberculosis (Level 2)	Males	γ_4	Standard deviation	0.284 (SE = 0.008)
By county	Respiratory infections and tuberculosis (Level 2)	Males	γ_4	Correlation parameter, County	0.964 (SE = 0.006)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Respiratory infections and tuberculosis (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.873 (SE = 0.007)
By county	Respiratory infections and tuberculosis (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.67 (SE = 0.019)
By county	Enteric infections (Level 2)	Females	γ_2	Standard deviation	0.054 (SE = 0.041)
By county	Enteric infections (Level 2)	Females	γ_2	Correlation parameter, County	0.624 (SE = 0.338)
By county	Enteric infections (Level 2)	Females	γ_3	Standard deviation	0.066 (SE = 0.007)
By county	Enteric infections (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Enteric infections (Level 2)	Females	γ_3	Correlation parameter, Age	0.973 (SE = 0.011)
By county	Enteric infections (Level 2)	Females	γ_4	Standard deviation	0.322 (SE = 0.019)
By county	Enteric infections (Level 2)	Females	γ_4	Correlation parameter, County	0.986 (SE = 0.004)
By county	Enteric infections (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.547 (SE = 0.043)
By county	Enteric infections (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.868 (SE = 0.019)
By county	Enteric infections (Level 2)	Males	γ_2	Standard deviation	0.074 (SE = 0.049)
By county	Enteric infections (Level 2)	Males	γ_2	Correlation parameter, County	0.587 (SE = 0.343)
By county	Enteric infections (Level 2)	Males	γ_3	Standard deviation	0.067 (SE = 0.007)
By county	Enteric infections (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Enteric infections (Level 2)	Males	γ_3	Correlation parameter, Age	0.968 (SE = 0.012)
By county	Enteric infections (Level 2)	Males	γ_4	Standard deviation	0.316 (SE = 0.022)
By county	Enteric infections (Level 2)	Males	γ_4	Correlation parameter, County	0.991 (SE = 0.003)
By county	Enteric infections (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.63 (SE = 0.049)
By county	Enteric infections (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.834 (SE = 0.026)
By county	Other infectious diseases (Level 2)	Females	γ_2	Standard deviation	0.044 (SE = 0.03)
By county	Other infectious diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.588 (SE = 0.322)
By county	Other infectious diseases (Level 2)	Females	γ_3	Standard deviation	0.03 (SE = 0.005)
By county	Other infectious diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Other infectious diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.954 (SE = 0.023)
By county	Other infectious diseases (Level 2)	Females	γ_4	Standard deviation	0.144 (SE = 0.017)
By county	Other infectious diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.995 (SE = 0.002)
By county	Other infectious diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.915 (SE = 0.02)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Other infectious diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.611 (SE = 0.066)
By county	Other infectious diseases (Level 2)	Males	γ_2	Standard deviation	0.087 (SE = 0.036)
By county	Other infectious diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.633 (SE = 0.289)
By county	Other infectious diseases (Level 2)	Males	γ_3	Standard deviation	0.033 (SE = 0.005)
By county	Other infectious diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Other infectious diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.96 (SE = 0.019)
By county	Other infectious diseases (Level 2)	Males	γ_4	Standard deviation	0.161 (SE = 0.017)
By county	Other infectious diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.993 (SE = 0.003)
By county	Other infectious diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.909 (SE = 0.02)
By county	Other infectious diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.553 (SE = 0.082)
By county	Maternal disorders (Level 3)	Females	γ_2	Standard deviation	0.055 (SE = 0.04)
By county	Maternal disorders (Level 3)	Females	γ_2	Correlation parameter, County	0.587 (SE = 0.349)
By county	Maternal disorders (Level 3)	Females	γ_3	Standard deviation	0.181 (SE = 0.019)
By county	Maternal disorders (Level 3)	Females	γ_3	Correlation parameter, Year	0.998 (SE = 0.001)
By county	Maternal disorders (Level 3)	Females	γ_3	Correlation parameter, Age	0.85 (SE = 0.05)
By county	Maternal disorders (Level 3)	Females	γ_4	Standard deviation	0.696 (SE = 0.036)
By county	Maternal disorders (Level 3)	Females	γ_4	Correlation parameter, County	0.993 (SE = 0.003)
By county	Maternal disorders (Level 3)	Females	γ_4	Correlation parameter, Year spline	0.136 (SE = 0.072)
By county	Maternal disorders (Level 3)	Females	γ_4	Correlation parameter, Age spline	0.084 (SE = 0.057)
By county	Neonatal disorders (Level 3)	Females	γ_2	Standard deviation	0.346 (SE = 0.016)
By county	Neonatal disorders (Level 3)	Females	γ_2	Correlation parameter, County	0.977 (SE = 0.012)
By county	Neonatal disorders (Level 3)	Females	γ_2	Standard deviation	0.057 (SE = 0.015)
By county	Neonatal disorders (Level 3)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Neonatal disorders (Level 3)	Females	γ_3	Correlation parameter, Age	0.205 (SE = 0.154)
By county	Neonatal disorders (Level 3)	Females	γ_3	Standard deviation	0.246 (SE = 0.026)
By county	Neonatal disorders (Level 3)	Females	γ_4	Correlation parameter, County	0.912 (SE = 0.039)
By county	Neonatal disorders (Level 3)	Females	γ_4	Correlation parameter, Year spline	0.275 (SE = 0.134)
By county	Neonatal disorders (Level 3)	Females	γ_4	Correlation parameter, Age spline	0.308 (SE = 0.241)
By county	Neonatal disorders (Level 3)	Males	γ_4	Standard deviation	0.318 (SE = 0.022)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Neonatal disorders (Level 3)	Males	γ_2	Correlation parameter, County	0.98 (SE = 0.011)
By county	Neonatal disorders (Level 3)	Males	γ_2	Standard deviation	0.058 (SE = 0.014)
By county	Neonatal disorders (Level 3)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Neonatal disorders (Level 3)	Males	γ_3	Correlation parameter, Age	0.211 (SE = 0.156)
By county	Neonatal disorders (Level 3)	Males	γ_3	Standard deviation	0.264 (SE = 0.018)
By county	Neonatal disorders (Level 3)	Males	γ_4	Correlation parameter, County	0.898 (SE = 0.049)
By county	Neonatal disorders (Level 3)	Males	γ_4	Correlation parameter, Year spline	0.56 (SE = 0.124)
By county	Neonatal disorders (Level 3)	Males	γ_4	Correlation parameter, Age spline	0.22 (SE = 0.172)
By county	Nutritional deficiencies (Level 2)	Females	γ_2	Standard deviation	0.282 (SE = 0.041)
By county	Nutritional deficiencies (Level 2)	Females	γ_2	Correlation parameter, County	0.993 (SE = 0.005)
By county	Nutritional deficiencies (Level 2)	Females	γ_3	Standard deviation	0.038 (SE = 0.006)
By county	Nutritional deficiencies (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Nutritional deficiencies (Level 2)	Females	γ_3	Correlation parameter, Age	0.983 (SE = 0.008)
By county	Nutritional deficiencies (Level 2)	Females	γ_4	Standard deviation	0.554 (SE = 0.03)
By county	Nutritional deficiencies (Level 2)	Females	γ_4	Correlation parameter, County	0.928 (SE = 0.019)
By county	Nutritional deficiencies (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.572 (SE = 0.043)
By county	Nutritional deficiencies (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.765 (SE = 0.036)
By county	Nutritional deficiencies (Level 2)	Males	γ_2	Standard deviation	0.103 (SE = 0.07)
By county	Nutritional deficiencies (Level 2)	Males	γ_2	Correlation parameter, County	0.568 (SE = 0.331)
By county	Nutritional deficiencies (Level 2)	Males	γ_3	Standard deviation	0.038 (SE = 0.006)
By county	Nutritional deficiencies (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Nutritional deficiencies (Level 2)	Males	γ_3	Correlation parameter, Age	0.984 (SE = 0.008)
By county	Nutritional deficiencies (Level 2)	Males	γ_4	Standard deviation	0.392 (SE = 0.029)
By county	Nutritional deficiencies (Level 2)	Males	γ_4	Correlation parameter, County	0.971 (SE = 0.009)
By county	Nutritional deficiencies (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.716 (SE = 0.032)
By county	Nutritional deficiencies (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.876 (SE = 0.021)
By county	Non-communicable diseases (Level 1)	Females	γ_2	Standard deviation	0.056 (SE = 0.011)
By county	Non-communicable diseases (Level 1)	Females	γ_2	Correlation parameter, County	0.081 (SE = 0.089)
By county	Non-communicable diseases (Level 1)	Females	γ_3	Standard deviation	0.015 (SE = 0.001)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Non-communicable diseases (Level 1)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Non-communicable diseases (Level 1)	Females	γ_3	Correlation parameter, Age	0.935 (SE = 0.019)
By county	Non-communicable diseases (Level 1)	Females	γ_4	Standard deviation	0.151 (SE = 0.002)
By county	Non-communicable diseases (Level 1)	Females	γ_4	Correlation parameter, County	0.988 (SE = 0.003)
By county	Non-communicable diseases (Level 1)	Females	γ_4	Correlation parameter, Year spline	0.932 (SE = 0.002)
By county	Non-communicable diseases (Level 1)	Females	γ_4	Correlation parameter, Age spline	0.317 (SE = 0.017)
By county	Non-communicable diseases (Level 1)	Males	γ_2	Standard deviation	0.075 (SE = 0.01)
By county	Non-communicable diseases (Level 1)	Males	γ_2	Correlation parameter, County	0.088 (SE = 0.066)
By county	Non-communicable diseases (Level 1)	Males	γ_3	Standard deviation	0.02 (SE = 0.001)
By county	Non-communicable diseases (Level 1)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Non-communicable diseases (Level 1)	Males	γ_3	Correlation parameter, Age	0.941 (SE = 0.017)
By county	Non-communicable diseases (Level 1)	Males	γ_4	Standard deviation	0.147 (SE = 0.002)
By county	Non-communicable diseases (Level 1)	Males	γ_4	Correlation parameter, County	0.992 (SE = 0.002)
By county	Non-communicable diseases (Level 1)	Males	γ_4	Correlation parameter, Year spline	0.947 (SE = 0.002)
By county	Non-communicable diseases (Level 1)	Males	γ_4	Correlation parameter, Age spline	0.215 (SE = 0.016)
By county	Neoplasms (Level 2)	Females	γ_2	Standard deviation	0.014 (SE = 0.009)
By county	Neoplasms (Level 2)	Females	γ_2	Correlation parameter, County	0.521 (SE = 0.383)
By county	Neoplasms (Level 2)	Females	γ_3	Standard deviation	0.012 (SE = 0.001)
By county	Neoplasms (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Neoplasms (Level 2)	Females	γ_3	Correlation parameter, Age	0.965 (SE = 0.013)
By county	Neoplasms (Level 2)	Females	γ_4	Standard deviation	0.104 (SE = 0.003)
By county	Neoplasms (Level 2)	Females	γ_4	Correlation parameter, County	0.978 (SE = 0.004)
By county	Neoplasms (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.935 (SE = 0.004)
By county	Neoplasms (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.376 (SE = 0.023)
By county	Neoplasms (Level 2)	Males	γ_2	Standard deviation	0.042 (SE = 0.008)
By county	Neoplasms (Level 2)	Males	γ_2	Correlation parameter, County	0.107 (SE = 0.091)
By county	Neoplasms (Level 2)	Males	γ_3	Standard deviation	0.013 (SE = 0.001)
By county	Neoplasms (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Neoplasms (Level 2)	Males	γ_3	Correlation parameter, Age	0.964 (SE = 0.014)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Neoplasms (Level 2)	Males	γ_4	Standard deviation	0.106 (SE = 0.003)
By county	Neoplasms (Level 2)	Males	γ_4	Correlation parameter, County	0.981 (SE = 0.004)
By county	Neoplasms (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.943 (SE = 0.003)
By county	Neoplasms (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.27 (SE = 0.026)
By county	Cardiovascular diseases (Level 2)	Females	γ_2	Standard deviation	0.056 (SE = 0.026)
By county	Cardiovascular diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.374 (SE = 0.558)
By county	Cardiovascular diseases (Level 2)	Females	γ_3	Standard deviation	0.014 (SE = 0.001)
By county	Cardiovascular diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Cardiovascular diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.971 (SE = 0.01)
By county	Cardiovascular diseases (Level 2)	Females	γ_4	Standard deviation	0.186 (SE = 0.003)
By county	Cardiovascular diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.978 (SE = 0.004)
By county	Cardiovascular diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.931 (SE = 0.003)
By county	Cardiovascular diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.416 (SE = 0.022)
By county	Cardiovascular diseases (Level 2)	Males	γ_2	Standard deviation	0.045 (SE = 0.008)
By county	Cardiovascular diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.067 (SE = 0.067)
By county	Cardiovascular diseases (Level 2)	Males	γ_3	Standard deviation	0.013 (SE = 0.001)
By county	Cardiovascular diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Cardiovascular diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.971 (SE = 0.01)
By county	Cardiovascular diseases (Level 2)	Males	γ_4	Standard deviation	0.151 (SE = 0.003)
By county	Cardiovascular diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.969 (SE = 0.005)
By county	Cardiovascular diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.942 (SE = 0.003)
By county	Cardiovascular diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.476 (SE = 0.021)
By county	Chronic respiratory diseases (Level 2)	Females	γ_2	Standard deviation	0.023 (SE = 0.017)
By county	Chronic respiratory diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.59 (SE = 0.343)
By county	Chronic respiratory diseases (Level 2)	Females	γ_3	Standard deviation	0.027 (SE = 0.002)
By county	Chronic respiratory diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Chronic respiratory diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.956 (SE = 0.017)
By county	Chronic respiratory diseases (Level 2)	Females	γ_4	Standard deviation	0.216 (SE = 0.005)
By county	Chronic respiratory diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.979 (SE = 0.004)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Chronic respiratory diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.94 (SE = 0.003)
By county	Chronic respiratory diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.489 (SE = 0.021)
By county	Chronic respiratory diseases (Level 2)	Males	γ_2	Standard deviation	0.037 (SE = 0.025)
By county	Chronic respiratory diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.571 (SE = 0.365)
By county	Chronic respiratory diseases (Level 2)	Males	γ_3	Standard deviation	0.022 (SE = 0.002)
By county	Chronic respiratory diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Chronic respiratory diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.956 (SE = 0.017)
By county	Chronic respiratory diseases (Level 2)	Males	γ_4	Standard deviation	0.188 (SE = 0.005)
By county	Chronic respiratory diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.973 (SE = 0.005)
By county	Chronic respiratory diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.943 (SE = 0.003)
By county	Chronic respiratory diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.508 (SE = 0.023)
By county	Digestive diseases (Level 2)	Females	γ_2	Standard deviation	0.139 (SE = 0.014)
By county	Digestive diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.966 (SE = 0.033)
By county	Digestive diseases (Level 2)	Females	γ_3	Standard deviation	0.029 (SE = 0.002)
By county	Digestive diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Digestive diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.925 (SE = 0.027)
By county	Digestive diseases (Level 2)	Females	γ_4	Standard deviation	0.167 (SE = 0.005)
By county	Digestive diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.991 (SE = 0.002)
By county	Digestive diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.945 (SE = 0.004)
By county	Digestive diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.31 (SE = 0.036)
By county	Digestive diseases (Level 2)	Males	γ_2	Standard deviation	0.142 (SE = 0.019)
By county	Digestive diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.835 (SE = 0.204)
By county	Digestive diseases (Level 2)	Males	γ_3	Standard deviation	0.033 (SE = 0.002)
By county	Digestive diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Digestive diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.896 (SE = 0.035)
By county	Digestive diseases (Level 2)	Males	γ_4	Standard deviation	0.186 (SE = 0.005)
By county	Digestive diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.991 (SE = 0.002)
By county	Digestive diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.942 (SE = 0.004)
By county	Digestive diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.278 (SE = 0.032)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Neurological disorders (Level 2)	Females	γ_2	Standard deviation	0.026 (SE = 0.019)
By county	Neurological disorders (Level 2)	Females	γ_2	Correlation parameter, County	0.583 (SE = 0.386)
By county	Neurological disorders (Level 2)	Females	γ_3	Standard deviation	0.009 (SE = 0.001)
By county	Neurological disorders (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Neurological disorders (Level 2)	Females	γ_3	Correlation parameter, Age	0.965 (SE = 0.015)
By county	Neurological disorders (Level 2)	Females	γ_4	Standard deviation	0.222 (SE = 0.005)
By county	Neurological disorders (Level 2)	Females	γ_4	Correlation parameter, County	0.77 (SE = 0.025)
By county	Neurological disorders (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.881 (SE = 0.005)
By county	Neurological disorders (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.663 (SE = 0.019)
By county	Neurological disorders (Level 2)	Males	γ_2	Standard deviation	0.027 (SE = 0.019)
By county	Neurological disorders (Level 2)	Males	γ_2	Correlation parameter, County	0.538 (SE = 0.385)
By county	Neurological disorders (Level 2)	Males	γ_3	Standard deviation	0.01 (SE = 0.001)
By county	Neurological disorders (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Neurological disorders (Level 2)	Males	γ_3	Correlation parameter, Age	0.956 (SE = 0.019)
By county	Neurological disorders (Level 2)	Males	γ_4	Standard deviation	0.146 (SE = 0.005)
By county	Neurological disorders (Level 2)	Males	γ_4	Correlation parameter, County	0.814 (SE = 0.024)
By county	Neurological disorders (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.946 (SE = 0.004)
By county	Neurological disorders (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.699 (SE = 0.019)
By county	Substance use disorders (Level 2)	Females	γ_2	Standard deviation	0.218 (SE = 0.065)
By county	Substance use disorders (Level 2)	Females	γ_2	Correlation parameter, County	0.772 (SE = 0.269)
By county	Substance use disorders (Level 2)	Females	γ_3	Standard deviation	0.05 (SE = 0.004)
By county	Substance use disorders (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Substance use disorders (Level 2)	Females	γ_3	Correlation parameter, Age	0.965 (SE = 0.012)
By county	Substance use disorders (Level 2)	Females	γ_4	Standard deviation	0.54 (SE = 0.016)
By county	Substance use disorders (Level 2)	Females	γ_4	Correlation parameter, County	0.987 (SE = 0.003)
By county	Substance use disorders (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.836 (SE = 0.012)
By county	Substance use disorders (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.601 (SE = 0.032)
By county	Substance use disorders (Level 2)	Males	γ_2	Standard deviation	0.05 (SE = 0.036)
By county	Substance use disorders (Level 2)	Males	γ_2	Correlation parameter, County	0.543 (SE = 0.364)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Substance use disorders (Level 2)	Males	γ_3	Standard deviation	0.047 (SE = 0.003)
By county	Substance use disorders (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Substance use disorders (Level 2)	Males	γ_3	Correlation parameter, Age	0.964 (SE = 0.013)
By county	Substance use disorders (Level 2)	Males	γ_4	Standard deviation	0.552 (SE = 0.011)
By county	Substance use disorders (Level 2)	Males	γ_4	Correlation parameter, County	0.992 (SE = 0.002)
By county	Substance use disorders (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.867 (SE = 0.006)
By county	Substance use disorders (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.59 (SE = 0.016)
By county	Diabetes and kidney diseases (Level 2)	Females	γ_2	Standard deviation	0.071 (SE = 0.018)
By county	Diabetes and kidney diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.108 (SE = 0.134)
By county	Diabetes and kidney diseases (Level 2)	Females	γ_3	Standard deviation	0.015 (SE = 0.002)
By county	Diabetes and kidney diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Diabetes and kidney diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.978 (SE = 0.009)
By county	Diabetes and kidney diseases (Level 2)	Females	γ_4	Standard deviation	0.198 (SE = 0.005)
By county	Diabetes and kidney diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.975 (SE = 0.005)
By county	Diabetes and kidney diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.942 (SE = 0.003)
By county	Diabetes and kidney diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.569 (SE = 0.027)
By county	Diabetes and kidney diseases (Level 2)	Males	γ_2	Standard deviation	0.066 (SE = 0.011)
By county	Diabetes and kidney diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.046 (SE = 0.043)
By county	Diabetes and kidney diseases (Level 2)	Males	γ_3	Standard deviation	0.016 (SE = 0.002)
By county	Diabetes and kidney diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Diabetes and kidney diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.982 (SE = 0.007)
By county	Diabetes and kidney diseases (Level 2)	Males	γ_4	Standard deviation	0.193 (SE = 0.006)
By county	Diabetes and kidney diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.962 (SE = 0.007)
By county	Diabetes and kidney diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.936 (SE = 0.004)
By county	Diabetes and kidney diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.623 (SE = 0.025)
By county	Skin and subcutaneous diseases (Level 2)	Females	γ_2	Standard deviation	0.071 (SE = 0.05)
By county	Skin and subcutaneous diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.65 (SE = 0.305)
By county	Skin and subcutaneous diseases (Level 2)	Females	γ_3	Standard deviation	0.028 (SE = 0.005)
By county	Skin and subcutaneous diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Skin and subcutaneous diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.959 (SE = 0.02)
By county	Skin and subcutaneous diseases (Level 2)	Females	γ_4	Standard deviation	0.208 (SE = 0.016)
By county	Skin and subcutaneous diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.995 (SE = 0.002)
By county	Skin and subcutaneous diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.885 (SE = 0.017)
By county	Skin and subcutaneous diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.728 (SE = 0.045)
By county	Skin and subcutaneous diseases (Level 2)	Males	γ_2	Standard deviation	0.089 (SE = 0.056)
By county	Skin and subcutaneous diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.646 (SE = 0.292)
By county	Skin and subcutaneous diseases (Level 2)	Males	γ_3	Standard deviation	0.03 (SE = 0.005)
By county	Skin and subcutaneous diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Skin and subcutaneous diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.954 (SE = 0.023)
By county	Skin and subcutaneous diseases (Level 2)	Males	γ_4	Standard deviation	0.2 (SE = 0.018)
By county	Skin and subcutaneous diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.994 (SE = 0.002)
By county	Skin and subcutaneous diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.882 (SE = 0.02)
By county	Skin and subcutaneous diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.774 (SE = 0.042)
By county	Musculoskeletal disorders (Level 2)	Females	γ_2	Standard deviation	0.023 (SE = 0.016)
By county	Musculoskeletal disorders (Level 2)	Females	γ_2	Correlation parameter, County	0.568 (SE = 0.343)
By county	Musculoskeletal disorders (Level 2)	Females	γ_3	Standard deviation	0.018 (SE = 0.003)
By county	Musculoskeletal disorders (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Musculoskeletal disorders (Level 2)	Females	γ_3	Correlation parameter, Age	0.987 (SE = 0.005)
By county	Musculoskeletal disorders (Level 2)	Females	γ_4	Standard deviation	0.178 (SE = 0.013)
By county	Musculoskeletal disorders (Level 2)	Females	γ_4	Correlation parameter, County	0.994 (SE = 0.002)
By county	Musculoskeletal disorders (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.958 (SE = 0.006)
By county	Musculoskeletal disorders (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.493 (SE = 0.037)
By county	Musculoskeletal disorders (Level 2)	Males	γ_2	Standard deviation	0.032 (SE = 0.023)
By county	Musculoskeletal disorders (Level 2)	Males	γ_2	Correlation parameter, County	0.565 (SE = 0.344)
By county	Musculoskeletal disorders (Level 2)	Males	γ_3	Standard deviation	0.023 (SE = 0.004)
By county	Musculoskeletal disorders (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Musculoskeletal disorders (Level 2)	Males	γ_3	Correlation parameter, Age	0.979 (SE = 0.01)
By county	Musculoskeletal disorders (Level 2)	Males	γ_4	Standard deviation	0.121 (SE = 0.02)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Musculoskeletal disorders (Level 2)	Males	γ_4	Correlation parameter, County	0.995 (SE = 0.002)
By county	Musculoskeletal disorders (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.97 (SE = 0.01)
By county	Musculoskeletal disorders (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.507 (SE = 0.064)
By county	Other non-communicable diseases (Level 2)	Females	γ_2	Standard deviation	0.027 (SE = 0.019)
By county	Other non-communicable diseases (Level 2)	Females	γ_2	Correlation parameter, County	0.544 (SE = 0.375)
By county	Other non-communicable diseases (Level 2)	Females	γ_3	Standard deviation	0.018 (SE = 0.002)
By county	Other non-communicable diseases (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Other non-communicable diseases (Level 2)	Females	γ_3	Correlation parameter, Age	0.958 (SE = 0.016)
By county	Other non-communicable diseases (Level 2)	Females	γ_4	Standard deviation	0.232 (SE = 0.007)
By county	Other non-communicable diseases (Level 2)	Females	γ_4	Correlation parameter, County	0.955 (SE = 0.008)
By county	Other non-communicable diseases (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.877 (SE = 0.008)
By county	Other non-communicable diseases (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.507 (SE = 0.026)
By county	Other non-communicable diseases (Level 2)	Males	γ_2	Standard deviation	0.07 (SE = 0.008)
By county	Other non-communicable diseases (Level 2)	Males	γ_2	Correlation parameter, County	0.038 (SE = 0.031)
By county	Other non-communicable diseases (Level 2)	Males	γ_3	Standard deviation	0.021 (SE = 0.002)
By county	Other non-communicable diseases (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Other non-communicable diseases (Level 2)	Males	γ_3	Correlation parameter, Age	0.943 (SE = 0.021)
By county	Other non-communicable diseases (Level 2)	Males	γ_4	Standard deviation	0.243 (SE = 0.008)
By county	Other non-communicable diseases (Level 2)	Males	γ_4	Correlation parameter, County	0.942 (SE = 0.01)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Other non-communicable diseases (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.854 (SE = 0.011)
By county	Other non-communicable diseases (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.529 (SE = 0.032)
By county	Transport injuries (Level 2)	Females	γ_2	Standard deviation	0.046 (SE = 0.03)
By county	Transport injuries (Level 2)	Females	γ_2	Correlation parameter, County	0.512 (SE = 0.379)
By county	Transport injuries (Level 2)	Females	γ_3	Standard deviation	0.032 (SE = 0.003)
By county	Transport injuries (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Transport injuries (Level 2)	Females	γ_3	Correlation parameter, Age	0.949 (SE = 0.018)
By county	Transport injuries (Level 2)	Females	γ_4	Standard deviation	0.191 (SE = 0.011)
By county	Transport injuries (Level 2)	Females	γ_4	Correlation parameter, County	0.98 (SE = 0.005)
By county	Transport injuries (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.924 (SE = 0.008)
By county	Transport injuries (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.727 (SE = 0.024)
By county	Transport injuries (Level 2)	Males	γ_2	Standard deviation	0.066 (SE = 0.012)
By county	Transport injuries (Level 2)	Males	γ_2	Correlation parameter, County	0.051 (SE = 0.049)
By county	Transport injuries (Level 2)	Males	γ_3	Standard deviation	0.026 (SE = 0.002)
By county	Transport injuries (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Transport injuries (Level 2)	Males	γ_3	Correlation parameter, Age	0.964 (SE = 0.012)
By county	Transport injuries (Level 2)	Males	γ_4	Standard deviation	0.196 (SE = 0.008)
By county	Transport injuries (Level 2)	Males	γ_4	Correlation parameter, County	0.976 (SE = 0.005)
By county	Transport injuries (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.941 (SE = 0.005)
By county	Transport injuries (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.626 (SE = 0.028)
By county	Unintentional injuries (Level 2)	Females	γ_2	Standard deviation	0.018 (SE = 0.013)
By county	Unintentional injuries (Level 2)	Females	γ_2	Correlation parameter, County	0.582 (SE = 0.343)
By county	Unintentional injuries (Level 2)	Females	γ_3	Standard deviation	0.029 (SE = 0.002)
By county	Unintentional injuries (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Unintentional injuries (Level 2)	Females	γ_3	Correlation parameter, Age	0.88 (SE = 0.042)
By county	Unintentional injuries (Level 2)	Females	γ_4	Standard deviation	0.317 (SE = 0.008)
By county	Unintentional injuries (Level 2)	Females	γ_4	Correlation parameter, County	0.973 (SE = 0.005)
By county	Unintentional injuries (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.853 (SE = 0.008)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Unintentional injuries (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.486 (SE = 0.024)
By county	Unintentional injuries (Level 2)	Females	γ_5	Standard deviation, County (2005)	0.614 (SE = 0.074)
By county	Unintentional injuries (Level 2)	Females	γ_6	Standard deviation, Age	0.052 (SE = 0.042)
By county	Unintentional injuries (Level 2)	Males	γ_2	Standard deviation	0.015 (SE = 0.011)
By county	Unintentional injuries (Level 2)	Males	γ_2	Correlation parameter, County	0.567 (SE = 0.345)
By county	Unintentional injuries (Level 2)	Males	γ_3	Standard deviation	0.03 (SE = 0.002)
By county	Unintentional injuries (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Unintentional injuries (Level 2)	Males	γ_3	Correlation parameter, Age	0.876 (SE = 0.037)
By county	Unintentional injuries (Level 2)	Males	γ_4	Standard deviation	0.248 (SE = 0.007)
By county	Unintentional injuries (Level 2)	Males	γ_4	Correlation parameter, County	0.964 (SE = 0.006)
By county	Unintentional injuries (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.918 (SE = 0.005)
By county	Unintentional injuries (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.393 (SE = 0.022)
By county	Unintentional injuries (Level 2)	Males	γ_5	Standard deviation, County (2005)	0.477 (SE = 0.059)
By county	Unintentional injuries (Level 2)	Males	γ_6	Standard deviation, Age	0.112 (SE = 0.038)
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_2	Standard deviation	0.038 (SE = 0.028)
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_2	Correlation parameter, County	0.583 (SE = 0.344)
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_3	Standard deviation	0.035 (SE = 0.003)
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_3	Correlation parameter, Age	0.851 (SE = 0.051)
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_4	Standard deviation	0.231 (SE = 0.011)
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_4	Correlation parameter, County	0.973 (SE = 0.006)
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_4	Correlation parameter, Year spline	0.92 (SE = 0.007)
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_4	Correlation parameter, Age spline	0.738 (SE = 0.019)

Model	Cause	Sex	Parameter		Mean (SE)*
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_5	Standard deviation, County (2001)	0.338 (SE = 0.032)
By county	Self-harm and interpersonal violence (Level 2)	Females	γ_6	Standard deviation, Age	0.049 (SE = 0.031)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_2	Standard deviation	0.025 (SE = 0.018)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_2	Correlation parameter, County	0.565 (SE = 0.353)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_3	Standard deviation	0.028 (SE = 0.002)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_3	Correlation parameter, Year	>0.999 (SE < 0.001)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_3	Correlation parameter, Age	0.907 (SE = 0.029)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_4	Standard deviation	0.229 (SE = 0.006)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_4	Correlation parameter, County	0.937 (SE = 0.01)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_4	Correlation parameter, Year spline	0.939 (SE = 0.003)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_4	Correlation parameter, Age spline	0.653 (SE = 0.015)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_5	Standard deviation, County (2001)	0.34 (SE = 0.025)
By county	Self-harm and interpersonal violence (Level 2)	Males	γ_6	Standard deviation, Age	0.113 (SE = 0.028)

*Estimates are reported by TMB on the log standard deviation and logit correlation parameter scale. For convenience, we have transformed these using a delta transformation for the standard error. SE = standard error; TMB = Template Model Builder package in R version 3.6.110.

3.7 County and racial–ethnic groups in the validation set

State	Merged county	Racial–ethnic group*
Alabama	Jefferson	All racial–ethnic groups, Black
	Madison	All racial–ethnic groups
	Mobile	All racial–ethnic groups, Black
Alaska	Anchorage Municipality	All racial–ethnic groups
Arizona	Maricopa	All racial–ethnic groups, Black, Latino, White
	Pima	All racial–ethnic groups, Latino
	Pinal	All racial–ethnic groups
Arkansas	Pulaski	All racial–ethnic groups
California	Alameda	All racial–ethnic groups, Latino
	Contra Costa	All racial–ethnic groups, White
	Fresno	All racial–ethnic groups, Latino
	Kern	All racial–ethnic groups, Latino, White
	Los Angeles	All racial–ethnic groups, Asian, Black, Latino, White
	Merced	All racial–ethnic groups
	Monterey	All racial–ethnic groups, Latino
	Orange	All racial–ethnic groups, Latino, White
	Riverside	All racial–ethnic groups, Latino, White
	Sacramento	All racial–ethnic groups
	San Bernardino	All racial–ethnic groups, Black, Latino
	San Diego	All racial–ethnic groups, Latino, White
	San Francisco	All racial–ethnic groups
	San Joaquin	All racial–ethnic groups, Latino
	San Mateo	All racial–ethnic groups
	Santa Clara	All racial–ethnic groups, Asian, Latino
	Solano	All racial–ethnic groups
	Sonoma	All racial–ethnic groups
	Stanislaus	All racial–ethnic groups
	Tulare	All racial–ethnic groups, Latino
	Ventura	All racial–ethnic groups
Colorado	Adams/Arapahoe/Boulder/Broomfield/Denver/Jefferson/Weld	All racial–ethnic groups, Latino, White
	El Paso	All racial–ethnic groups
Connecticut	Fairfield	All racial–ethnic groups, White
	Hartford	All racial–ethnic groups
	New Haven	All racial–ethnic groups, White
District of Columbia	District of Columbia	All racial–ethnic groups, Black

State	Merged county	Racial–ethnic group*
Florida	Brevard	All racial–ethnic groups
	Broward	All racial–ethnic groups, Black, White
	Miami-Dade	All racial–ethnic groups, Black, Latino
	Duval	All racial–ethnic groups, Black, White
	Hillsborough	All racial–ethnic groups, Black, Latino, White
	Lee	All racial–ethnic groups
	Orange	All racial–ethnic groups
	Palm Beach	All racial–ethnic groups, Latino, White
	Pasco	All racial–ethnic groups
	Pinellas	All racial–ethnic groups
	Polk	All racial–ethnic groups
	Seminole	All racial–ethnic groups
Georgia	Bibb	All racial–ethnic groups
	Cobb	All racial–ethnic groups, White
	DeKalb	All racial–ethnic groups, Black
	Fulton	All racial–ethnic groups, Black, White
	Gwinnett	All racial–ethnic groups
Hawaii	Honolulu	All racial–ethnic groups, Asian
Illinois	Cook	All racial–ethnic groups, Black, Latino, White
	DuPage	All racial–ethnic groups
	Kane	All racial–ethnic groups
	Lake	All racial–ethnic groups
	Will	All racial–ethnic groups, White
Indiana	Allen	All racial–ethnic groups
	Elkhart	All racial–ethnic groups
	Lake	All racial–ethnic groups, Black
	Marion	All racial–ethnic groups, Black, White
Iowa	Polk	All racial–ethnic groups
Kansas	Sedgwick	All racial–ethnic groups, White
Kentucky	Jefferson	All racial–ethnic groups, White
Louisiana	Caddo	All racial–ethnic groups
	East Baton Rouge	All racial–ethnic groups, Black
	Jefferson	All racial–ethnic groups
	Orleans	All racial–ethnic groups, Black
Maryland	Anne Arundel	All racial–ethnic groups
	Baltimore	All racial–ethnic groups
	Baltimore City	All racial–ethnic groups, Black
	Montgomery/Prince George's	All racial–ethnic groups, Black
Massachusetts	Bristol	All racial–ethnic groups

State	Merged county	Racial–ethnic group*
	Essex	All racial–ethnic groups
	Hampden	All racial–ethnic groups
	Middlesex	All racial–ethnic groups, White
	Suffolk	All racial–ethnic groups
	Worcester	All racial–ethnic groups
Michigan	Genesee	All racial–ethnic groups
	Kent	All racial–ethnic groups
	Macomb	All racial–ethnic groups, White
	Oakland	All racial–ethnic groups
	Wayne	All racial–ethnic groups, Black, White
Minnesota	Hennepin	All racial–ethnic groups, White
	Ramsey	All racial–ethnic groups
Mississippi	Hinds	All racial–ethnic groups, Black
Missouri	Jackson	All racial–ethnic groups, White
	Saint Louis	All racial–ethnic groups, Black, White
Nebraska	Douglas	All racial–ethnic groups
Nevada	Clark	All racial–ethnic groups, Latino, White
	Washoe	All racial–ethnic groups
New Jersey	Bergen	All racial–ethnic groups, White
	Burlington	All racial–ethnic groups
	Camden	All racial–ethnic groups
	Essex	All racial–ethnic groups, Black
	Hudson	All racial–ethnic groups
	Mercer	All racial–ethnic groups
	Middlesex	All racial–ethnic groups
	Monmouth	All racial–ethnic groups, White
	Ocean	All racial–ethnic groups, White
	Passaic	All racial–ethnic groups
	Union	All racial–ethnic groups
New Mexico	Bernalillo	All racial–ethnic groups, Latino
	Dona Ana	All racial–ethnic groups
	San Juan	All racial–ethnic groups
New York	Bronx	All racial–ethnic groups, Black, Latino
	Erie	All racial–ethnic groups, White
	Kings	All racial–ethnic groups, Black, Latino, White
	Monroe	All racial–ethnic groups, White
	Nassau	All racial–ethnic groups, White
	New York	All racial–ethnic groups, Latino
	Onondaga	All racial–ethnic groups

State	Merged county	Racial–ethnic group*
	Queens	All racial–ethnic groups, Asian, Black, Latino
	Suffolk	All racial–ethnic groups, White
	Westchester	All racial–ethnic groups, White
North Carolina	Durham	All racial–ethnic groups
	Forsyth	All racial–ethnic groups
	Mecklenburg	All racial–ethnic groups, White
	Wake	All racial–ethnic groups, White
Ohio	Cuyahoga	All racial–ethnic groups, Black, White
	Franklin	All racial–ethnic groups, Black
	Hamilton	All racial–ethnic groups, Black, White
	Lucas	All racial–ethnic groups
	Montgomery	All racial–ethnic groups, White
Oklahoma	Oklahoma	All racial–ethnic groups, White
	Tulsa	All racial–ethnic groups, White
Oregon	Multnomah	All racial–ethnic groups
Pennsylvania	Allegheny	All racial–ethnic groups, Black, White
	Chester	All racial–ethnic groups, White
	Delaware	All racial–ethnic groups, White
	Lancaster	All racial–ethnic groups, White
	Montgomery	All racial–ethnic groups, White
	Philadelphia	All racial–ethnic groups, Black, Latino, White
Rhode Island	Providence	All racial–ethnic groups, White
South Carolina	Greenville	All racial–ethnic groups, White
	Spartanburg	All racial–ethnic groups
Tennessee	Davidson	All racial–ethnic groups, Black
	Knox	All racial–ethnic groups
	Montgomery	All racial–ethnic groups
	Shelby	All racial–ethnic groups, Black
Texas	Bell	All racial–ethnic groups
	Bexar	All racial–ethnic groups, Latino, White
	Cameron	All racial–ethnic groups, Latino
	Collin	All racial–ethnic groups, White
	Dallas	All racial–ethnic groups, Black, Latino, White
	Denton	All racial–ethnic groups, White
	El Paso	All racial–ethnic groups, Latino
	Fort Bend	All racial–ethnic groups
	Galveston	All racial–ethnic groups
	Harris	All racial–ethnic groups, Black, Latino, White
	Hidalgo	All racial–ethnic groups, Latino

State	Merged county	Racial–ethnic group*
	Jefferson	All racial–ethnic groups
	McLennan	All racial–ethnic groups
	Montgomery	All racial–ethnic groups
	Tarrant	All racial–ethnic groups, Latino, White
	Travis	All racial–ethnic groups, White
	Webb	All racial–ethnic groups, Latino
Utah	Salt Lake	All racial–ethnic groups, White
	Utah	All racial–ethnic groups, White
Virginia	Chesapeake City	All racial–ethnic groups
	Fairfax/Fairfax City	All racial–ethnic groups
	Norfolk City	All racial–ethnic groups
	York/Newport News City	All racial–ethnic groups
Washington	Clark	All racial–ethnic groups
	King	All racial–ethnic groups, White
	Pierce	All racial–ethnic groups, White
	Spokane	All racial–ethnic groups
	Yakima	All racial–ethnic groups
Wisconsin	Milwaukee	All racial–ethnic groups, Black, White
	Rock	All racial–ethnic groups

* “All racial–ethnic groups” was validated separately from individual racial–ethnic groups.

3.8 Model validation results

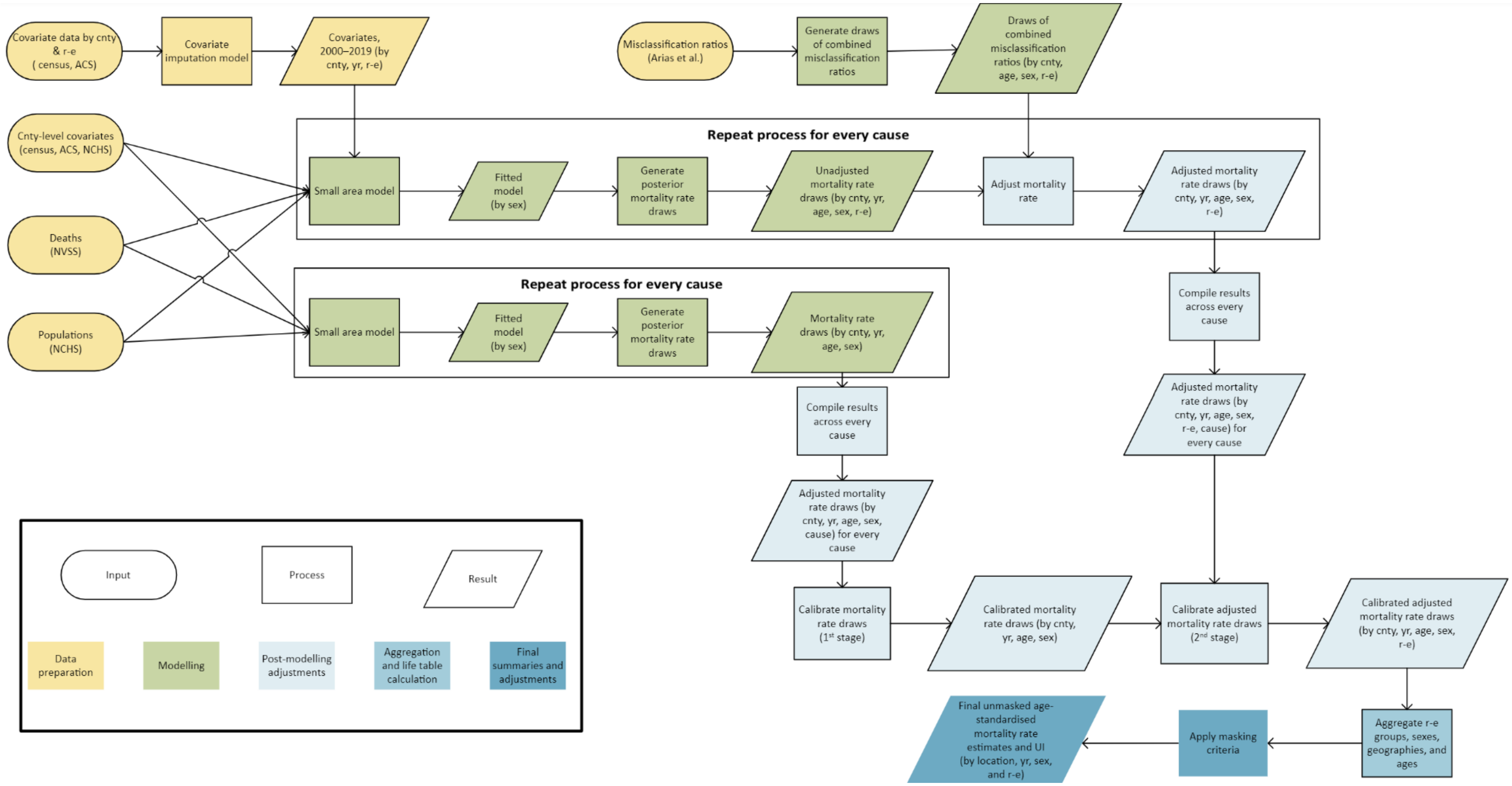
Racial–ethnic group	Size	Model 1			Model 2			Model 3		
		Mean relative error (%)	Mean absolute relative error (%)	Coverage (%)	Mean relative error (%)	Mean absolute relative error (%)	Coverage (%)	Mean relative error (%)	Mean absolute relative error (%)	Coverage (%)
Across all racial–ethnic groups	10	1·15	6·73	99·03	-0·1	6·61	99·72	0·07	6·65	99·41
	100	1·13	6·7	98·83	-0·02	6·85	99·62	0·2	6·74	99·18
	1000	0·44	6	97·09	0·04	6·42	97·59	-0·02	6·4	97·45
	3000	0·69	5	95·94	0·43	5·29	96·23	0·46	5·27	96·16
	5000	0·3	4·55	94·8	0·11	4·72	94·88	0·15	4·72	94·93
	10 000	0·29	3·73	94·42	0·19	3·8	94·55	0·2	3·83	94·68
	25 000	0·16	2·9	92·87	0·04	2·97	92·89	0·13	2·97	93·01
	100 000	-0·05	2·05	87·56	-0·05	2·08	87·05	-0·04	2·09	87·23
Asian	10	8·67	8·72	100	7·77	7·99	100	6·98	7·4	100
	100	8·23	8·51	100	6·8	7·57	100	6·29	7·17	100
	1000	5·33	6·2	98·24	5·54	7·51	98·53	4·42	6·42	98·38
	3000	3·26	4·37	97·94	1·98	4·33	98·09	2·44	4·35	98·09
	5000	2·66	4·9	97·79	1·79	5·51	98·09	2·04	5·16	98·68
	10 000	1·71	3·99	96·62	1·1	4·15	96·91	1·43	4·18	96·32
	25 000	0·59	3·13	96·32	0·15	3·13	96·91	0·42	3·14	96·32
	100 000	0·07	2·28	91·18	0·1	2·35	90·74	0·15	2·35	90·59
Black	10	2·9	7·32	99·17	0·58	6·63	99·95	1·25	7·29	99·64
	100	2·81	7·31	99·2	0·72	6·98	99·77	1·32	7·53	99·56
	1000	1·31	6·31	96·54	0·46	6·43	96·8	0·48	6·5	96·67
	3000	0·86	5·27	95·57	0·24	5·29	95·52	0·32	5·29	96·08
	5000	0·56	4·54	94·53	0·11	4·48	94·62	0·2	4·49	95·11
	10 000	0·56	3·87	93·69	0·34	3·77	94·1	0·39	3·85	94·54
	25 000	0·35	2·98	91·54	0·25	2·91	91·96	0·29	2·96	92·34

		Model 1			Model 2			Model 3		
Racial–ethnic group	Size	Mean relative error (%)	Mean absolute relative error (%)	Coverage (%)	Mean relative error (%)	Mean absolute relative error (%)	Coverage (%)	Mean relative error (%)	Mean absolute relative error (%)	Coverage (%)
	100 000	0·02	1·99	87·08	-0·01	1·99	86·26	0·01	2	86·81
Latino	10	2·57	8·77	99·53	-0·5	7·66	99·97	1·03	7·62	100
	100	2·71	8·78	99·39	0	7·7	99·86	1·51	7·88	99·98
	1000	1·12	7·45	97·66	-0·32	7·21	98·3	0·51	7·89	98·74
	3000	1·68	6·54	97·92	1	6·78	97·21	1·49	7·16	97·51
	5000	0·94	5·83	96·97	0·48	5·95	96·3	0·79	6·2	96·96
	10 000	0·17	4·84	96·37	-0·12	4·87	95·16	0·04	5·06	95·81
	25 000	0·18	3·79	94·86	0	4·01	92·84	0·14	3·98	94·46
	100 000	-0·09	2·78	89·78	-0·13	2·82	88·04	-0·11	2·85	89·33
White	10	-1·07	5·19	98·63	-0·76	5·95	99·44	-1·54	5·72	98·93
	100	-1·09	5·13	98·24	-0·87	6·29	99·38	-1·51	5·66	98·48
	1000	-0·71	5·04	97·03	-0·35	5·92	97·6	-0·86	5·56	97·15
	3000	-0·1	4·08	94·97	0·15	4·56	95·98	-0·13	4·32	95·38
	5000	-0·32	3·86	93·62	-0·18	4·15	94·06	-0·35	4·03	93·51
	10 000	0·11	3·05	93·65	0·22	3·23	94·34	0·11	3·16	94·06
	25 000	0·01	2·38	92·35	-0·06	2·44	93·2	0	2·43	92·41
	100 000	-0·06	1·69	86·42	-0·05	1·72	86·73	-0·05	1·71	86·13

*"Across all racial–ethnic groups" indicates that errors and coverage were calculated across all racial–ethnic groups.

