

Supplementary Materials for

Exposure to air pollution and COVID-19 mortality in

the United States: A nationwide cross-sectional study

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S.1 Data

Health data

The Johns Hopkins University Center for Systems Science and Engineering (JHU-CSSE) created and maintains a platform hosting worldwide coronavirus case and death count data at the national and sub-national level that are updated in real time. For the US, these data are provided by the US Centers for Disease Control and Prevention (CDC) and state government at the county level. As of April 20, 2020, the CDC reports that COVID-19 testing is being conducted at 97 public health laboratories across the US and territories. The CDC website (1) says that COVID-19 deaths are identified using the International Statistical Classification of Diseases and Related Health Problems (ICD) codes for cause of death recorded on death certificates. The ICD-10 code indicating a COVID-19 related death is U07.1. The CDC notes that deaths reported with this code “can include laboratory confirmed cases, as well as cases without laboratory confirmation.” They also note that the data may be affected by delays in reporting and by differential reporting practices across states (1).

Pollution data

We rely on modeled $\text{PM}_{2.5}$ exposure estimates rather than monitored observations alone, because air pollution monitors are sparsely distributed across the US, with a large majority of counties not containing a monitor. Our primary $\text{PM}_{2.5}$ modeled exposure estimates are produced by van Donkelaar et al (2019) (2). They are created by fusing $\text{PM}_{2.5}$ measures from three different sources: ground-based monitors, GEOS-Chem chemical transport models (CTM), and satellite observations. In short, CTM and satellite data are combined to estimate a high-resolution $\text{PM}_{2.5}$ surface across the whole US, then this surface is bias-corrected for ground-monitor $\text{PM}_{2.5}$ observations using a geographically-weighted regression. The cross-validated R^2 for these models in the US was reported to be 0.61, although the accuracy varies across regions. For the primary analysis, the gridded data were aggregated to the

county level using area-aggregation and then were averaged across the years 2000-2016. For sensitivity analyses, we also considered the county-average $\text{PM}_{2.5}$ on the year 2016 only, created using an analogous procedure.

To assess the sensitivity of our results to the specific $\text{PM}_{2.5}$ prediction model used to generate exposure estimates, we also collect the estimated daily $\text{PM}_{2.5}$ modeled exposure at a high spatio-temporal resolution of $1 \text{ km} \times 1 \text{ km}$ grid network across the whole US using another well-validated ensemble-based prediction model (3). This model used ensemble learning approaches to combine three machine learning models; a random forest regression, a gradient boosting machine, and an artificial neural network. These machine learning algorithms used more than 100 predictor variables from satellite data, land-use information, weather variables, and output from chemical transport model simulations. We use the same area-aggregation approach to aggregate the gridded data to the county level and then were averaged across the years 2000-2016.

Potential Confounders

To adjust for confounding bias in the nationwide observational study, we use county level variables from numerous public sources. Multiple socioeconomic and demographic variables were collected from the 2000 and 2010 Census (<https://www.census.gov>), the 2005–2016 American Community Surveys (<https://www.census.gov/programs-surveys/acs/>) and the 2009–2016 CDC Compressed Mortality File (https://www.cdc.gov/nchs/data_access/cmf.htm). Specifically, we collect the following 11 county level census variables: proportion of residents older than 65, proportion of residents 45-64, proportion of residents 15-44, proportion of Hispanic residents, proportion of Black residents, median household income, median home value, proportion of residents in poverty, proportion of residents with a high school diploma, population density, and proportion of residents that own their house. We also collect two county-level health risk factors: proportion of residents obese and proportion of residents that are current smokers from the Robert Wood

Johnson Foundation’s 2020 County Health Rankings (<https://www.countyhealthrankings.org/explore-health-rankings/rankings-data-documentation>).