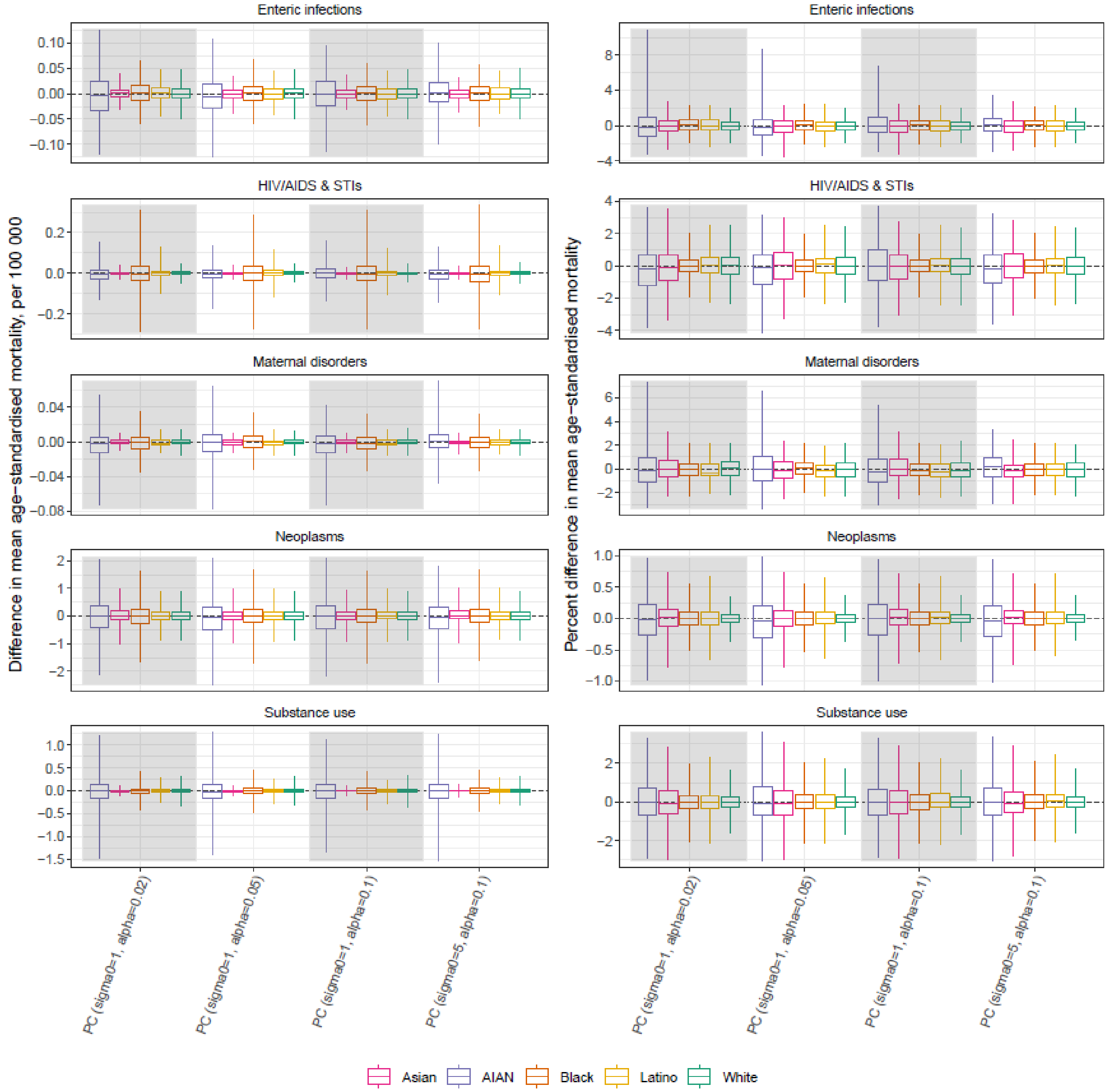
4 Supplemental Methods Figures

4.1 Analysis flow chart

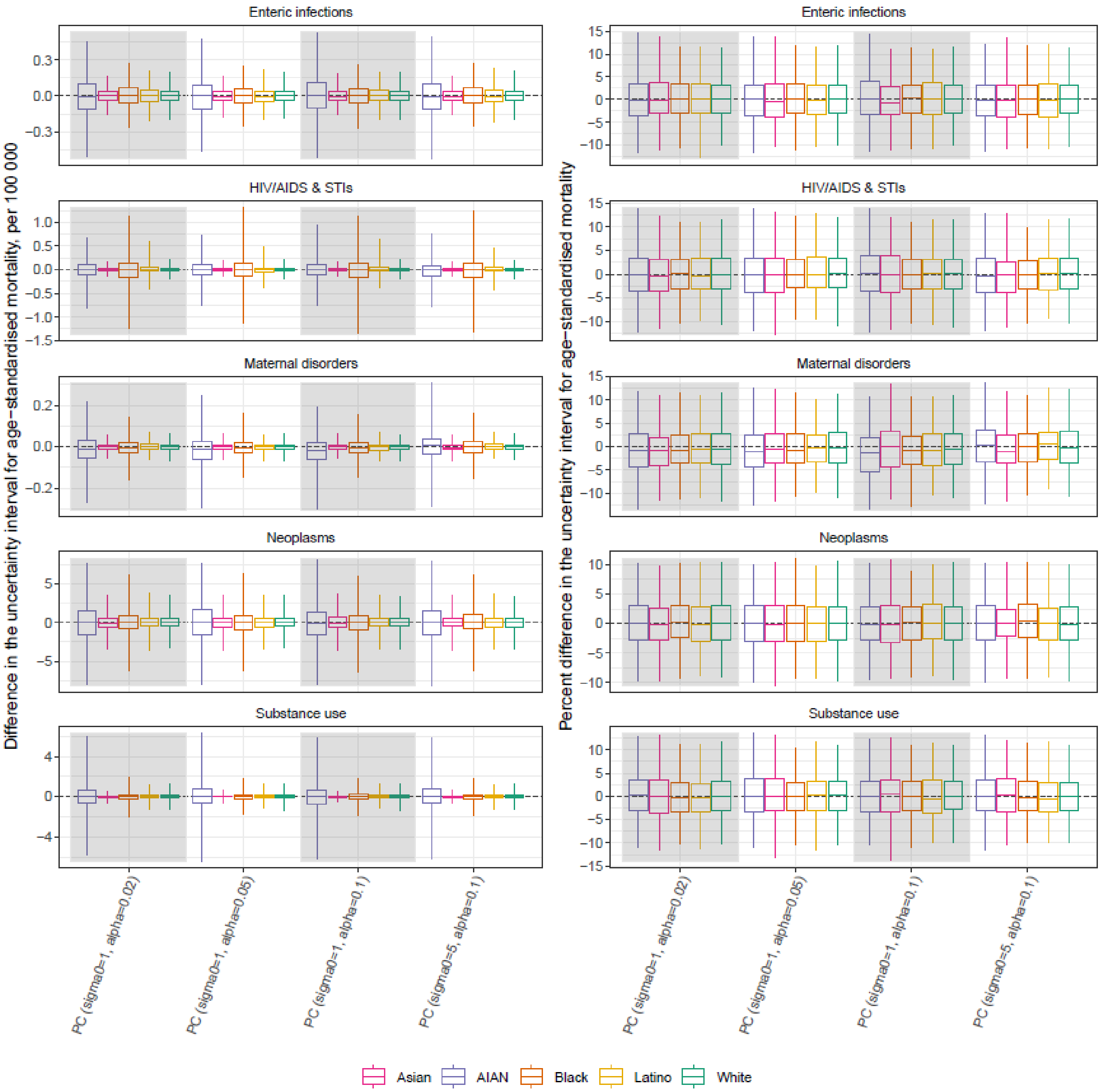


ACS = American Community Survey; cnty = county; NCHS = National Center for Health Statistics; NVSS = National Vital Statistics System; r-e = race–ethnicity; UI = uncertainty interval; yr = year.

4.2 Hyperprior sensitivity analysis results

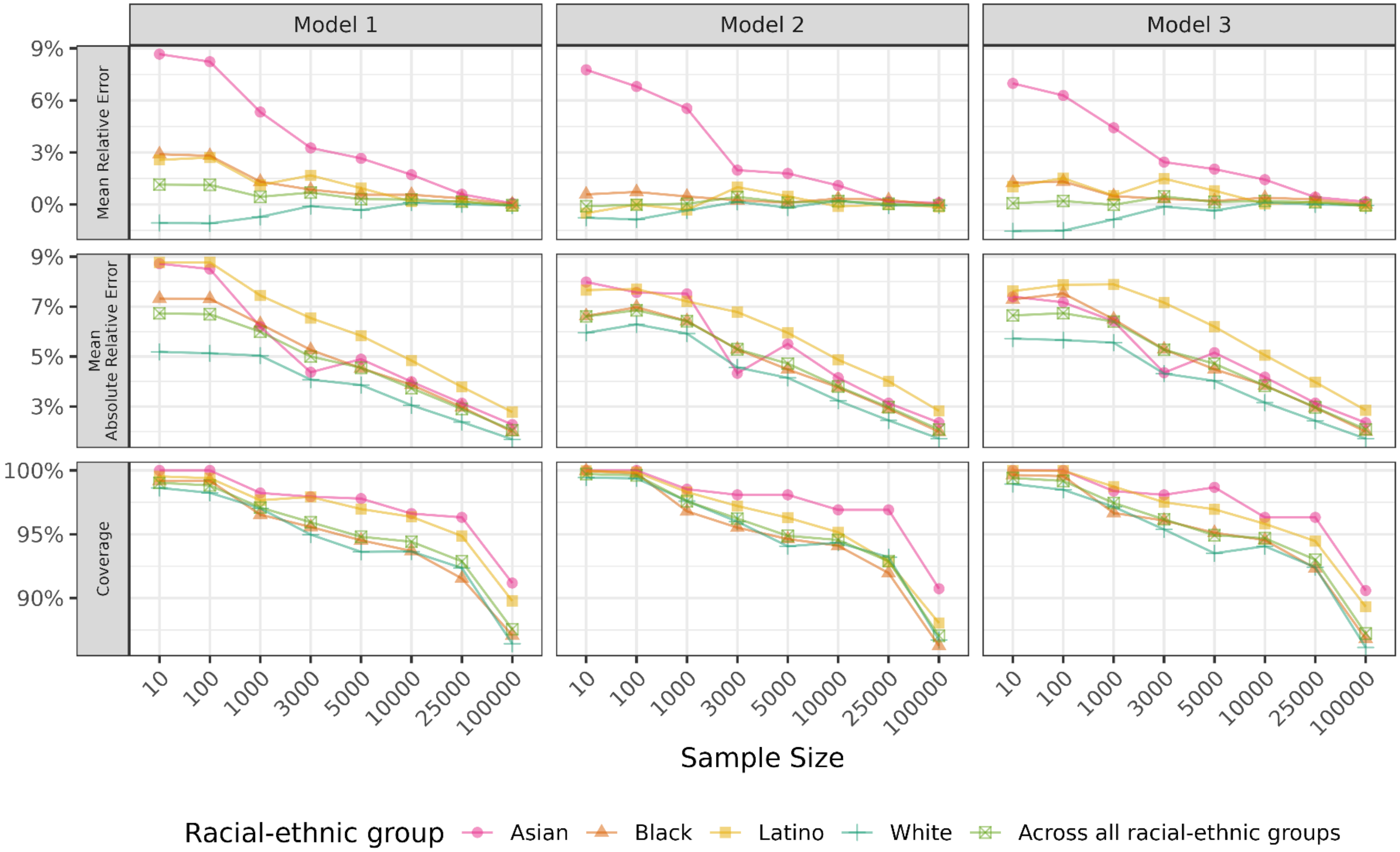


Population-weighted summary of differences (left: absolute differences; right: percent difference) in age-standardised mortality by county and racial–ethnic group for males and females combined in 2000, 2010, and 2019 compared with that of the model used in this analysis (penalised complexity models, $\sigma_0 = 5, \alpha = 0.05$). Boxes show the IQR, while the whiskers extend to 1st and 99th percentiles, weighted by the average population across all years in each county and racial–ethnic group combination. The data shown are for both masked and unmasked data. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.



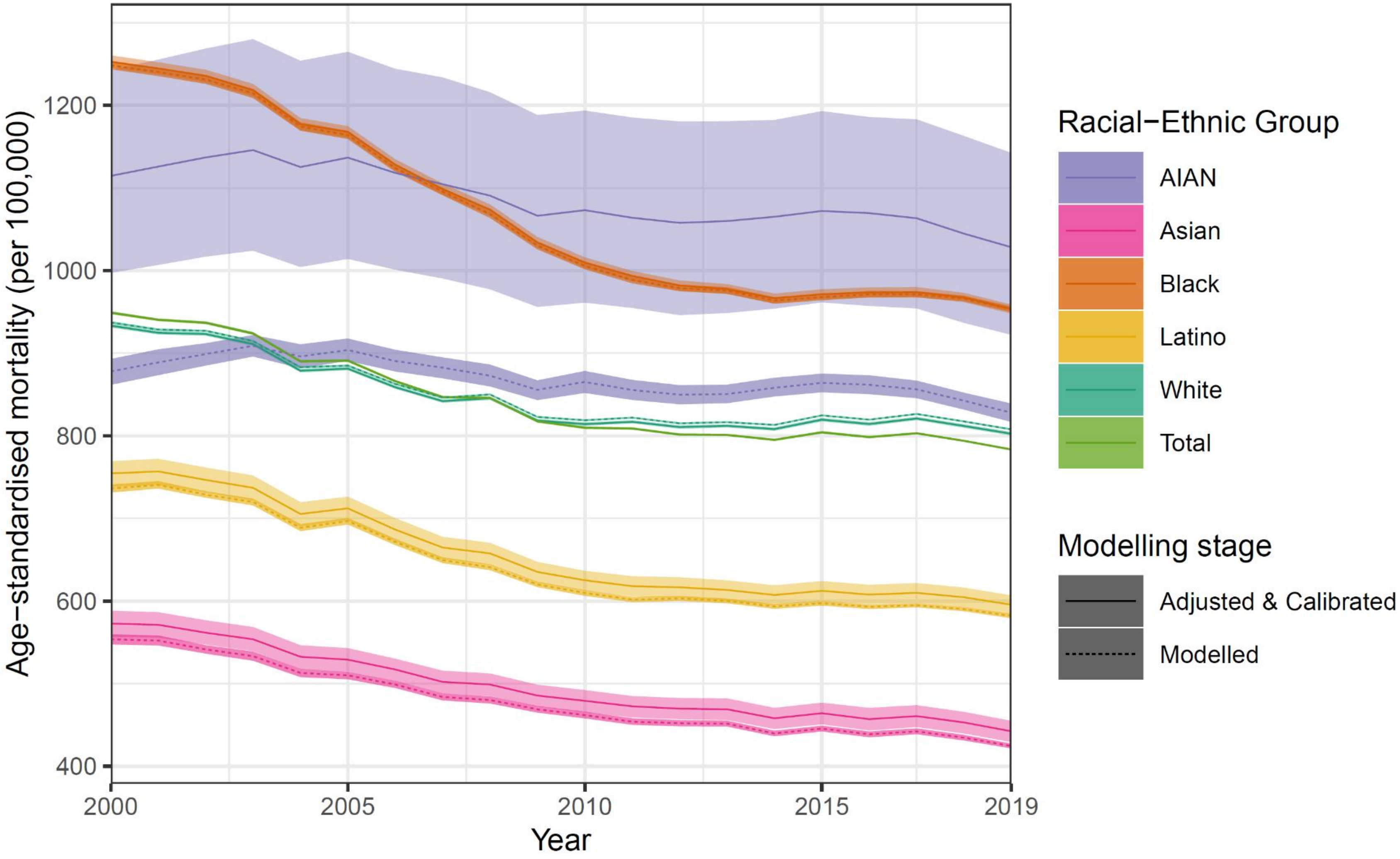
Population-weighted summary of differences in the uncertainty intervals (UI) of differences (left: absolute differences in UI; right: percent difference in UI) for age-standardised mortality by county and racial–ethnic group for males and females combined in 2000, 2010, and 2019 compared with that of the model used in this analysis (penalised complexity models, $\sigma_0 = 5, \alpha = 0.05$). Boxes show the IQR, while the whiskers extend to 1st and 99th percentiles, weighted by the average population across all years in each county and racial–ethnic group combination. The data shown are for both masked and unmasked data. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

4.3 Model validation results



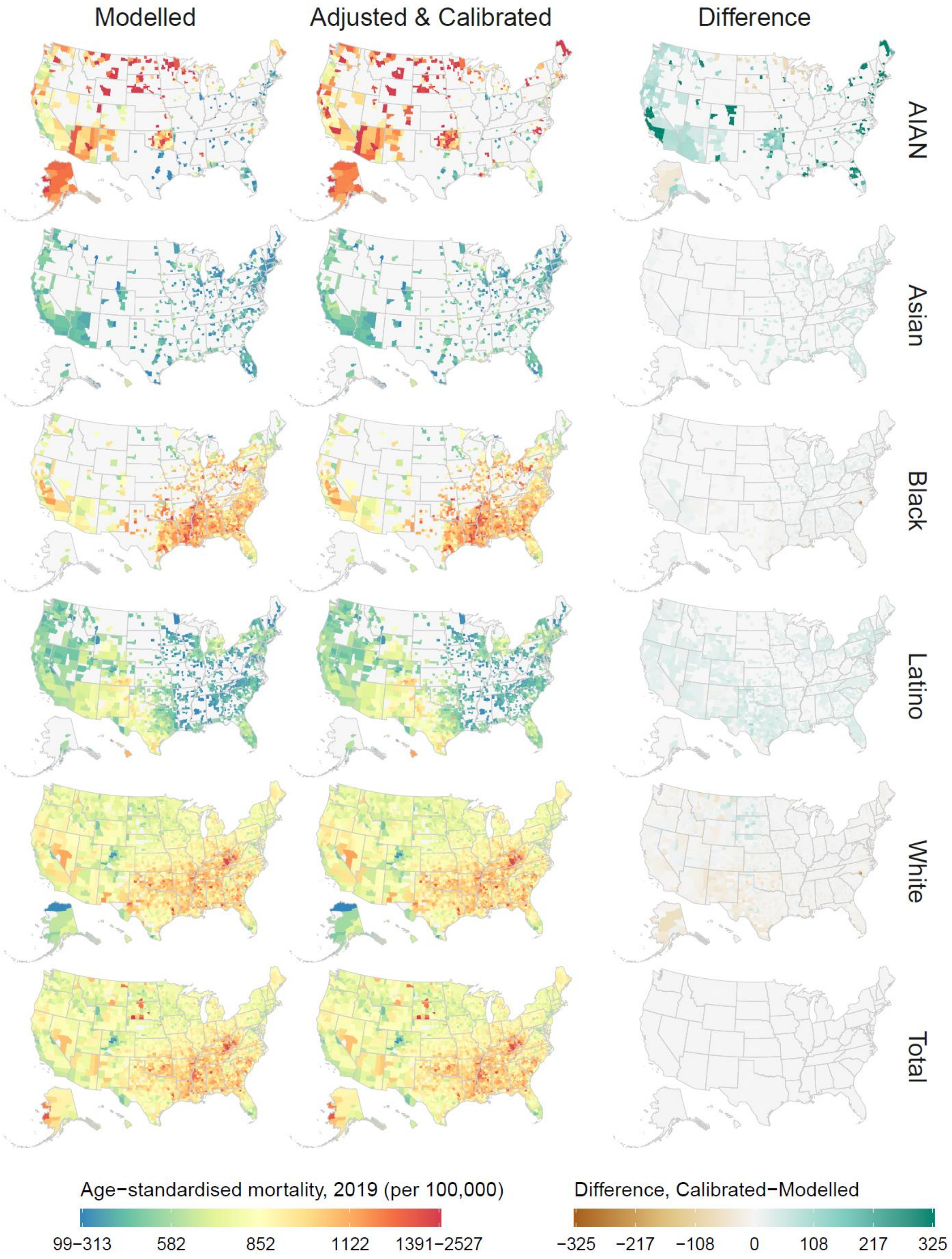
*"Across all racial–ethnic groups" means that errors and coverage were calculated across all racial–ethnic groups.

4.4 Impact of misclassification adjustment on national age-standardised all-cause mortality



National age-standardised all-cause mortality estimates before adjustment for misclassification (“Modelled”) and after adjustment and calibration (“Adjusted & Calibrated”)—ie, the final estimates.

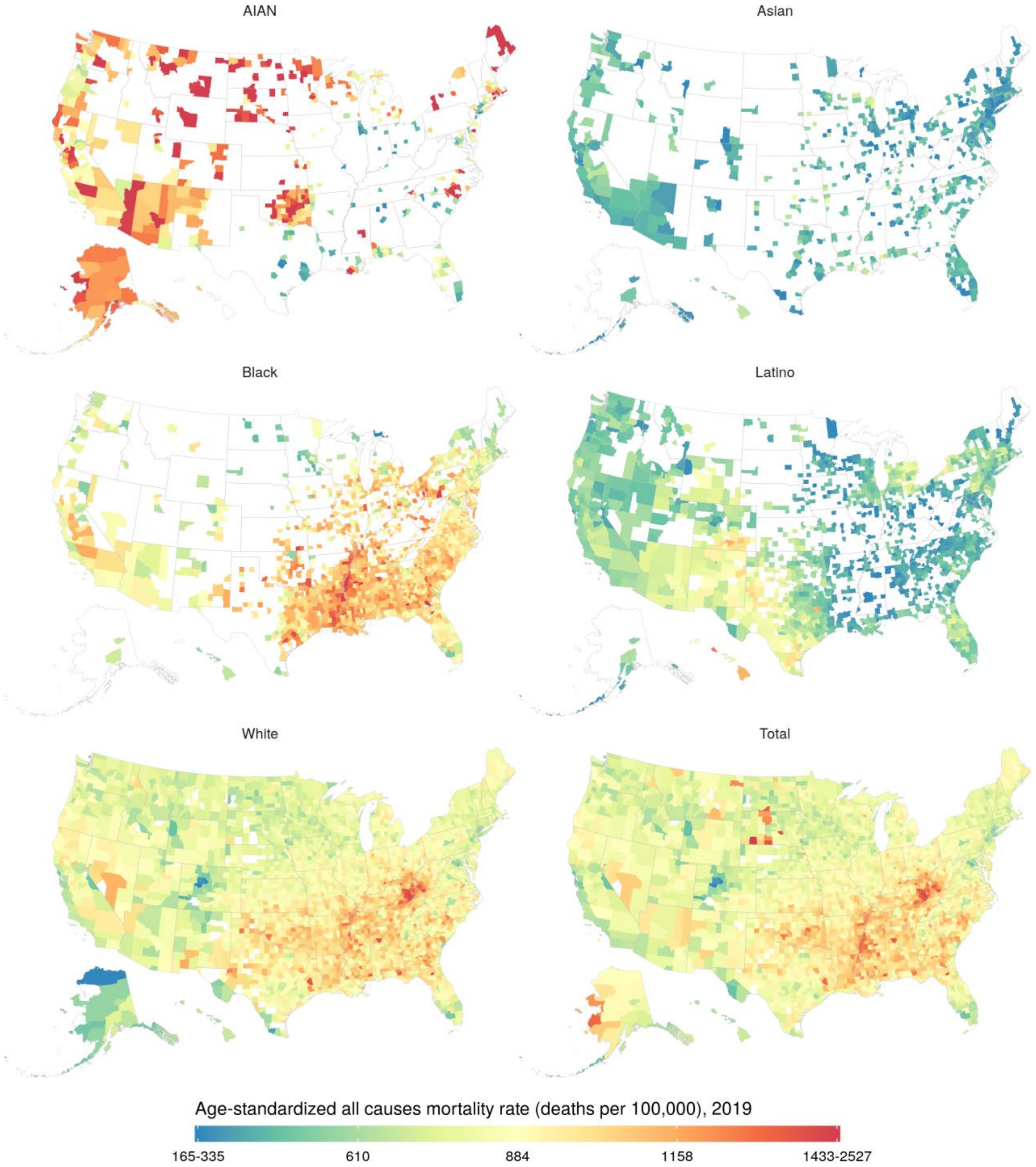
4.5 Impact of misclassification adjustment on county age-standardised all-cause mortality estimates



County age-standardised all-cause mortality estimates before adjustment for misclassification ("Modelled") and after adjustment and calibration ("Adjusted & Calibrated")—ie, the final estimates. Estimates have been masked for county and racial–ethnic groups with a mean annual population fewer than 1000 people because model performance declined notably below this threshold. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

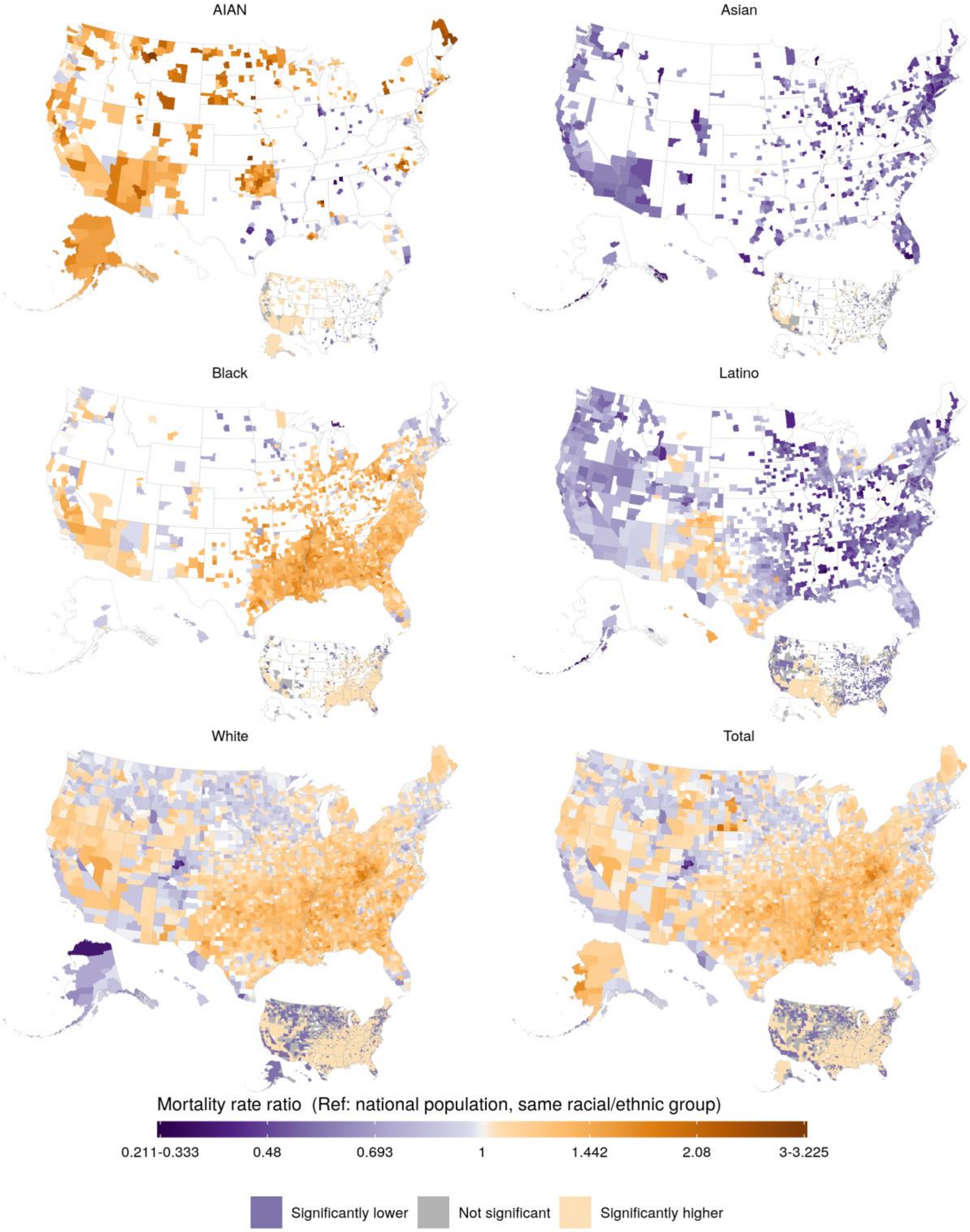
5 Supplemental Results Figures

eFigure 1: Age-standardised mortality rate, all causes, 2019



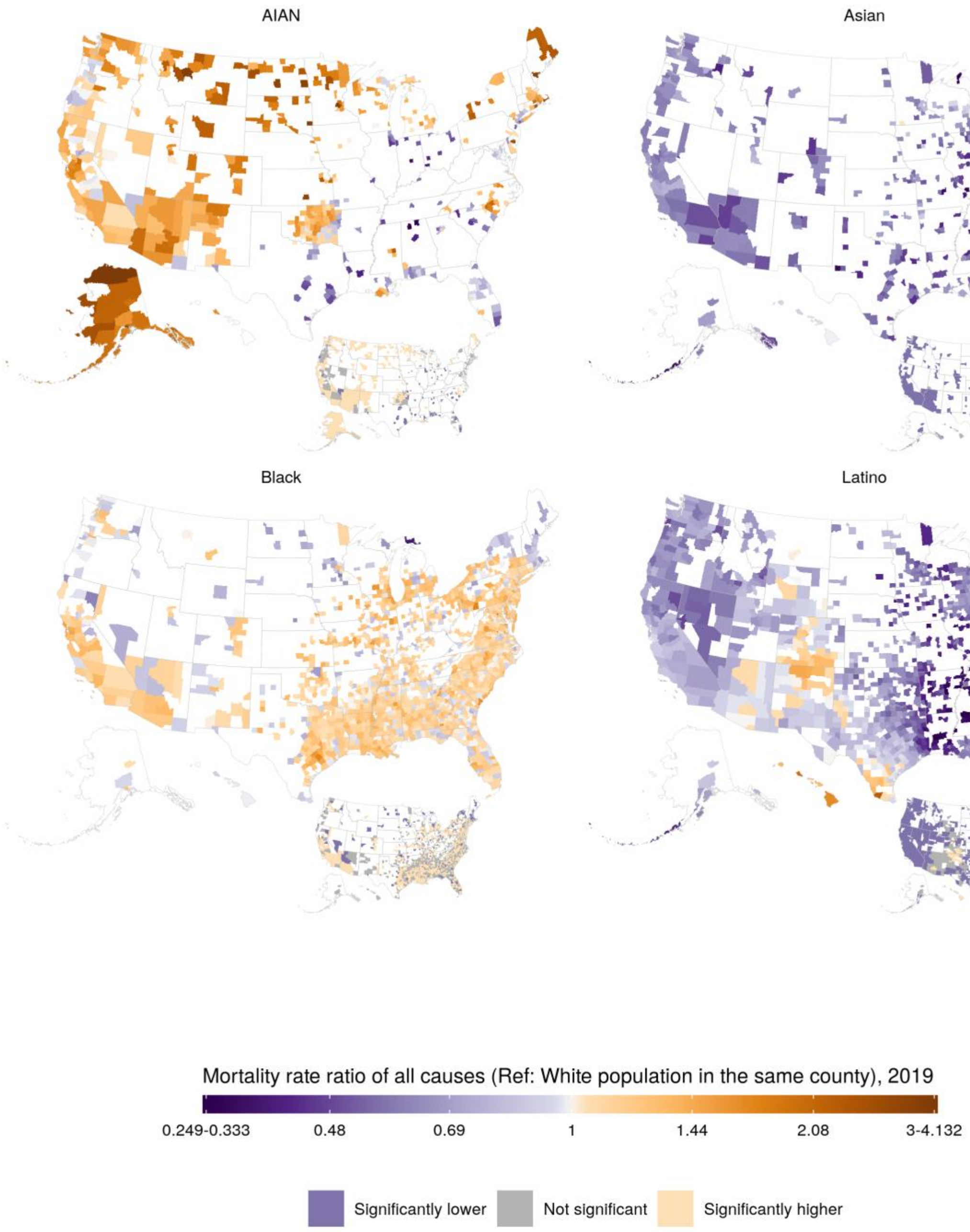
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 2: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, all causes, 2019



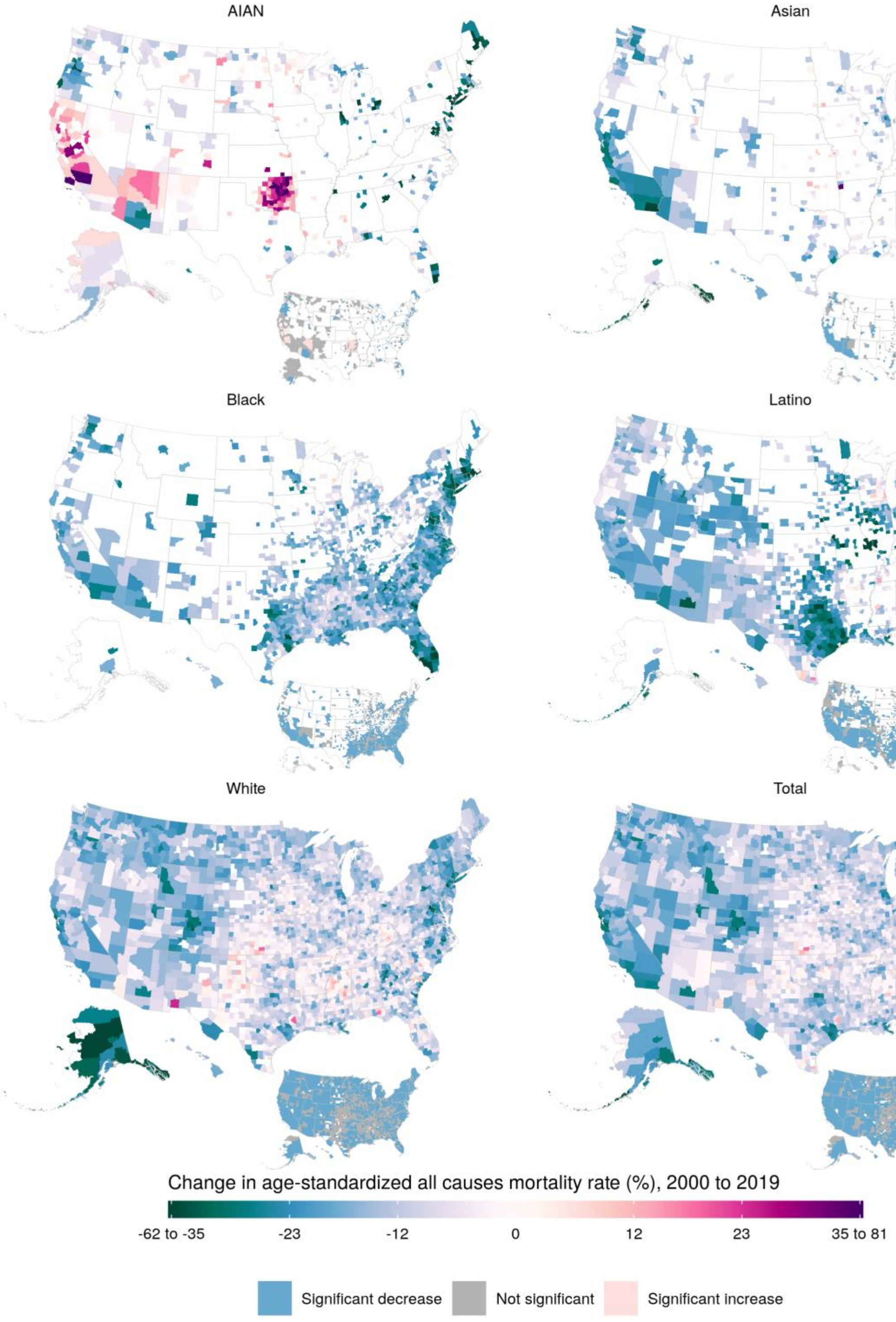
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 3: Age-standardised mortality rate ratio compared to the White population in the same county, all causes, 2019



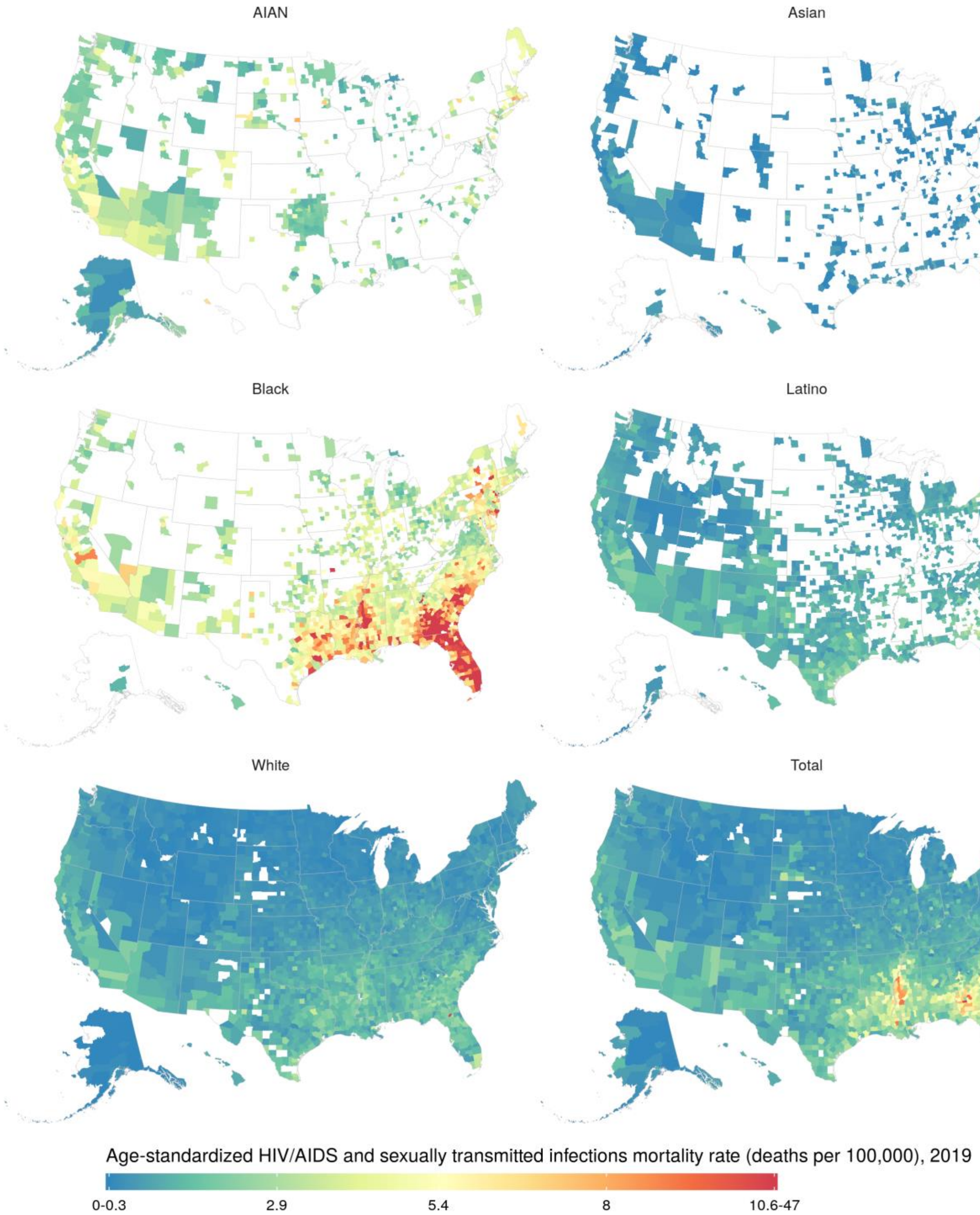
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 4: Change in age-standardised mortality rate, all causes, 2000–2019



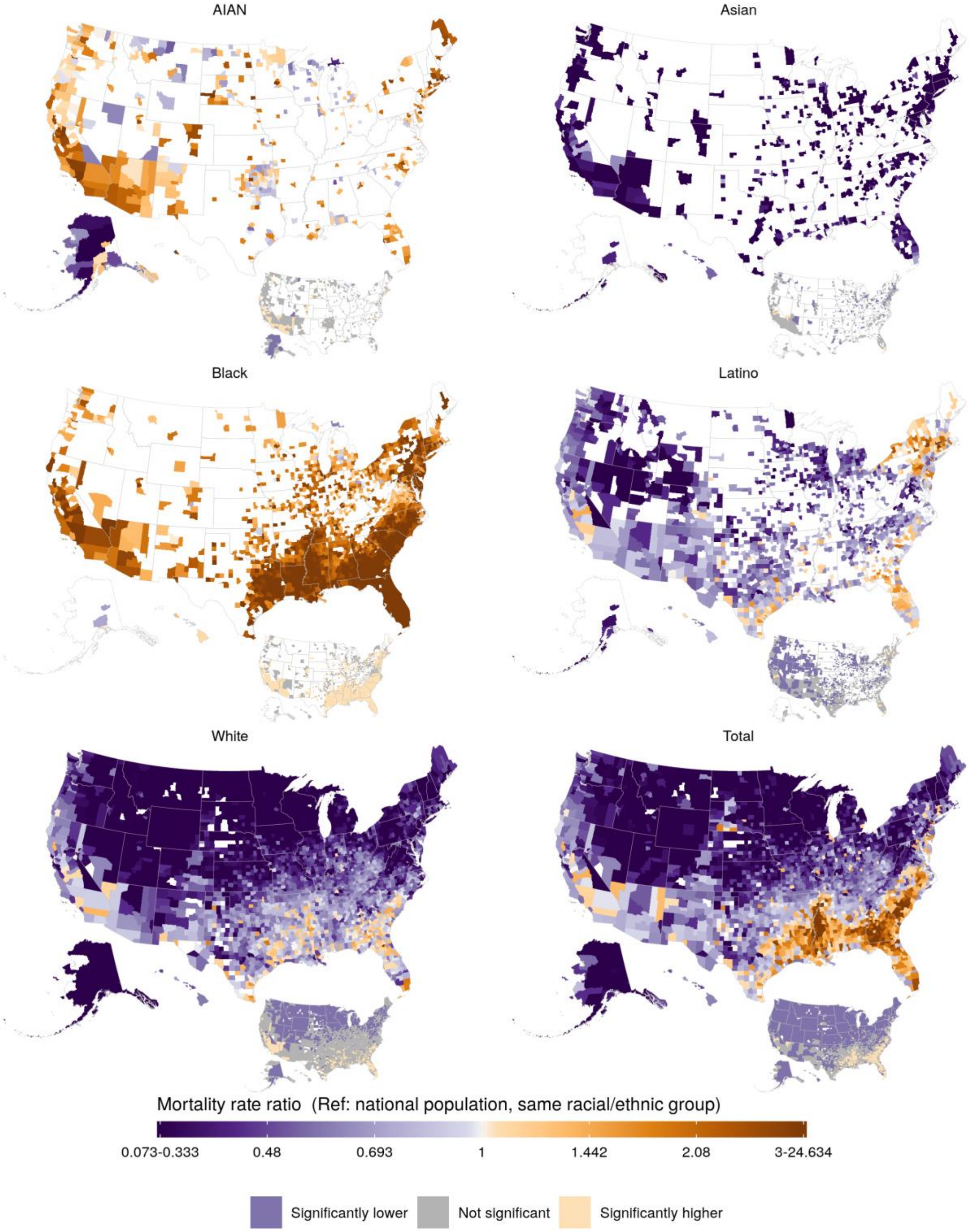
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 5: Age-standardised mortality rate, HIV/AIDS and sexually transmitted infections, 2019



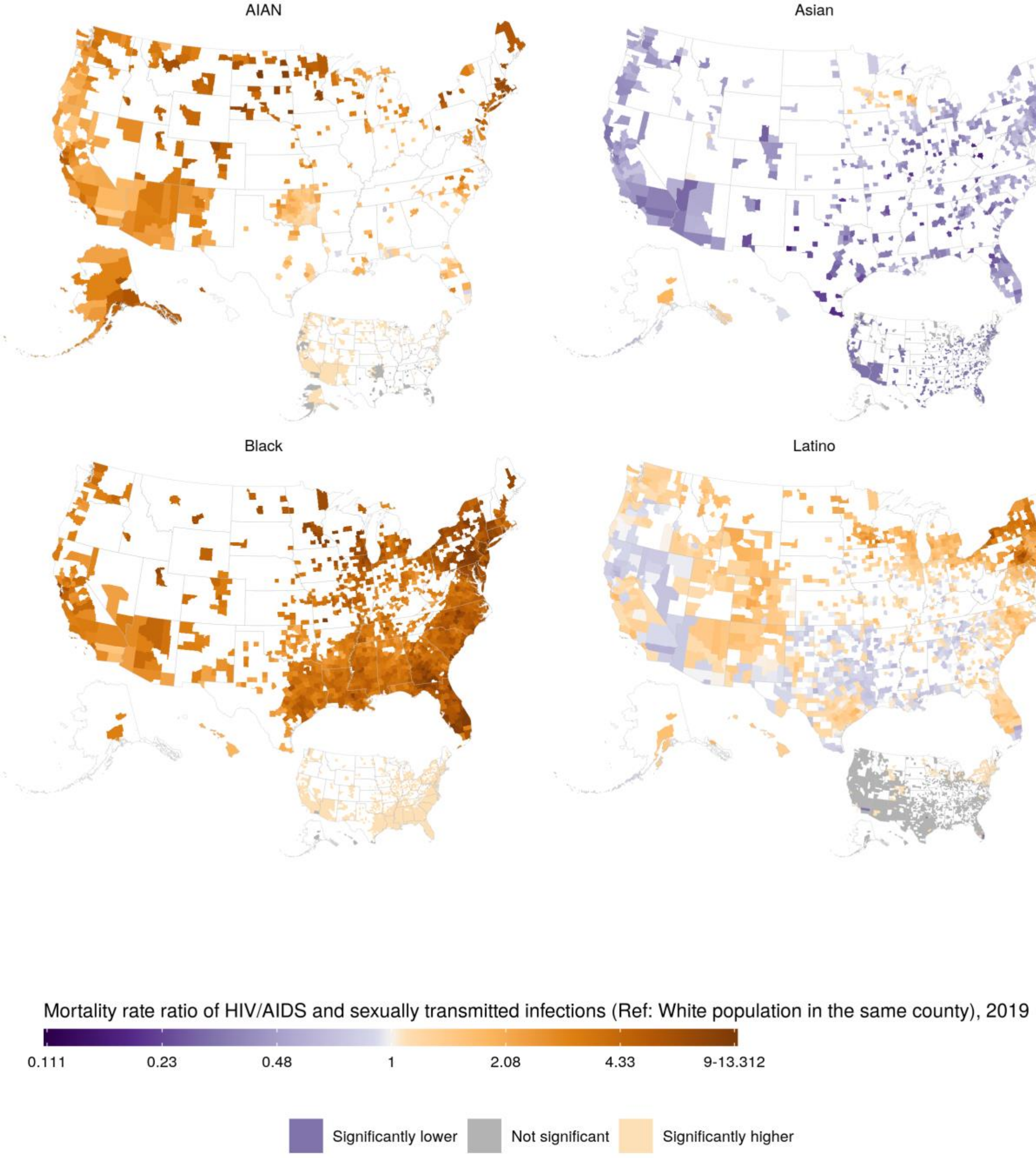
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 6: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, HIV/AIDS and sexually transmitted infections, 2019



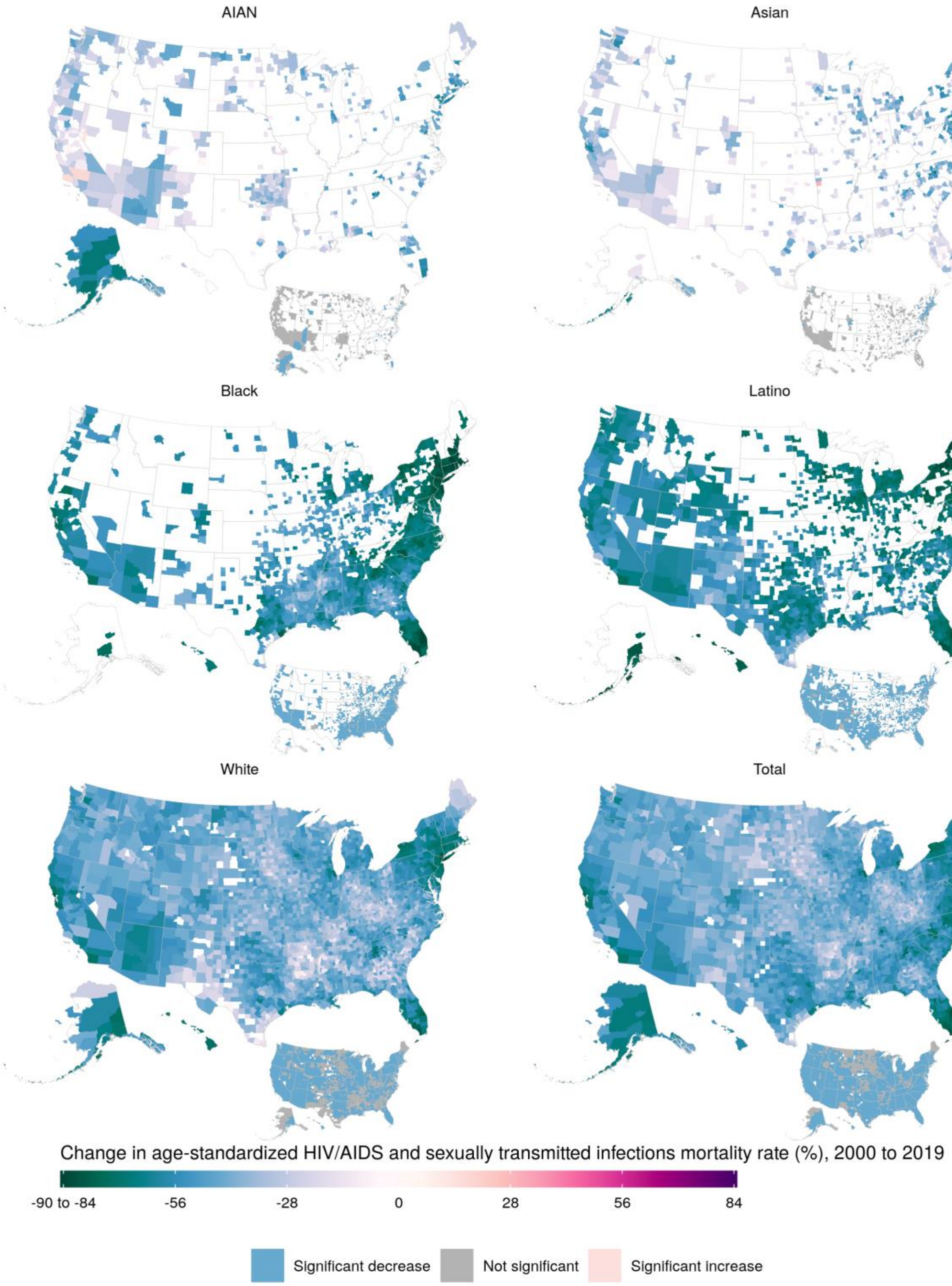
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 7: Age-standardised mortality rate ratio compared to the White population in the same county, HIV/AIDS and sexually transmitted infections, 2019



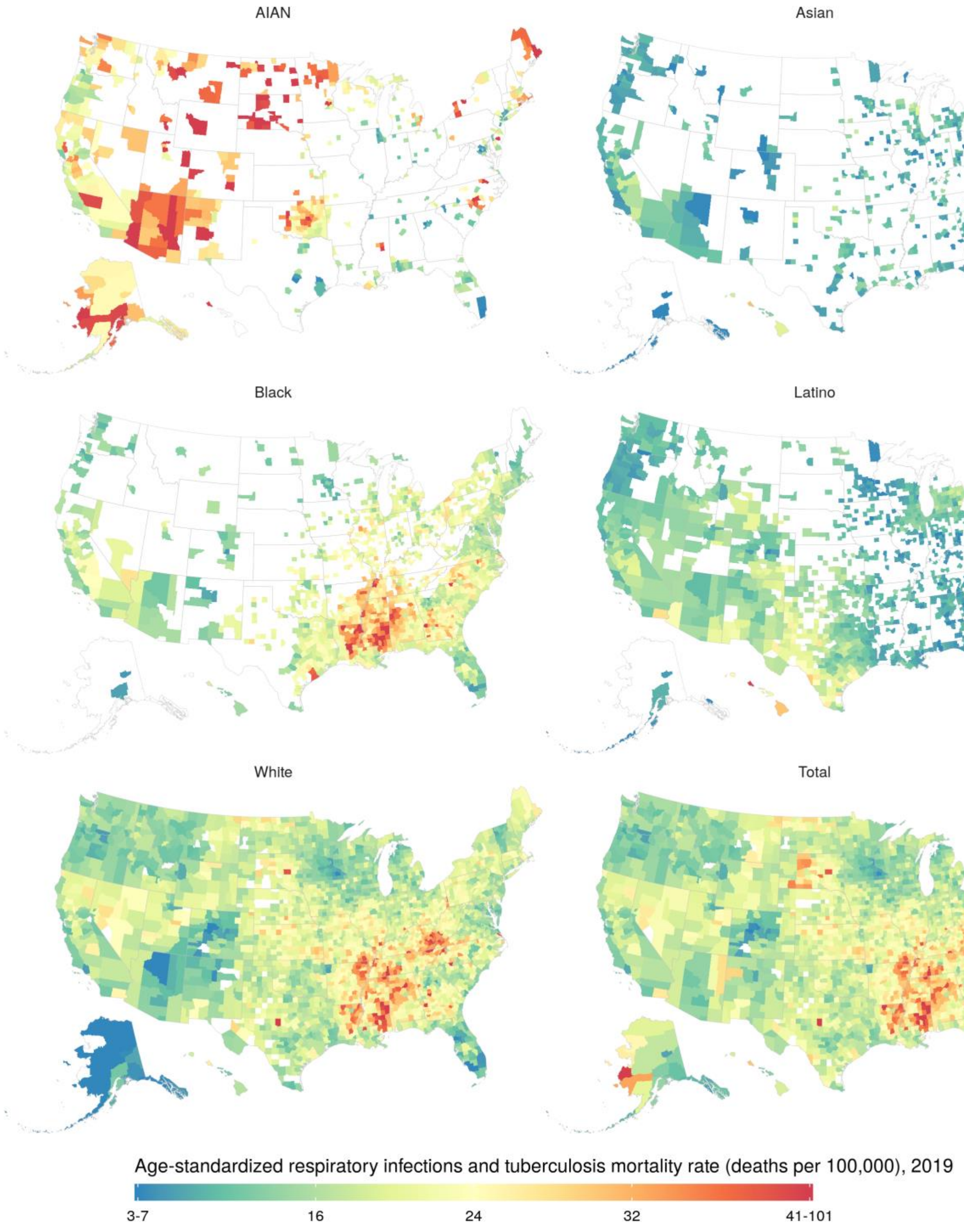
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 8: Change in age-standardised mortality rate, HIV/AIDS and sexually transmitted infections, 2000–2019



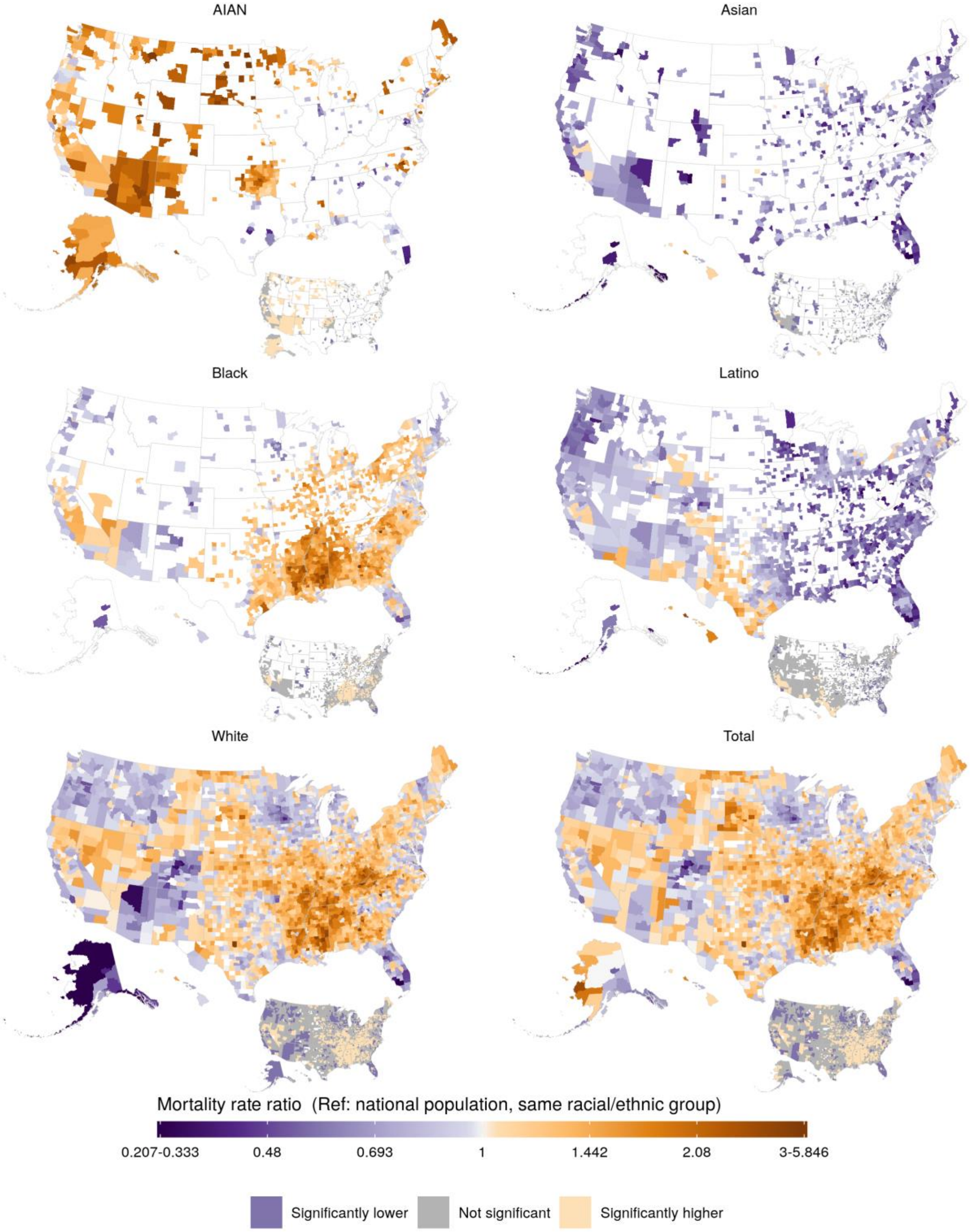
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 9: Age-standardised mortality rate, respiratory infections and tuberculosis, 2019



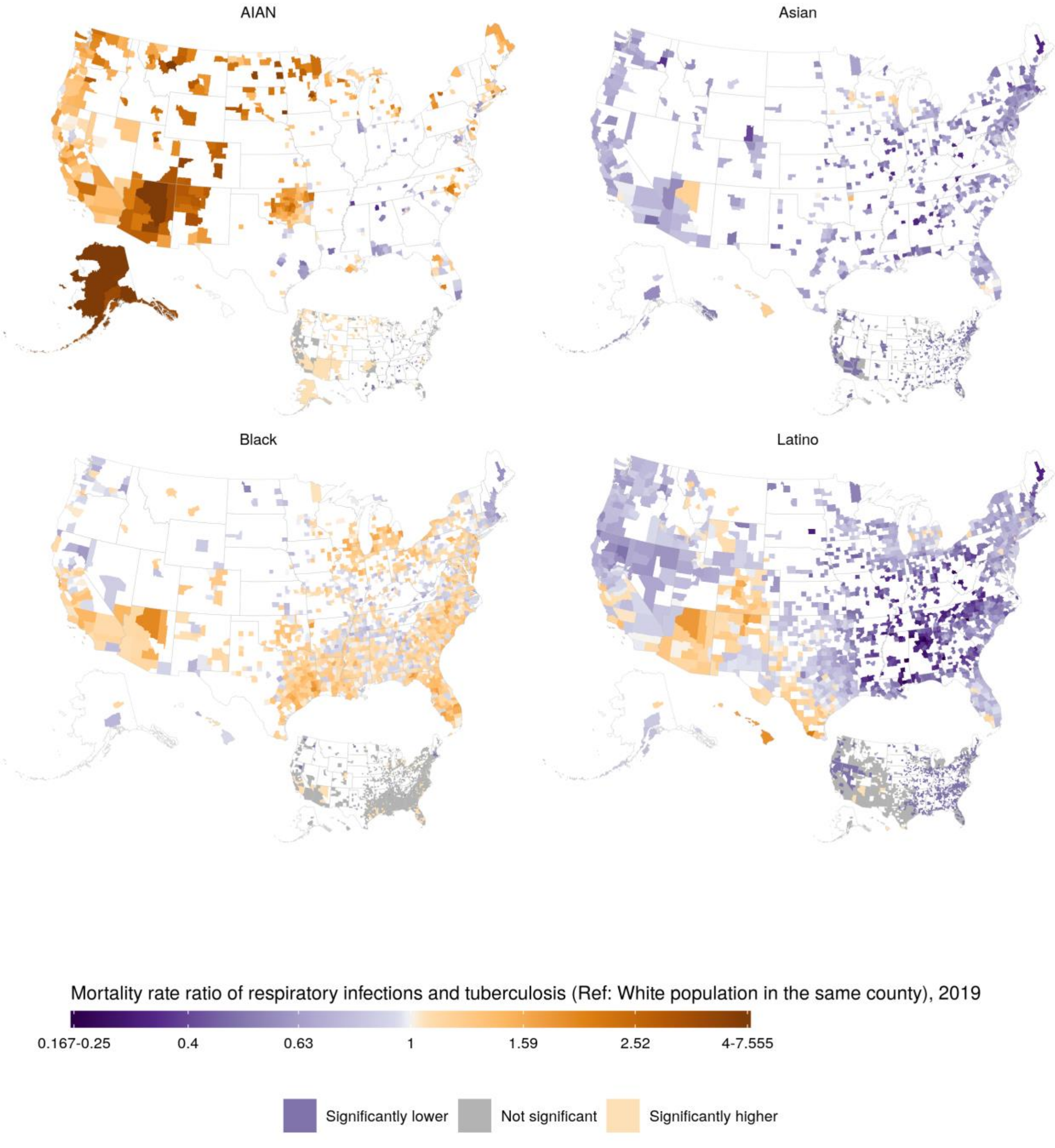
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 10: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, respiratory infections and tuberculosis, 2019



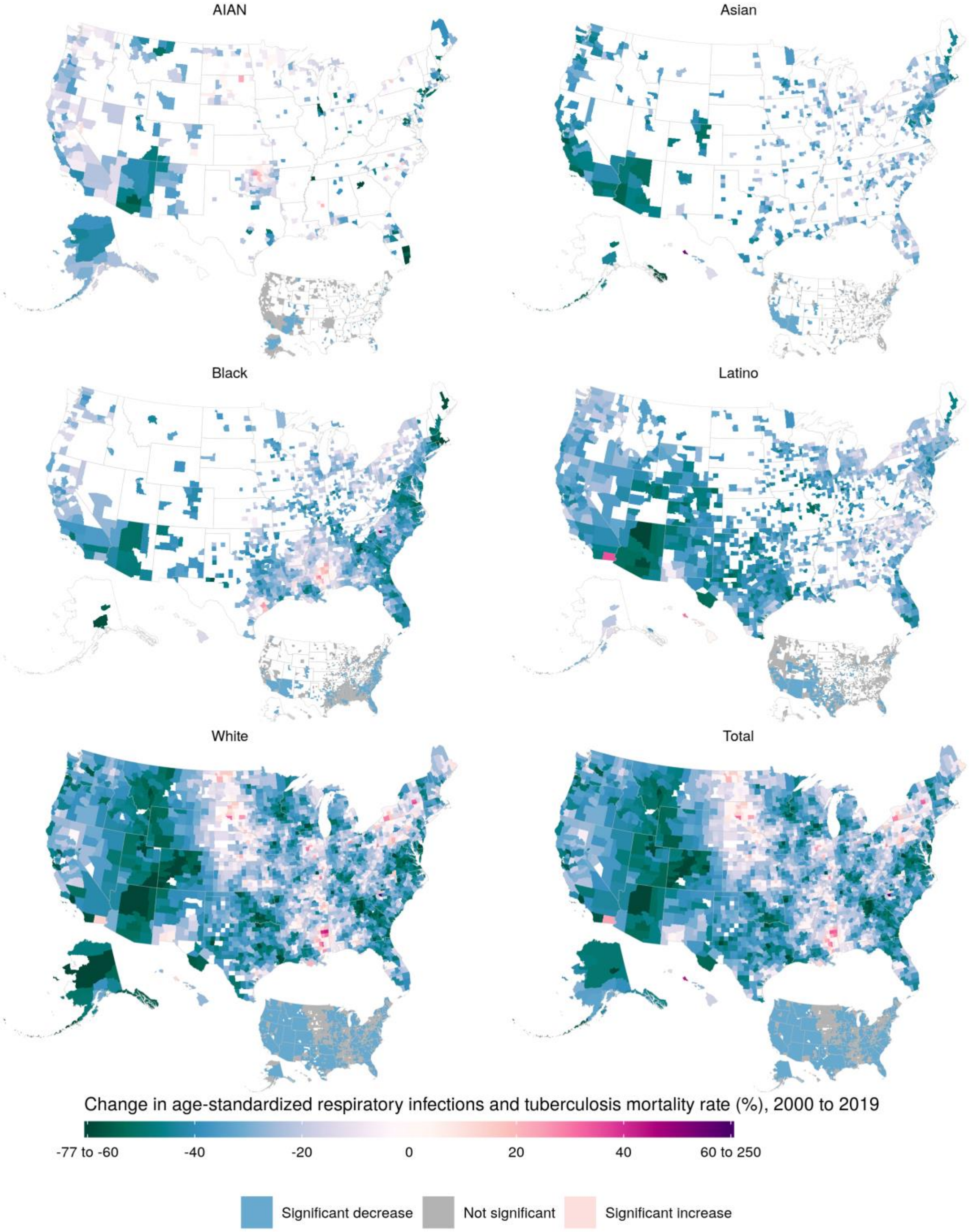
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 11: Age-standardised mortality rate ratio compared to the White population in the same county, respiratory infections and tuberculosis, 2019



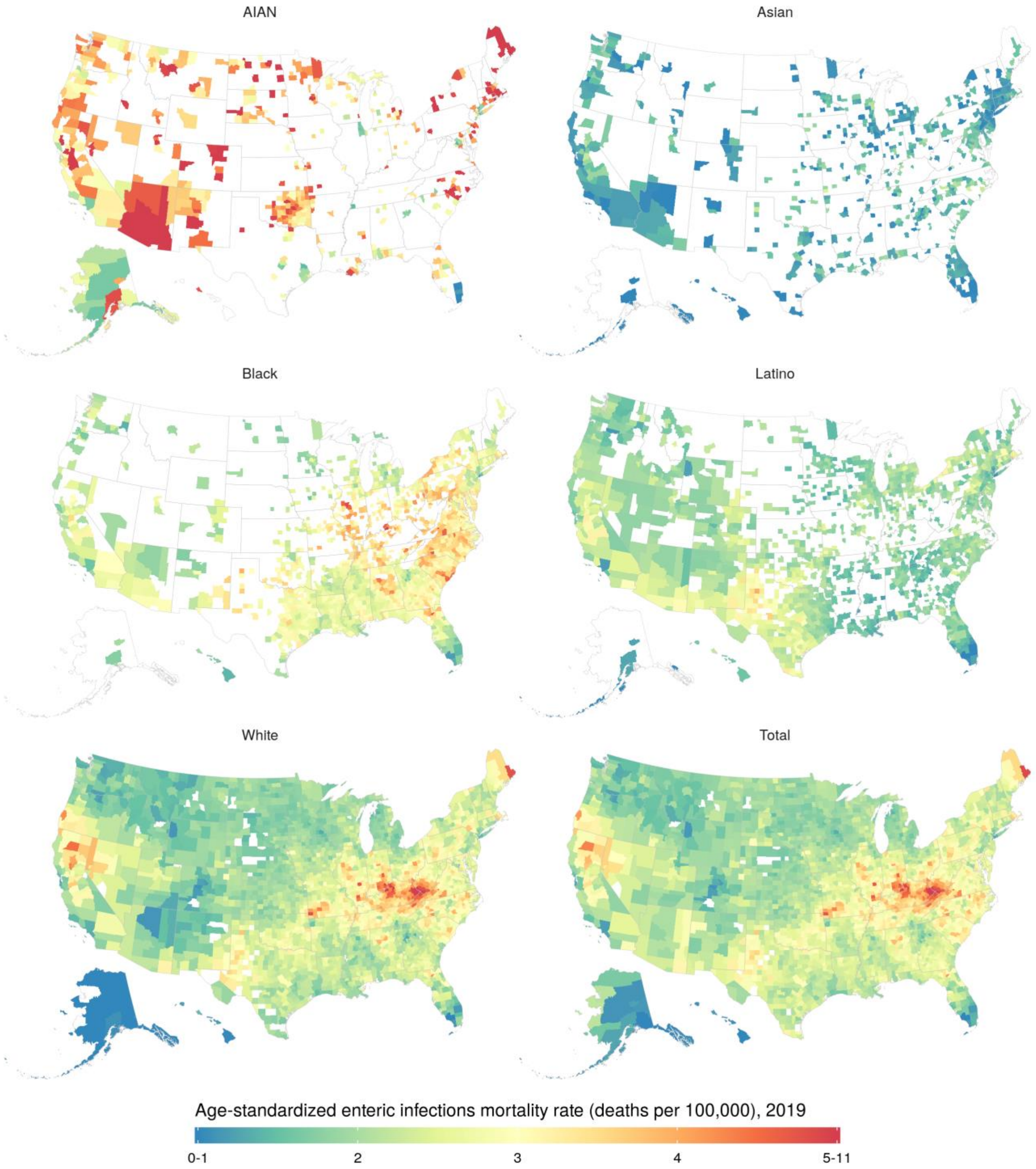
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 12: Change in age-standardised mortality rate, respiratory infections and tuberculosis, 2000–2019



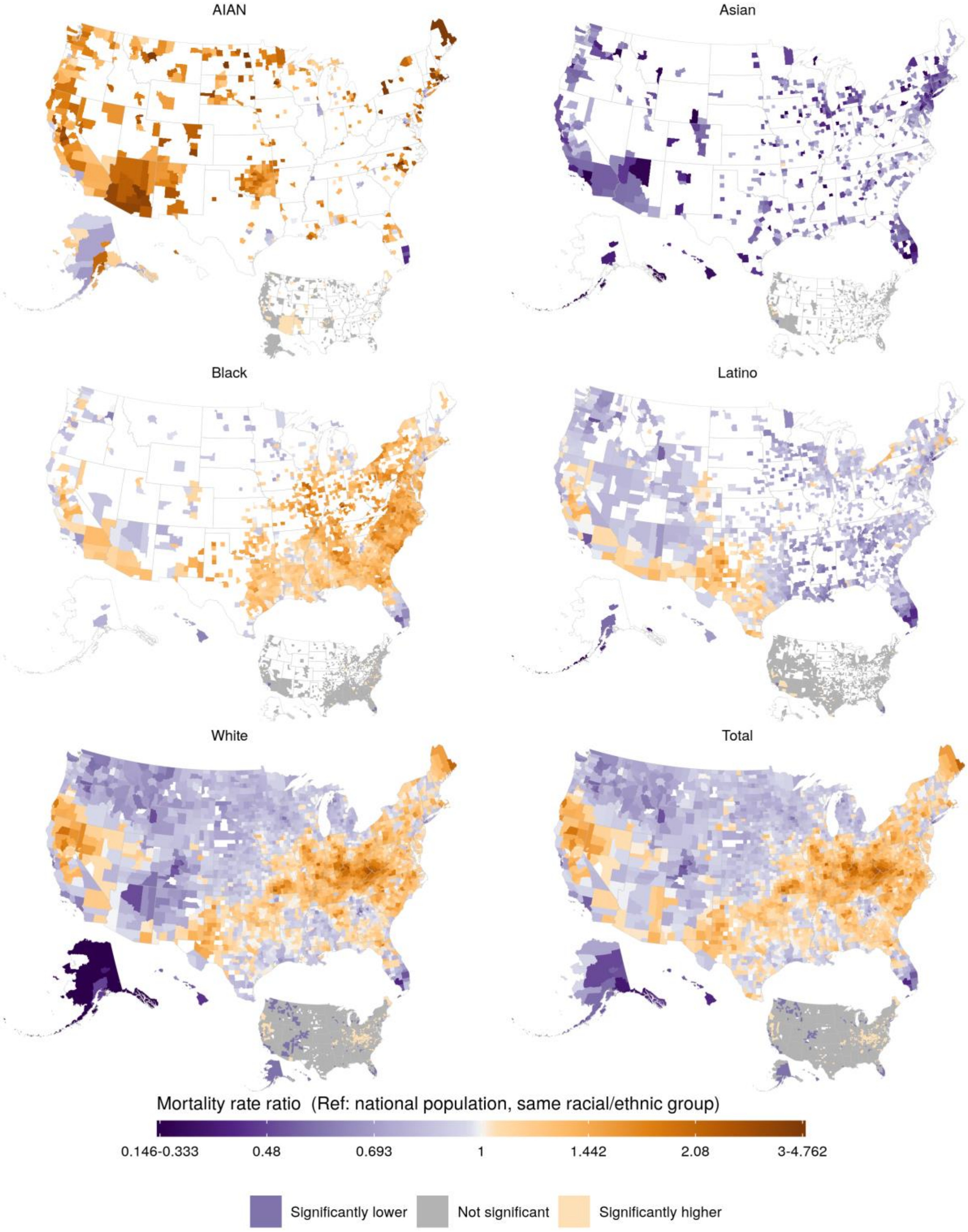
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 13: Age-standardised mortality rate, enteric infections, 2019



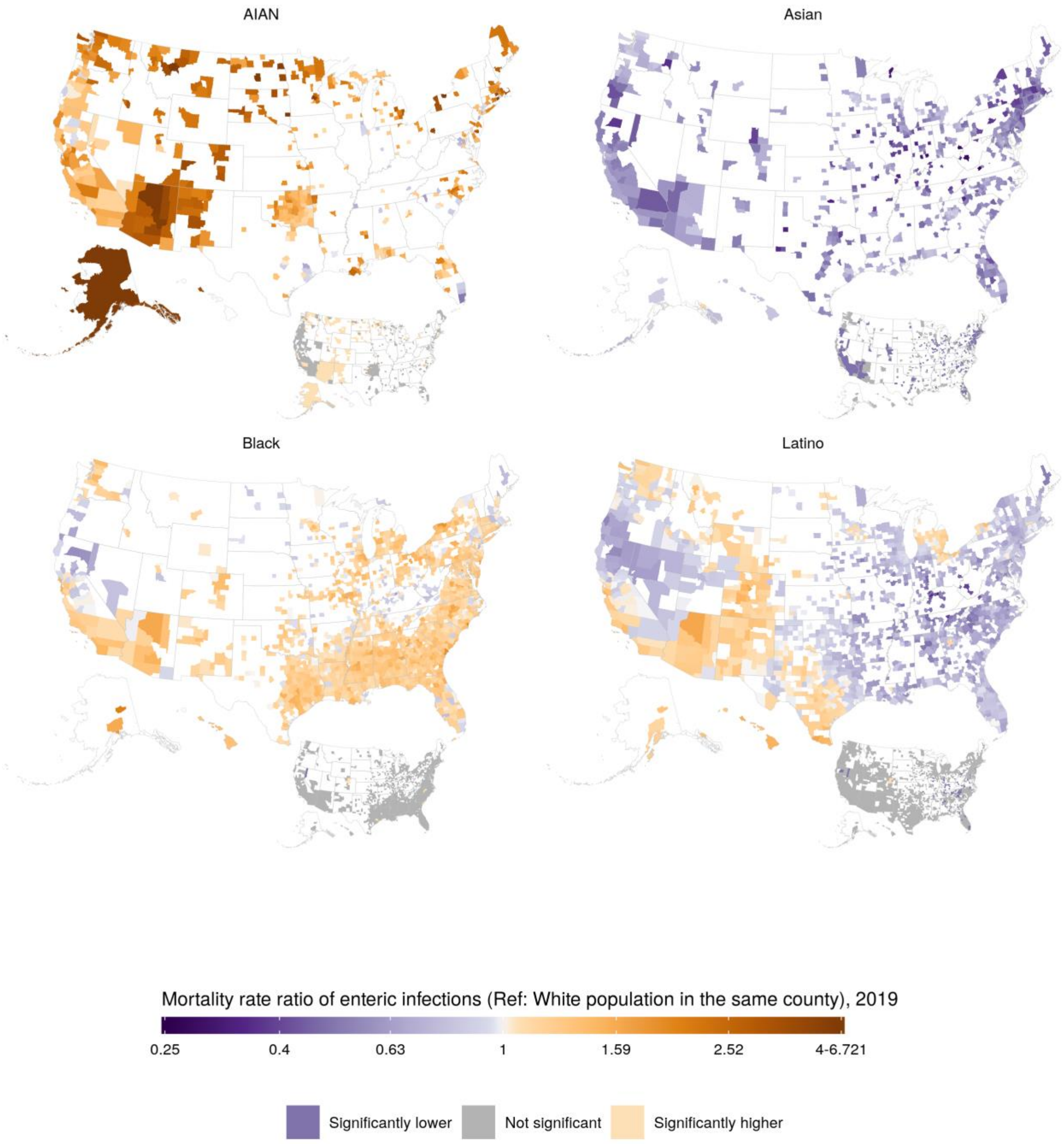
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 14: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, enteric infections, 2019



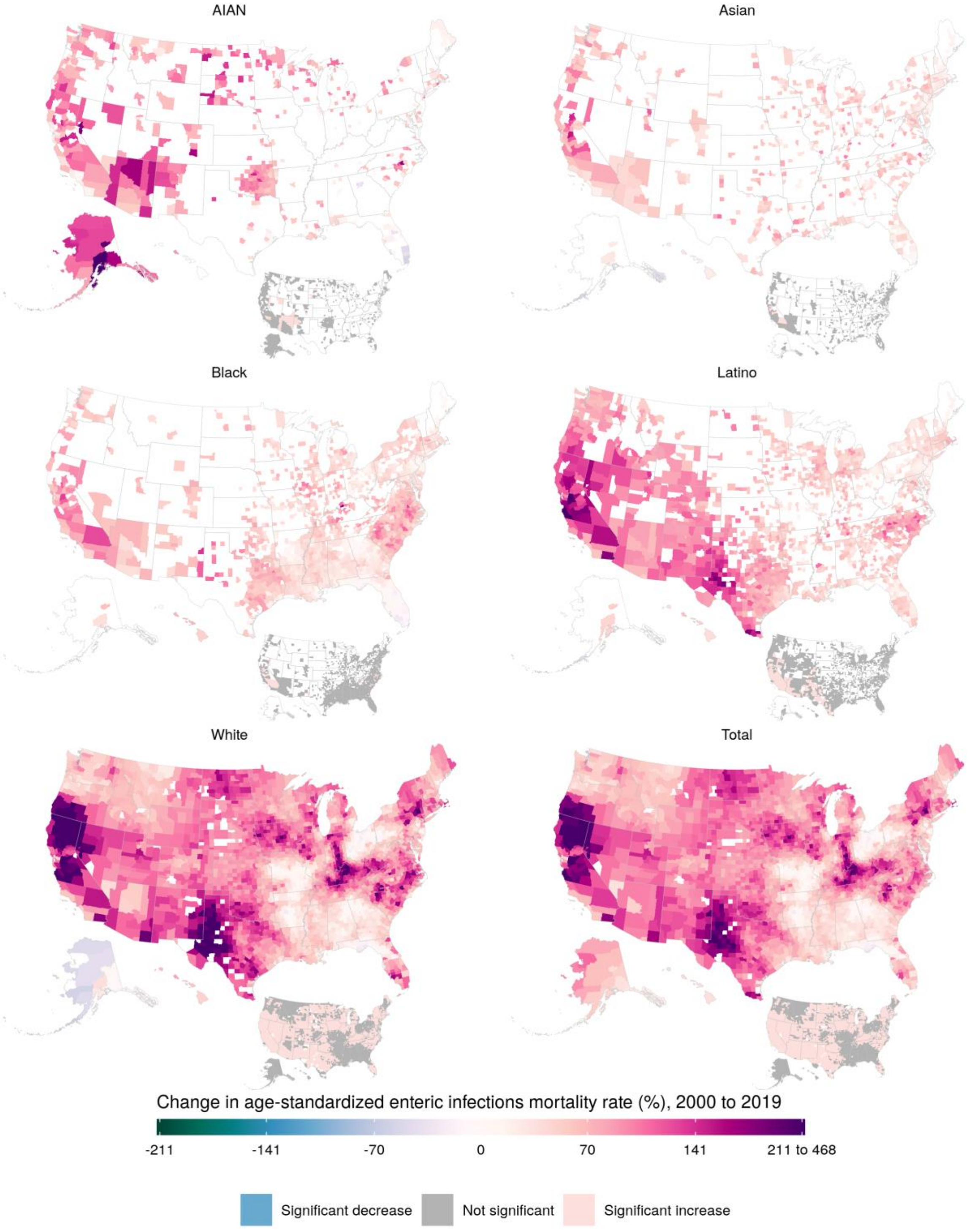
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 15: Age-standardised mortality rate ratio compared to the White population in the same county, enteric infections, 2019



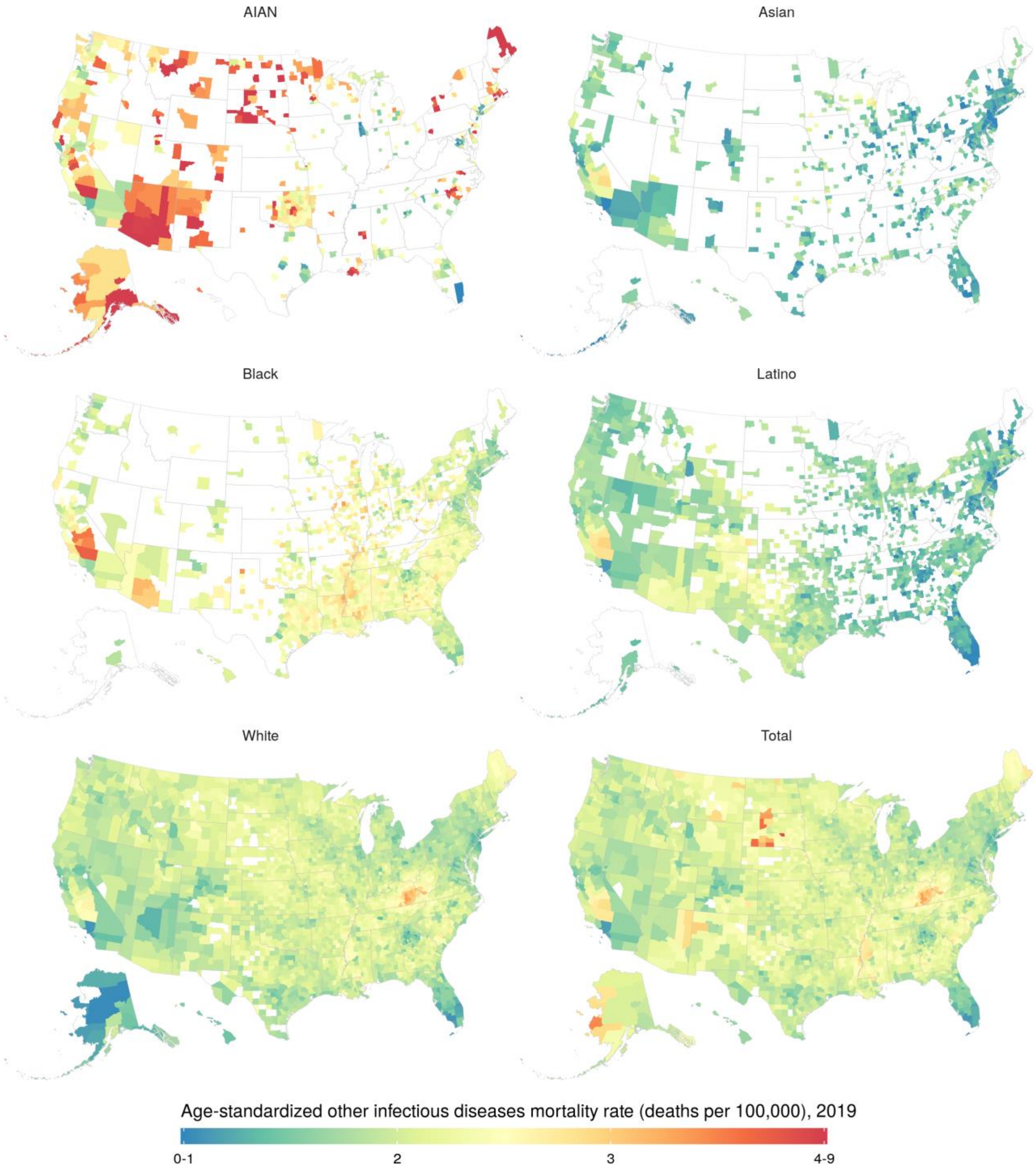
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 16: Change in age-standardised mortality rate, enteric infections, 2000–2019



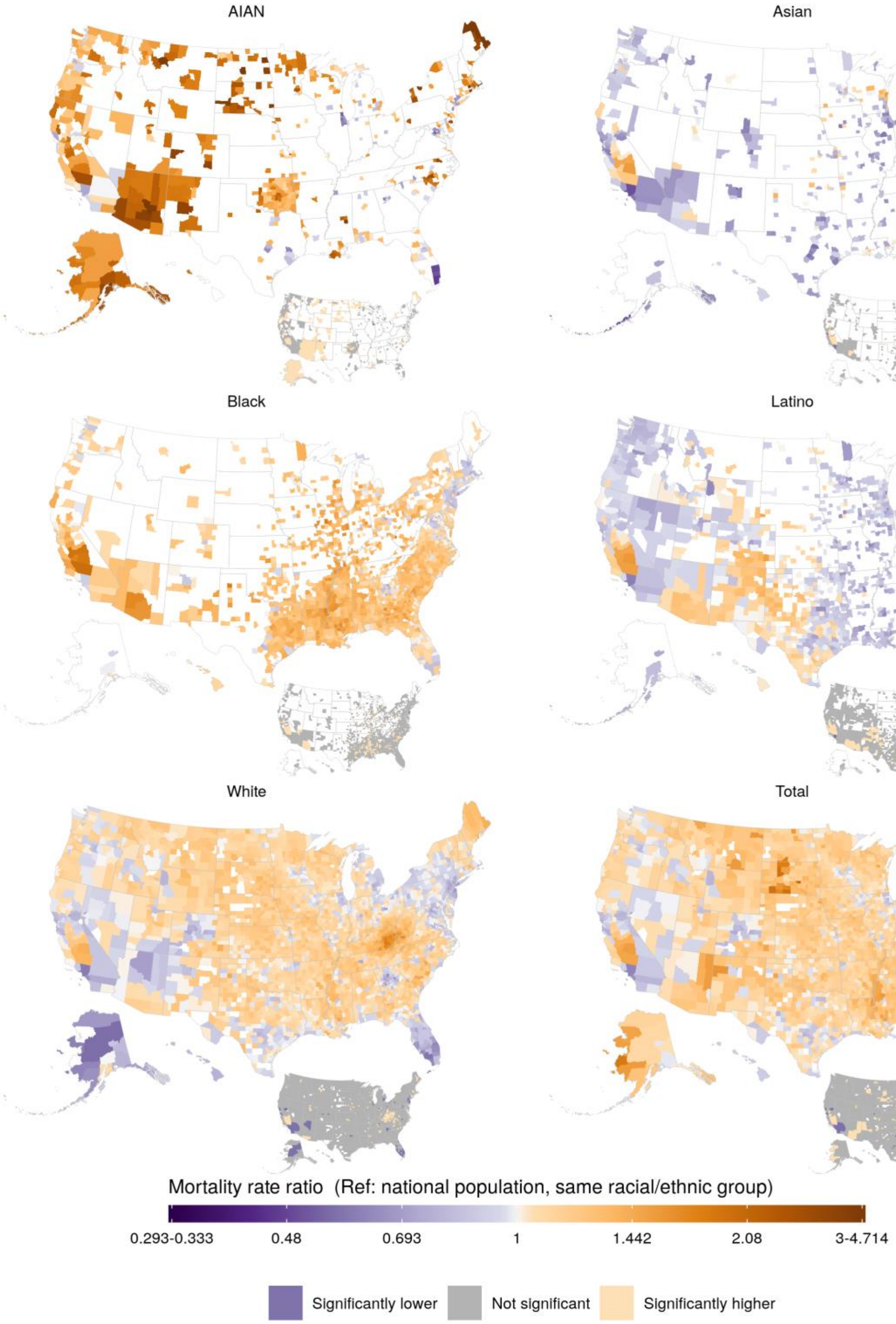
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 17: Age-standardised mortality rate, other infectious diseases, 2019



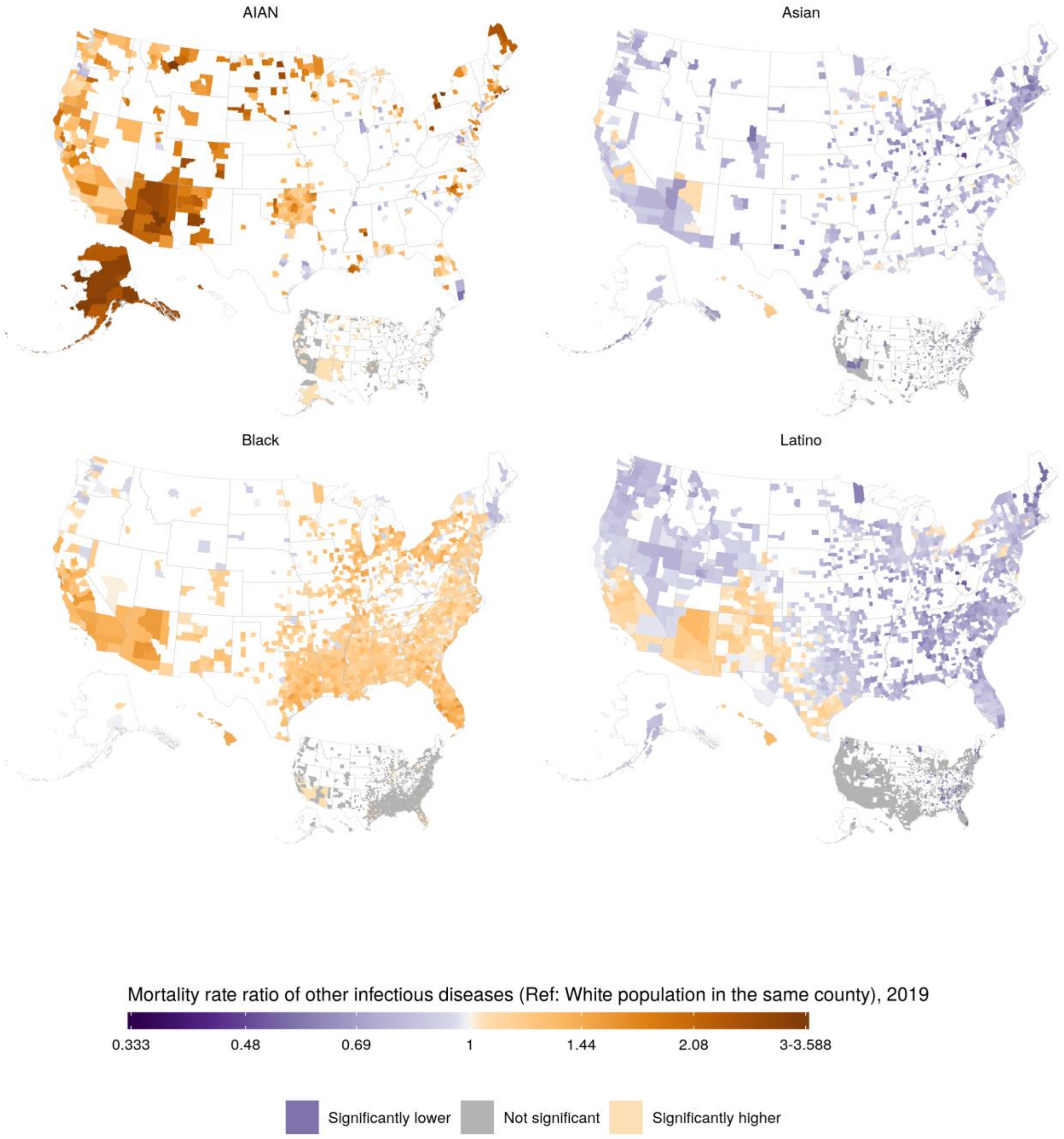
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 18: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, other infectious diseases, 2019