Certain features of the counties’ COVID-19 outbreaks and response and the accessibility of health care may also confound the relationship between $PM_{2.5}$ and COVID-19 mortality. One particularly important feature is the county’s point on the epidemic curve at the time of analysis. Although this feature is difficult to accurately measure, we approximate it using time since first reported COVID-19 case. This information is also extracted from the JHU-CSSE database (the same source used for the COVID-19 death counts). The database records county-level case counts starting on March 22, 2020, meaning that our measure of time since first COVID-19 case will be truncated by this date. Thus, the time since first COVID-19 case variable is formally defined as “days between April 22, 2020 and the later of March 22, 2020 of the date of the first COVID-19 case reported in the county”. States also issued “stay-at-home/shelter-in-place” orders in response to the outbreak at different times, which likely affected infection rates and could also be associated with $PM_{2.5}$. Thus, we also adjust our models for state-level time since implementation of stay-at-home/shelter-in-place order, obtained from COVID-19 US state policy database (www.tinyurl.com/statepolicies). During the course of COVID-19 outbreak, the availability of adequate hospital resources and of testing resources likely influence COVID-19 outcomes and these may also be more widely available in urban areas where $PM_{2.5}$ is also higher. We collect county-level information on number of hospital beds available in 2019 from Homeland Infrastructure Foundation-Level Data (HIFLD) and state-level information on number of COVID-19 tests performed up to April 22, 2020 from the COVID tracking project (<https://covidtracking.com/>).

Meteorological variables are commonly adjusted for when studying the health impacts of air pollution. We obtain meteorological variables on maximum daily temperature and relative humidity data on 4km x 4km gridded rasters from Gridmet via Google Earth Engine (https://developers.google.com/earth-engine/datasets/catalog/IDAHO_EPSCOR_GRIDMET). We average daily temperature and relative humidity for the summer (June-September) and win-

ter (December-February) period respectively across the period 2000-2016 and average across grid rasters in each county. We adjust for all four of these weather variables in our main models. The data used for this study are publicly available and sources are listed in Table 1 of the main manuscript.

S.2 Statistical Modeling

For our main and secondary analyses, we fit Negative Binomial regression models with a state-specific random intercept (4; 5). All potential confounders are centered and scaled prior to analysis. Letting $E[\cdot]$ denote an expected value, the main model takes the form

$$\begin{aligned} \log(E[\text{COVID-19 deaths}]) = & \beta_0 + \beta_1 \text{PM}_{2.5} + \beta_2 \text{population density} + \beta_3 \text{percent} \\ & \text{of the population} \geq 65 + \beta_4 \text{percent of the population 45-64} + \beta_5 \text{percent of the} \\ & \text{population 15-44} + \beta_6 \text{percent living in poverty} + \beta_7 \text{median household income} + \\ & \beta_8 \text{percent black} + \beta_9 \text{percent hispanic} + \beta_{10} \text{percent of adults with less than a} \\ & \text{high school education} + \beta_{11} \text{median house value} + \beta_{12} \text{percent of owner-occupied} \\ & \text{housing} + \beta_{13} \text{percent obese} + \beta_{14} \text{percent smokers} + \beta_{15} \text{days since first case} + \\ & \beta_{16} \text{days since stay at home order} + \beta_{17} \text{number of hospital beds} + \beta_{18} \text{average} \\ & \text{summer temperature} + \beta_{19} \text{average summer relative humidity} + \beta_{20} \text{average winter} \\ & \text{temperature} + \beta_{21} \text{average winter relative humidity} + \text{offset}(\log(\text{population size})) \\ & + \text{random intercept}(\text{State}) \end{aligned}$$

We report the mortality rate ratios (MRR) and 95% CIs for $\text{PM}_{2.5}$, corresponding to the exponentiated parameter estimate ($e^{\hat{\beta}_1}$). The MRR can be interpreted as the multiplicative increase in the COVID-19 death rate associated with a $1 \mu\text{g}/\text{m}^3$ increase in long-term average $\text{PM}_{2.5}$ exposure.

Model Assumption Diagnostics

Poisson regression models are a common choice for modeling count data, but the Poisson distribution is restrictive in that it assumes that the mean is equal to the variance. In our setting, because most counties have experienced few or no COVID-19 deaths thus far, the mean of our outcome data is small ($\mu = 14.84$); however the variance is large due to the large death counts in several outbreak epicenters ($\sigma^2 = 278.61$). Among the counties with non-zero deaths, the mean of our outcome data is still relative small ($\mu = 35.57$); however the variance is large ($\sigma^2 = 430.56$). The dispersion parameter for the quasi-Poisson family is estimated to be 20.87, which indicates substantial over-dispersion. Thus, the Poisson distributional assumption is likely to be inappropriate. The negative binomial distribution provides more flexibility by introducing an additional parameter that allows the count outcome variable with variance larger than mean. This flexibility also better accounts for the large number of zeros in our outcome, without requiring the use of zero-inflated models, which are more complex and less interpretable.