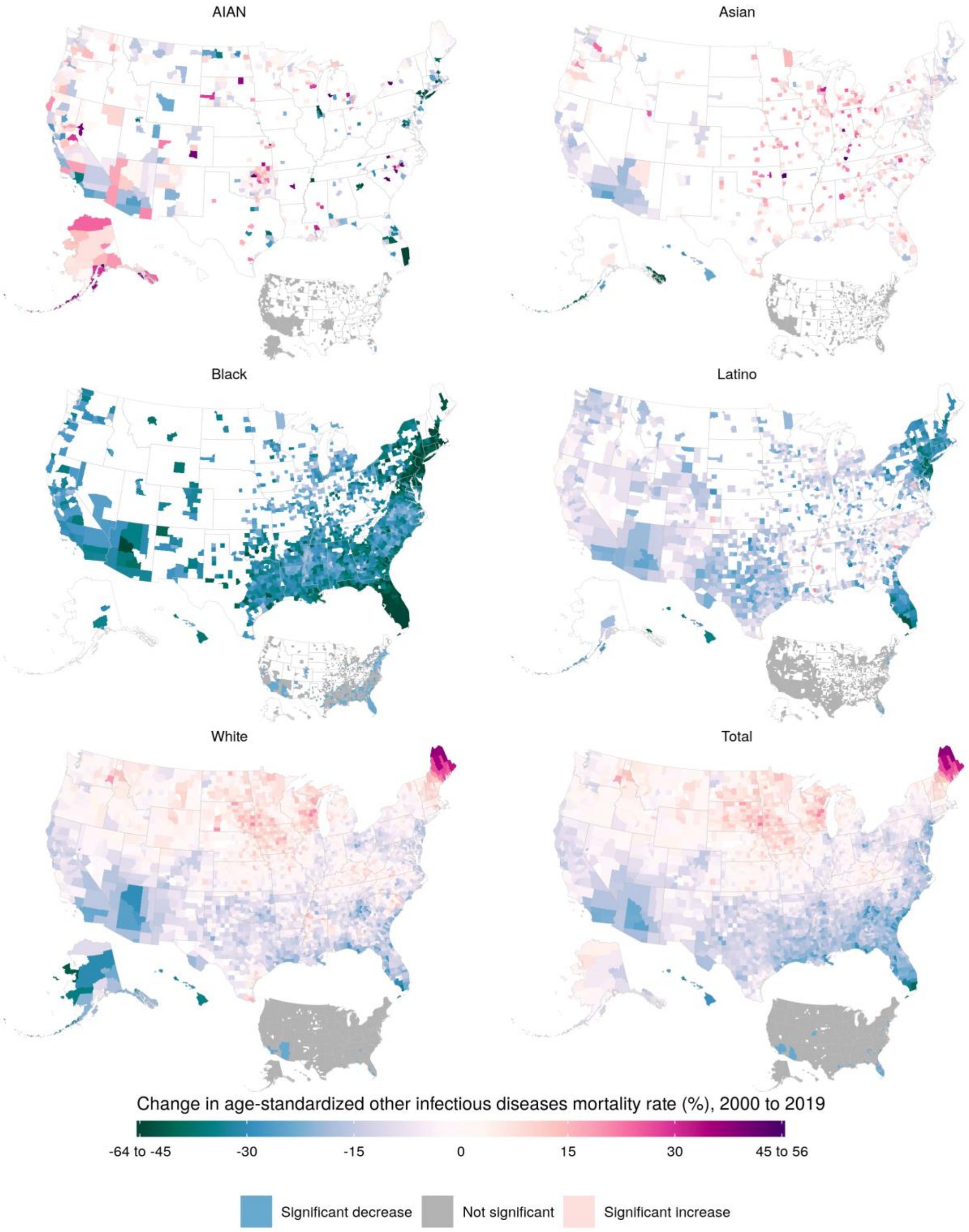
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 19: Age-standardised mortality rate ratio compared to the White population in the same county, other infectious diseases, 2019



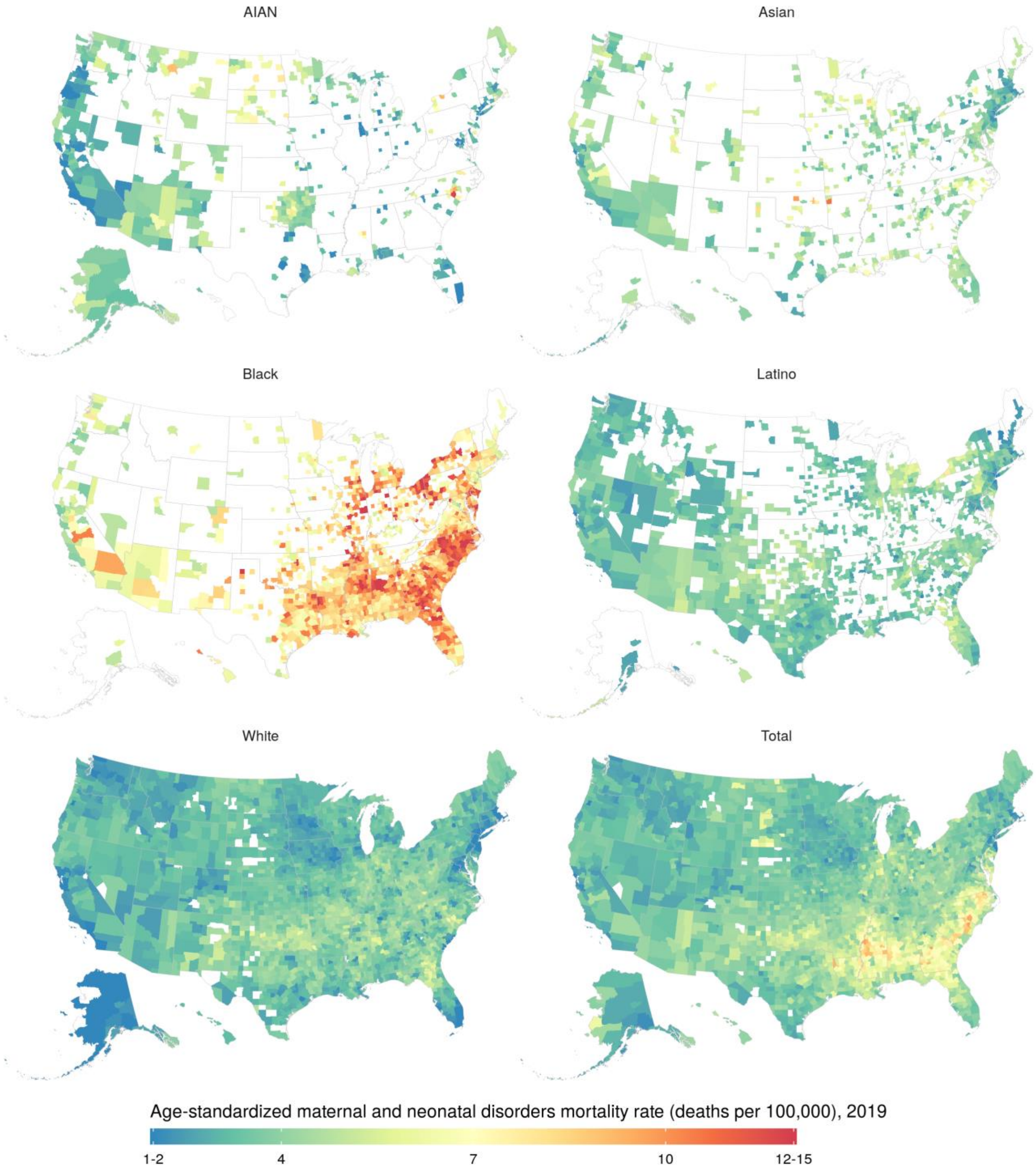
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 20: Change in age-standardised mortality rate, other infectious diseases, 2000–2019



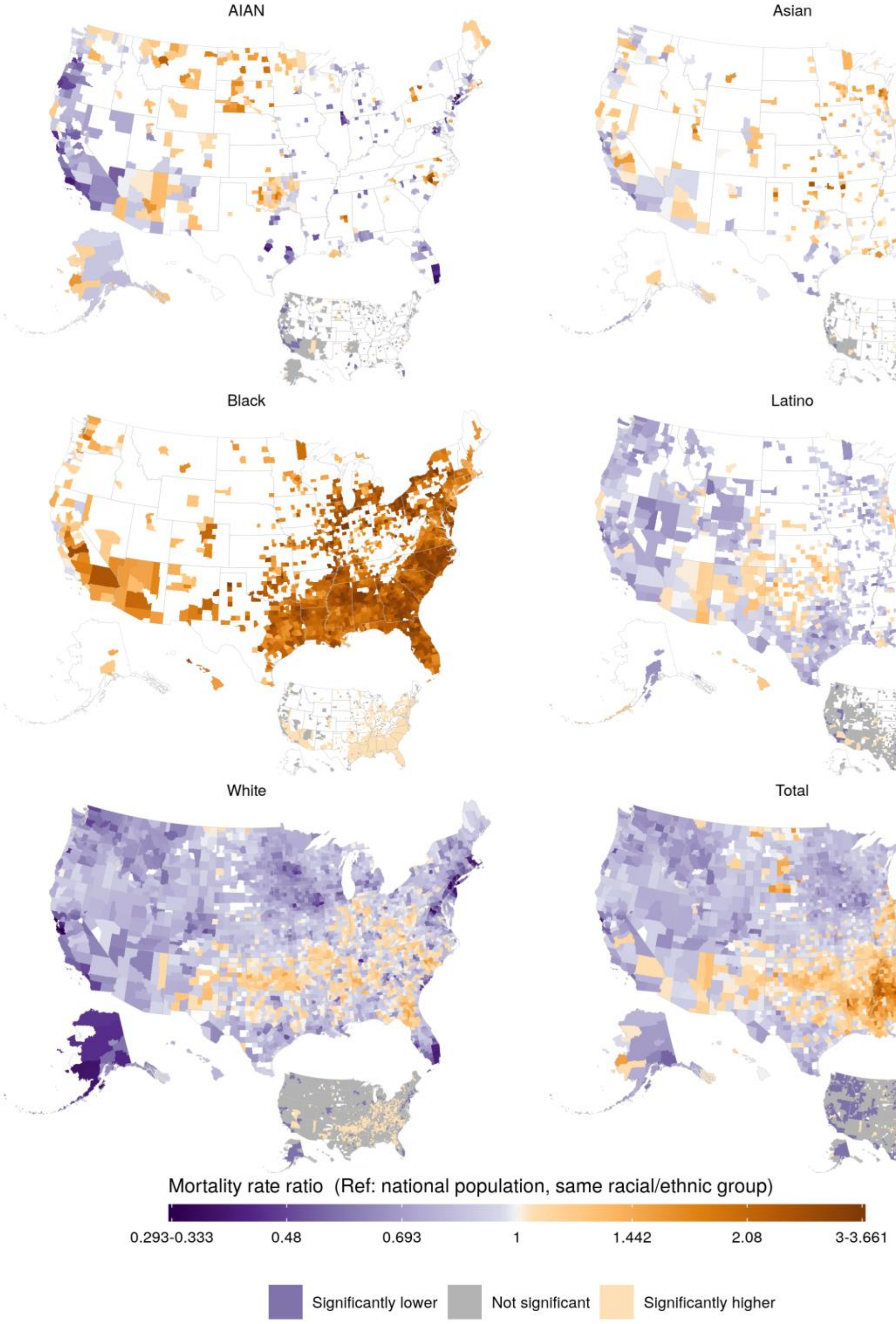
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 21: Age-standardised mortality rate, maternal and neonatal disorders, 2019



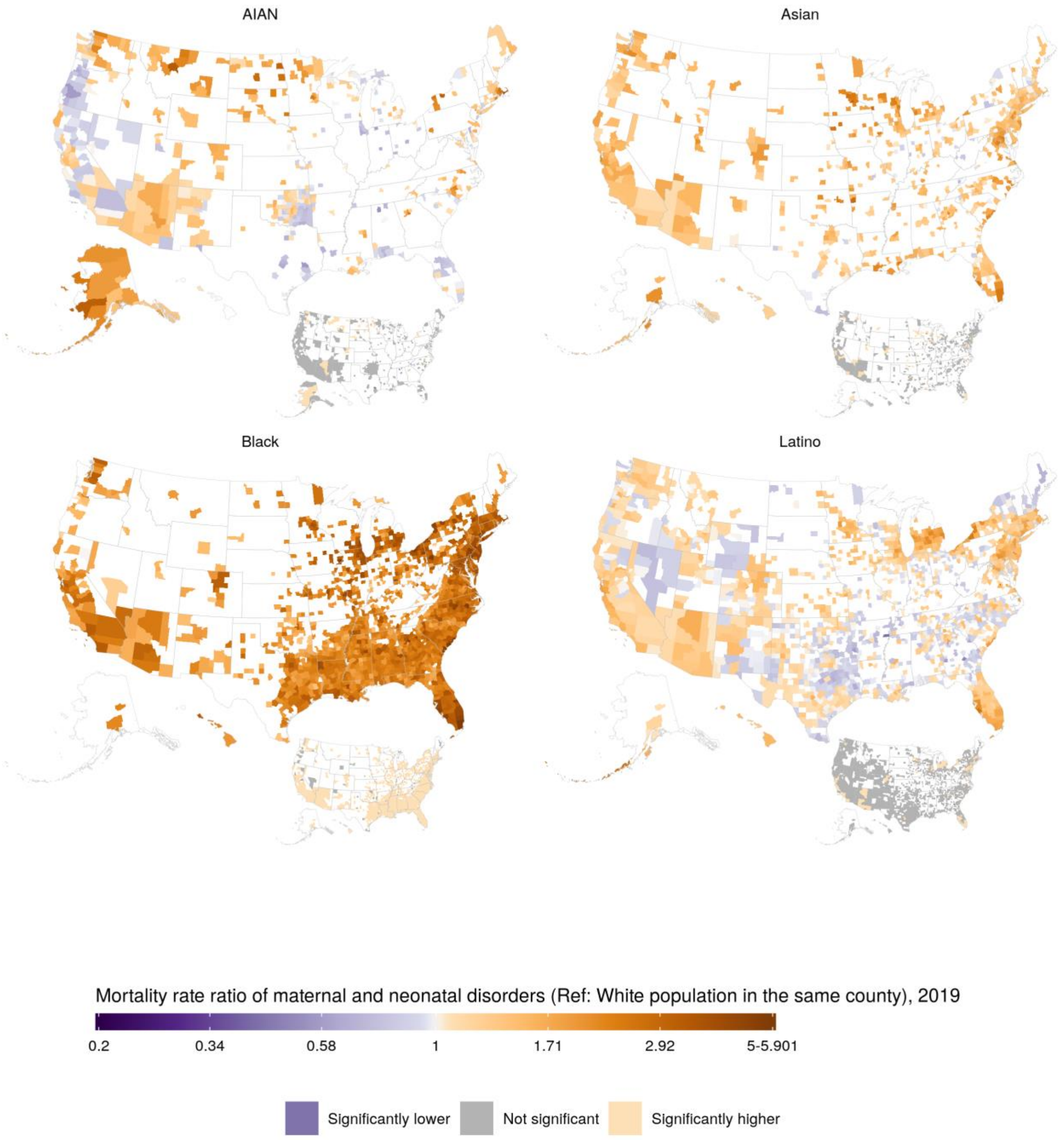
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 22: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, maternal and neonatal disorders, 2019



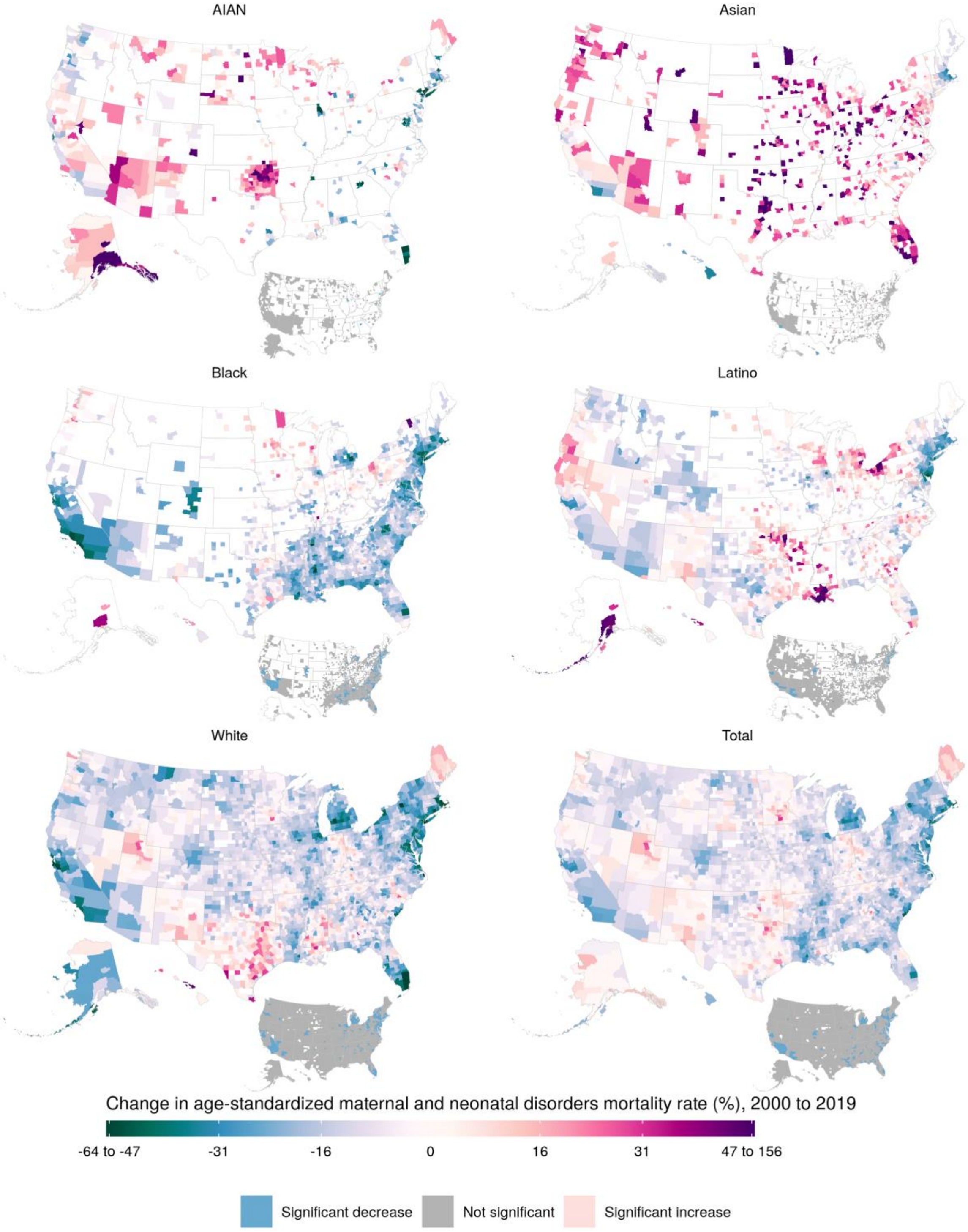
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 23: Age-standardised mortality rate ratio compared to the White population in the same county, maternal and neonatal disorders, 2019



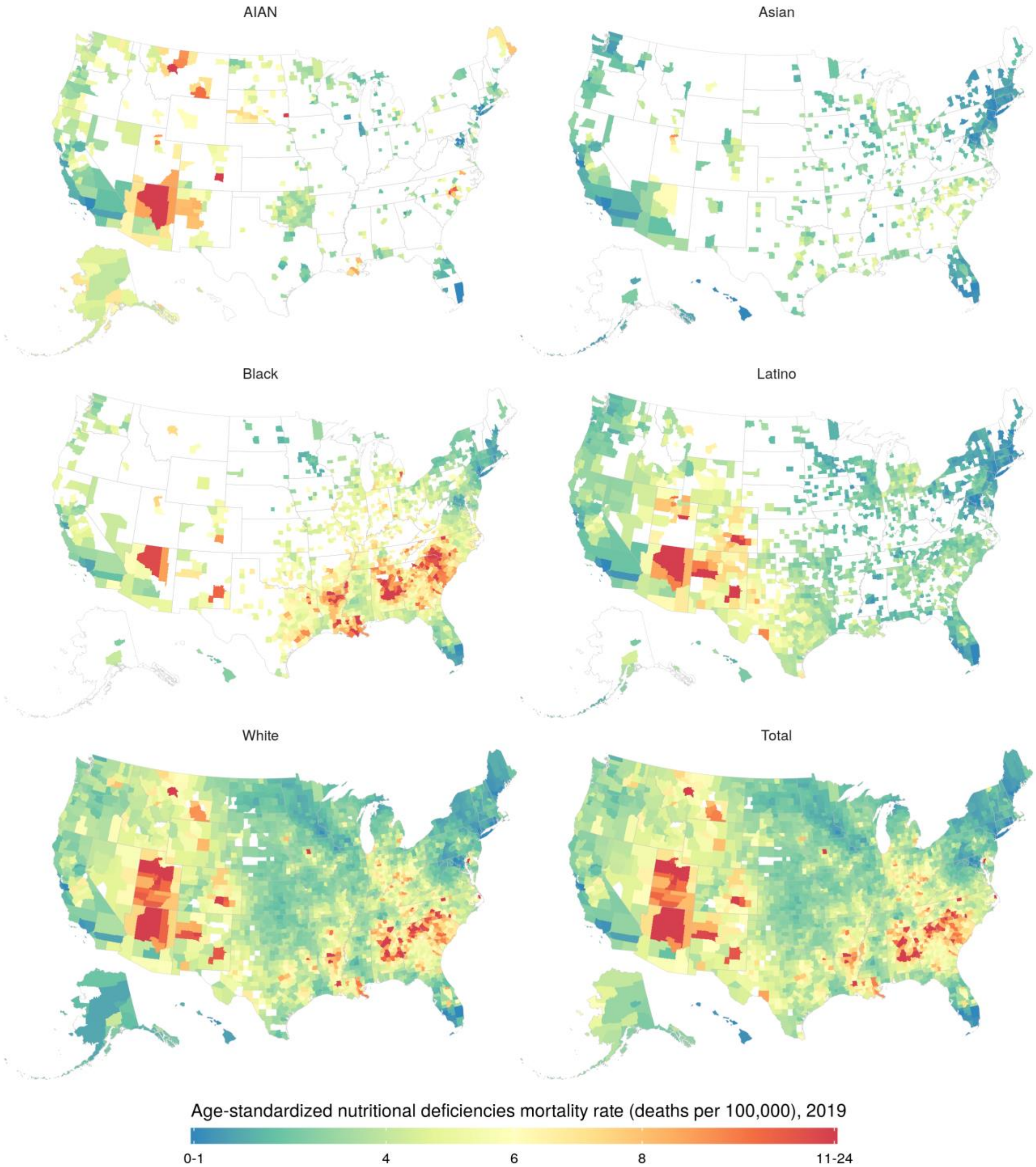
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 24: Change in age-standardised mortality rate, maternal and neonatal disorders, 2000–2019



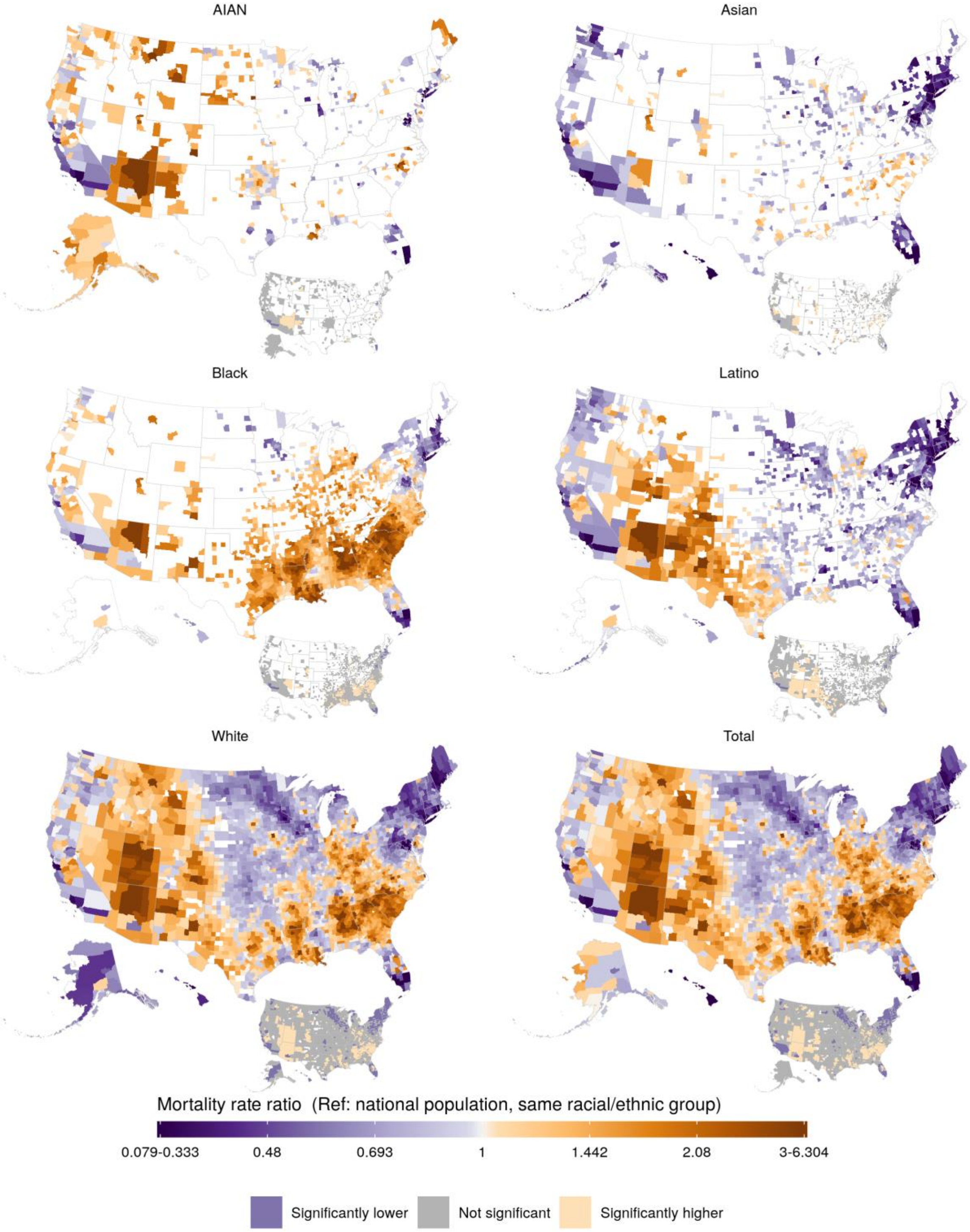
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 25: Age-standardised mortality rate, nutritional deficiencies, 2019



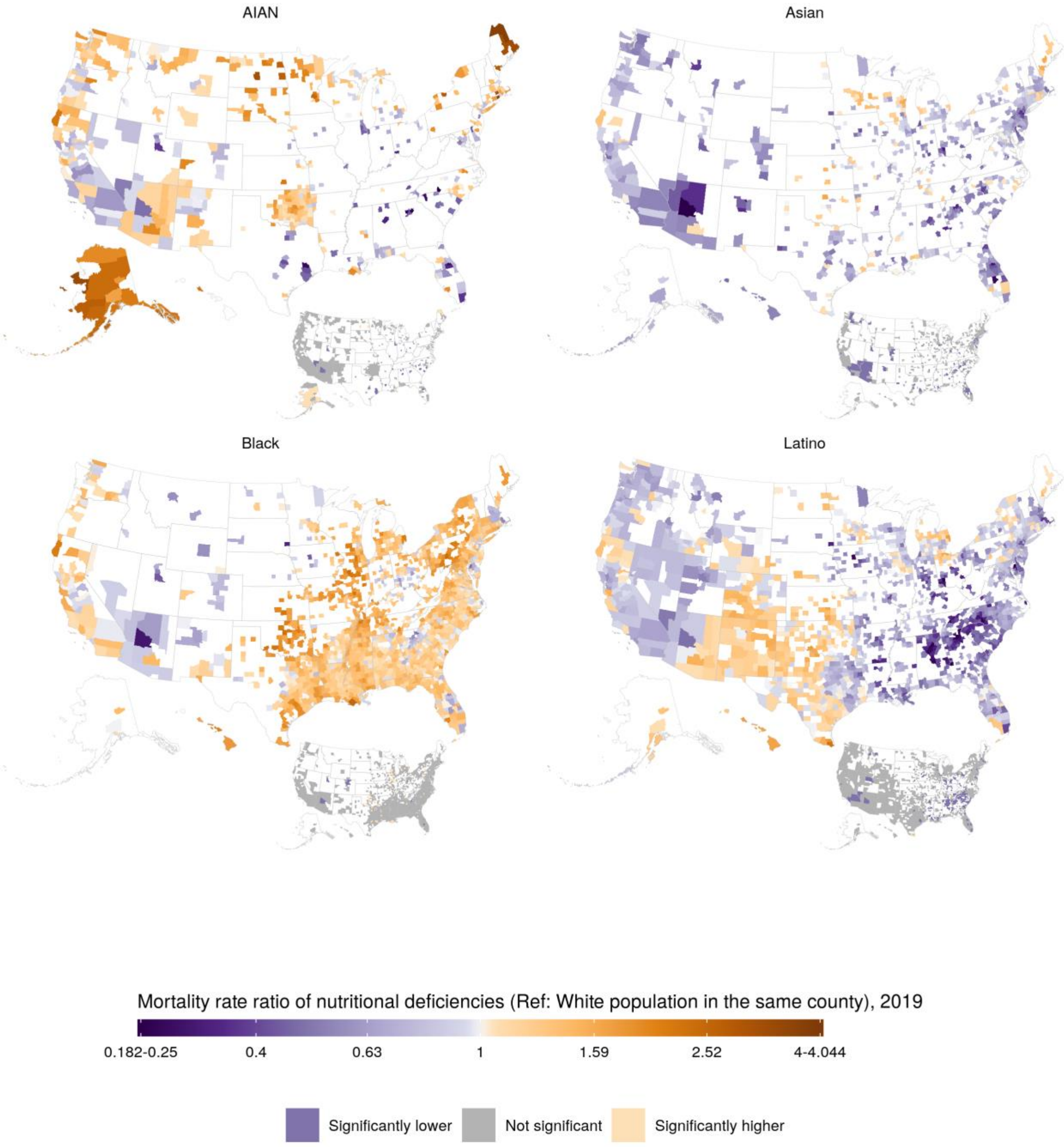
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 26: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, nutritional deficiencies, 2019



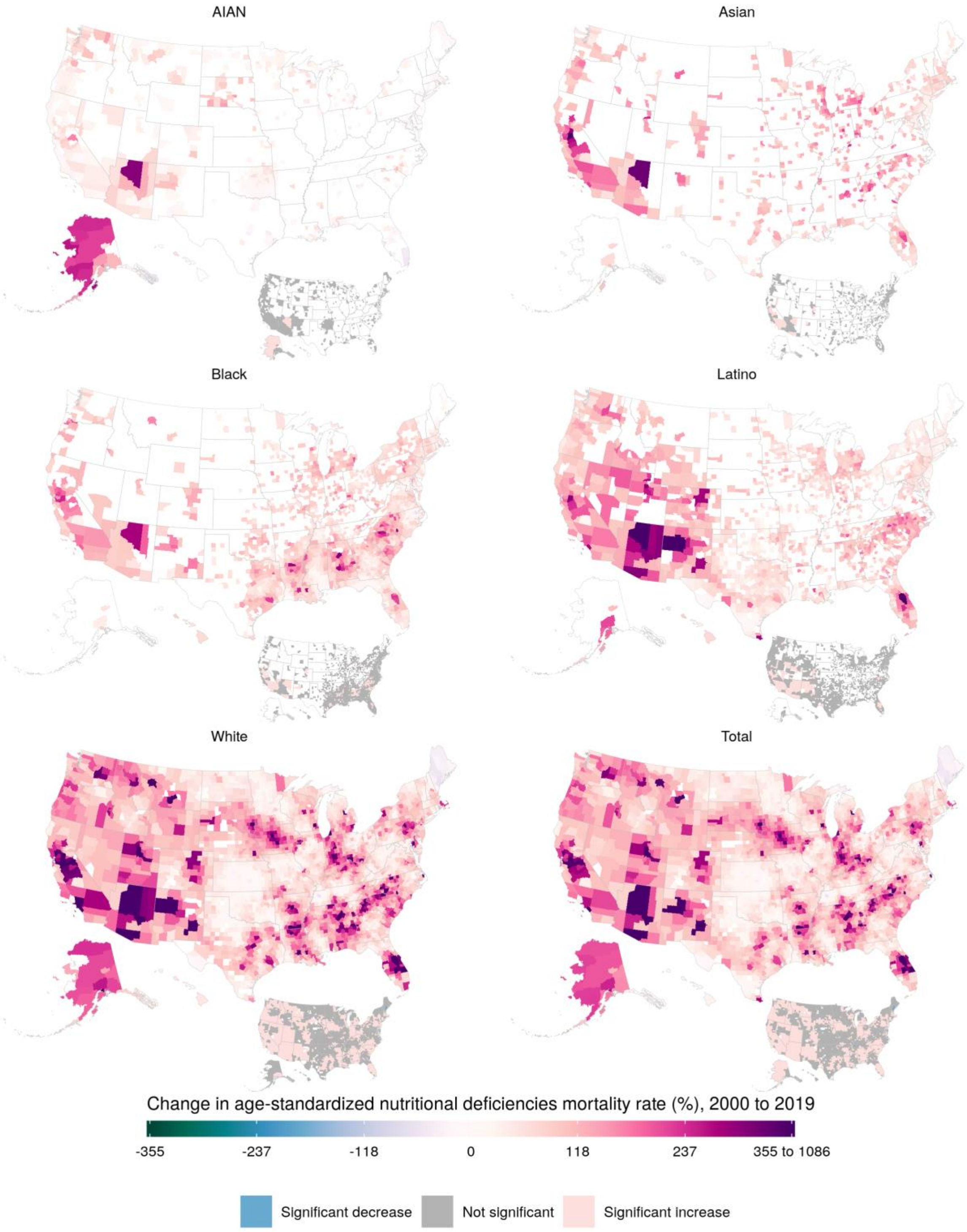
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 27: Age-standardised mortality rate ratio compared to the White population in the same county, nutritional deficiencies, 2019



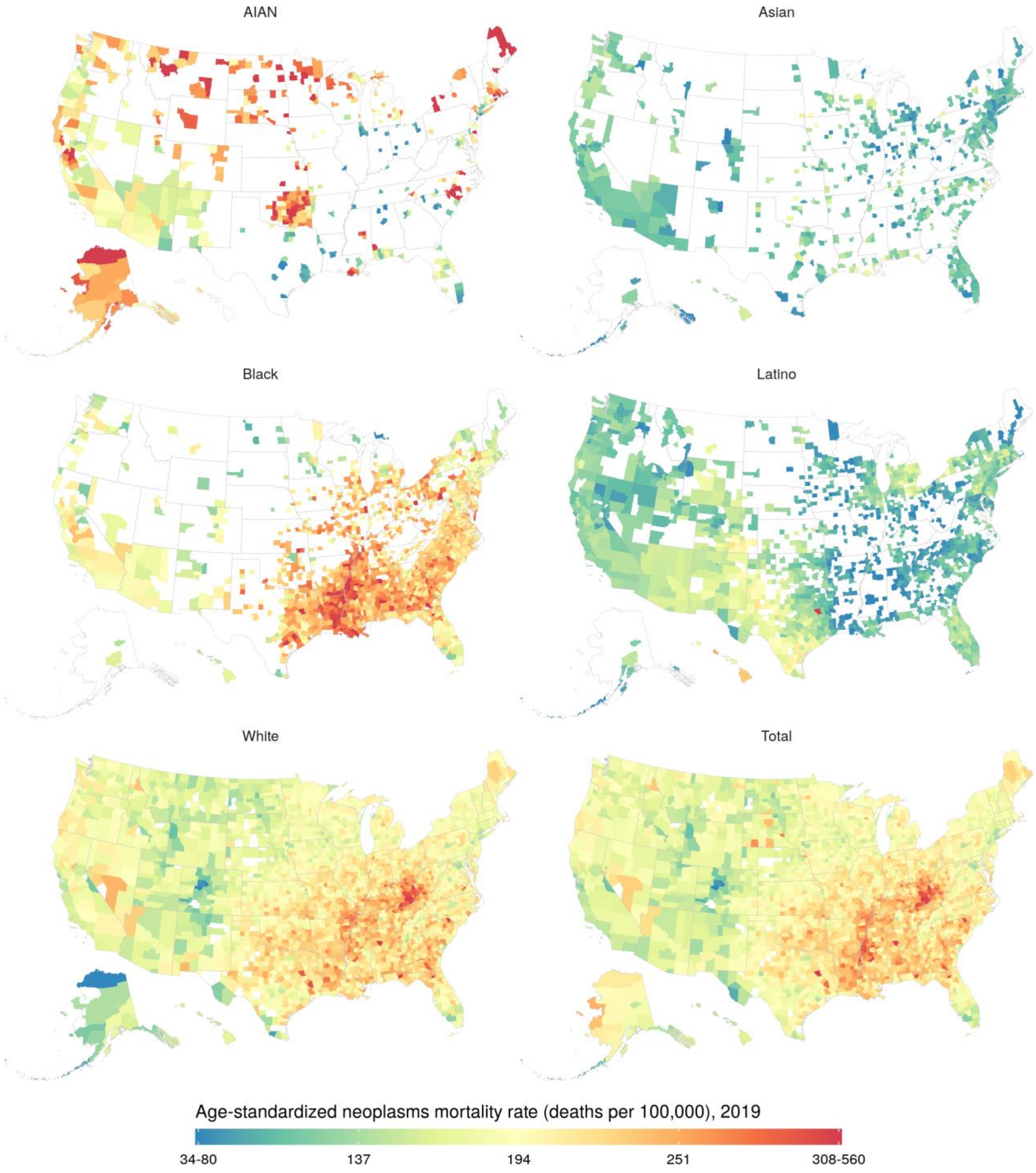
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 28: Change in age-standardised mortality rate, nutritional deficiencies, 2000–2019



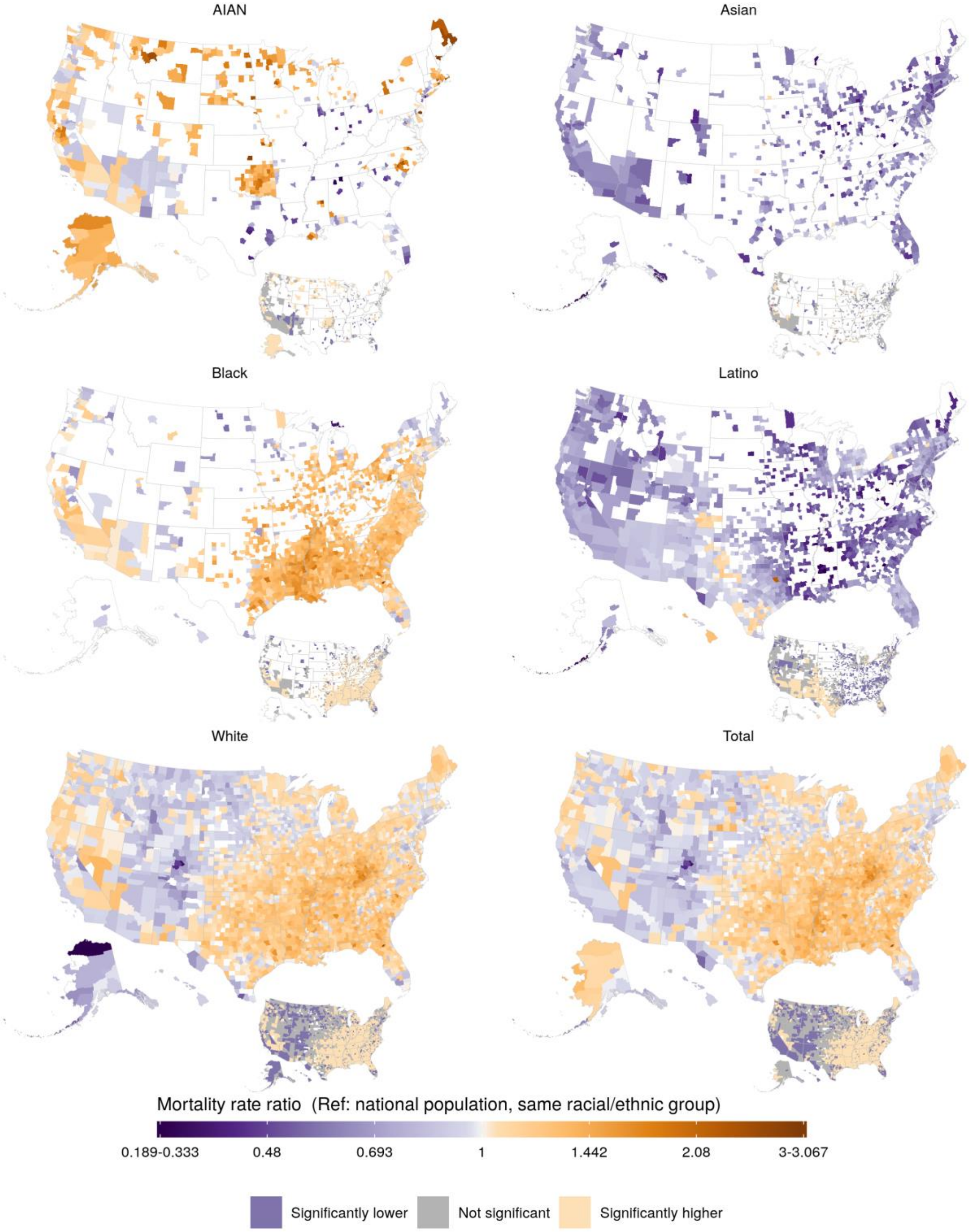
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 29: Age-standardised mortality rate, neoplasms, 2019



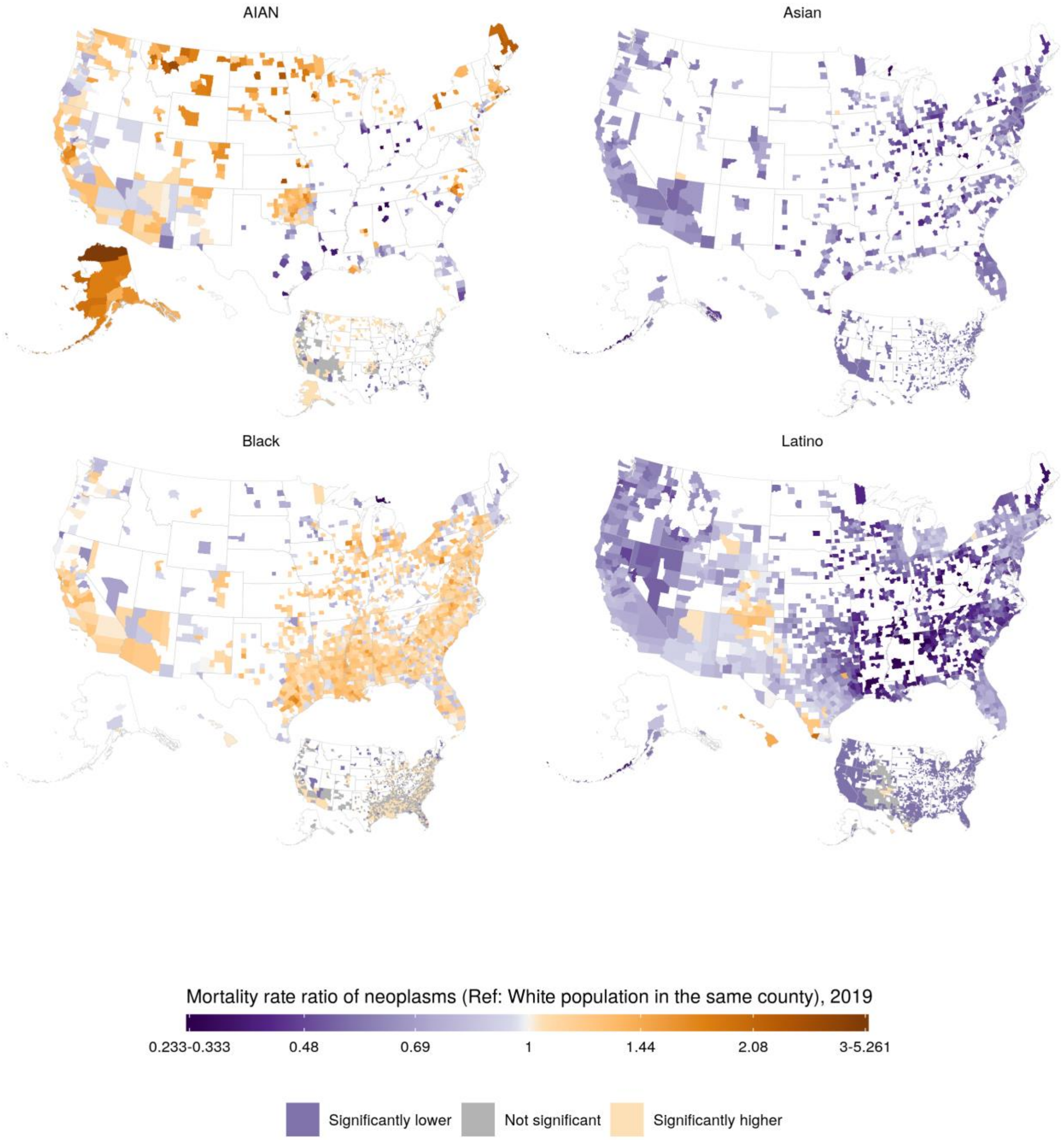
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 30: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, neoplasms, 2019



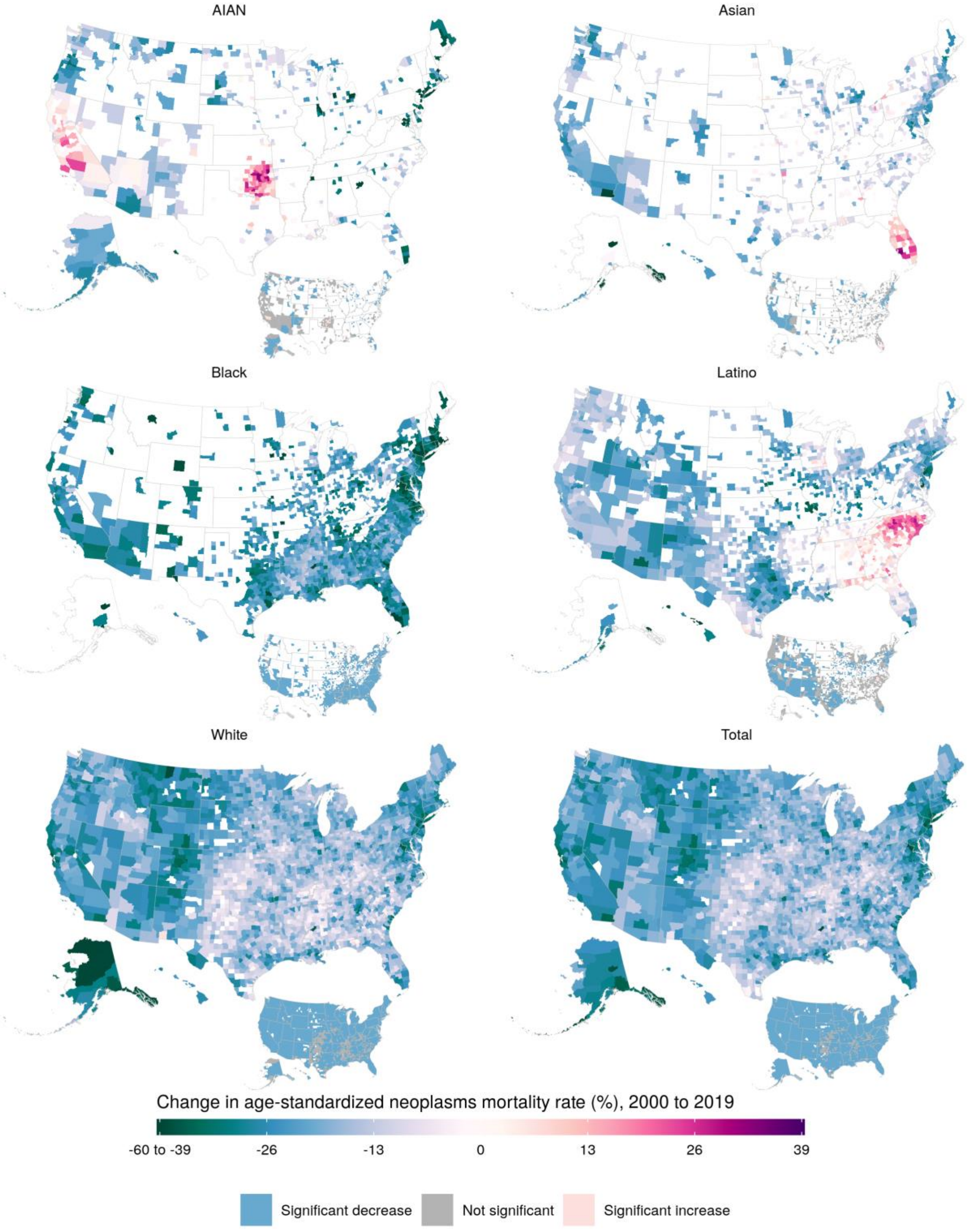
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 31: Age-standardised mortality rate ratio compared to the White population in the same county, neoplasms, 2019



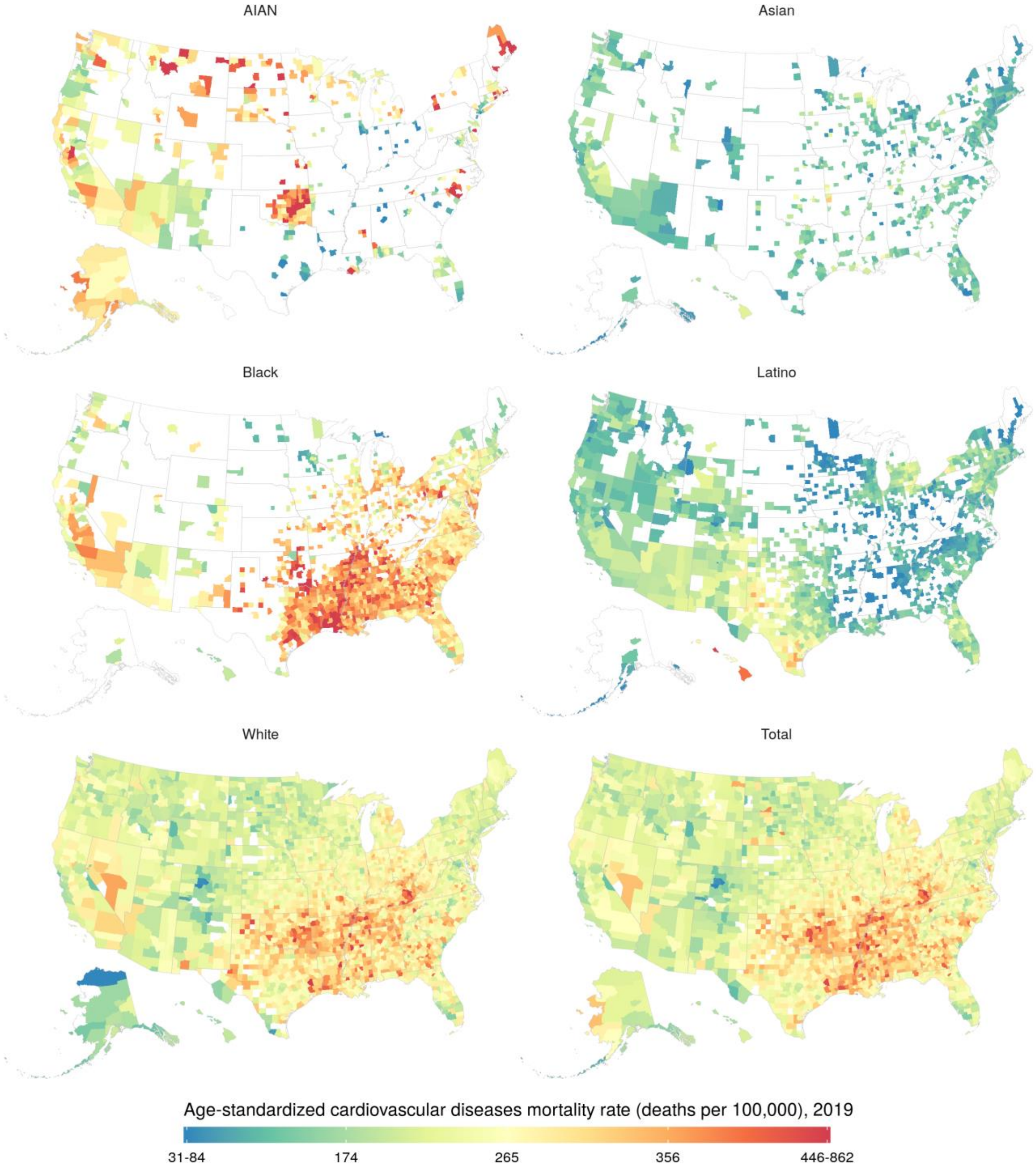
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 32: Change in age-standardised mortality rate, neoplasms, 2000–2019



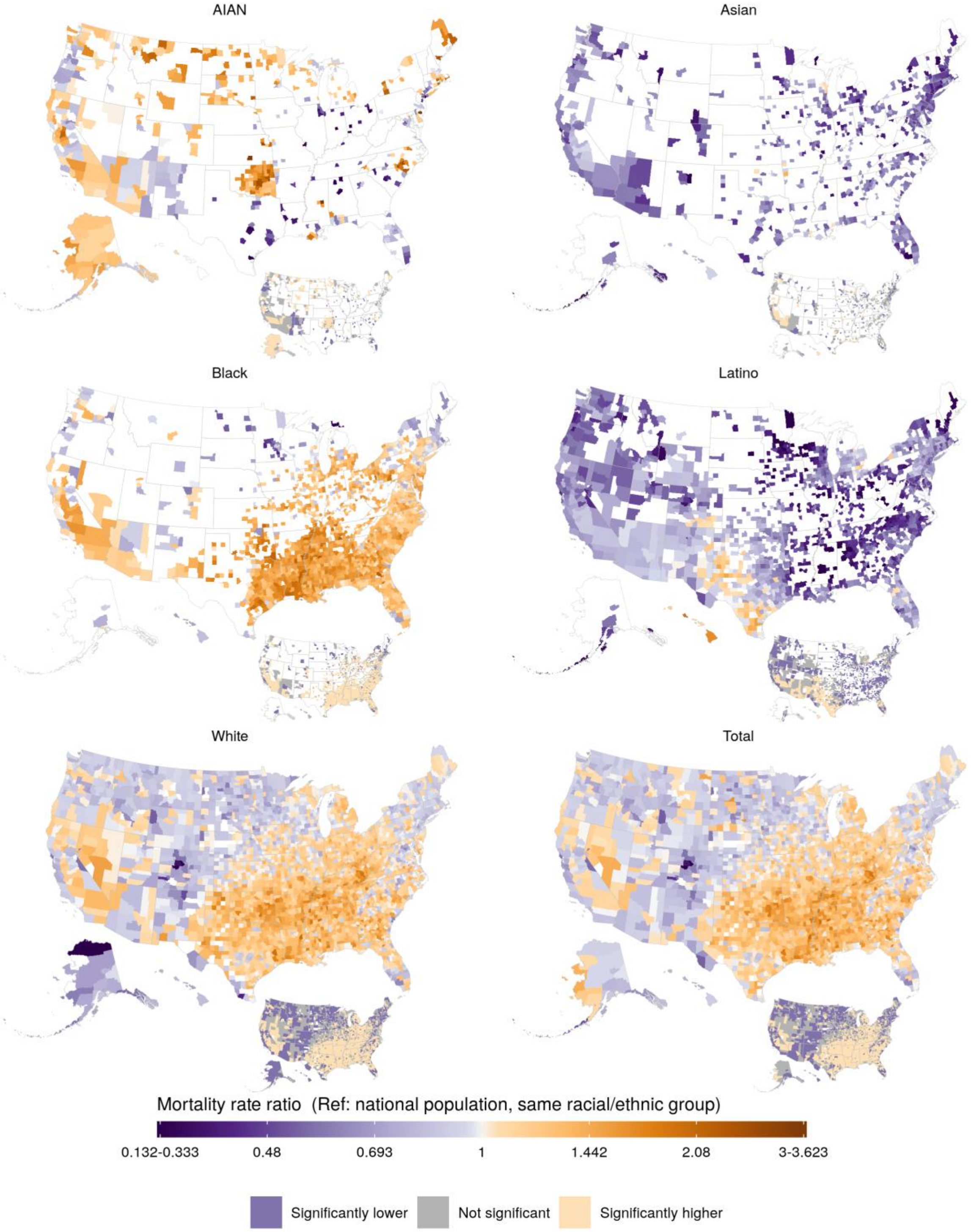
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 33: Age-standardised mortality rate, cardiovascular diseases, 2019



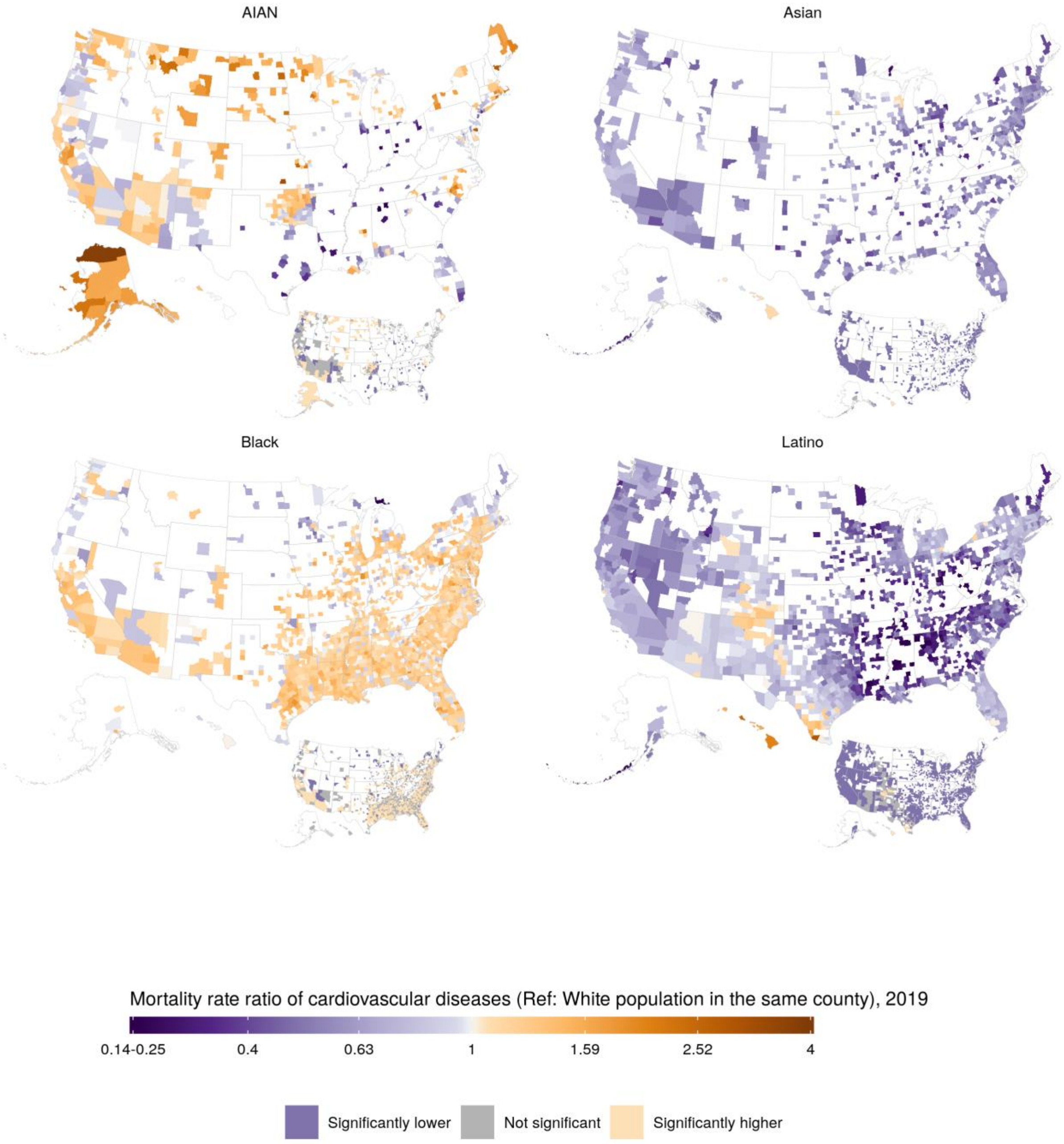
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 34: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, cardiovascular diseases, 2019



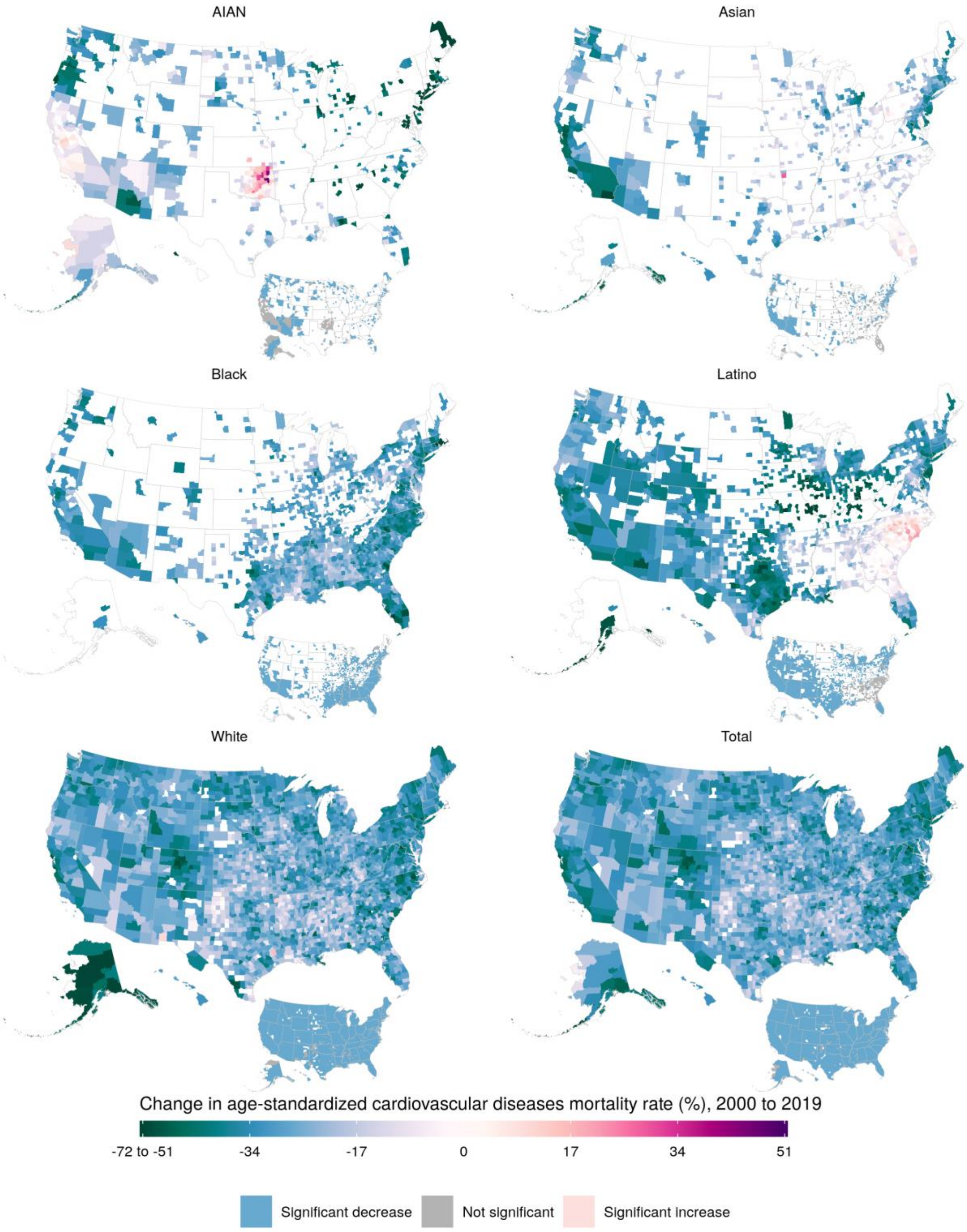
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 35: Age-standardised mortality rate ratio compared to the White population in the same county, cardiovascular diseases, 2019



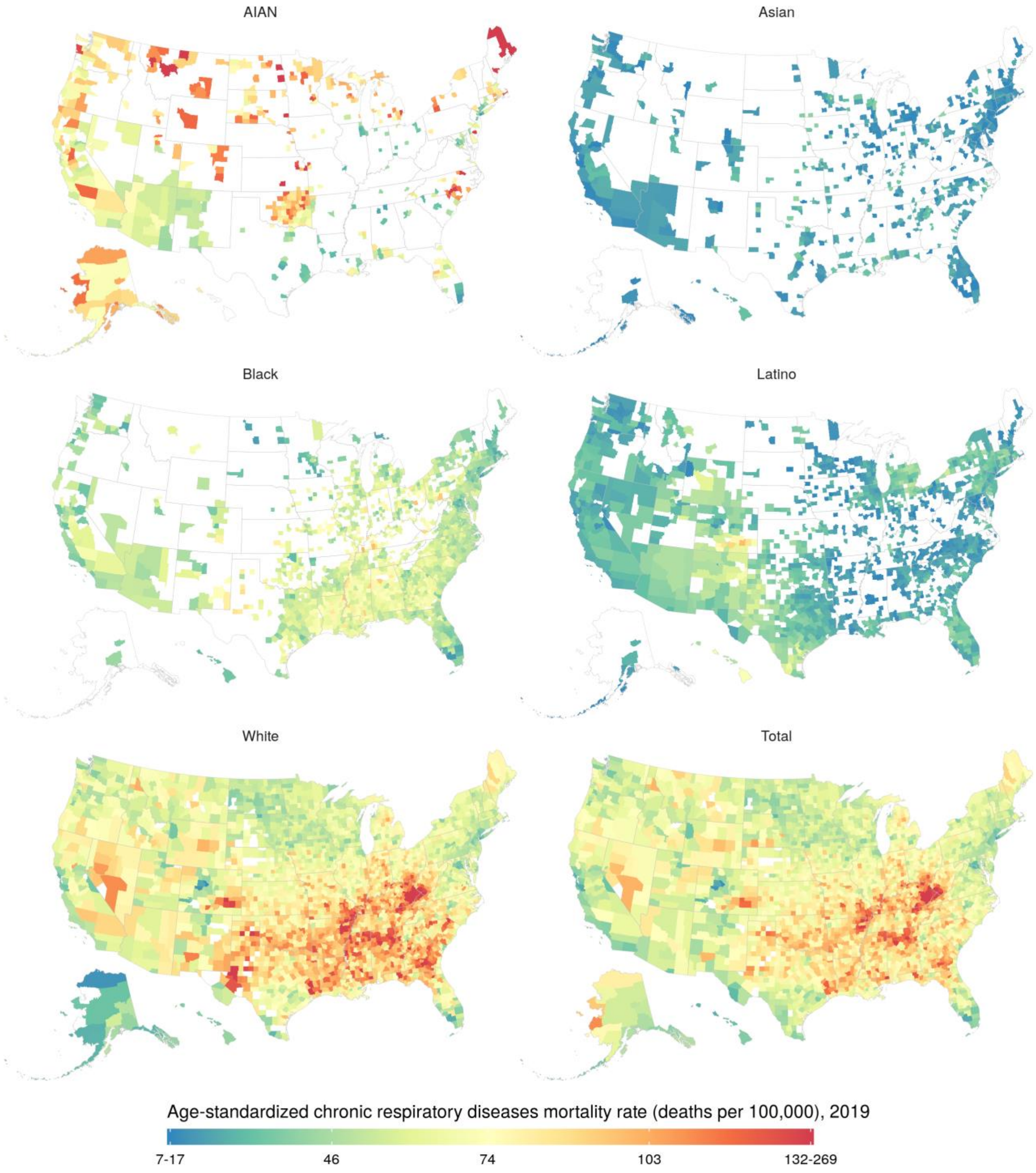
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 36: Change in age-standardised mortality rate, cardiovascular diseases, 2000–2019



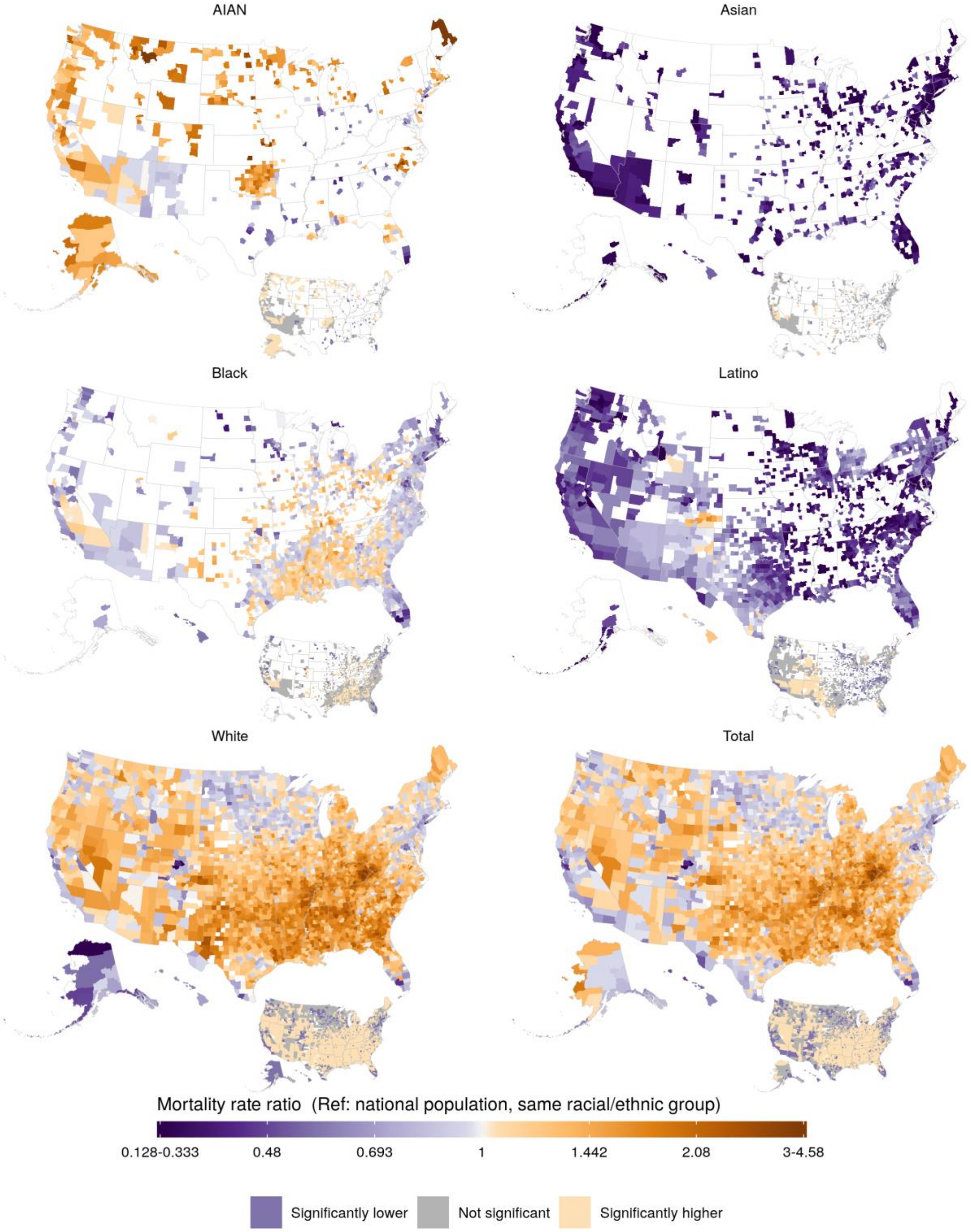
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 37: Age-standardised mortality rate, chronic respiratory diseases, 2019



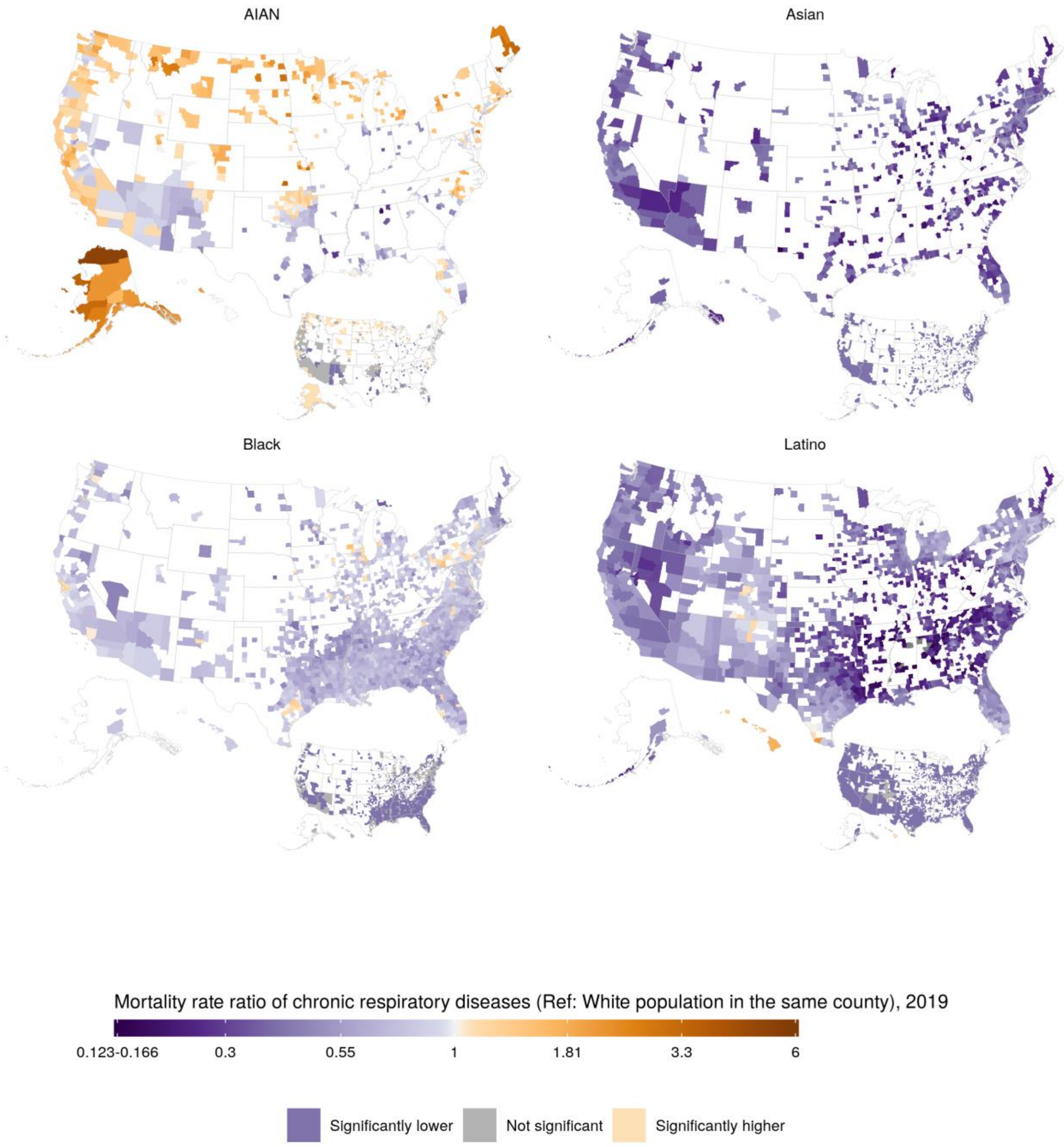
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 38: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, chronic respiratory diseases, 2019



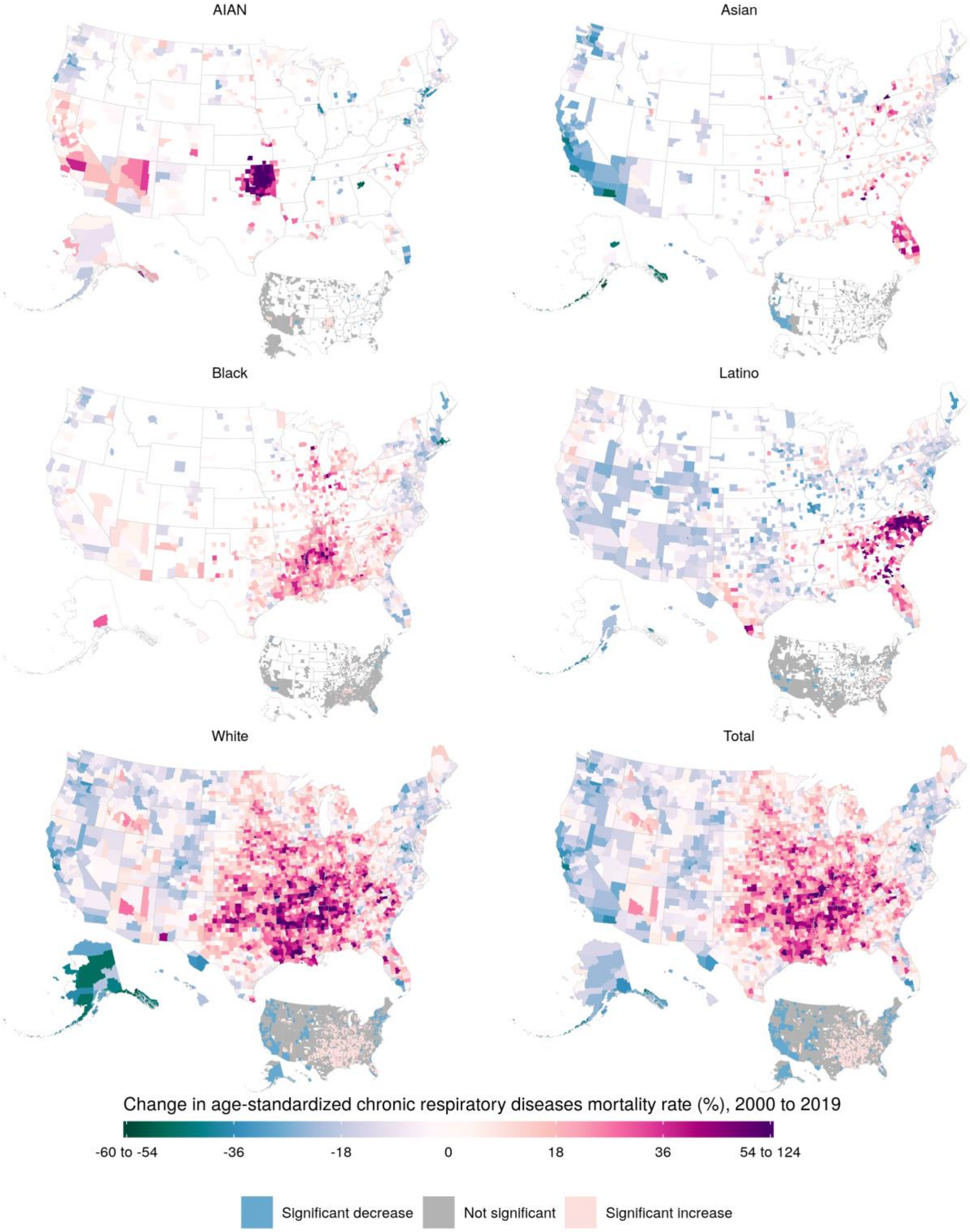
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 39: Age-standardised mortality rate ratio compared to the White population in the same county, chronic respiratory diseases, 2019



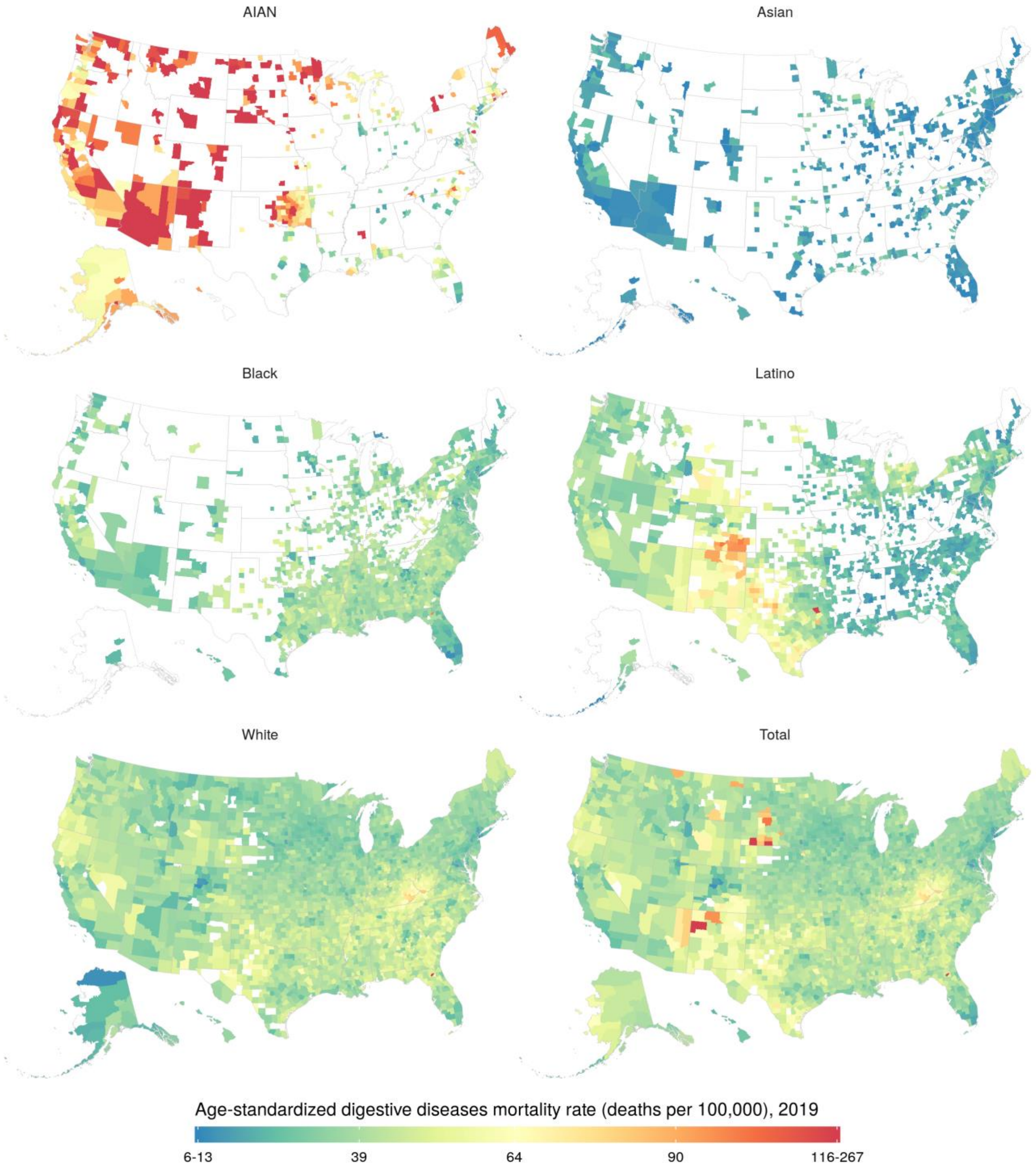
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 40: Change in age-standardised mortality rate, chronic respiratory diseases, 2000–2019



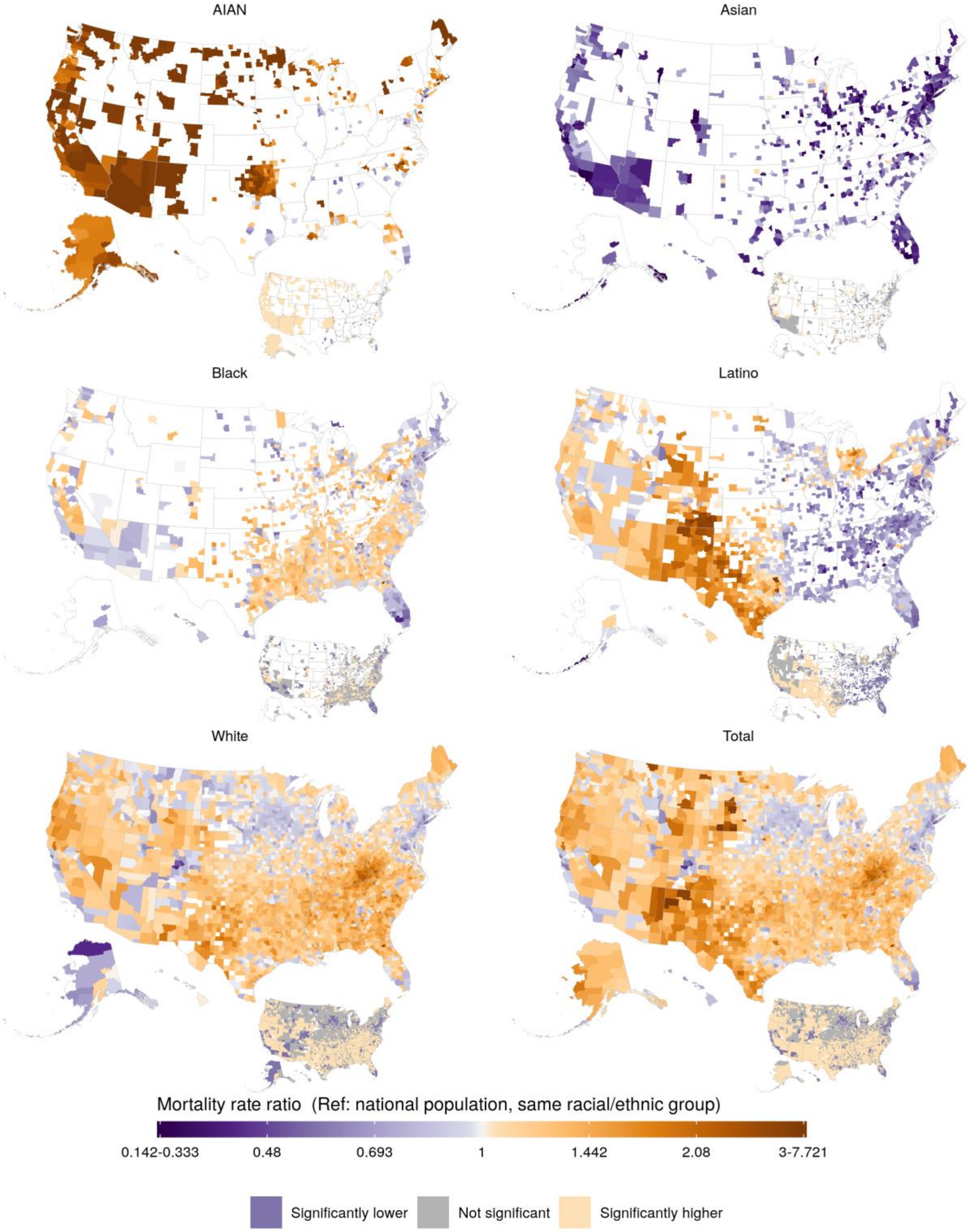
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 41: Age-standardised mortality rate, digestive diseases, 2019



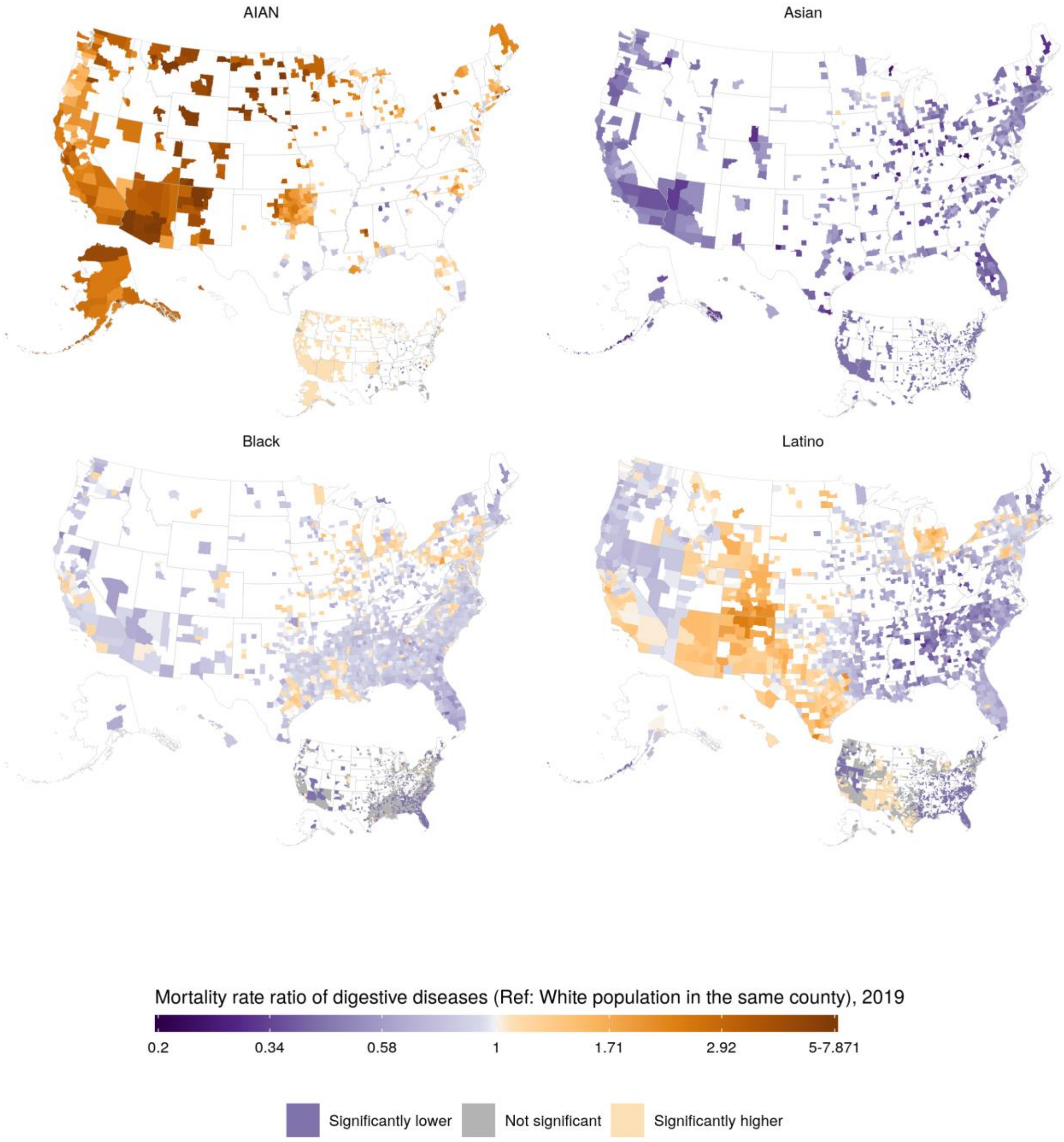
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 42: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, digestive diseases, 2019



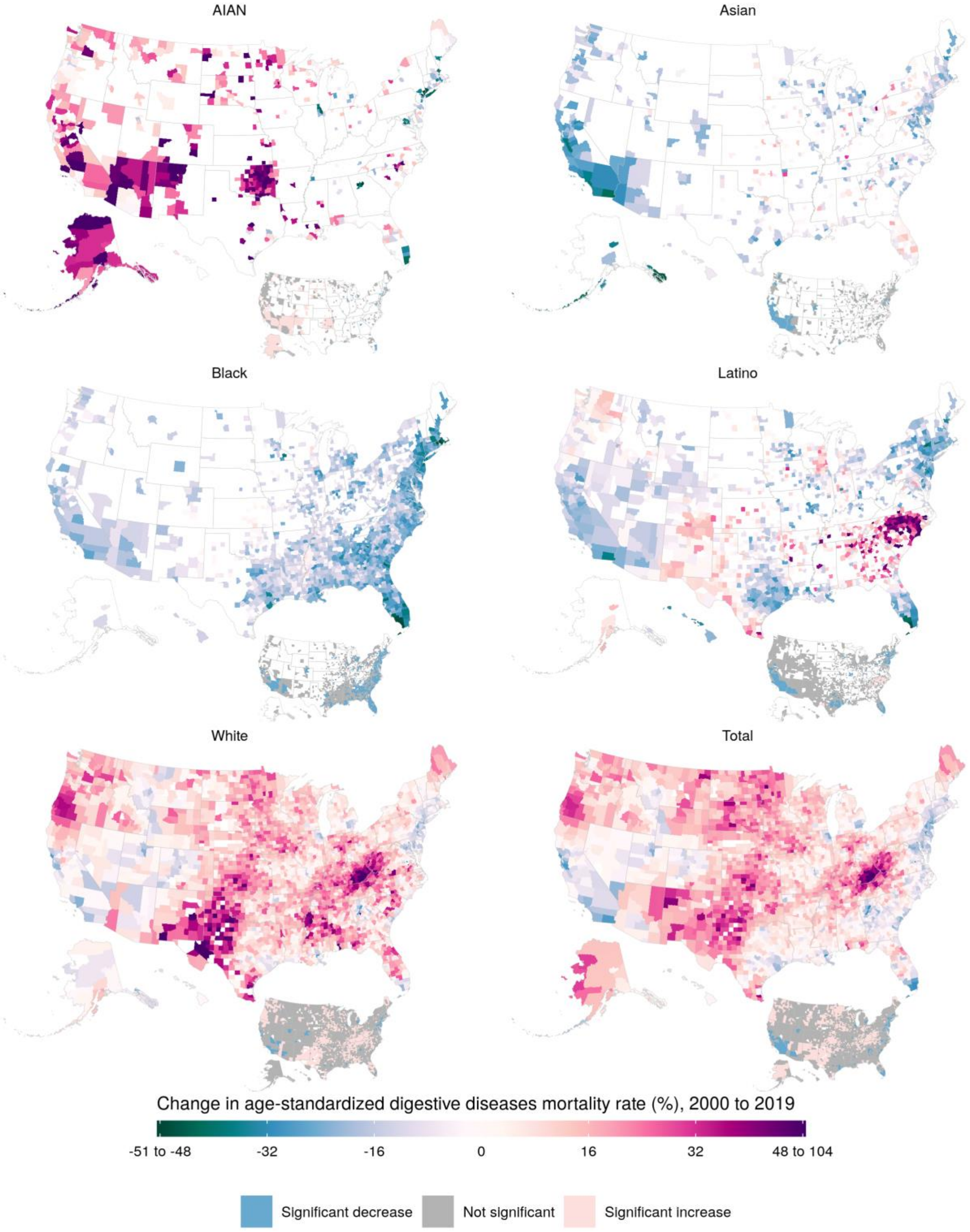
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 43: Age-standardised mortality rate ratio compared to the White population in the same county, digestive diseases, 2019