To assess the model fit of the standard Negative Binomial regression model comparing to a zero-inflated Negative Binomial regression model, we conduct an Vuong closeness test for the goodness-of-fit (6). We found no statistically significant improvement of model fit for a zero-inflated Negative Binomial regression model (P-Value = 0.22). The AIC of the standard Negative Binomial regression model is even slightly lower (AIC= 9498.5 vs. 9499.0), which suggests a better model fit.

Unmeasured Confounding Sensitivity Analysis

We conducted a sensitivity analysis to evaluate the robustness of our results to unmeasured confounding by calculating the E-value (7). The E-value for the point estimate of interest (in our case the MRR) can be defined as the minimal strength of association, on the risk ratio scale, that an unmeasured confounder would need to have with both the exposure and outcome, conditional on the covariates already included in the model, to fully

explain the observed association under the null. We calculated the E-values for our reported MRRs per 1 $\mu\text{g}/\text{m}^3$ increase of long-term exposure to $\text{PM}_{2.5}$. The calculation of E-values can be implemented through the E-value calculator by Mathur et al (8), available at <https://www.evalue-calculator.com/>.

For our main analysis, we found that for an unmeasured confounder U to fully account for the estimated effects of the exposure E on the outcome Y , it would have to be associated with both long-term $\text{PM}_{2.5}$ exposure (E) and with mortality (Y) by a risk ratio of at least 1.37-fold each, through pathways independent of all covariates already included in the model. In other words, if we were to adjust for this U in our model, the estimated MRR for $\text{PM}_{2.5}$ would be reduced to 1 (the null value). A 1.37 risk ratio means that U would need to meet the following two criteria: 1) a 1-unit increase in U would need to lead to a 37% increase in the risk of mortality (Y); *and* 2) a 1-unit increase in U would need to be associated with a 37% increase in $\text{PM}_{2.5}$ exposure levels.

S.3 Additional Analysis Results

The detailed results are presented in Table S1-S4 and Figure S1-S2.

Alternative $\text{PM}_{2.5}$ Estimates

To evaluate the sensitivity of our results to the approach used to calculate long-term pollution exposure measure, we repeat our analyses using four relevant sets of exposure data. Using the modeled exposure estimates of van Donkelaar et al (2), we test the 17-year average concentrations (2000-2016), i.e., the primary analysis results, and the one-year average concentrations using the most recent available year (2016), and we refer to the analyses using these exposures as P-1 and P-2, respectively. Using the modeled exposure estimates of Di et al (2019) (3), we test the 17-year average concentrations (2000-2016) and the one-year average concentrations using the most recent available year (2016), referred to

as P-3 and P-4 respectively. In each analysis, we adjust for the set of potential confounders described in the main text and in Section S1. The finding that long-term exposure to $\text{PM}_{2.5}$ is positively associated with increased COVID-19 mortality holds regardless of which pollution data are used. When adjusted for the full confounder set, analyses using 17-year average concentrations (2000-2016) (P-1 and P-3) give similar point estimates for $\text{PM}_{2.5}$ and attain statistical significance using different pollution data sources. We note the fact that one year average estimates to $\text{PM}_{2.5}$ exposure are less reliable than 17-year average. In particular, the analysis results using P-2 and P-4 are less agreed with each other, i.e., P-2 is notably lower, yet P-4 is notably higher. The analysis using single year exposure data P-2, in which though shows positive associations between long-term exposure to $\text{PM}_{2.5}$ and increased mortality for COVID-19 yet remain statistical insignificance. Because the focus of our study is to assess the cumulative chronic effect of long-term exposure to $\text{PM}_{2.5}$, we use 17-year mean exposure data in our main report.

Differing Confounder Sets

For each of these pollution data sources, we evaluate the model sensitivity to the set of confounders adjusted for by individually omitting each of the following from the confounder set: 1) days since first reported COVID-19 case; 2) number of hospital beds in the county; 3) behavioral risk factors, i.e., population obesity rate and percent of population who are current smokers; and 4) meteorological (weather) variables, i.e., summer and winter temperature and relative humidity. We also conduct analyses adjusting for the following additional variables (separately): 1) the total number of COVID-19 tests performed up to April 22, 2020 in each state and 2) the estimated percentage of people with COVID-19 symptoms in each county. Effect estimates are presented as mortality rate ratio (MRR) per $1 \mu\text{g}/\text{m}^3$ increase in annual $\text{PM}_{2.5}$.