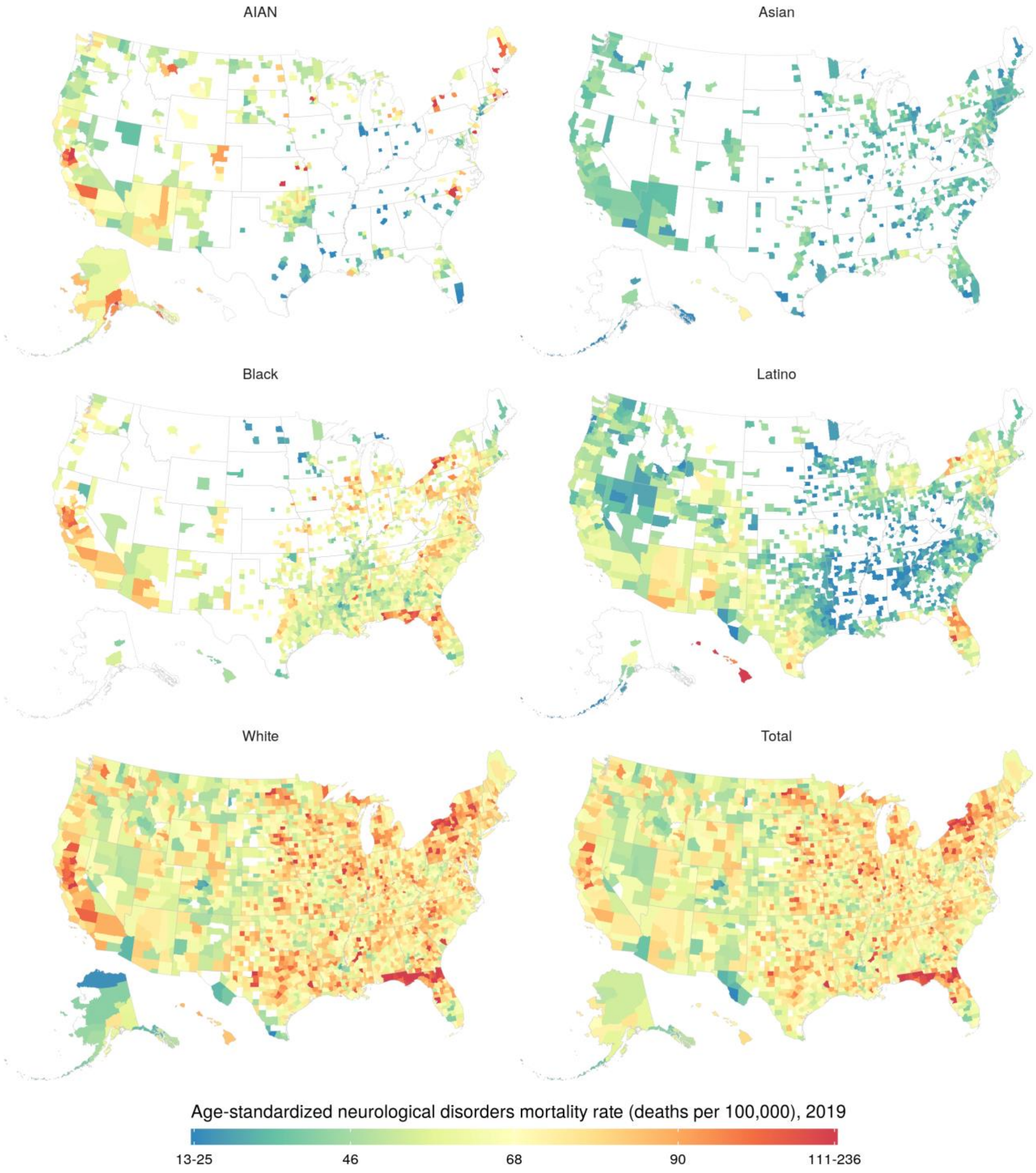
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 44: Change in age-standardised mortality rate, digestive diseases, 2000–2019



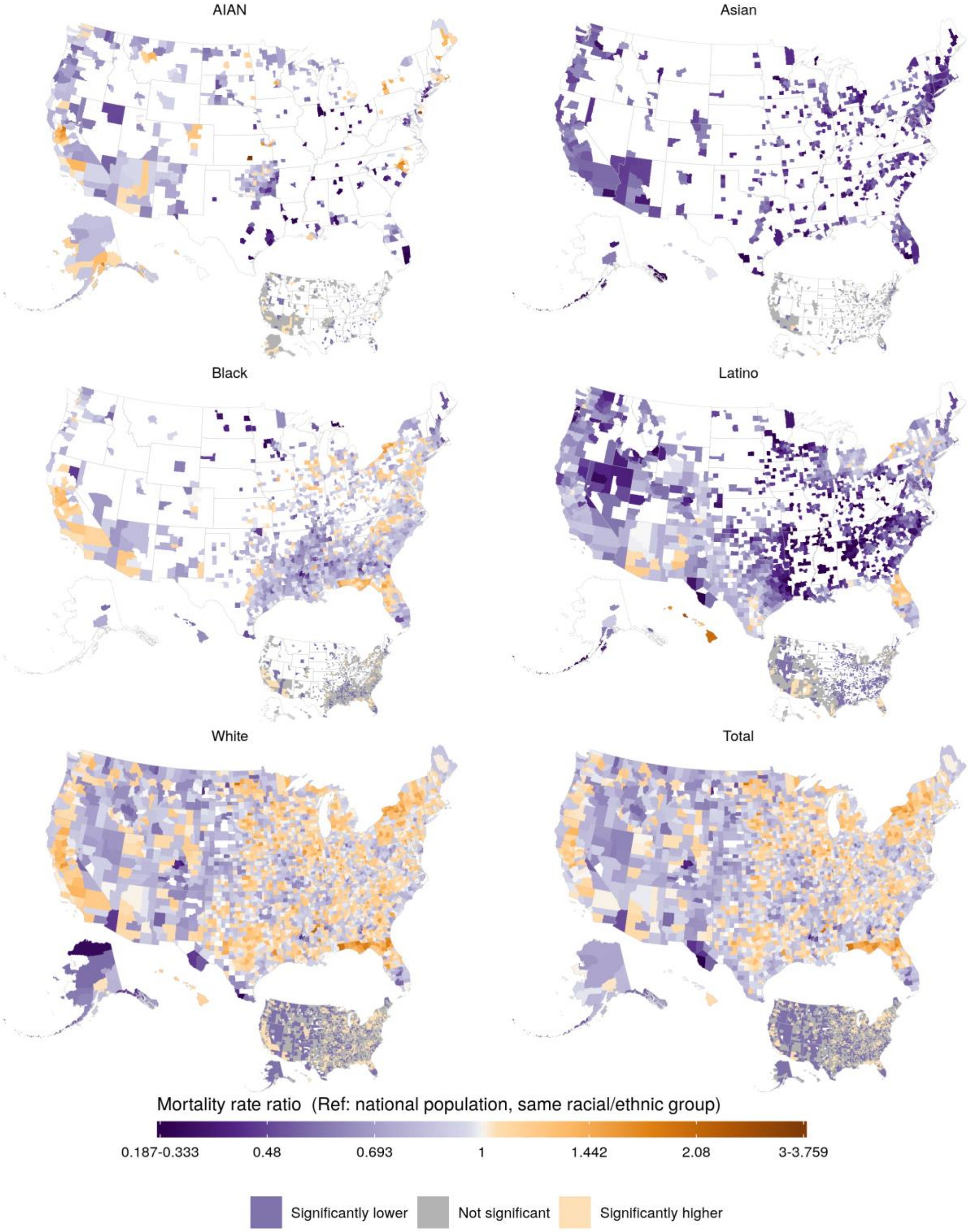
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 45: Age-standardised mortality rate, neurological disorders, 2019



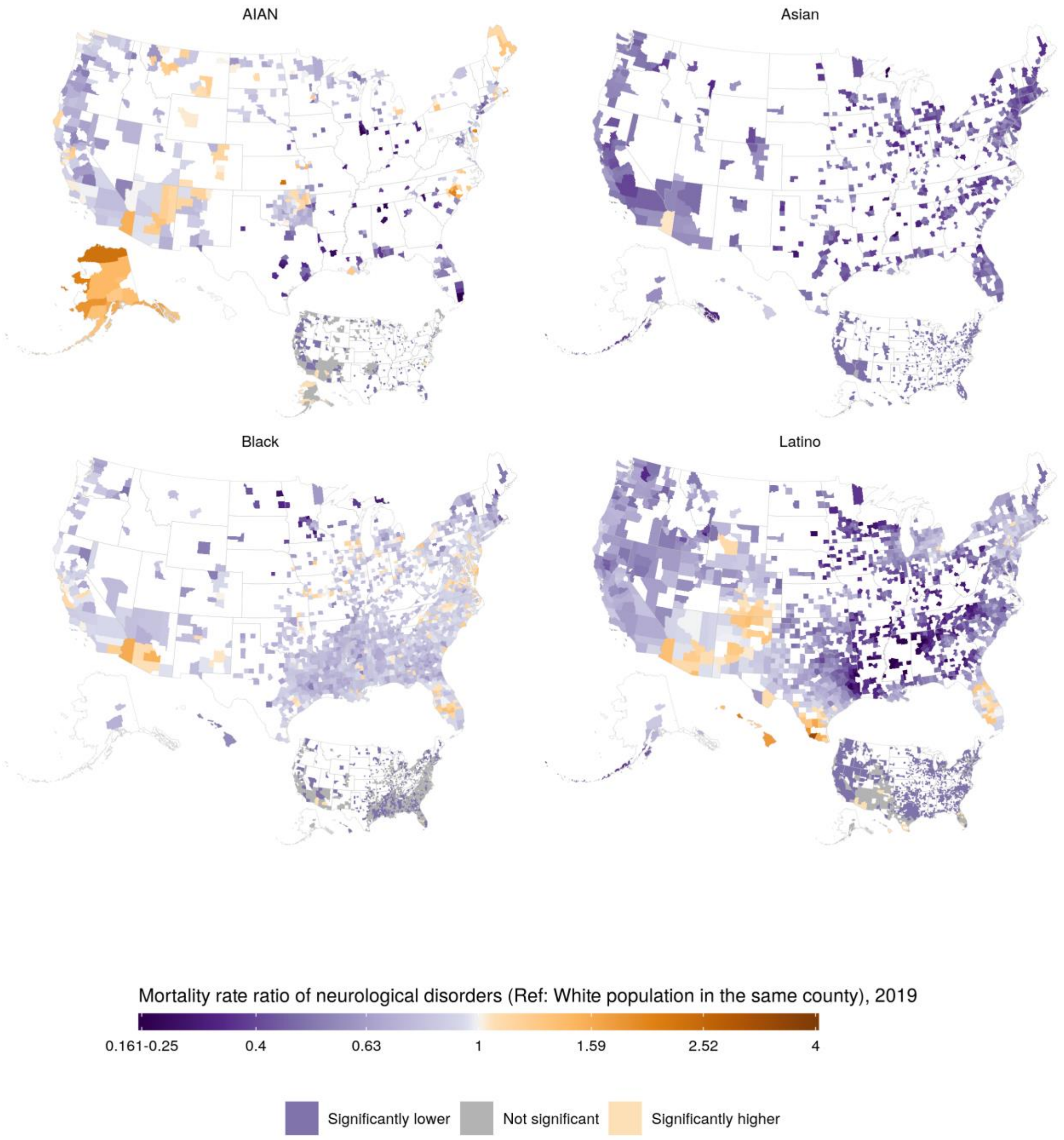
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 46: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, neurological disorders, 2019



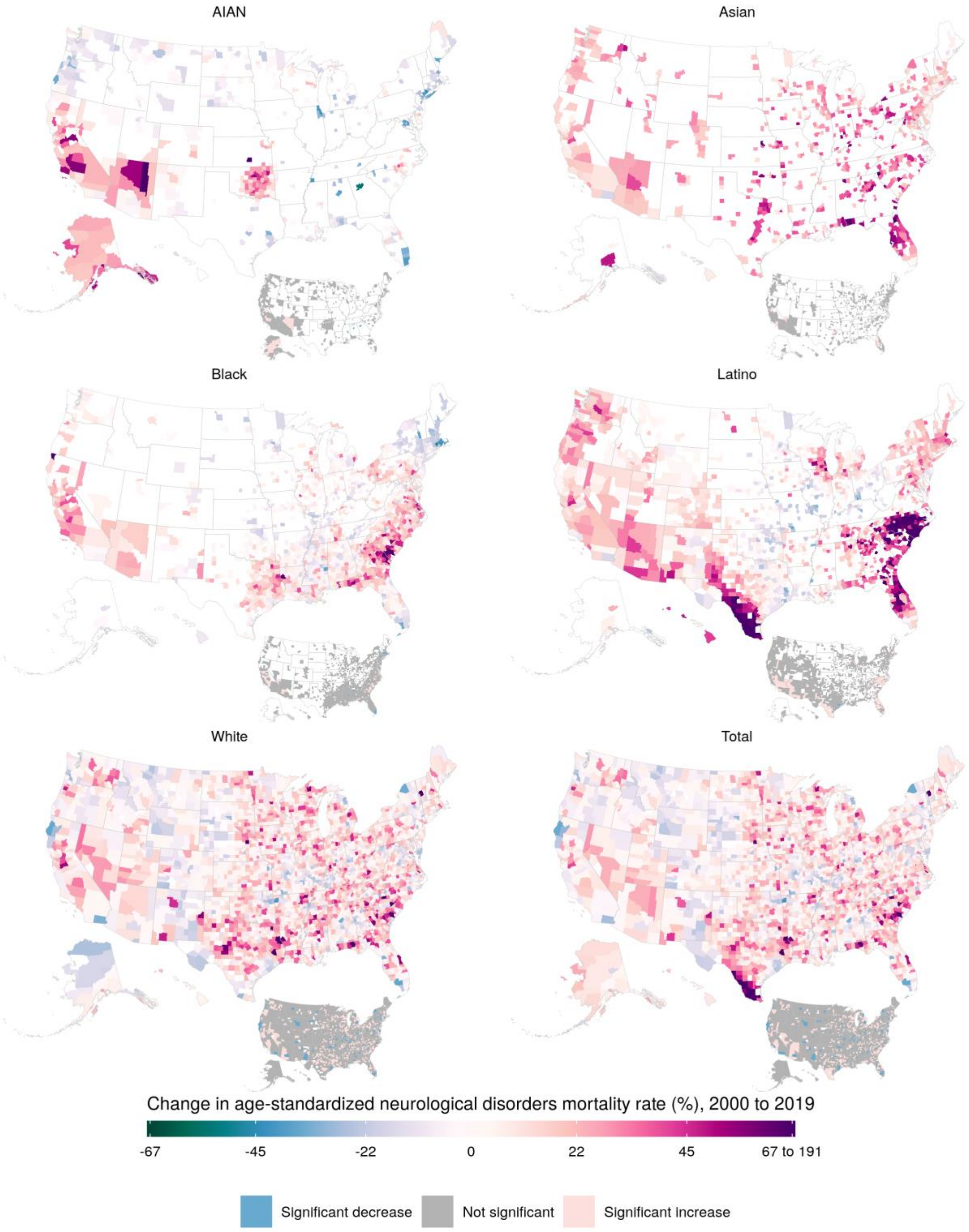
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 47: Age-standardised mortality rate ratio compared to the White population in the same county, neurological disorders, 2019



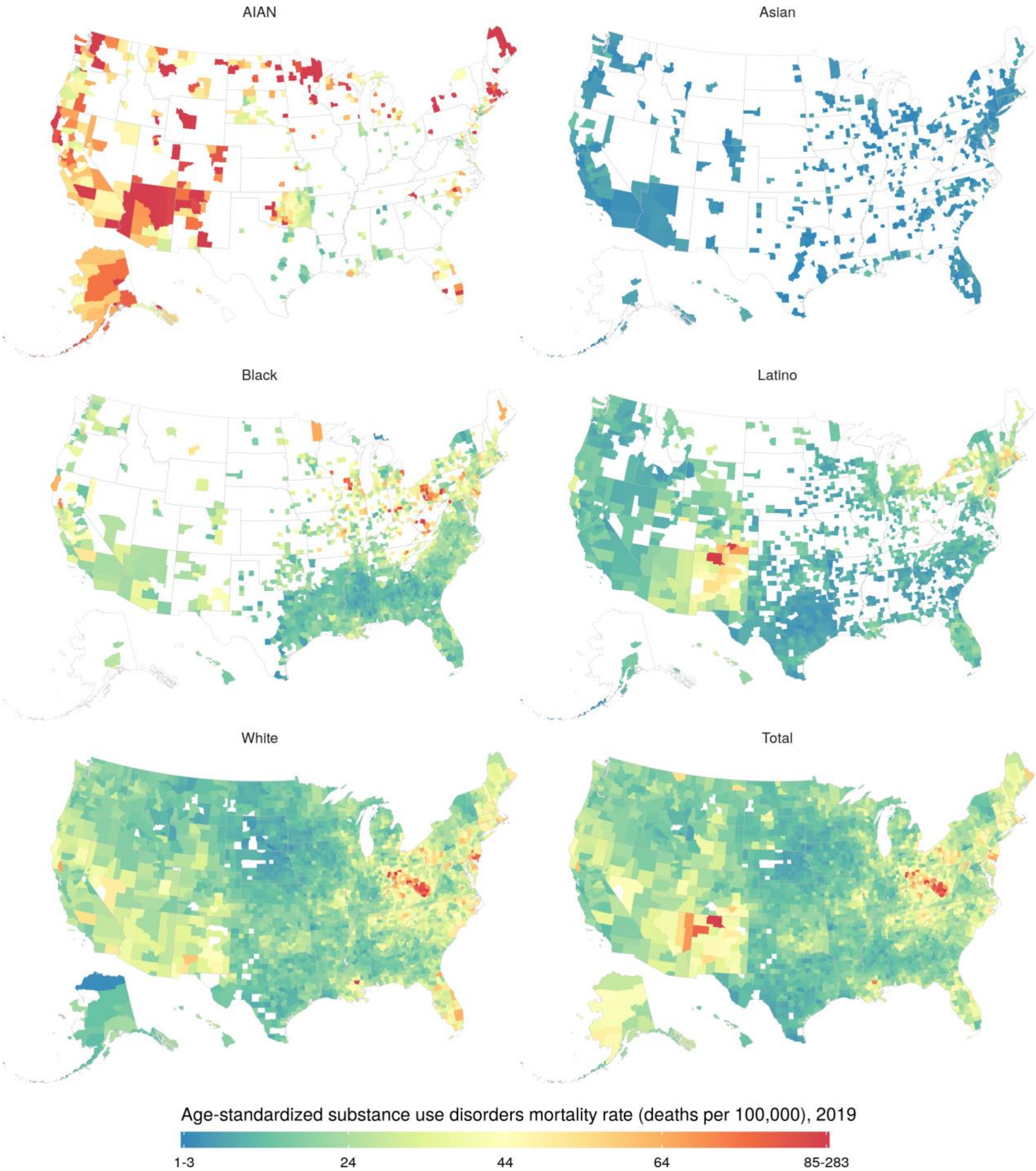
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 48: Change in age-standardised mortality rate, neurological disorders, 2000–2019



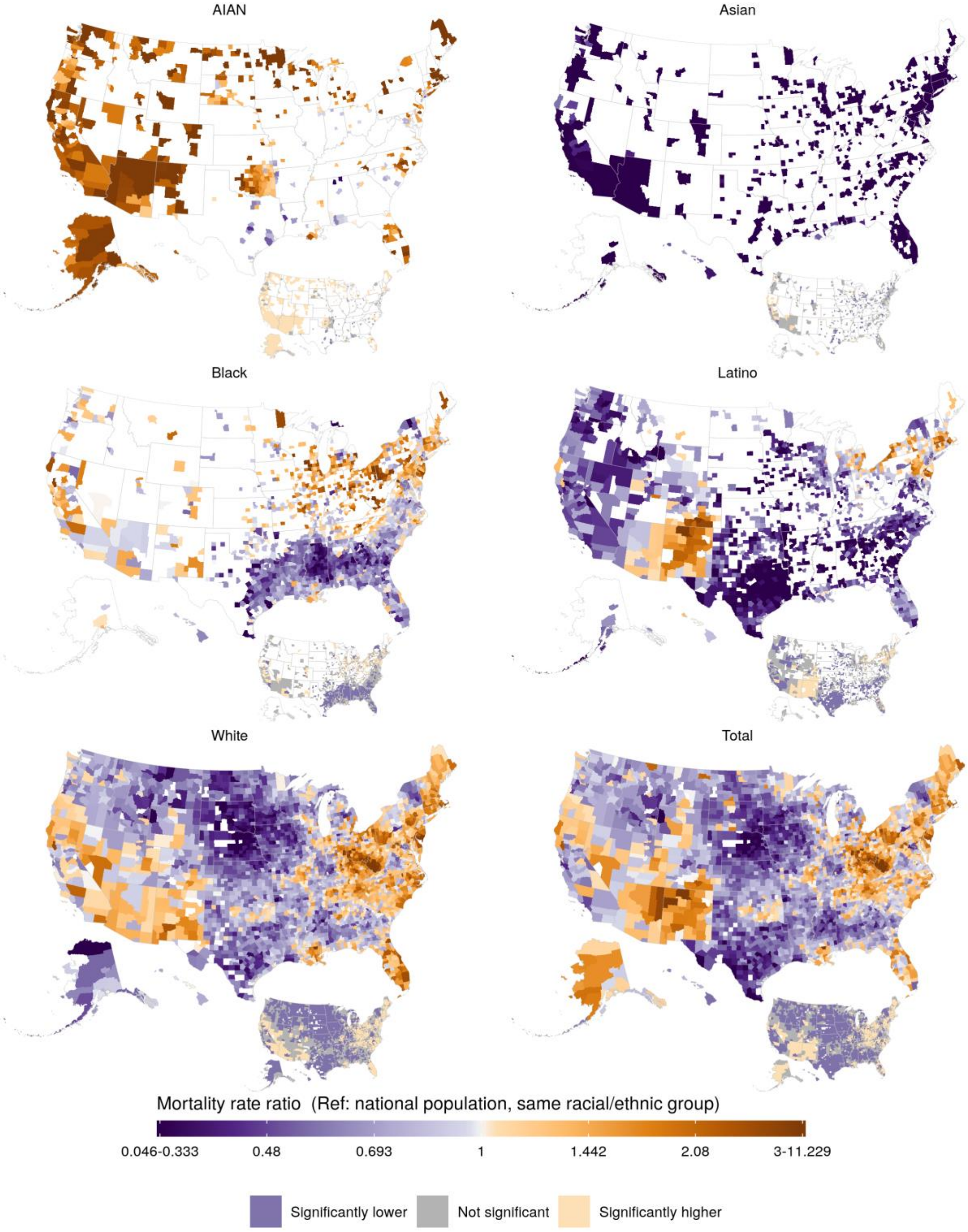
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 49: Age-standardised mortality rate, substance use disorders, 2019



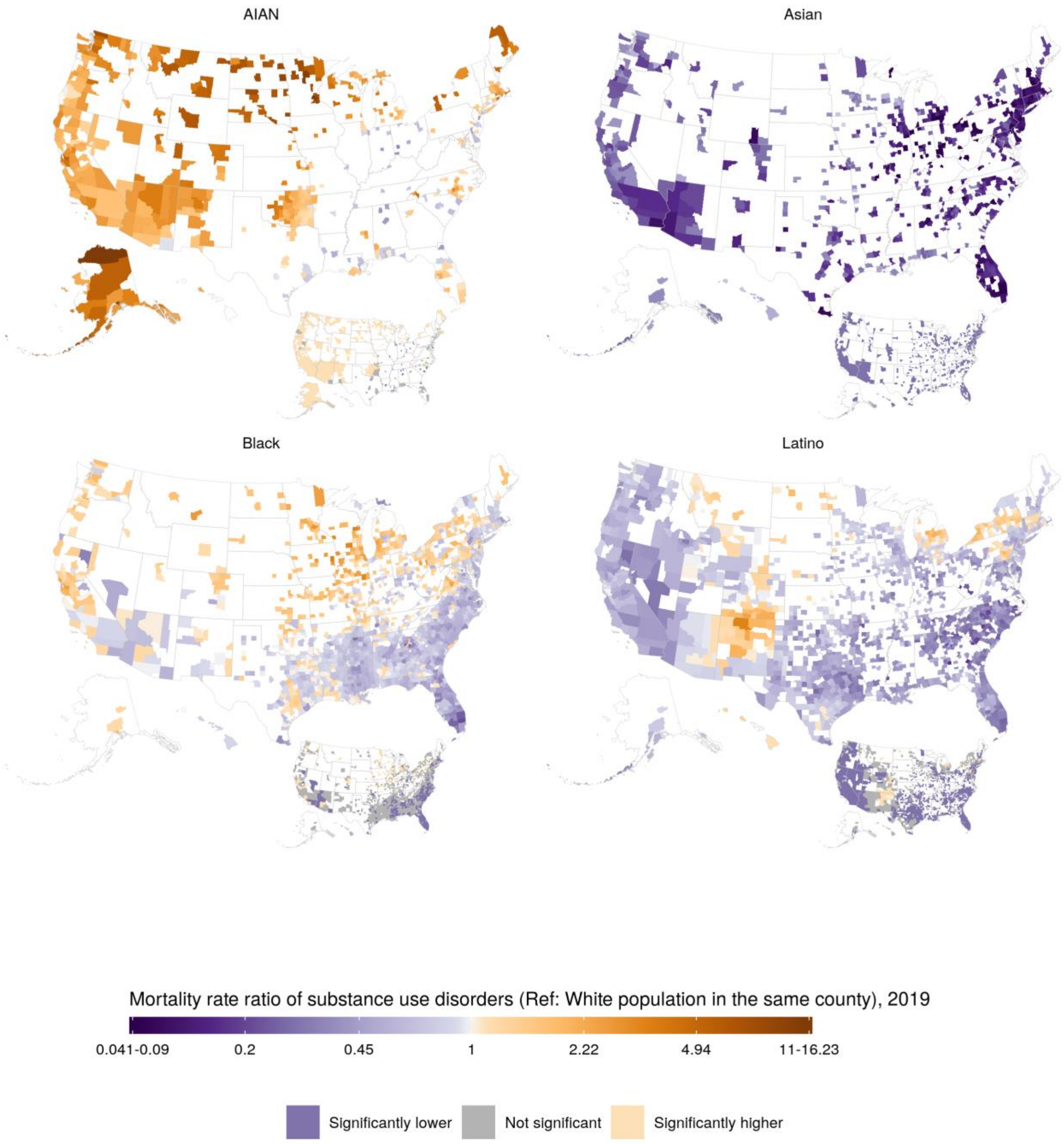
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 50: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, substance use disorders, 2019



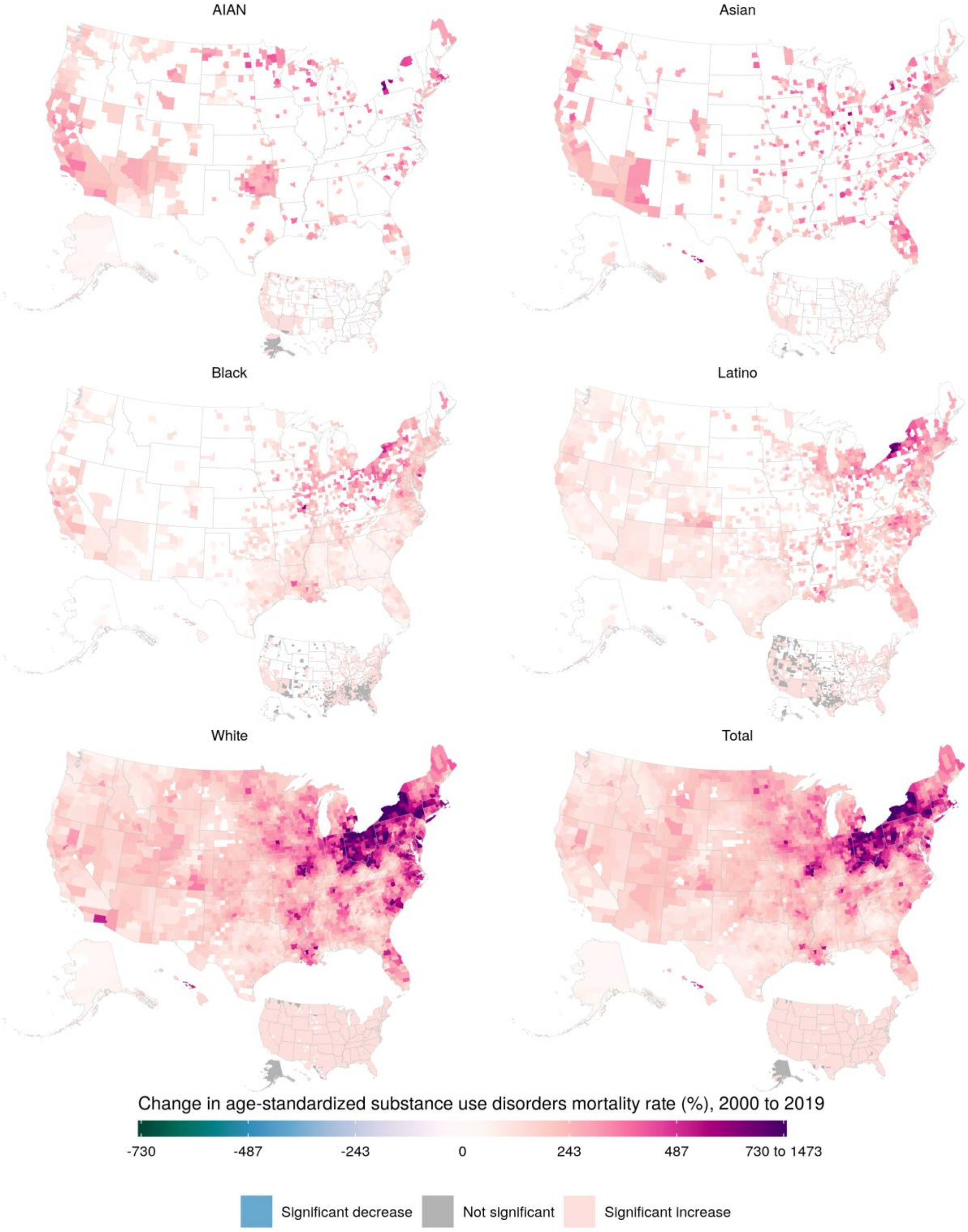
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 51: Age-standardised mortality rate ratio compared to the White population in the same county, substance use disorders, 2019



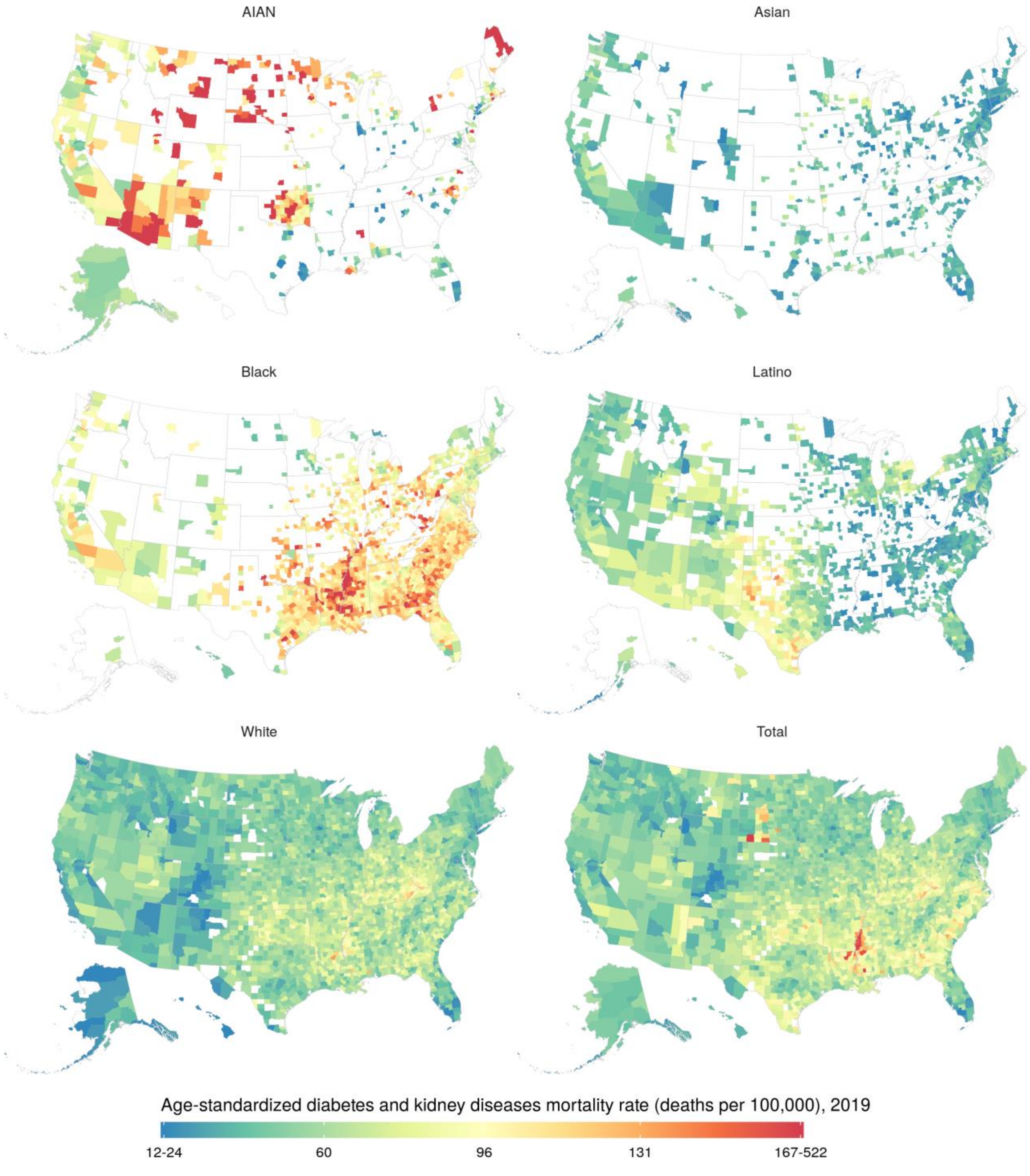
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 52: Change in age-standardised mortality rate, substance use disorders, 2000–2019



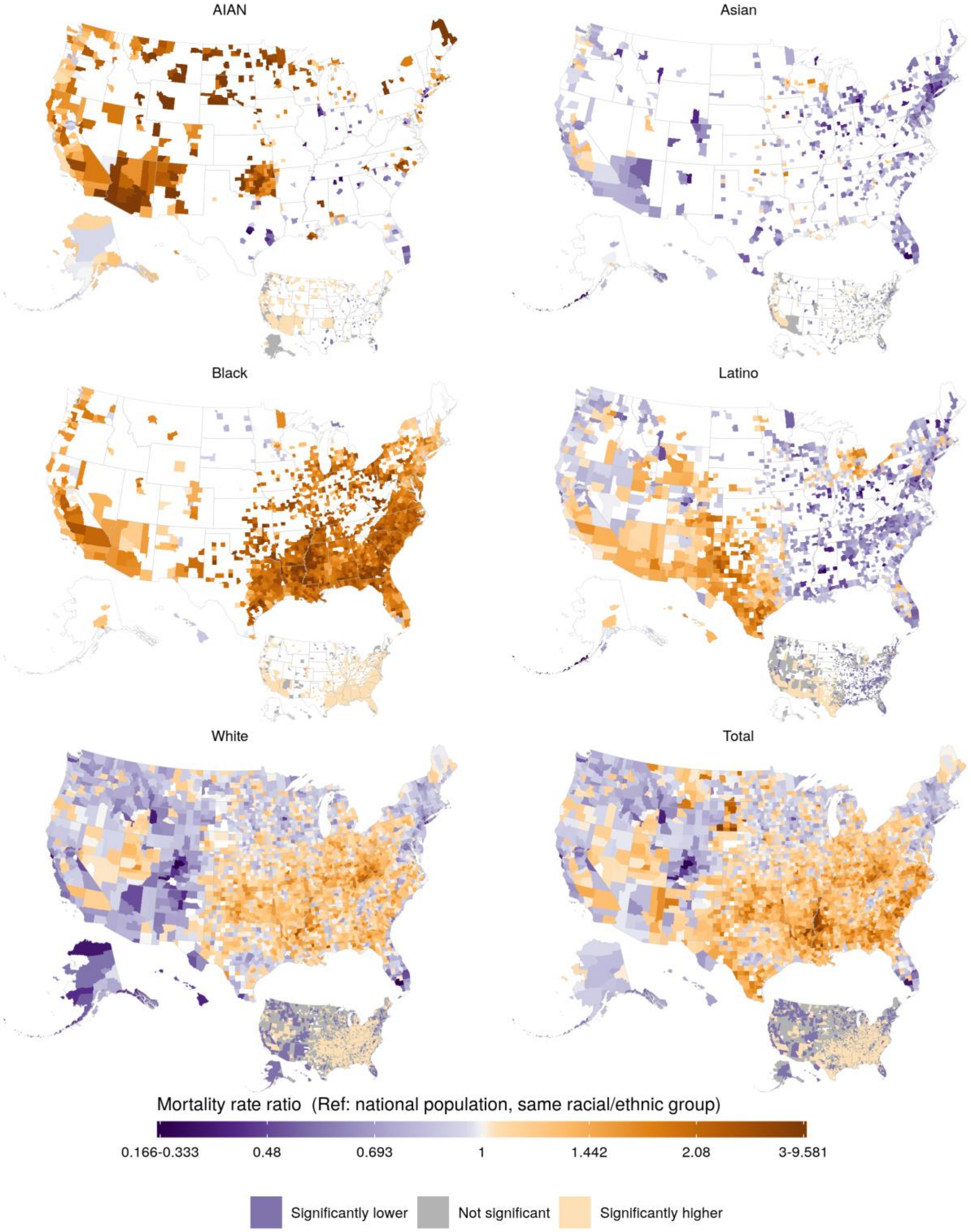
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 53: Age-standardised mortality rate, diabetes and kidney diseases, 2019



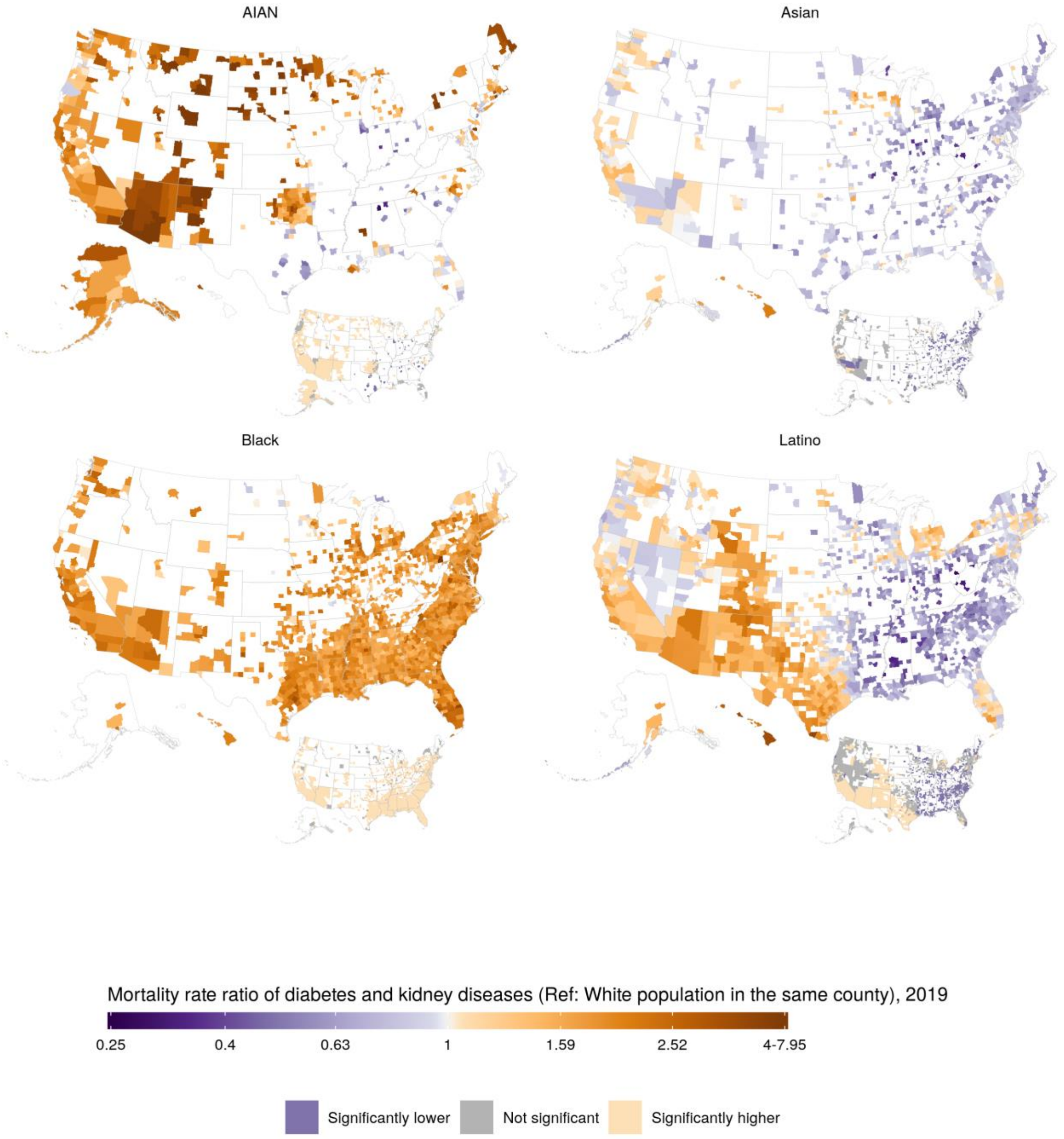
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 54: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, diabetes and kidney diseases, 2019



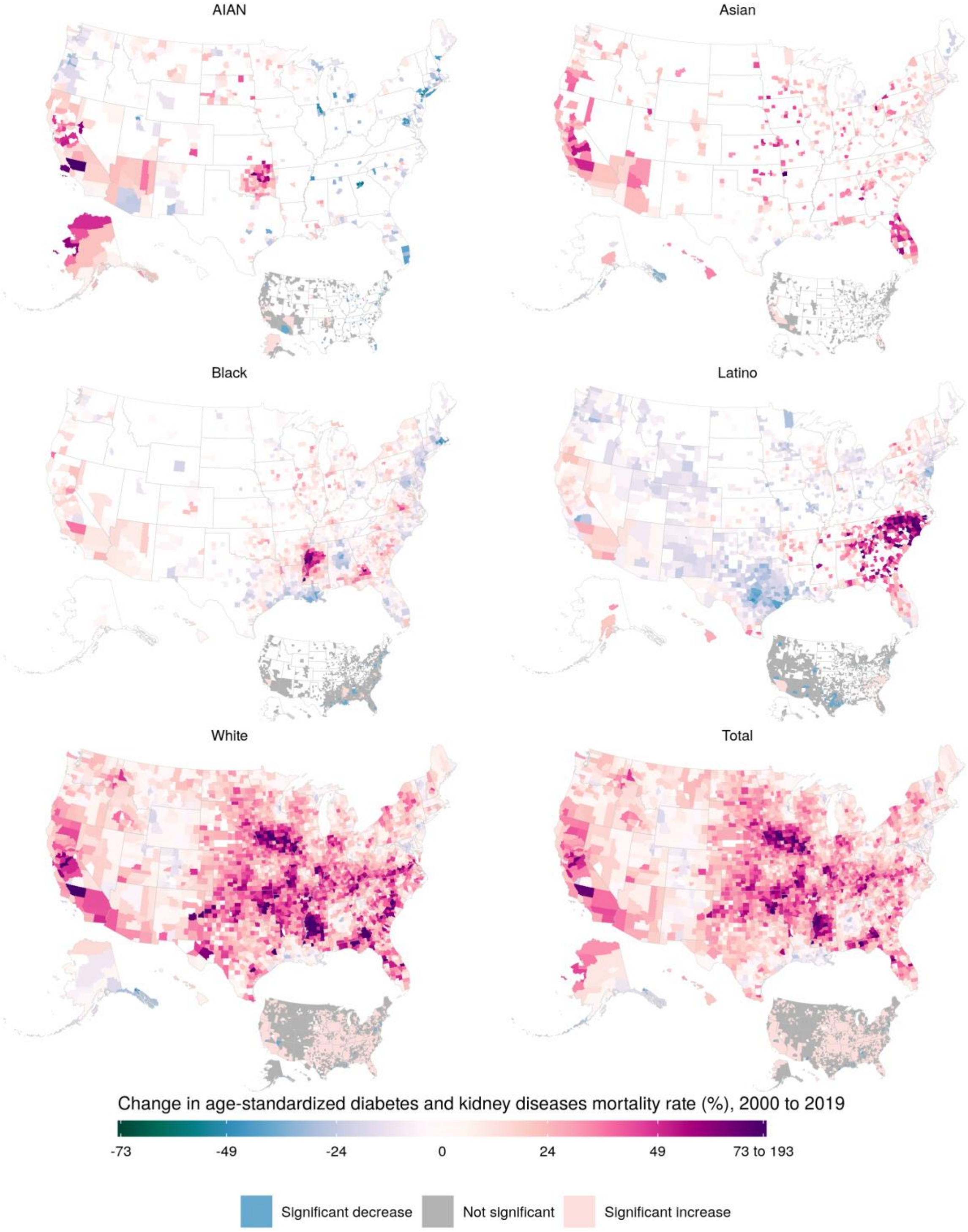
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 55: Age-standardised mortality rate ratio compared to the White population in the same county, diabetes and kidney diseases, 2019



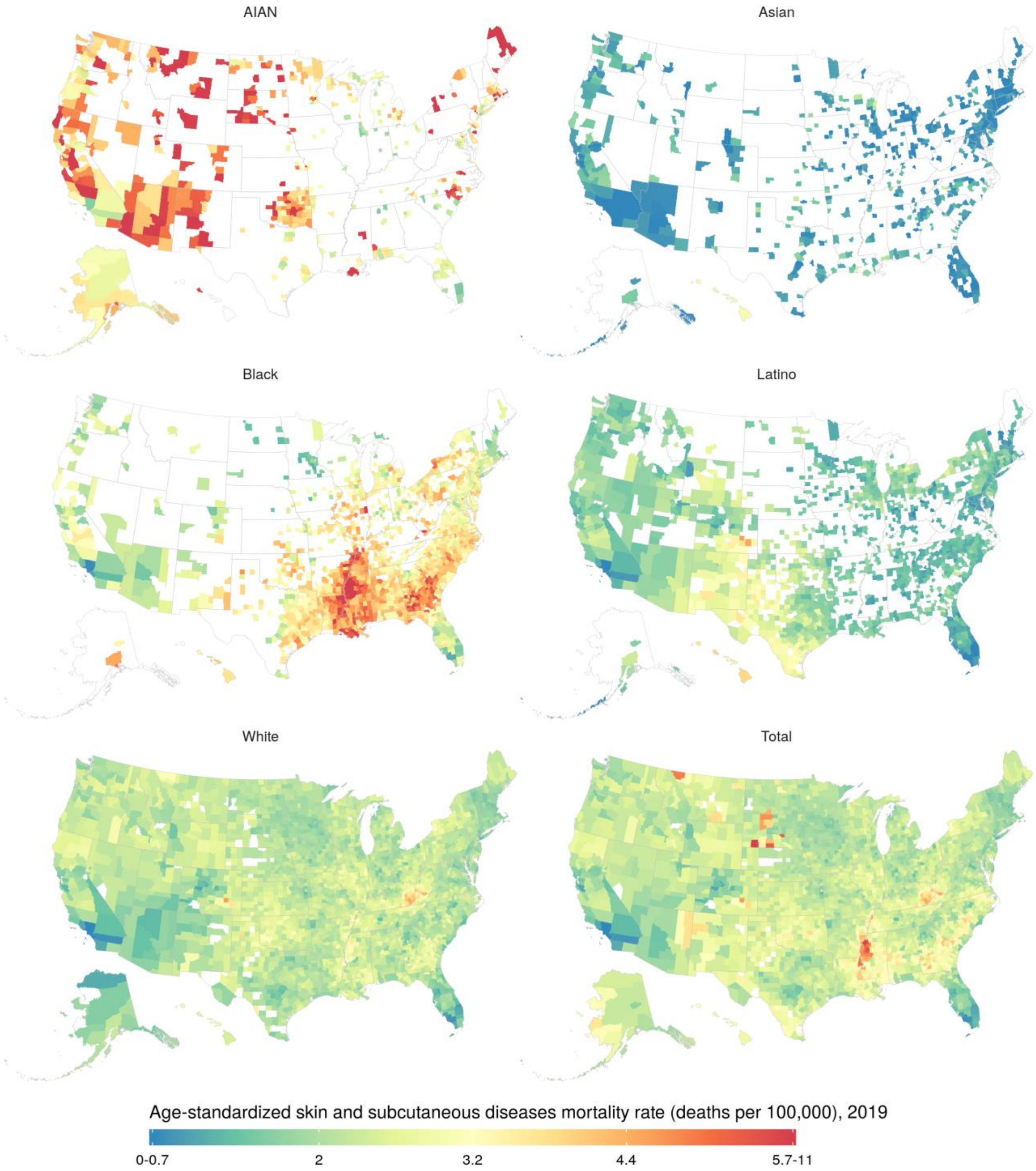
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 56: Change in age-standardised mortality rate, diabetes and kidney diseases, 2000–2019



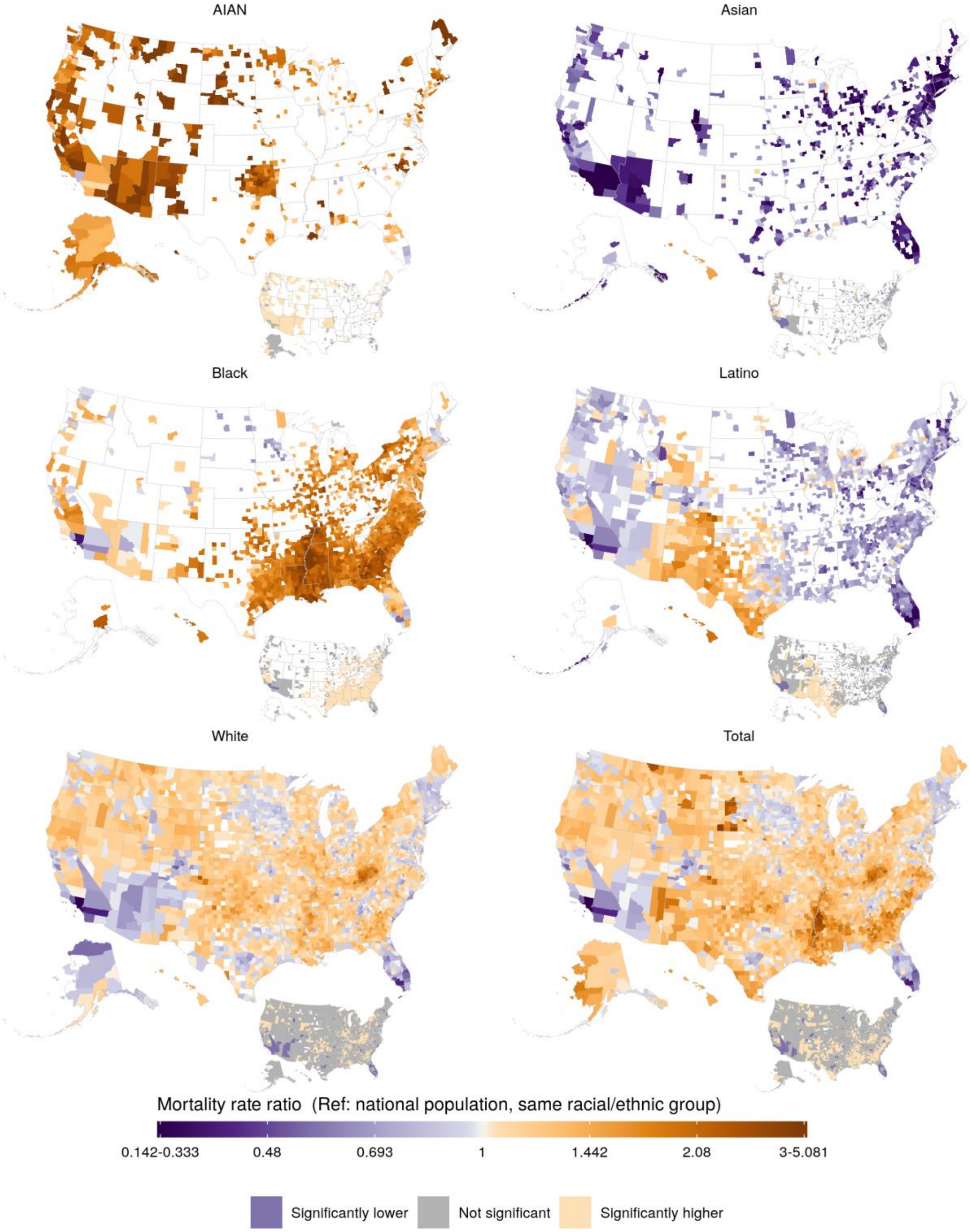
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 57: Age-standardised mortality rate, skin and subcutaneous diseases, 2019



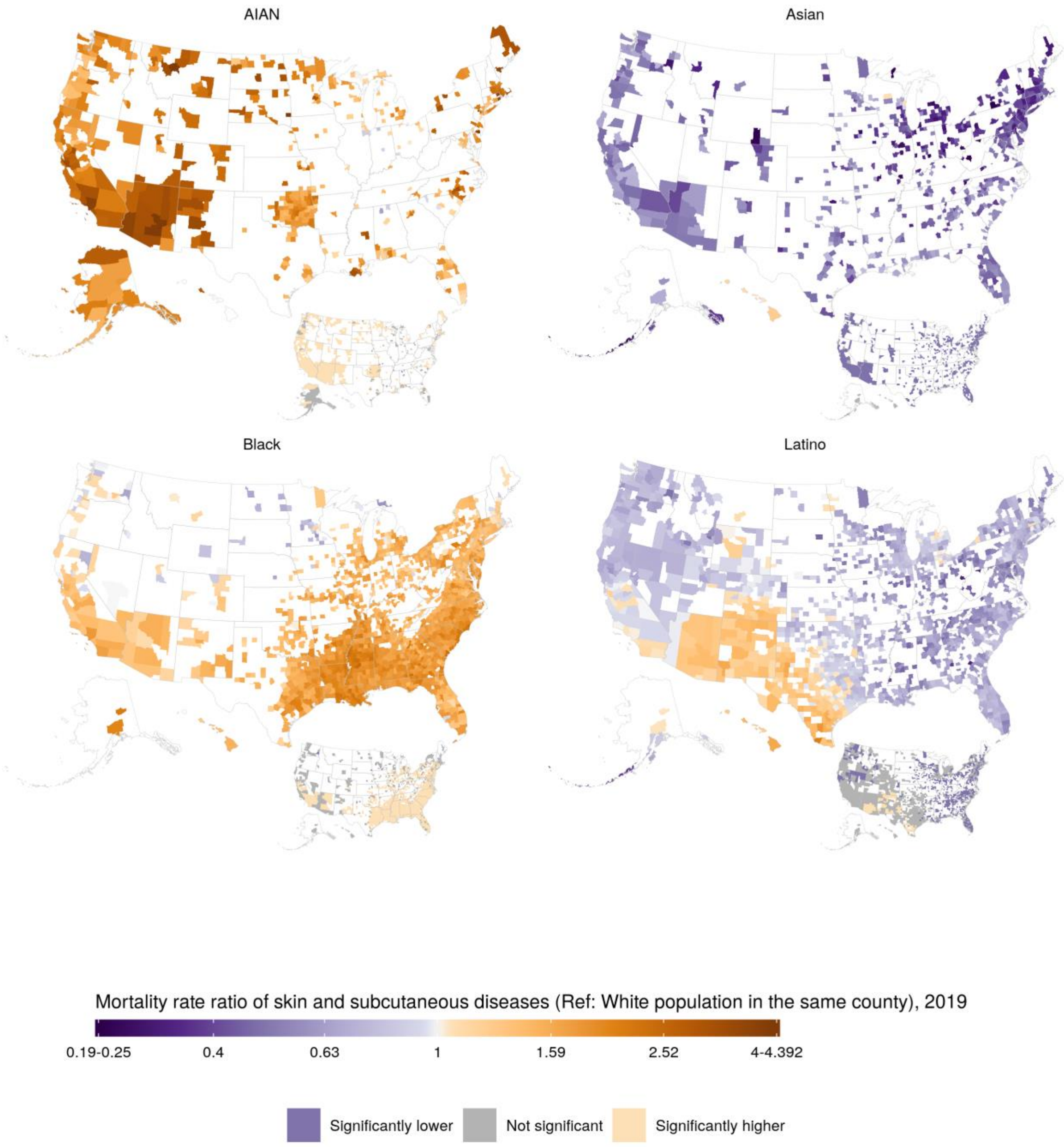
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 58: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, skin and subcutaneous diseases, 2019



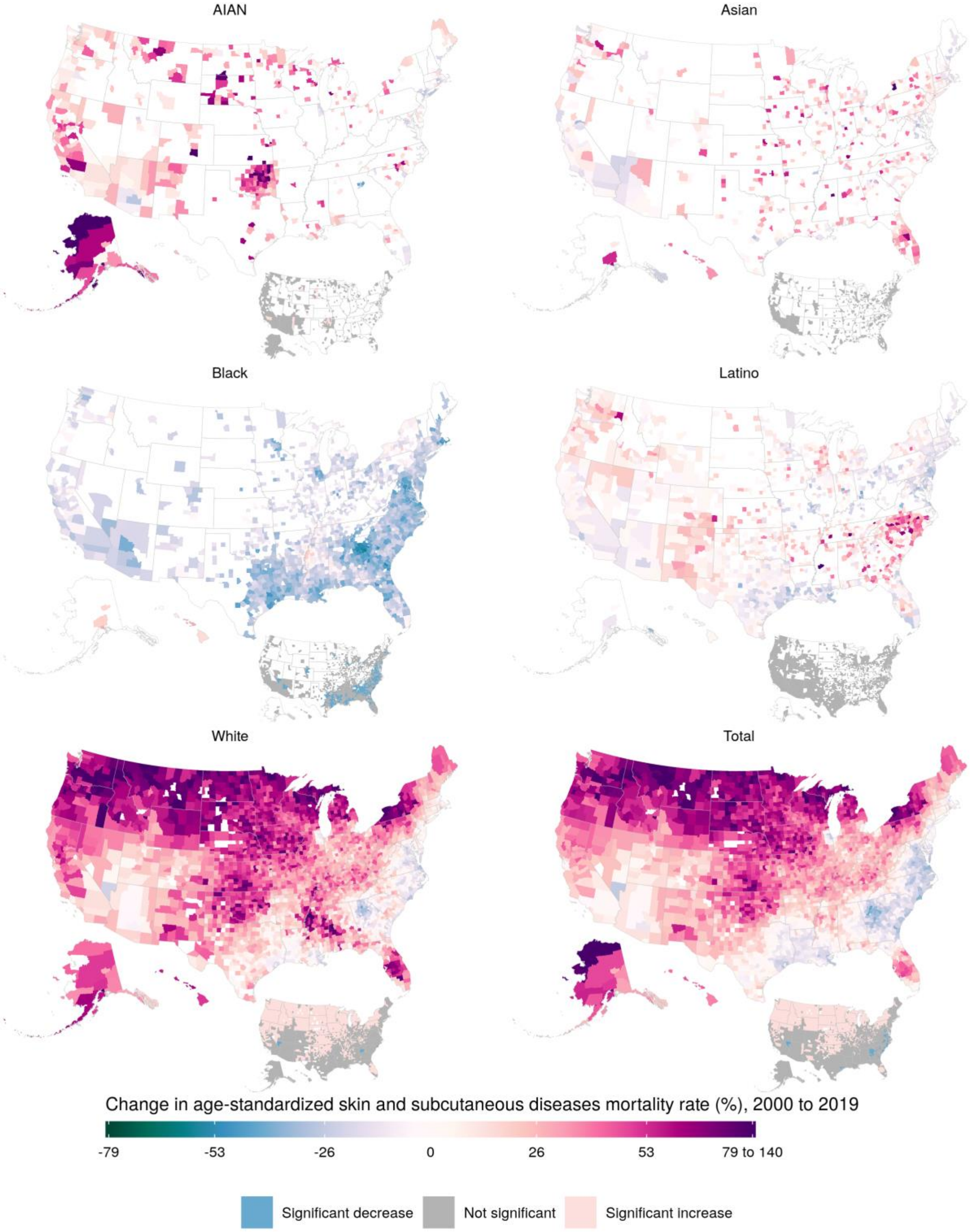
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 59: Age-standardised mortality rate ratio compared to the White population in the same county, skin and subcutaneous diseases, 2019



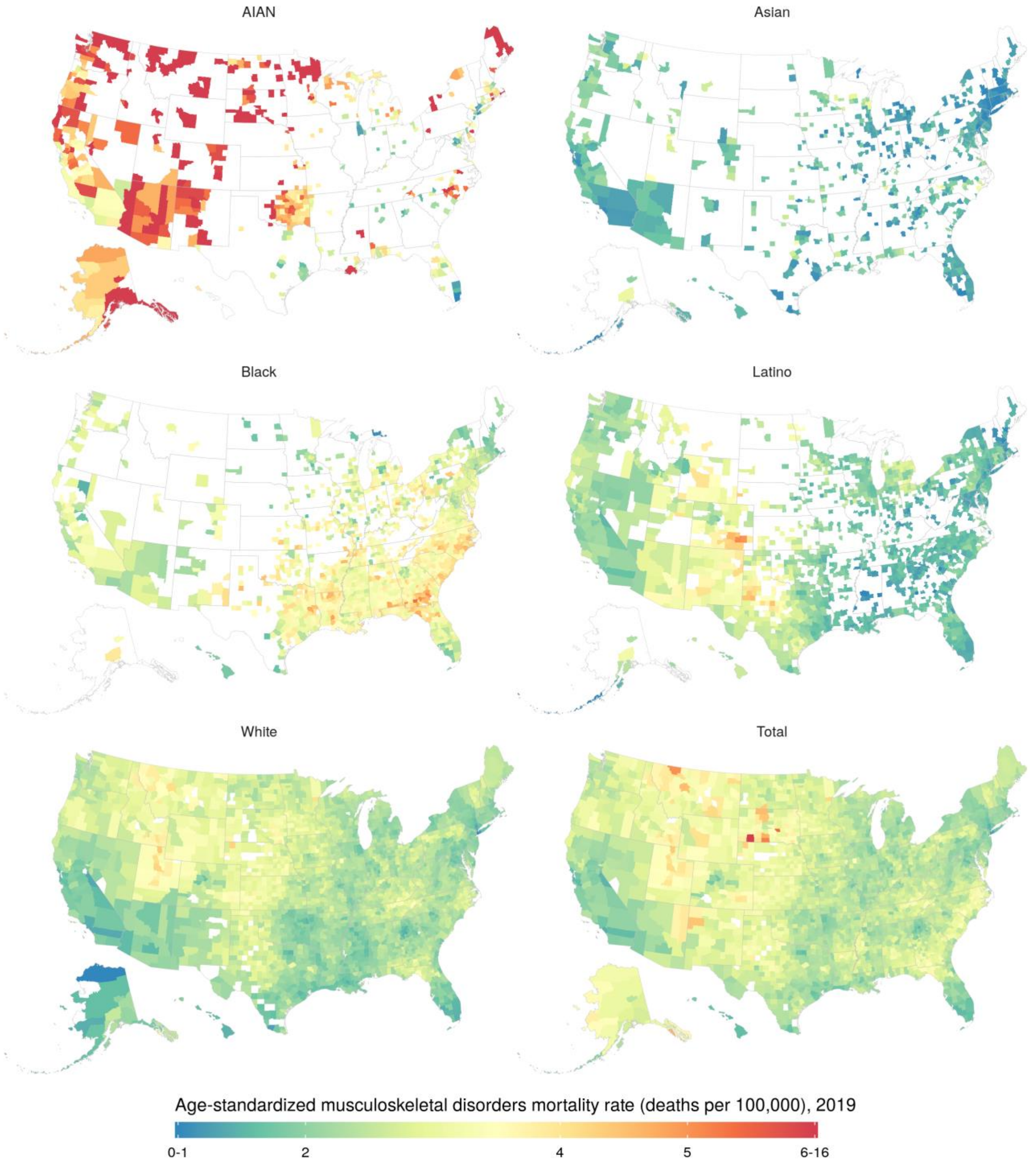
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 60: Change in age-standardised mortality rate, skin and subcutaneous diseases, 2000–2019



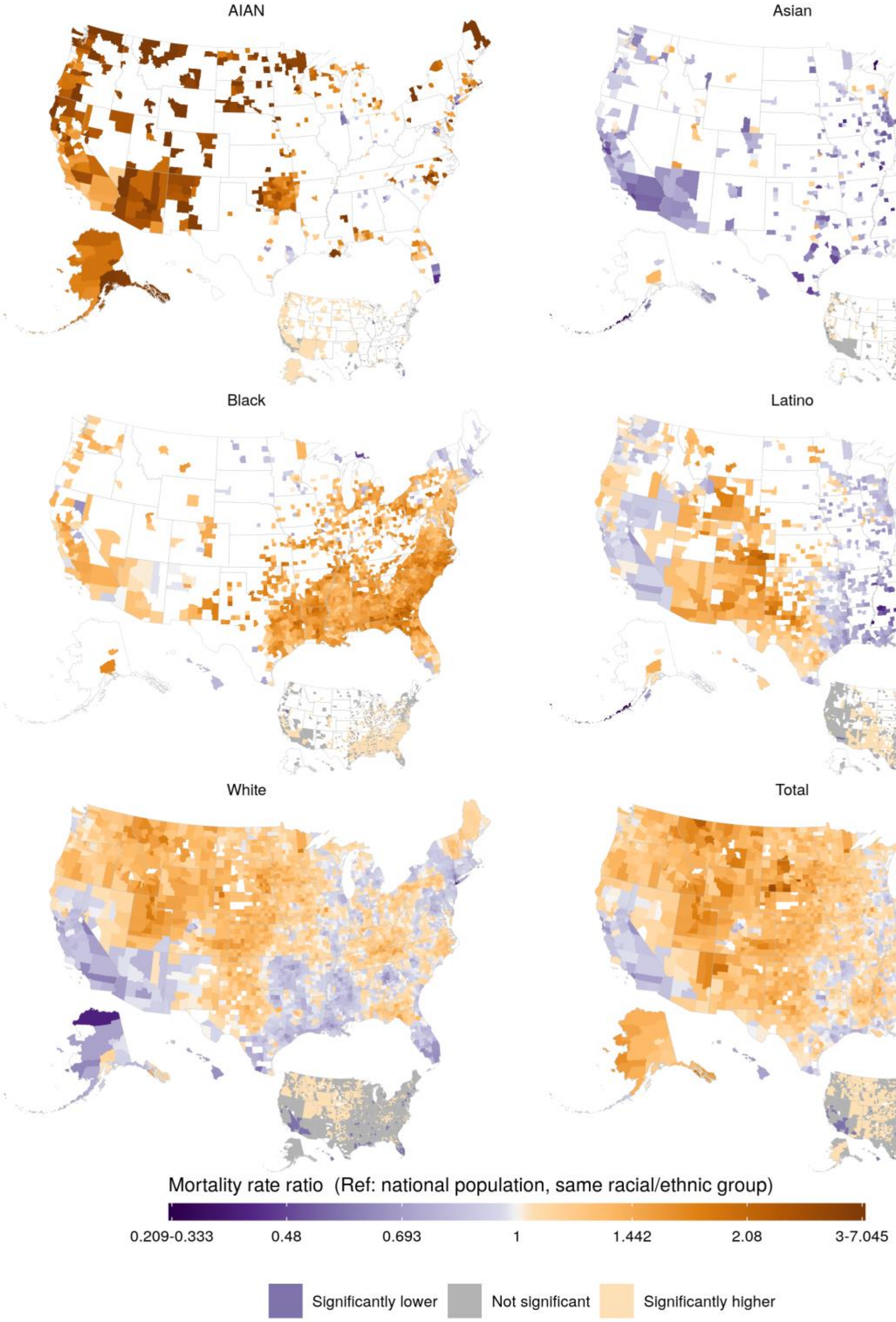
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 61: Age-standardised mortality rate, musculoskeletal disorders, 2019



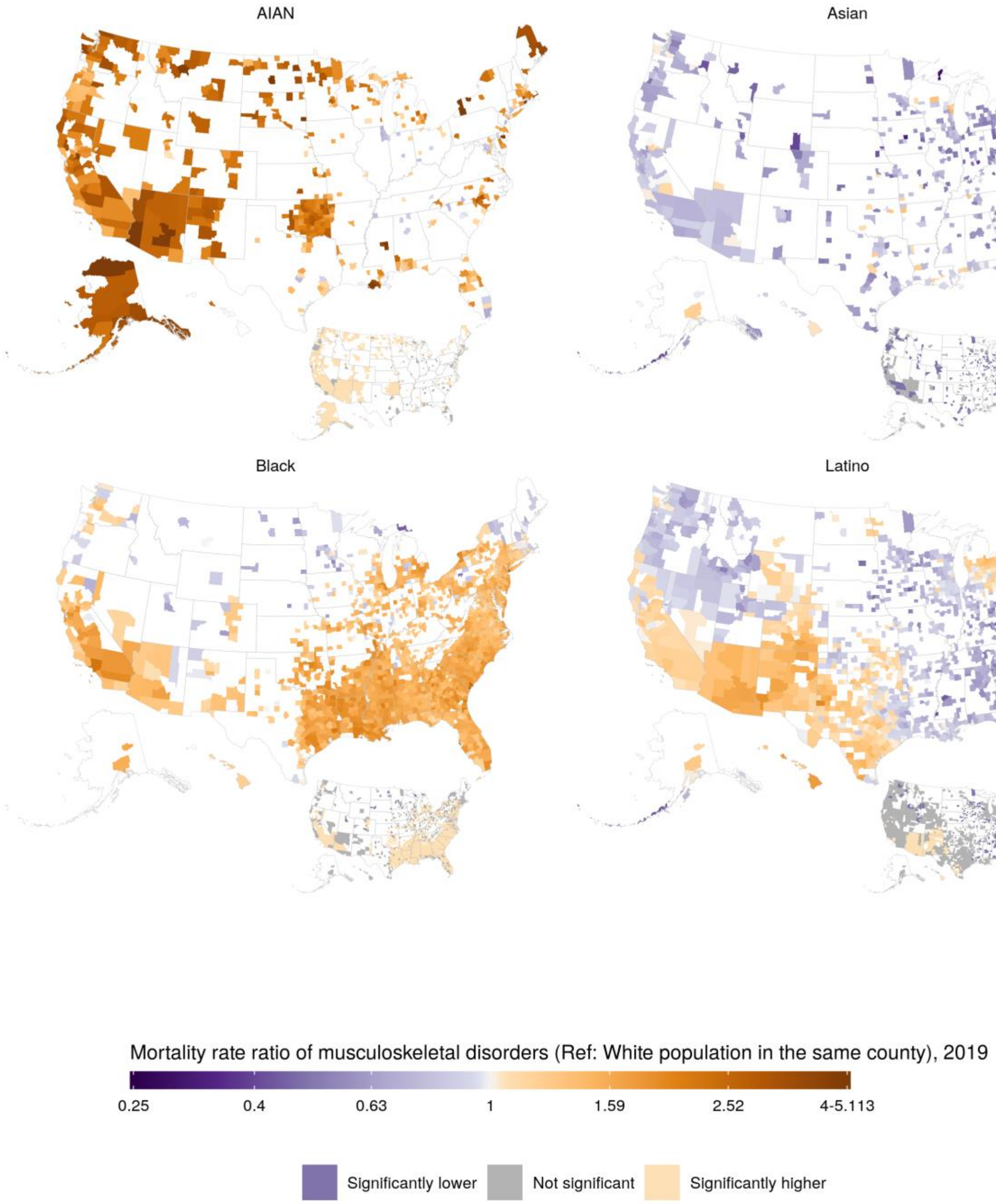
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 62: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, musculoskeletal disorders, 2019



Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 63: Age-standardised mortality rate ratio compared to the White population in the same county, musculoskeletal disorders, 2019

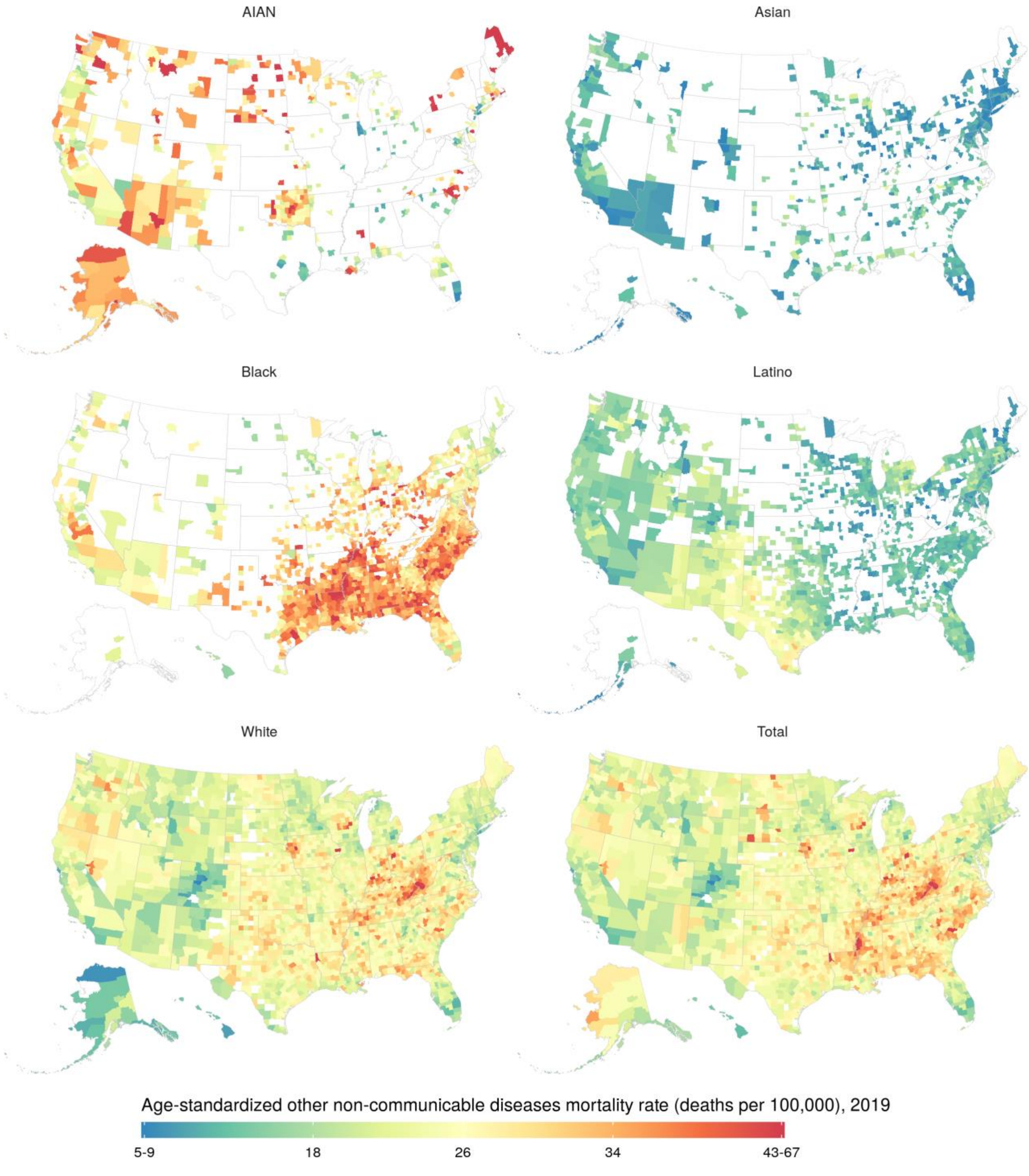


Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 64: Change in age-standardised mortality rate, musculoskeletal disorders, 2000–2019

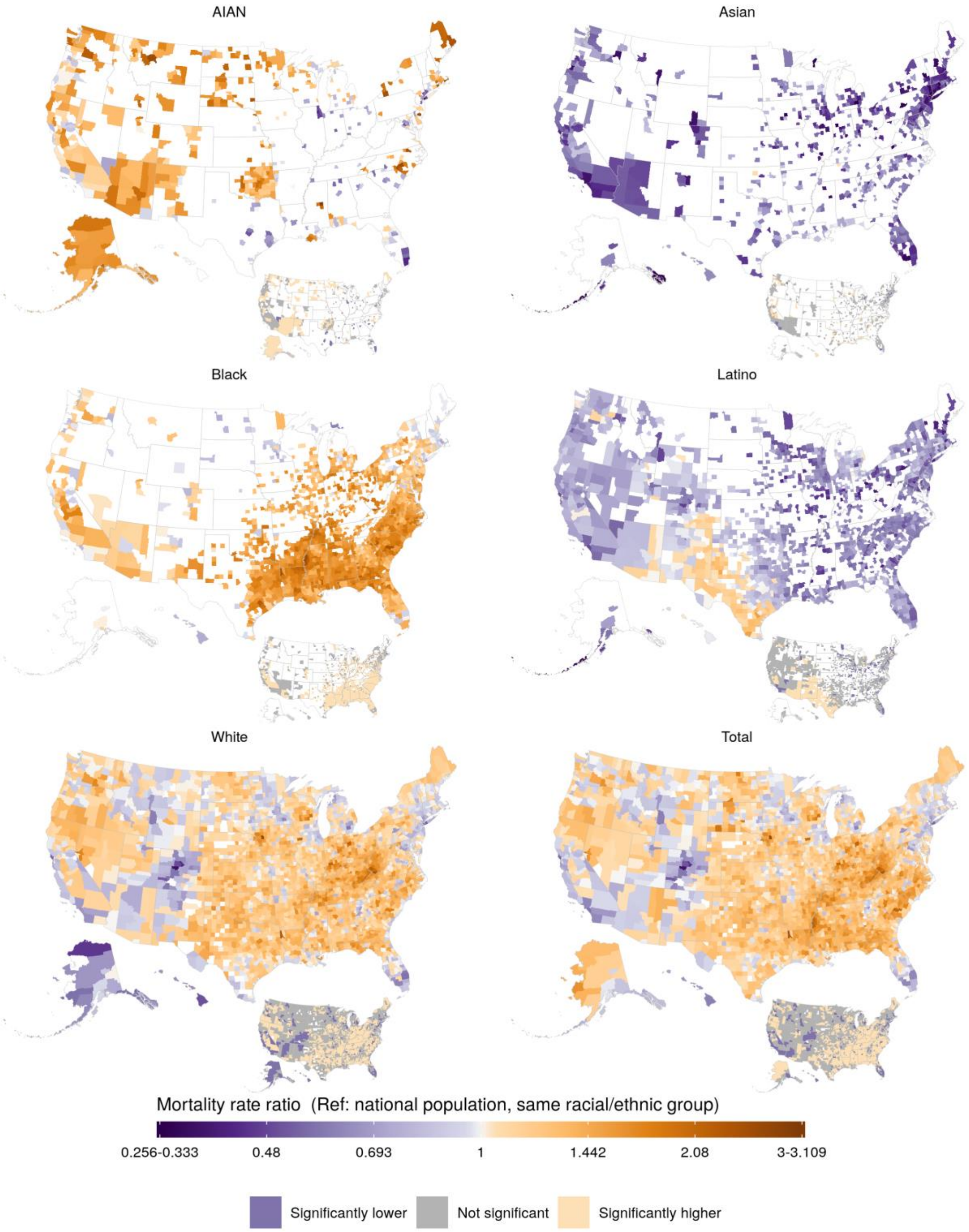
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 65: Age-standardised mortality rate, other non-communicable diseases, 2019



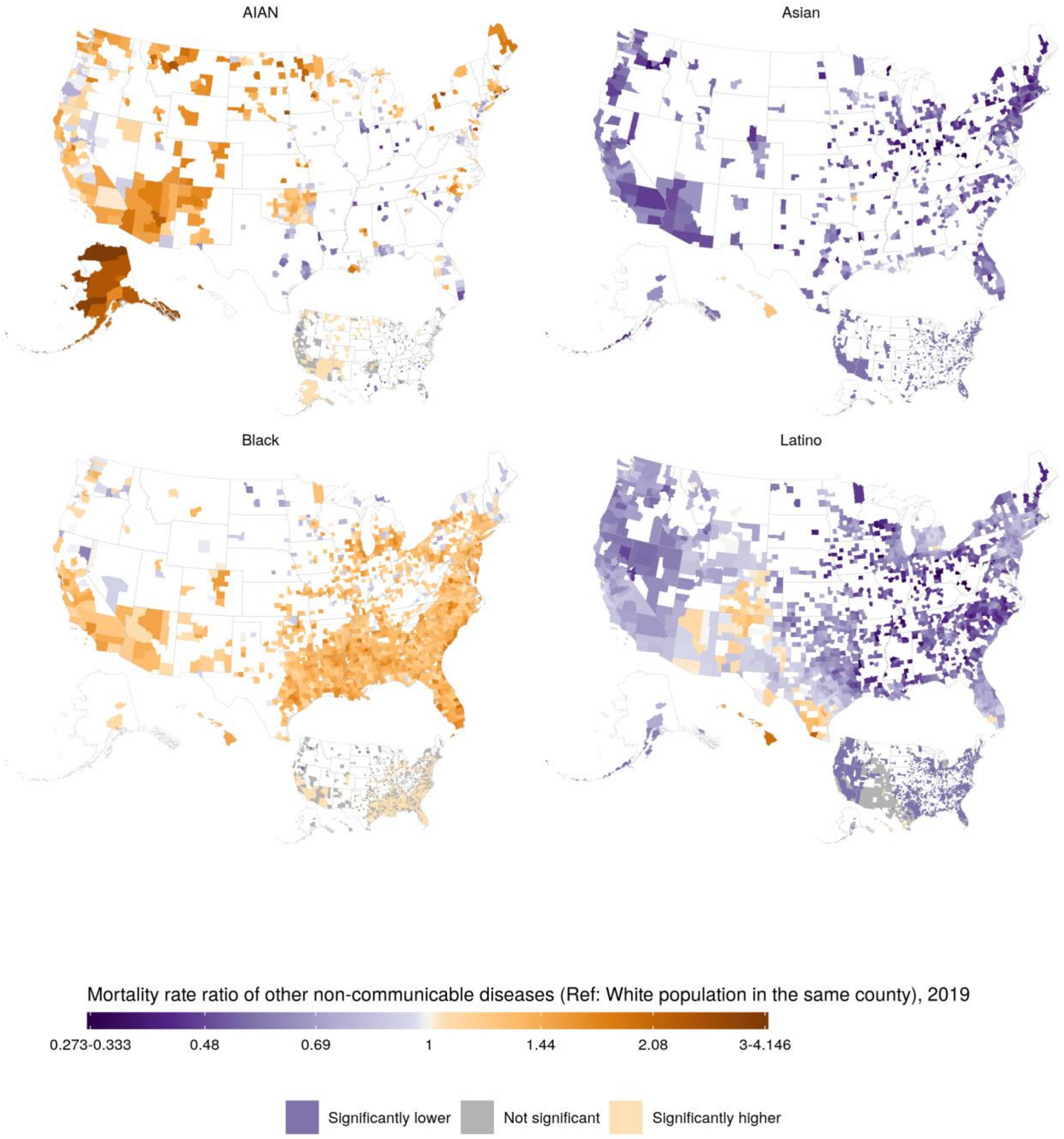
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 66: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, other non-communicable diseases, 2019



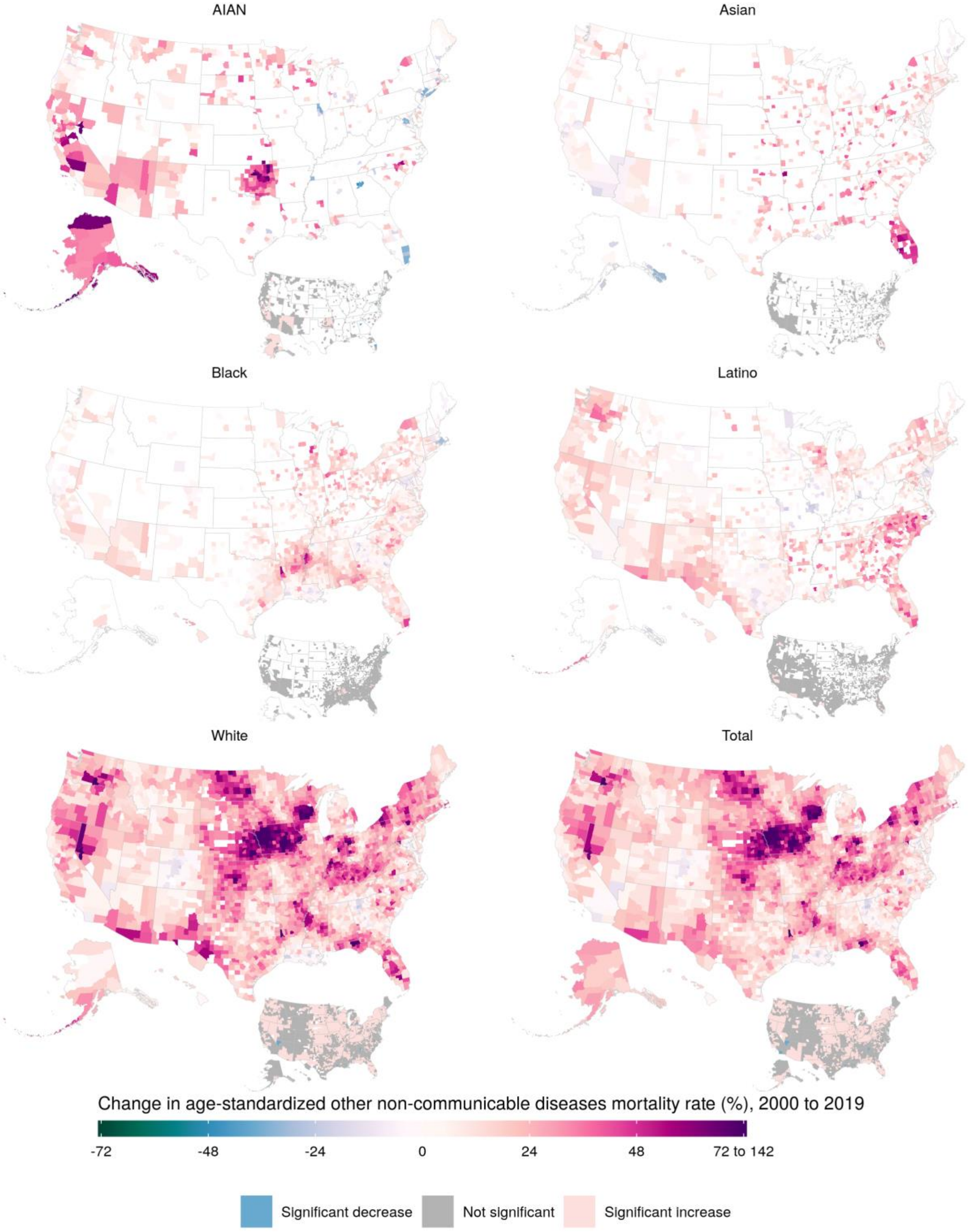
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 67: Age-standardised mortality rate ratio compared to the White population in the same county, other non-communicable diseases, 2019



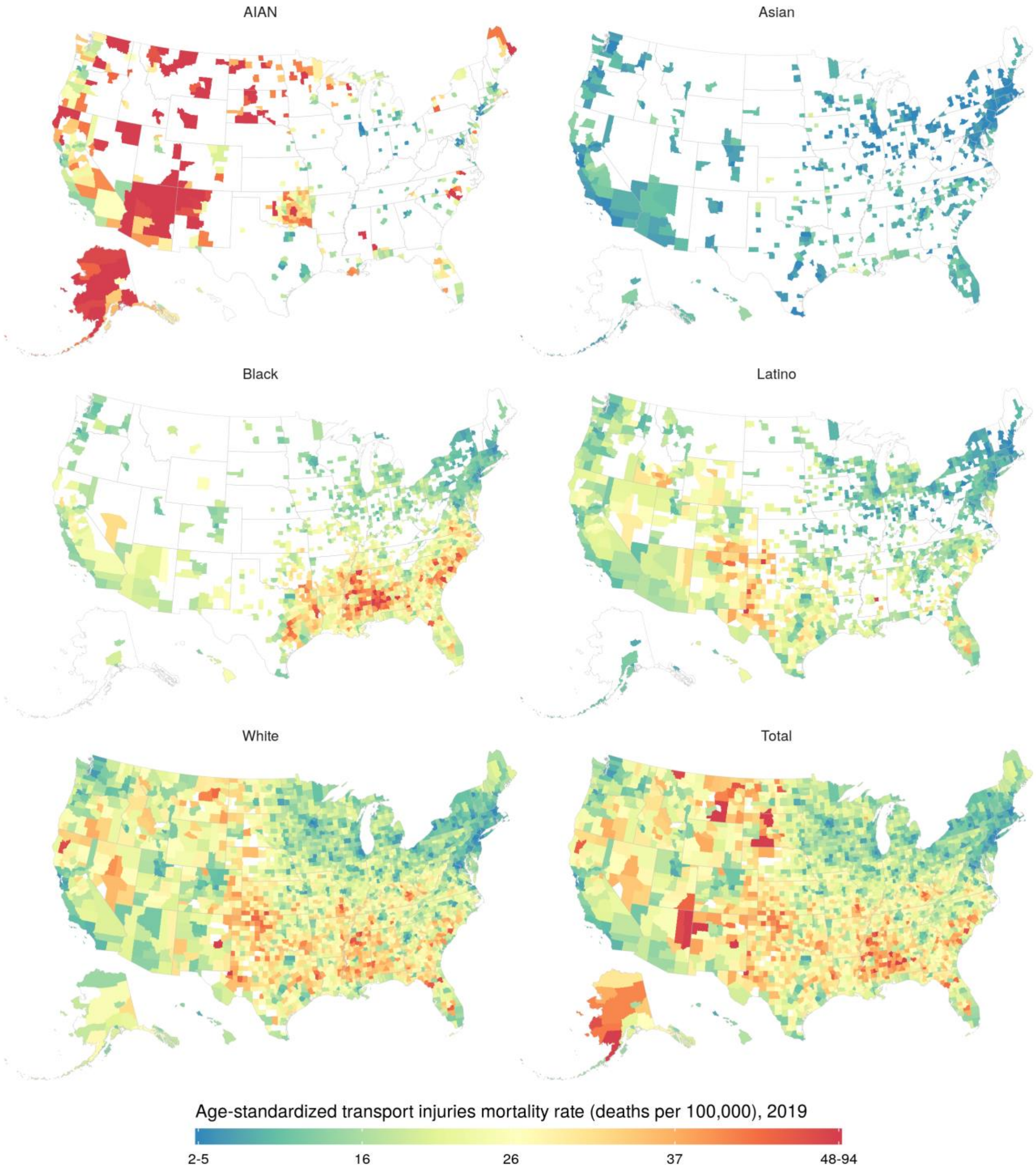
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 68: Change in age-standardised mortality rate, other non-communicable diseases, 2000–2019



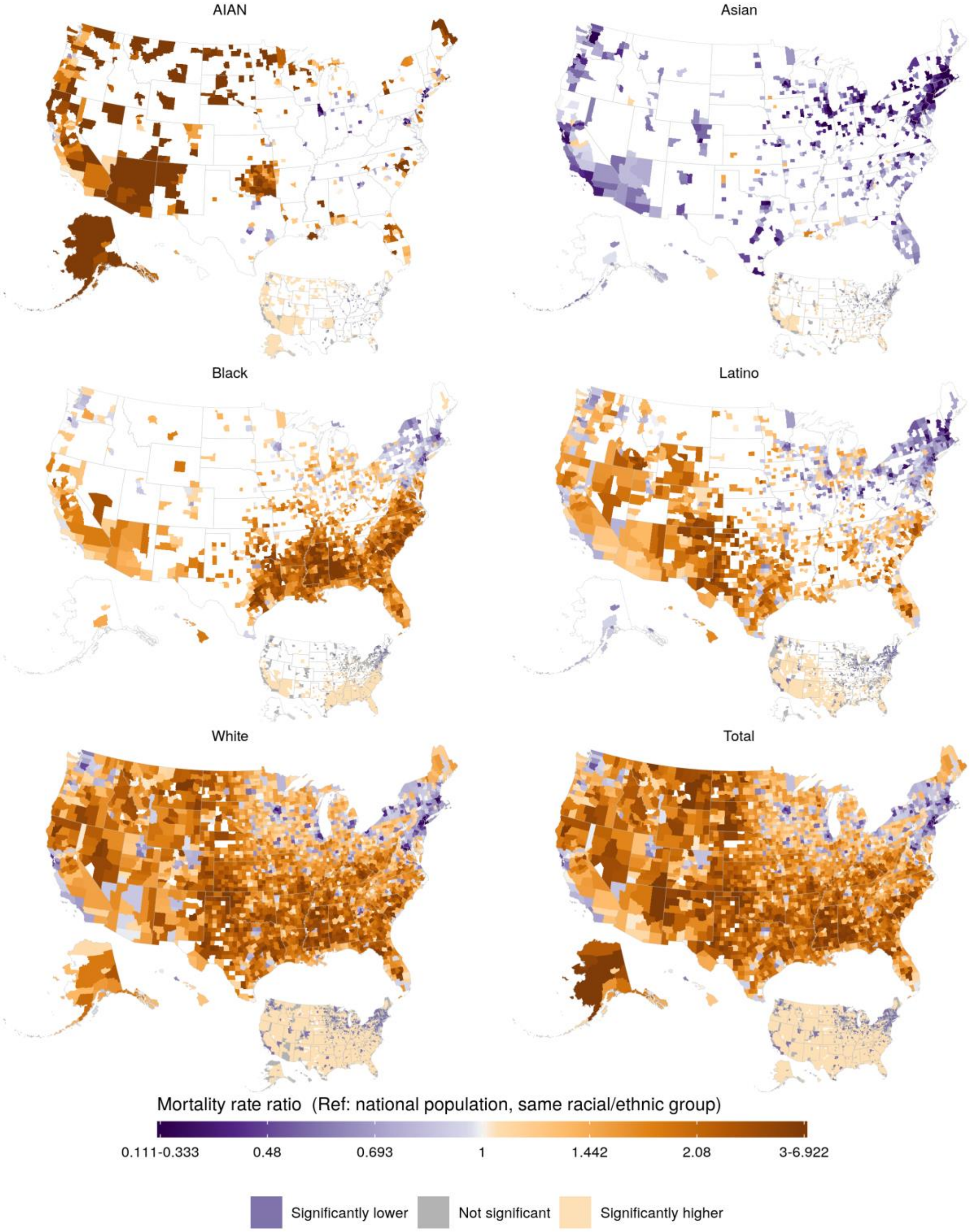
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 69: Age-standardised mortality rate, transport injuries, 2019