We find consistent positive associations between long-term exposure to $\text{PM}_{2.5}$ and increased mortality for COVID-19 in these analyses, with MRR between 1.08 – 1.10 across

P-1 models that adjust for different potential confounders (similar results for P-2, P-3, and P-4). The removal of days since first reported COVID-19 case from the confounder set consistently elevates the $PM_{2.5}$ point estimates and increases the statistical significance. This suggests that days since first reported COVID-19 case is a strong confounder, as it captures the different stages on the epidemic curve of each county.

Assessing the Impact of Outbreak Size

To evaluate the possible impact of confounding bias due to epidemic outbreak sizes, which are not accurately captured by current data, we conduct analyses 1) excluding counties in New York metropolitan area where the major outbreak is happening 2) excluding counties with less than 10 confirmed COVID-19 cases. In the analysis that excludes counties in New York metropolitan area, we still find a statistically significant association between long-term exposure to $PM_{2.5}$ and increased mortality for COVID-19 with MRR 1.07 and 95% confidence interval (1.01, 1.14) for P-1. In the analysis that excludes counties with less than 10 confirmed COVID-19 cases, we also find a positive association with increased mortality of COVID-19 with magnitude of MRR 1.06 and 95% confidence interval (1.00, 1.13) for P-1. The loss of statistical significance, however, is partially due to dramatically reduced sample size (1692 counties only).

Differing Model Specifications

To evaluate the sensitivity to modeling choices (e.g., distributional assumptions or assumptions of linearity), we conduct sensitivity analyses by 1) treating $PM_{2.5}$ as a categorical variable (categorized at empirical quintiles), 2) adjusting for population density under a logarithm transformation rather than a categorical variable, 3) using a zero-inflated negative binomial mixed model, 4) using a fixed effect negative binomial model, 5) adjusting for population size as a covariate, rather than as an offset. We also conducted stratified analyses based on county urban/rural status. Counties' classifications are obtained from

the National Center for Health Statistics Urban-Rural Classification Scheme for Counties (9), which assigns each US county to one of six urban-rural categories: Large central metro, Large fringe metro, Medium metro, Small metro, Micropolitan, and Non-core. Based on this, we create a two-level urban/rural variable, with Micropolitan and Non-core defined as rural, and all other types defined as urban. We then conduct the main analysis separately for urban counties and rural counties.

In the analysis that treats $PM_{2.5}$ as a categorical variable, we found the magnitude of the MRRs increases dramatically and monotonically as the quintile of $PM_{2.5}$ exposures increases for P-1. Similar results are found when using P-2, P-3, and P-4. Such findings suggest that the assumption of a linear effect of $PM_{2.5}$ on COVID-19 mortality rate is reasonable and that there is no threshold for the effect of long-term exposure to $PM_{2.5}$ on COVID-19 mortality. In the analysis that adjusts for population density under a logarithm transformation, we again find a statistically significant positive association with increased COVID-19 mortality with MRR 1.08 for P-1. In the analysis that uses a negative binomial model accounting for zero-inflation, we find very similar results as of our main analyses. In the analysis that uses a fixed effect negative binomial model, we find a slightly reduced effect size compared to our main analyses. In the analysis that adjusts for population size directly, rather than as an offset, we find long-term exposure to $PM_{2.5}$ is still significantly positively associated with the number of COVID-19 deaths, although here the MRR refers to the increase in the mortality count ratio of COVID-19 per unit increase of $PM_{2.5}$, rather than the increase in the mortality rate ratio.

The results of the urban/rural stratified analyses suggest an interesting pattern– the positive association between $PM_{2.5}$ and COVID-19 mortality appears to be approximately the same in rural counties (MRR 1.06, 95% CI 0.95, 1.19) and in urban counties (MRR 1.06, 95% CI 0.98, 1.13) for P-1. This confirms that our results are not dominated only by large urban areas where the most severe outbreaks have been reported (and often tend to be highly polluted). While the results from the stratified analyses are not statistically

significant, likely due to smaller sample sizes and lower power, the magnitude of the effect sizes is large.

S.4 Code

We provide code for all analyses reported in the paper. The completed code can be found on https://github.com/wxwx1993/PM_COVID.

S.5 Figures

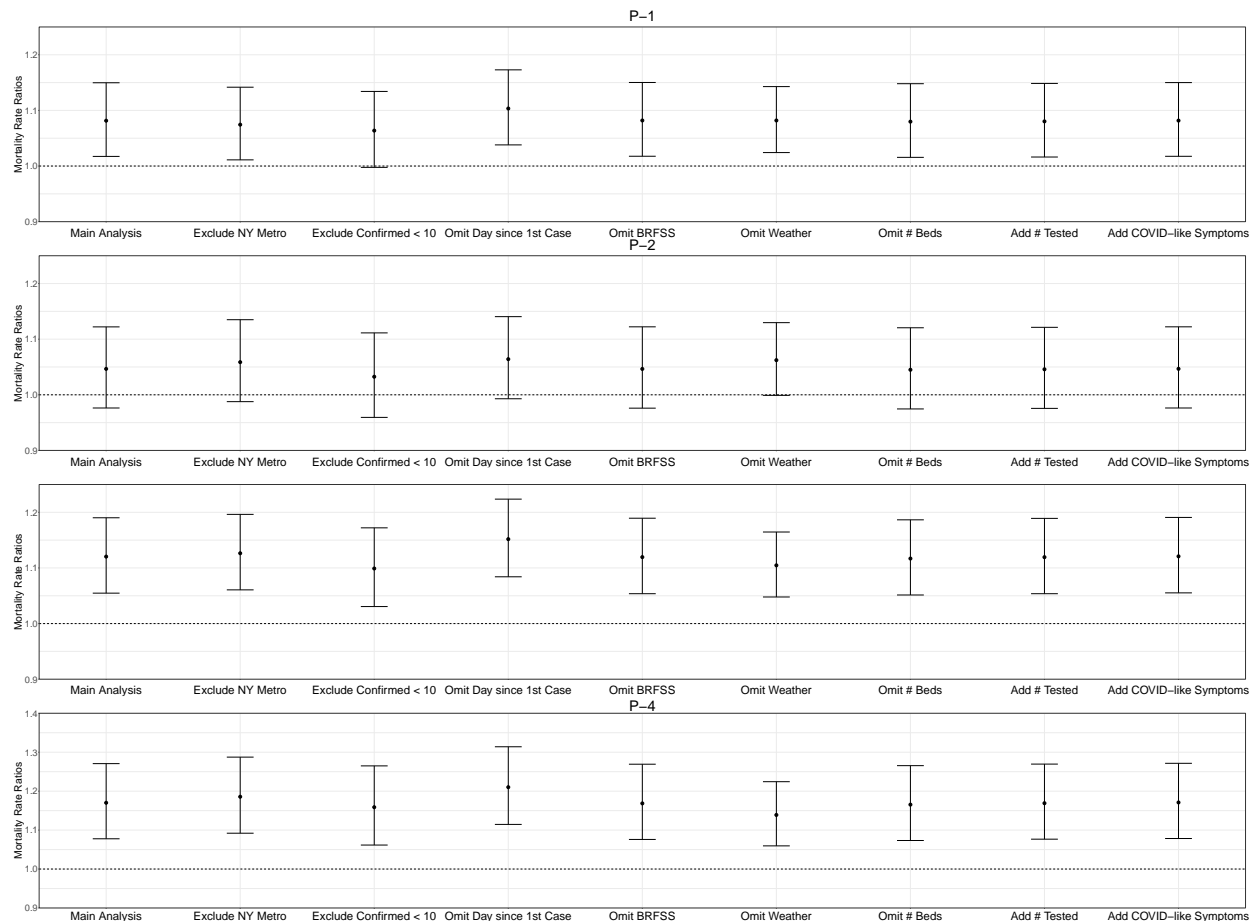


Figure S1: COVID-19 mortality rate ratios (MRR) per 1 $\mu\text{g}/\text{m}^3$ increase in $\text{PM}_{2.5}$ and 95% CI. The main analyses were adjusted for 20 socioeconomic, demographic, behavioral, climate, and healthcare confounders. In addition to the main analysis, we fit models excluding counties from NY metropolitan area, and excluding counties with < 10 confirmed cases. We also conduct analyses omitting the following variables from the adjustment set: days since first COVID-19 case (day since 1st case), smoking rate and obesity rate (BRFSS), seasonal temperature and humidity variables (weather), and number of hospital beds. We conduct analyses adjusting for two additional variables (separately): the total number of COVID-19 tests performed up to April 22, 2020 and the estimated percent of people with COVID-19 symptoms. We repeat our analyses using four relevant sets of exposure data (P-1, P-2, P-3 and P-4).