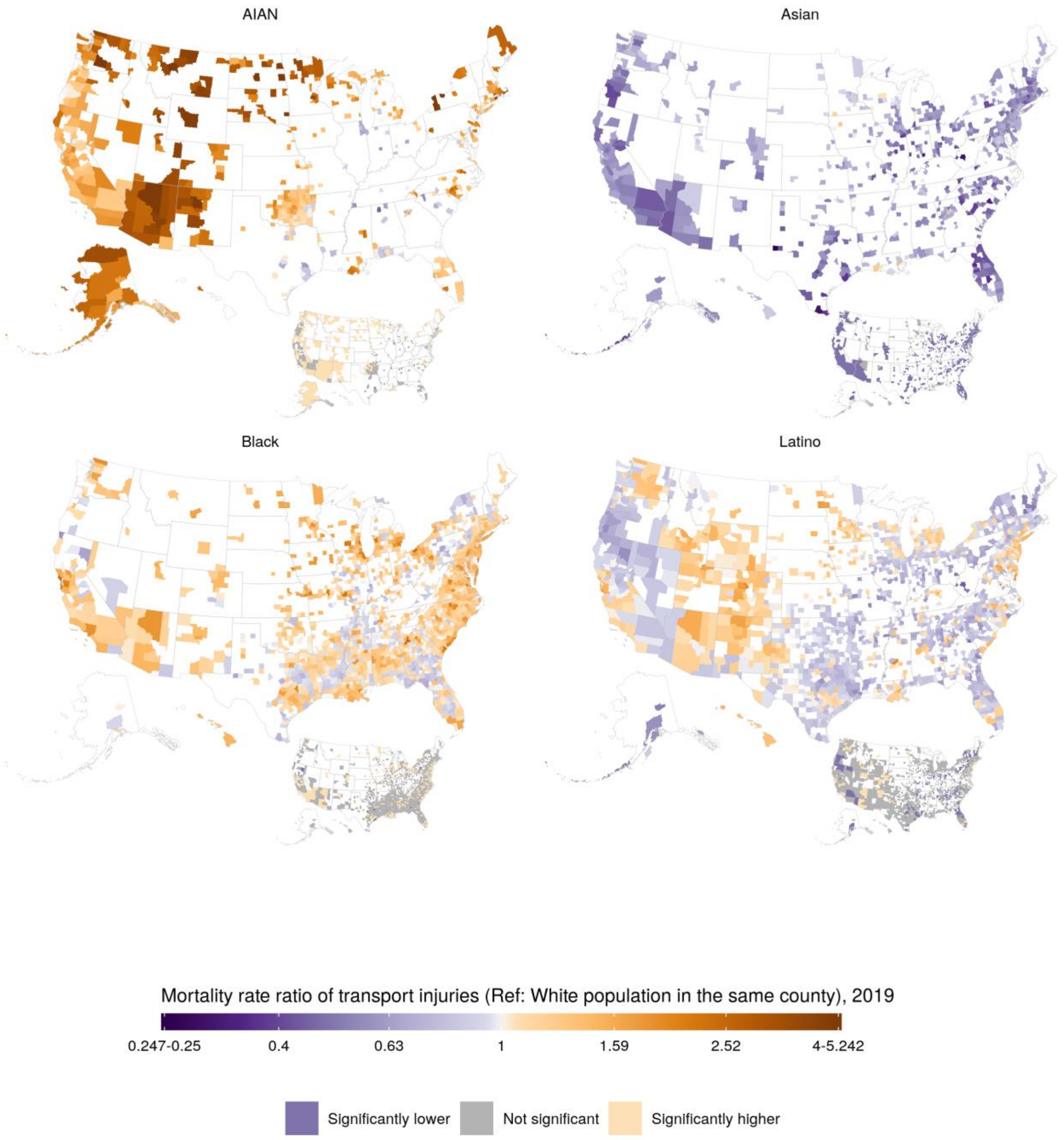
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 70: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, transport injuries, 2019



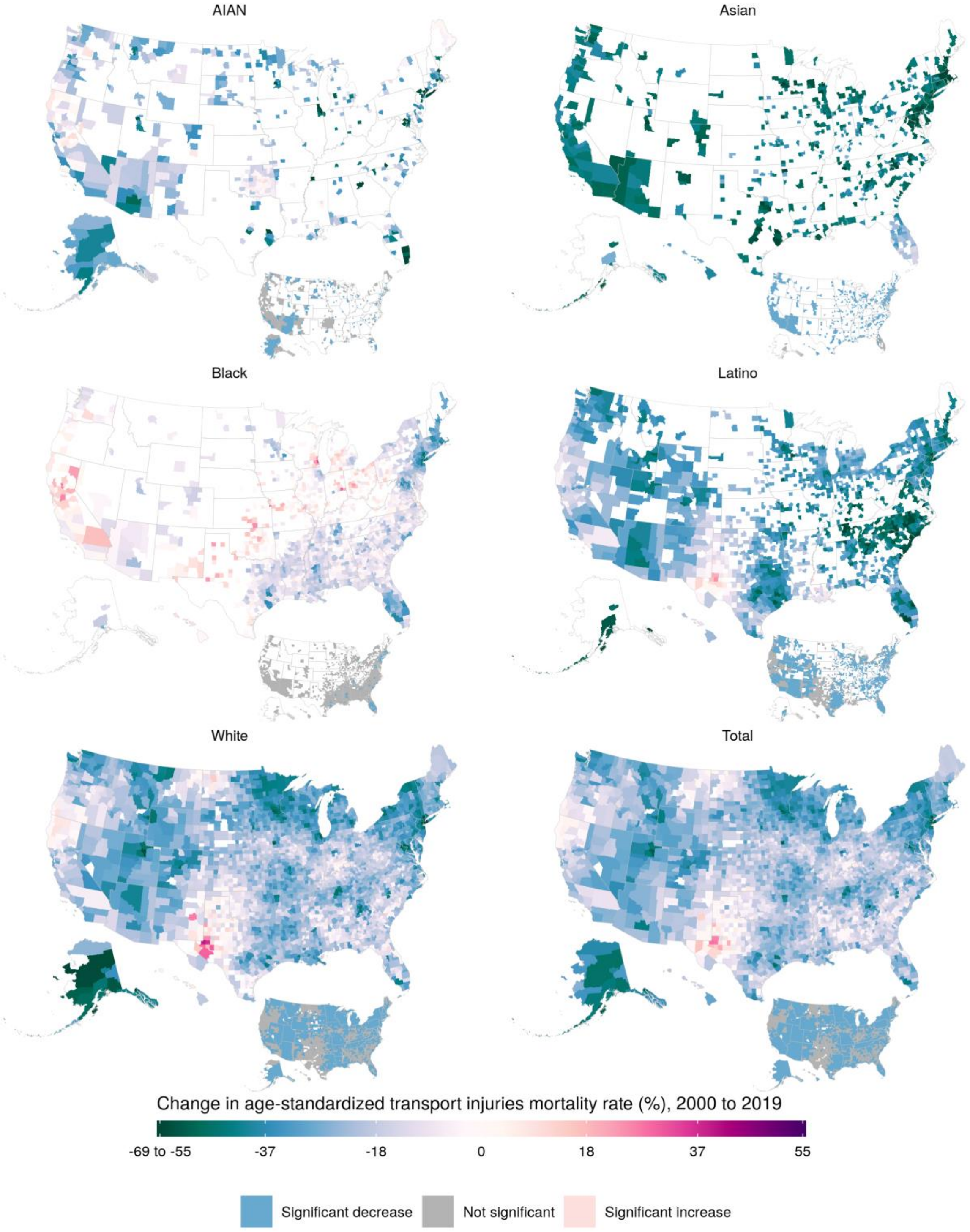
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 71: Age-standardised mortality rate ratio compared to the White population in the same county, transport injuries, 2019



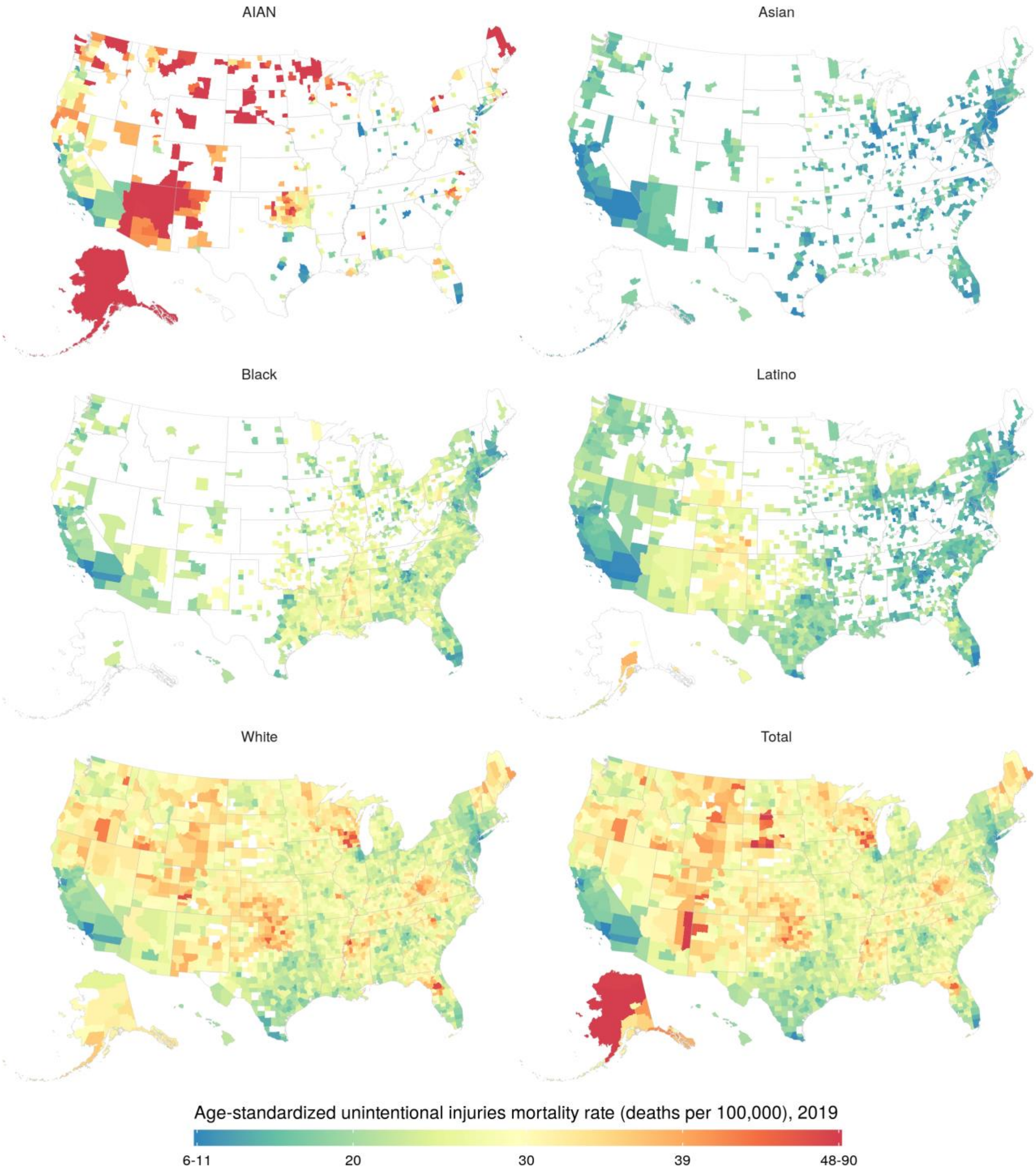
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 72: Change in age-standardised mortality rate, transport injuries, 2000–2019



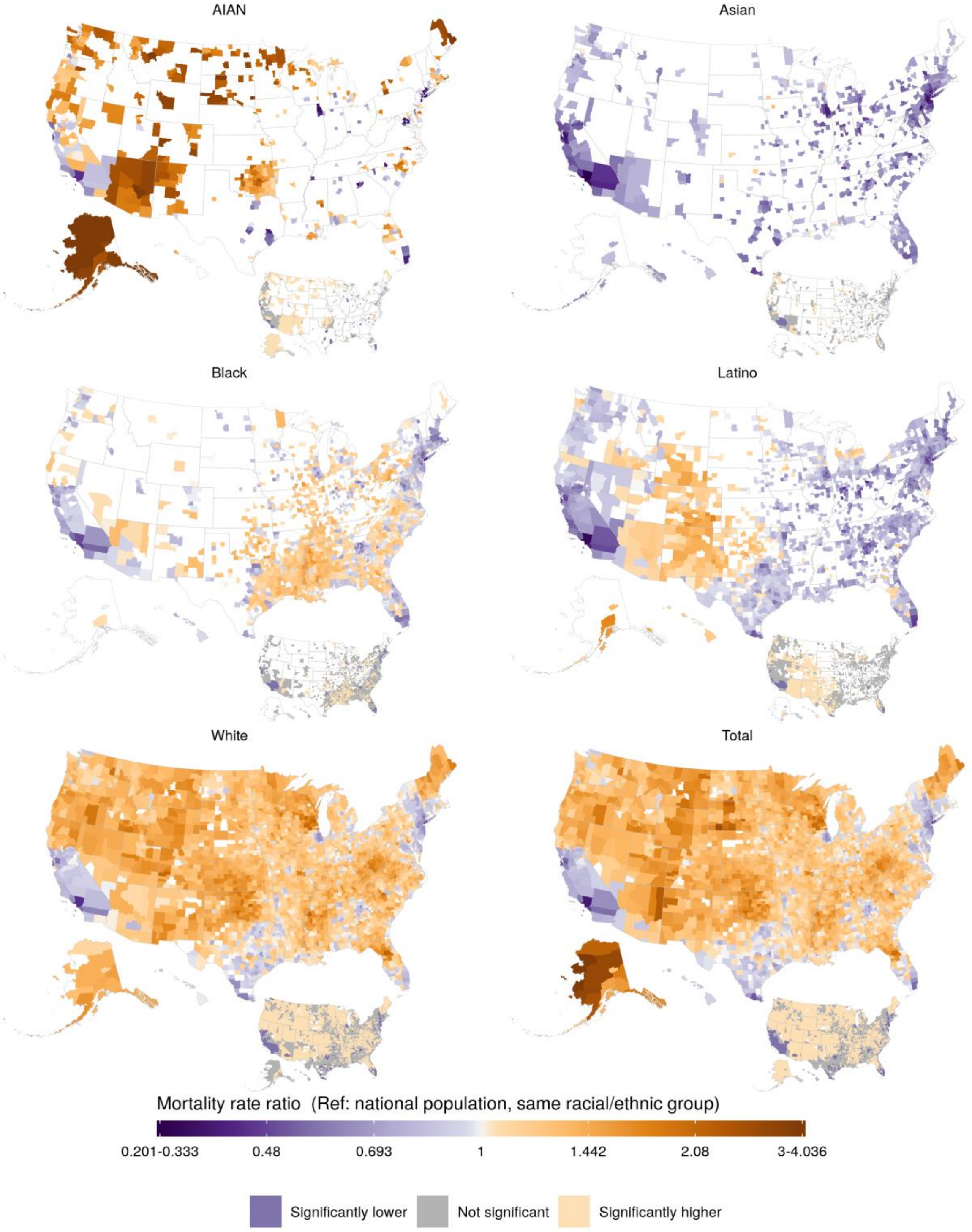
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 73: Age-standardised mortality rate, unintentional injuries, 2019



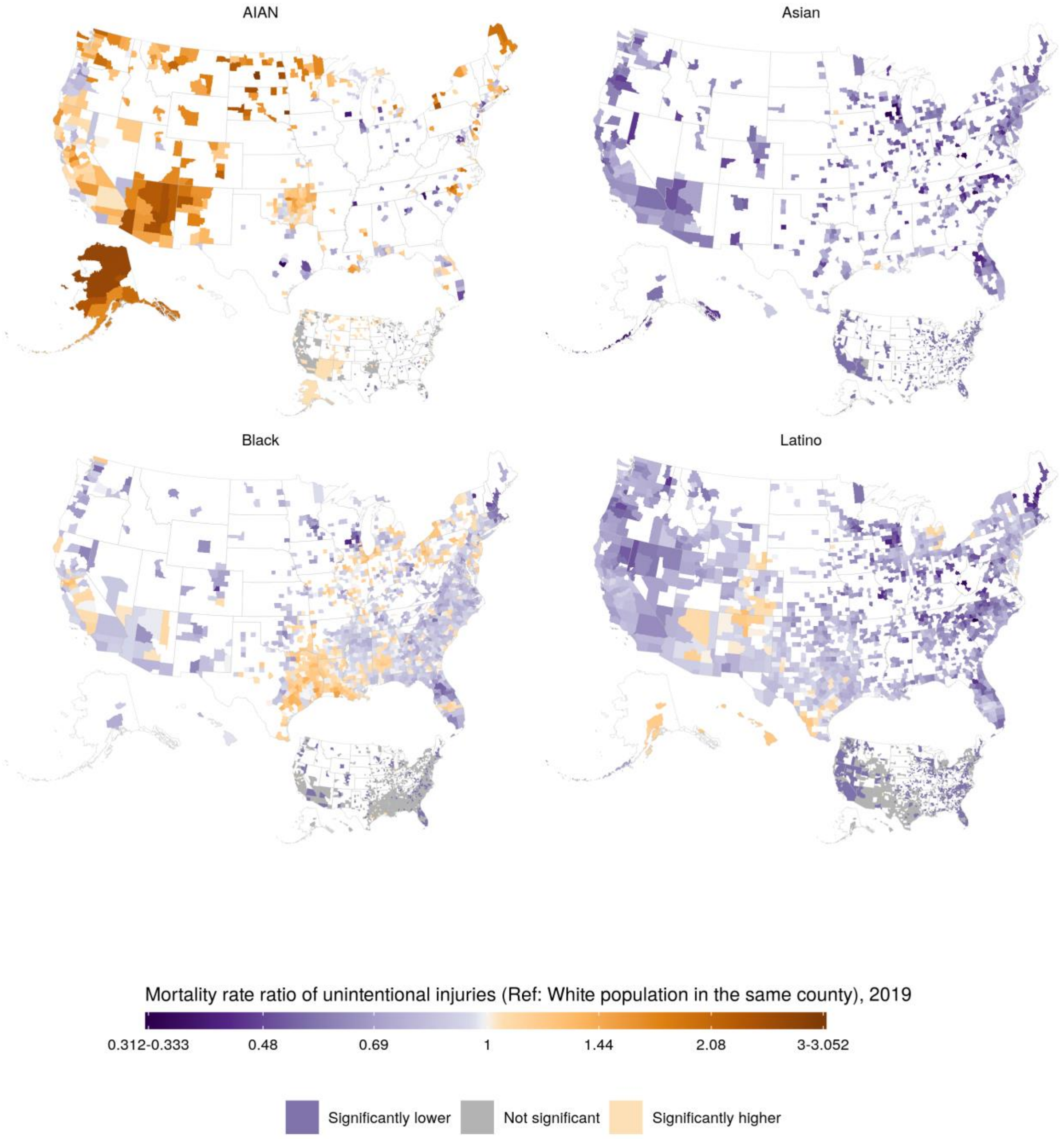
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 74: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, unintentional injuries, 2019



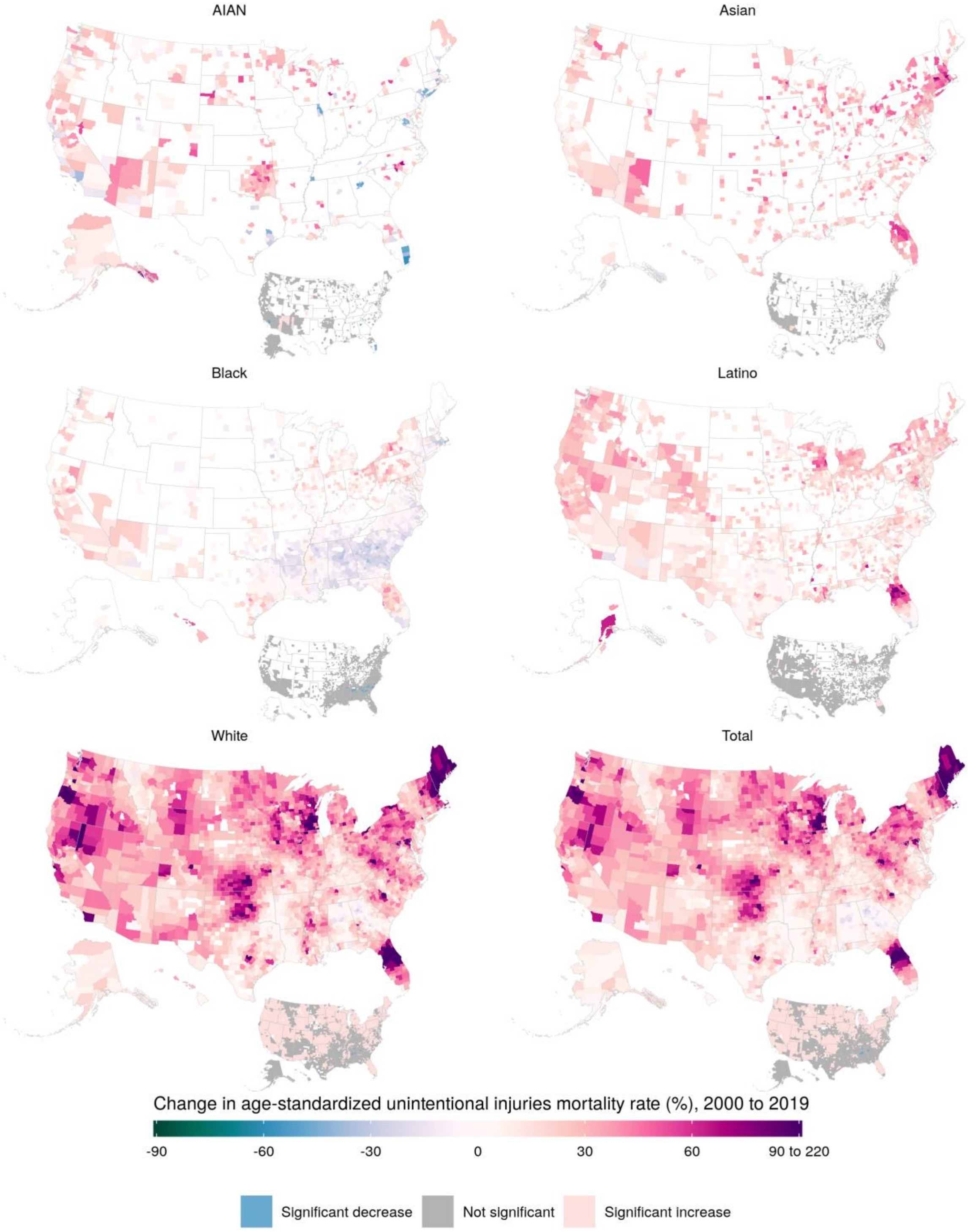
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 75: Age-standardised mortality rate ratio compared to the White population in the same county, unintentional injuries, 2019



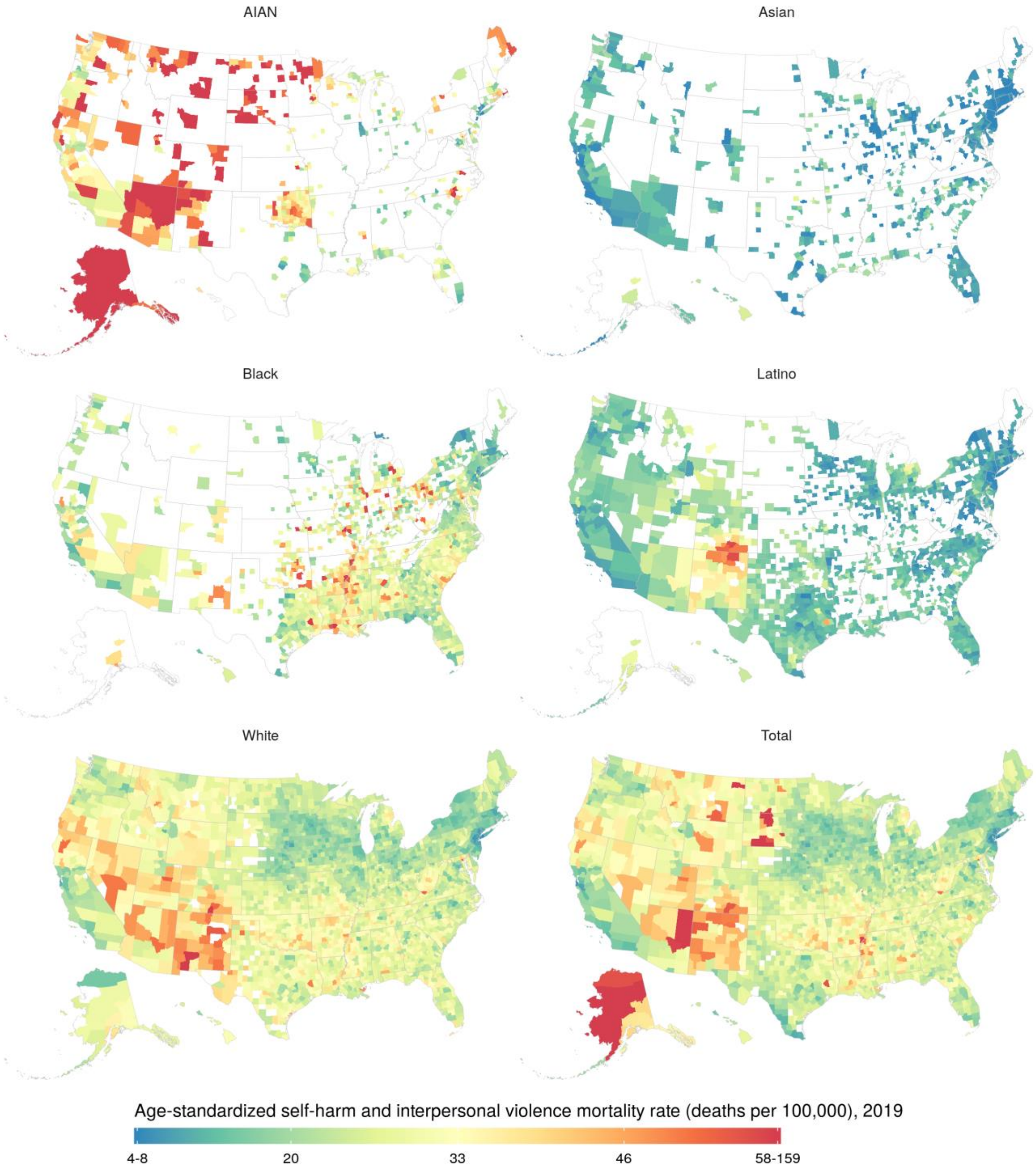
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 76: Change in age-standardised mortality rate, unintentional injuries, 2000–2019



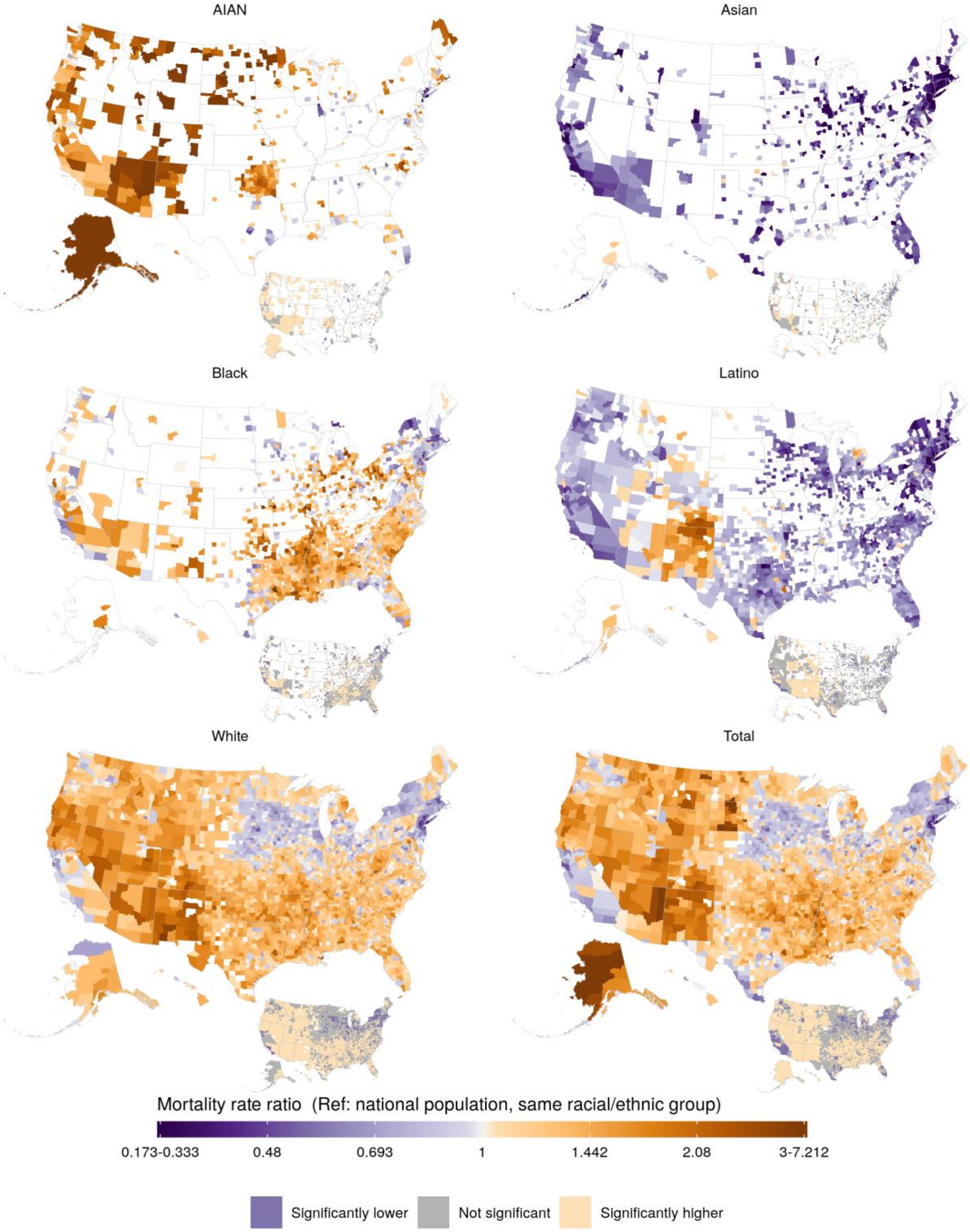
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 77: Age-standardised mortality rate, self-harm and interpersonal violence, 2019



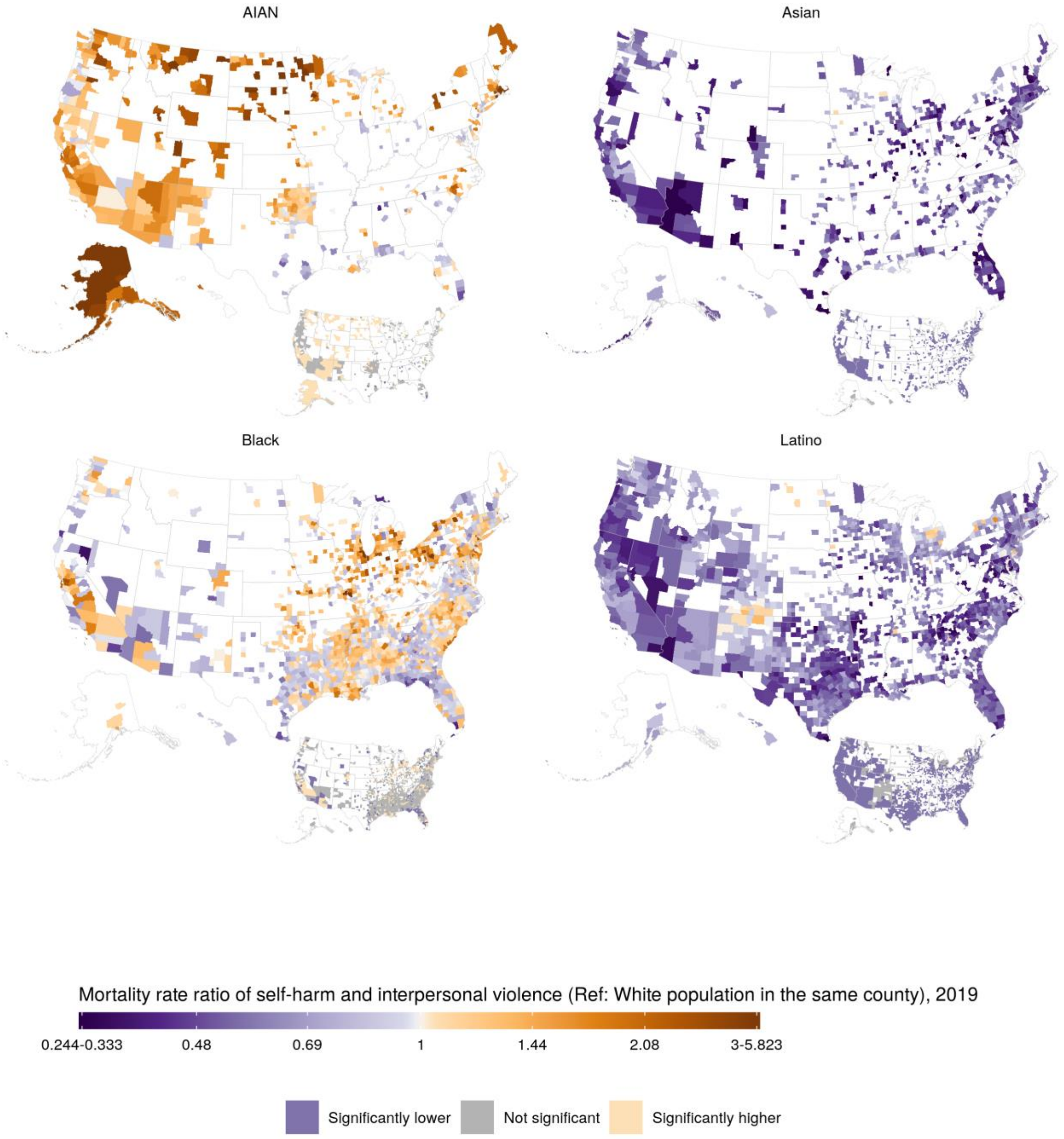
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 78: Age-standardised mortality rate ratio compared to the national population for the same racial–ethnic group, self-harm and interpersonal violence, 2019



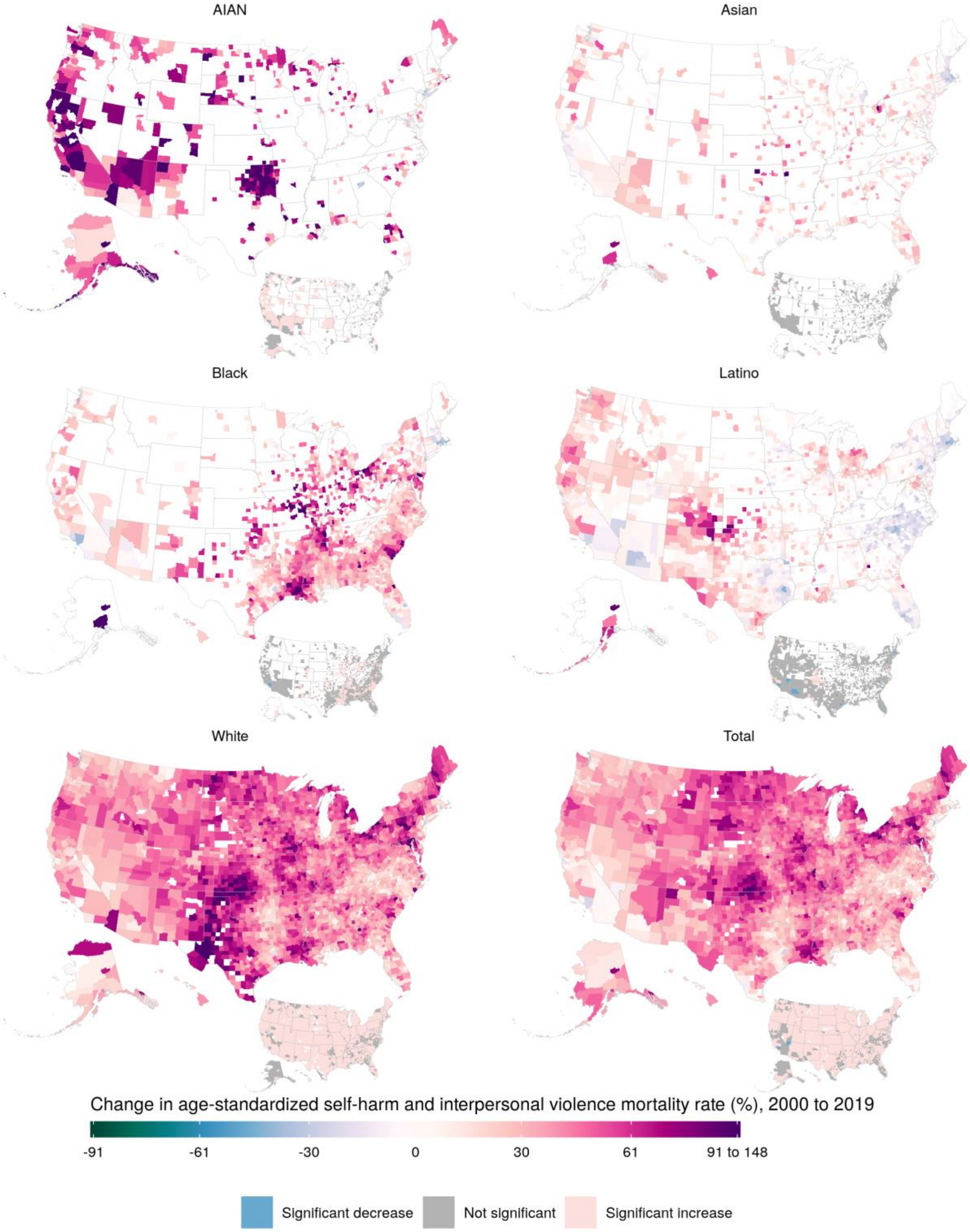
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 79: Age-standardised mortality rate ratio compared to the White population in the same county, self-harm and interpersonal violence, 2019



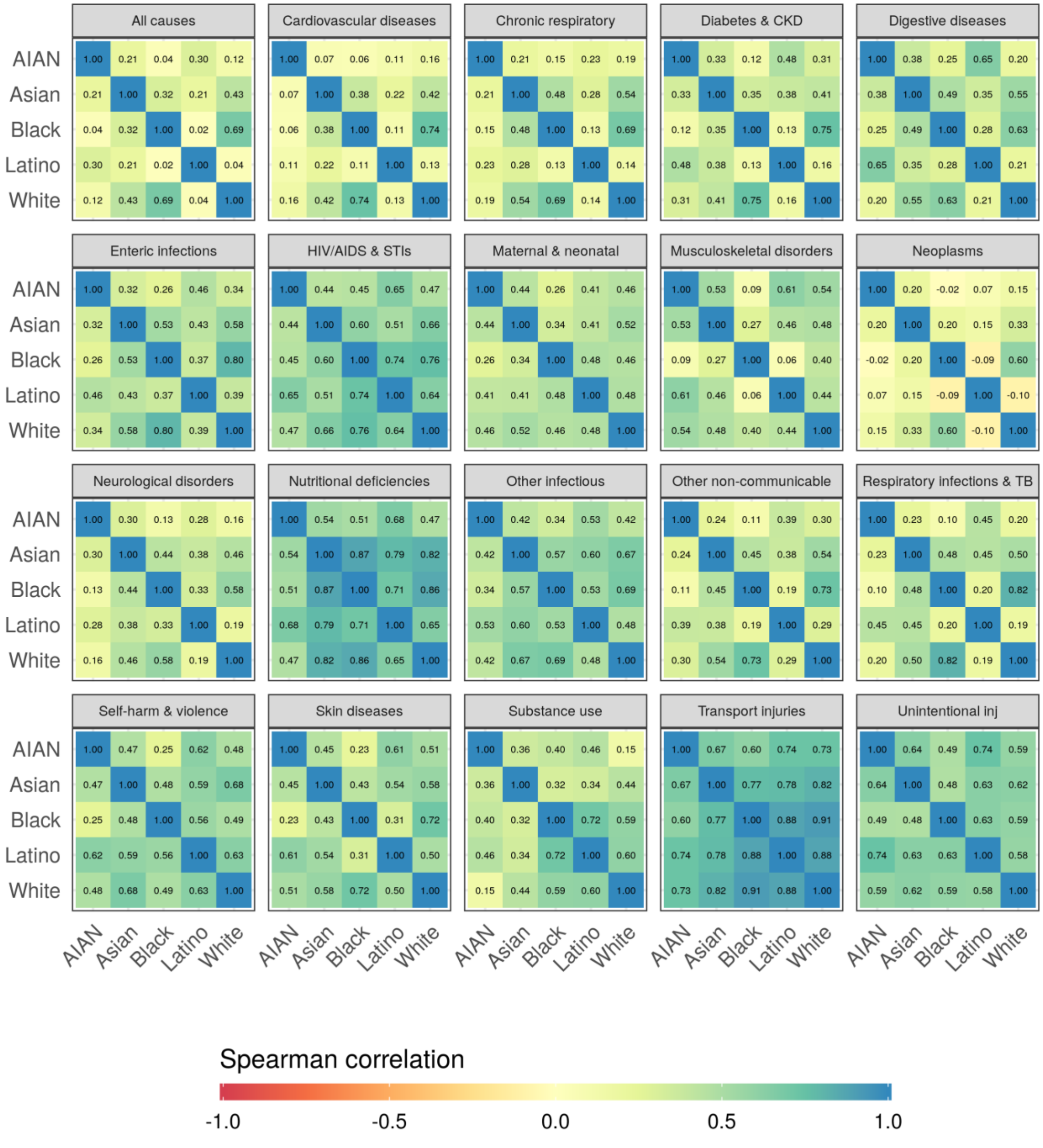
Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 80: Change in age-standardised mortality rate, self-harm and interpersonal violence, 2000–2019



Note: estimates have been masked for county and racial–ethnic group combinations with a mean annual population of fewer than 1000 people. AIAN = non-Latino and non-Hispanic American Indian or Alaska Native.

eFigure 81: Spearman correlation among racial–ethnic groups (across counties), 2019



All causes

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.21	0.04	0.30	0.12
Asian	0.21	1.00	0.32	0.21	0.43
Black	0.04	0.32	1.00	0.02	0.69
Latino	0.30	0.21	0.02	1.00	0.04
White	0.12	0.43	0.69	0.04	1.00

Cardiovascular diseases

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.07	0.06	0.11	0.16
Asian	0.07	1.00	0.38	0.22	0.42
Black	0.06	0.38	1.00	0.11	0.74
Latino	0.11	0.22	0.11	1.00	0.13
White	0.16	0.42	0.74	0.13	1.00

Chronic respiratory

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.21	0.15	0.23	0.19
Asian	0.21	1.00	0.48	0.28	0.54
Black	0.15	0.48	1.00	0.13	0.69
Latino	0.23	0.28	0.13	1.00	0.14
White	0.19	0.54	0.69	0.14	1.00

Diabetes & CKD

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.33	0.12	0.48	0.31
Asian	0.33	1.00	0.35	0.38	0.41
Black	0.12	0.35	1.00	0.13	0.75
Latino	0.48	0.38	0.13	1.00	0.16
White	0.31	0.41	0.75	0.16	1.00

Digestive diseases

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.38	0.25	0.65	0.20
Asian	0.38	1.00	0.49	0.35	0.55
Black	0.25	0.49	1.00	0.28	0.63
Latino	0.65	0.35	0.28	1.00	0.21
White	0.20	0.55	0.63	0.21	1.00

Enteric infections

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.32	0.26	0.46	0.34
Asian	0.32	1.00	0.53	0.43	0.58
Black	0.26	0.53	1.00	0.37	0.80
Latino	0.46	0.43	0.37	1.00	0.39
White	0.34	0.58	0.80	0.39	1.00

HIV/AIDS & STIs

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.44	0.45	0.65	0.47
Asian	0.44	1.00	0.60	0.51	0.66
Black	0.45	0.60	1.00	0.74	0.76
Latino	0.65	0.51	0.74	1.00	0.64
White	0.47	0.66	0.76	0.64	1.00

Maternal & neonatal

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.44	0.26	0.41	0.46
Asian	0.44	1.00	0.34	0.41	0.52
Black	0.26	0.34	1.00	0.48	0.46
Latino	0.41	0.41	0.48	1.00	0.48
White	0.46	0.52	0.46	0.48	1.00

Musculoskeletal disorders

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.53	0.09	0.61	0.54
Asian	0.53	1.00	0.27	0.46	0.48
Black	0.09	0.27	1.00	0.06	0.40
Latino	0.61	0.46	0.06	1.00	0.44
White	0.54	0.48	0.40	0.44	1.00

Neoplasms

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.20	-0.02	0.07	0.15
Asian	0.20	1.00	0.20	0.15	0.33
Black	-0.02	0.20	1.00	-0.09	0.60
Latino	0.07	0.15	-0.09	1.00	-0.10
White	0.15	0.33	0.60	-0.10	1.00

Neurological disorders

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.30	0.13	0.28	0.16
Asian	0.30	1.00	0.44	0.38	0.46
Black	0.13	0.44	1.00	0.33	0.58
Latino	0.28	0.38	0.33	1.00	0.19
White	0.16	0.46	0.58	0.19	1.00

Nutritional deficiencies

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.54	0.51	0.68	0.47
Asian	0.54	1.00	0.87	0.79	0.82
Black	0.51	0.87	1.00	0.71	0.86
Latino	0.68	0.79	0.71	1.00	0.65
White	0.47	0.82	0.86	0.65	1.00

Other infectious

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.42	0.34	0.53	0.42
Asian	0.42	1.00	0.57	0.60	0.67
Black	0.34	0.57	1.00	0.53	0.69
Latino	0.53	0.60	0.53	1.00	0.48
White	0.42	0.67	0.69	0.48	1.00

Other non-communicable

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.24	0.11	0.39	0.30
Asian	0.24	1.00	0.45	0.38	0.54
Black	0.11	0.45	1.00	0.19	0.73
Latino	0.39	0.38	0.19	1.00	0.29
White	0.30	0.54	0.73	0.29	1.00

Respiratory infections & TB

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.23	0.10	0.45	0.20
Asian	0.23	1.00	0.48	0.45	0.50
Black	0.10	0.48	1.00	0.20	0.82
Latino	0.45	0.45	0.20	1.00	0.19
White	0.20	0.50	0.82	0.19	1.00

Self-harm & violence

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.47	0.25	0.62	0.48
Asian	0.47	1.00	0.48	0.59	0.68
Black	0.25	0.48	1.00	0.56	0.49
Latino	0.62	0.59	0.56	1.00	0.63
White	0.48	0.68	0.49	0.63	1.00

Skin diseases

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.45	0.23	0.61	0.51
Asian	0.45	1.00	0.43	0.54	0.58
Black	0.23	0.43	1.00	0.31	0.72
Latino	0.61	0.54	0.31	1.00	0.50
White	0.51	0.58	0.72	0.50	1.00

Substance use

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.36	0.40	0.46	0.15
Asian	0.36	1.00	0.32	0.34	0.44
Black	0.40	0.32	1.00	0.72	0.59
Latino	0.46	0.34	0.72	1.00	0.60
White	0.15	0.44	0.59	0.60	1.00

Transport injuries

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.67	0.60	0.74	0.73
Asian	0.67	1.00	0.77	0.78	0.82
Black	0.60	0.77	1.00	0.88	0.91
Latino	0.74	0.78	0.88	1.00	0.88
White	0.73	0.82	0.91	0.88	1.00

Unintentional inj

	AIAN	Asian	Black	Latino	White
AIAN	1.00	0.64	0.49	0.74	0.59
Asian	0.64	1.00	0.48	0.63	0.62
Black	0.49	0.48	1.00	0.63	0.59
Latino	0.74	0.63	0.63	1.00	0.58
White	0.59	0.62	0.59	0.58	1.00

AIAN = non-Latino and non-Hispanic American Indian or Alaska Native; CKD = chronic kidney disease (kidney diseases); inj = injuries; STIs = sexually transmitted infections; TB = tuberculosis.