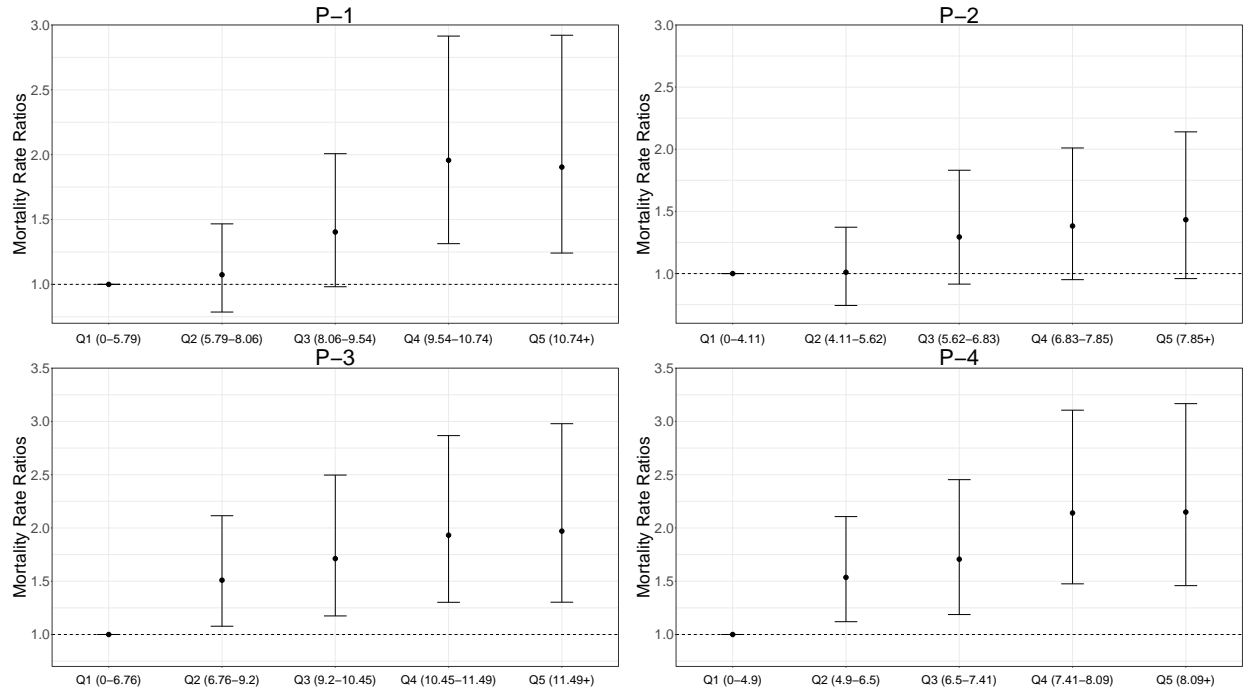


Figure S2: COVID-19 mortality rate ratios (MRR) per empirical quintile increase in PM_{2.5} and 95% CI. The MRR can be interpreted as the percentage increase in the COVID-19 death rate associated with each empirical quintile increase of long-term average PM_{2.5} compared to the baseline quintile (Q1). We repeat our analyses using four relevant sets of exposure data (P-1, P-2, P-3 and P-4).

S.6 Tables

Table S1: Main, secondary and sensitivity analysis results for P-1, i.e., PM_{2.5} exposure measured as the 17-year average concentration 2000-2016 by van Donekelaar et al (2019) (2). Point estimates, 95 % confidence intervals, and p-values for the mortality rate ratio (MRR) for PM_{2.5} .

Analysis	N Counties	MRR (CI)	P-Value
Main analysis	3087	1.08(1.02, 1.15)	0.01
Omit number of hospital beds	3087	1.08(1.02, 1.15)	0.01
Omit behavioral	3087	1.08(1.02, 1.15)	0.01
Omit weather	3087	1.08(1.02, 1.14)	0.00
Omit days since first case	3087	1.10(1.04, 1.17)	0.00
Exclude counties in New York Metropolitan	3060	1.07(1.01, 1.14)	0.02
Exclude counties with <10 confirmed cases	1692	1.06(1.00, 1.13)	0.06
Rural counties	1940	1.06(0.95, 1.19)	0.27
Urban counties	1147	1.06(0.98, 1.13)	0.12
Categorize PM into quintiles	3087		
Q1 (0-5.79 $\mu\text{g}/\text{m}^3$)		1.00	
Q2 (5.79-8.06 $\mu\text{g}/\text{m}^3$)		1.07(0.79, 1.47)	0.65
Q3 (8.06-9.54 $\mu\text{g}/\text{m}^3$)		1.40(0.98, 2.01)	0.06
Q4 (9.54-10.74 $\mu\text{g}/\text{m}^3$)		1.96(1.31, 2.91)	0.00
Q5 (10.74+ $\mu\text{g}/\text{m}^3$)		1.90(1.24, 2.92)	0.00
Add number tested	3087	1.08(1.02, 1.15)	0.01
Add percent with COVID symptoms	3087	1.08(1.02, 1.15)	0.01
Adjust log(population density) as covariate	3087	1.08(1.01, 1.15)	0.02
Adjust log(population) as covariate	3087	1.12(1.05, 1.19)	0.00
Adjust population as covariate	3087	1.17(1.09, 1.25)	0.00
Zero inflated Negative Binomial model	3087	1.08(1.02, 1.15)	0.01
Fixed effects Negative Binomial model	3087	1.06(1.00, 1.13)	0.06

1. Five boroughs of New York City are considered as one county aligning with COVID-19 statistics.
2. "Rural" represents "Micropolitan" and "Non-core" counties defined by 2013 NCHS Urban-Rural Classification Scheme.

Table S2: Main, secondary and sensitivity analysis results for P-2, i.e., PM_{2.5} exposure measured as 2016 average by van Donekelaar et al (2019) (2). Point estimates, 95 % confidence intervals, and p-values for the mortality rate ratio (MRR) for PM_{2.5} .

Analysis	<i>N</i> counties	MRR (CI)	P-Value
Main analysis	3087	1.05(0.98, 1.12)	0.20
Omit number of hospital beds	3087	1.05(0.97, 1.12)	0.22
Omit behavioral	3087	1.05(0.98, 1.12)	0.20
Omit weather	3087	1.06(1.00, 1.13)	0.05
Omit days since first case	3087	1.06(0.99, 1.14)	0.08
Exclude counties in New York Metropolitan	3060	1.06(0.99, 1.13)	0.11
Exclude counties with <10 confirmed cases	1692	1.03(0.96, 1.11)	0.39
Rural counties	1940	1.05(0.92, 1.19)	0.49
Urban counties	1147	1.04(0.96, 1.12)	0.37
Categorize PM into quintiles	3087		
Q1 (0-4.11 $\mu\text{g}/\text{m}^3$)		1.00	
Q2 (4.11-5.62 $\mu\text{g}/\text{m}^3$)		1.01(0.74, 1.37)	0.95
Q3 (5.62-6.83 $\mu\text{g}/\text{m}^3$)		1.29(0.92, 1.83)	0.14
Q4 (6.83-7.85 $\mu\text{g}/\text{m}^3$)		1.38(0.95, 2.01)	0.09
Q5 (7.85+ $\mu\text{g}/\text{m}^3$)		1.43(0.96, 2.14)	0.08
Add number tested	3087	1.05(0.98, 1.12)	0.21
Add percent with COVID symptoms	3087	1.05(0.98, 1.12)	0.20
Adjust log(population density) as covariate	3087	1.04(0.96, 1.11)	0.35
Adjust log(population) as covariate	3087	1.09(1.01, 1.17)	0.02
Adjust population as covariate	3087	1.14(1.06, 1.23)	0.00
Zero inflated Negative Binomial model	3087	1.05(0.98, 1.12)	0.20
Fixed effects Negative Binomial model	3087	1.02(0.95, 1.09)	0.60

Table S3: Main, secondary and sensitivity analysis results for P-3, i.e., PM_{2.5} exposure measured as the 17-year average concentrations 2000-2016 by Di et al (2019) (3). Point estimates, 95 % confidence intervals, and p-values for the mortality rate ratio (MRR) for PM_{2.5} .

Analysis	<i>N</i> counties	MRR (CI)	P-Value
Main analysis	3087	1.12(1.05, 1.19)	0.00
Omit number of hospital beds	3087	1.12(1.05, 1.19)	0.00
Omit behavioral	3087	1.12(1.05, 1.19)	0.00
Omit weather	3113	1.10(1.05, 1.16)	0.00
Omit days since first case	3087	1.15(1.08, 1.22)	0.00
Exclude counties in New York Metropolitan	3060	1.13(1.06, 1.20)	0.00
Exclude counties with <10 confirmed cases	1692	1.10(1.03, 1.17)	0.00
Rural counties	1940	1.15(1.03, 1.27)	0.01
Urban counties	1147	1.07(0.99, 1.15)	0.07
Categorize PM into quintiles	3087		
Q1 (0-6.76 μ g/m ³)		1.00	
Q2 (6.76-9.2 μ g/m ³)		1.51(1.08, 2.11)	0.02
Q3 (9.2-10.45 μ g/m ³)		1.71(1.17, 2.50)	0.01
Q4 (10.45-11.49 μ g/m ³)		1.93(1.30, 2.87)	0.00
Q5 (11.49+ μ g/m ³)		1.97(1.30, 2.98)	0.00
Add number tested	3087	1.12(1.05, 1.19)	0.00
Add precent with COVID symptoms	3087	1.12(1.06, 1.19)	0.00
Adjust log(population density) as covariate	3087	1.12(1.05, 1.19)	0.00
Adjust log(population) as covariate	3087	1.14(1.08, 1.21)	0.00
Adjust population as covariate	3087	1.15(1.14, 1.16)	0.00
Zero inflated Negative Binomial model	3087	1.12(1.05, 1.19)	0.00
Fixed effects Negative Binomial model	3087	1.11(1.04, 1.18)	0.00

Table S4: Main, secondary and sensitivity analysis results for P-4, i.e., PM_{2.5} exposure measured as 2016 average by Di et al (2019) (3). Point estimates, 95 % confidence intervals, and p-values for the mortality rate ratio (MRR) for PM_{2.5} .

Analysis	<i>N</i> counties	MRR (CI)	P-Value
Main analysis	3087	1.17(1.08, 1.27)	0.00
Omit number of hospital beds	3087	1.17(1.07, 1.27)	0.00
Omit behavioral	3087	1.17(1.08, 1.27)	0.00
Omit weather	3113	1.14(1.06, 1.22)	0.00
Omit days since first case	3087	1.21(1.11, 1.31)	0.00
Exclude counties in New York Metropolitan	3060	1.19(1.09, 1.29)	0.00
Exclude counties with <10 confirmed cases	1692	1.16(1.06, 1.26)	0.00
Rural counties	1940	1.22(1.05, 1.42)	0.01
Urban counties	1147	1.14(1.03, 1.26)	0.01
Categorize PM into quintiles	3087		
Q1 (0-4.9 μ g/m ³)		1.00	
Q2 (4.9-6.5 μ g/m ³)		1.54(1.12, 2.11)	0.01
Q3 (6.5-7.41 μ g/m ³)		1.71(1.19, 2.45)	0.00
Q4 (7.41-8.09 μ g/m ³)		2.14(1.48, 3.11)	0.00
Q5 (8.09+ μ g/m ³)		2.15(1.46, 3.17)	0.00
Add number tested	3087	1.17(1.08, 1.27)	0.00
Add percent with COVID symptoms	3087	1.17(1.08, 1.27)	0.00
Adjust log(population density) as covariate	3087	1.16(1.07, 1.27)	0.00
Adjust log(population) as covariate	3087	1.20(1.10, 1.30)	0.00
Adjust population as covariate	3087	1.20(1.10, 1.31)	0.00
Zero inflated Negative Binomial model	3087	1.17(1.08, 1.27)	0.00
Fixed effects Negative Binomial model	3087	1.15(1.06, 1.25)	0.00

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