# **Supplementary material**

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**Supplement Figure 01**. Study Group 2 zip codes and the matched controls for the Group 2 zip codes.

**Supplement Table 01**. The summaries of five matching variables used to match the study Group 2 with the control zip codes. See Table S1 of Kravchenko et al., (2018) for the compatible table.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Variable** | **Group 2 zipcodes** | **Matched Control zipcodes for Group 2** |
| 1 | Percent of African Americans | 29.23 ± 15.47 | 29.33 ± 16.05 |
| 2 | Percent of children (aged 0-10) | 19.10 ± 1.02 | 18.25 ± 2.83 |
| 3 | Percent of people aged 65+ | 11.05 ± 2.35 | 12.94 ± 10.04 |
| 4 | Median household income | $37,111.17 ± 7304.96 | $40,540. 63 ± 11, 686. 90 |
| 5 | Percent of people with high school or higher education in people aged 25+ | 18.57 ± 3.18 | 17.54 ± 5.01 |

**Supplement Table 02**. The International Classification of Diseases (ICD) codes used to extract relevant disease diagnostics from the H-CUP database. See Appendix 1 of Kravchenko et al., (2018) for the compatible table.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Disease Condition** | **ICD-9 Codes** | **ICD-10 Codes** |
| 1 | Anemia | 280-285 | D50-D53, D55-D59, D60-D64 |
| 2 | Kidney Disease | 580-589 | N00-N19 |
| 3 | Tuberculosis | 010-018 | A15-A19 |
| 4 | Septicemia | 038, 995.91 | A40-A41 |
| 5 | Low Birth Weight | V21.3 | P07.1 |
| 6 | HIV | 042 | B20 |
| 7 | Diabetes | 250 | E10-E11, E13 |

**Supplement Table 03.** Testing for confounding. Results of logistic regression indicating odds ratios and the percent change of odds ratios when each of the six confounding variable was introduced to the model one-by-one and collectively. The table summarizes the association of exposure Group 1 (compared to the controls) for hospitalizations due to kidney diseases and septicemia.



**Supplement Table 04.** Sensitivity analysis with and without the urban zipcodes. Odds ratios (OR) of mortalities related to the eight conditions are compared. There were no changes in the OR.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Negative health outcome** | **With urban areas** | **Without urban areas** |
| **Mortality** | **Anemia** | 1.165 | 1.165 |
| 95% CI & P | (0.748-1.813; p=0.499) | (0.748-1.813; p=0.499) |
| **Kidney Dz** | 1.179 | 1.179 |
| 95% CI & P | (1.057-1.315; p=0.003) | (1.057-1.315; p=0.003) |
| **Tuberculosis** | 0.741 | 0.741 |
| 95% CI & P | (0.193-2.847; p=0.66) | (0.193-2.847; p=0.66) |
| **Septicemia** | 1.070 | 1.070 |
| 95% CI & P | (1.036-1.106; p<0.0001) | (1.036-1.106; p<0.0001) |
| **HIV** | 1.092 | 1.092 |
| 95% CI & P | (0.723-1.647; p=0.676) | (0.723-1.647; p=0.676) |
| **Diabetes** | 0.913 | 0.913 |
| 95% CI & P | (0.726-1.148; p=0.438) | (0.726-1.148; p=0.438) |
| **All-cause** | 0.913 | 0.913 |
| 95% CI & P | (0.726-1.148; p=0.438) | (0.726-1.148; p=0.438) |

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**Supplementary Fig 02.** Mapped summaries of the hospitalizations, emergency department visits, and the rates of selected disease conditions. H-CUP data from 2007 – 2014 were used in the summaries. Each variable is categorized in to three based on the natural breaks (Jenks) if the variable.

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**Supplementary Fig 03.** Point density map of hog CAFOs in North Carolina weighted by hog counts. The zip code map is overlaid on the point density map and the areas with zero density is separated as an independent category.

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**Supplementary Fig 04**. Map of Co-Kriging using two variables: Var 1) the 10-log of hog counts and Var 2) number of lagoons. The predicted exposure levels are classified into five based on quantiles in which class 5 represents the highest exposure and class 1 the lowest. Co-Kriging is a geostatistical method and the distance between CAFOs and the spatial dependence is accounted for in the calculation. Further details on co-Kriging method are found elsewhere (Isaaks and Srivastava, 1989; Kanankege et al., 2020).

**Supplementary documents: SAS codes**

/\*SAS Code used for logistic regression and odds ratio determination; Code below uses the Kidney Disease variable as an example\*/

**data** hcup;

set hcup.hcup0714;

**run**;

/\*Group 1 DX1 Comparison Code\*/

ods select parameterestimates oddsratios; /\*Select output\*/

**proc** **logistic** data=hcup; /\*Logistic regression procedure\*/

class studyG1 (desc); /\*studyG1 is a character variable that indicates zip codes as either 1 (Study Group 1) or 0 (Control)\*/

model died (event='1') = studyG1 AHRF\_Primary\_Care AHRF\_Health\_Insurance BRFSS\_Smoking2012 Age MedianHHIncome Education; /\*Defines the logistic regression model and includes confounding variables\*/

where DX1\_Kidney = **1**; /\*Only analyzes cases of primary diagnosis of kidney disease\*/

title 'Death: DX1 Kidney - Group 1';

**run**;

ods select parameterestimates oddsratios;

**proc** **logistic** data=hcup;

class studyG1 (desc);

model DX1\_Kidney (event='1') = studyG1 AHRF\_Primary\_Care AHRF\_Health\_Insurance BRFSS\_Smoking2017 Age MedianHHIncome Education;

where Hospital = **1**;

title 'Hospitalizations: DX1 Kidney - Group 1';

**run**;

ods select parameterestimates oddsratios;

**proc** **logistic** data=hcup;

class studyG1 (desc);

model DX1\_Kidney (event='1') = studyG1 AHRF\_Primary\_Care AHRF\_Health\_Insurance BRFSS\_Smoking2017 Age MedianHHIncome Education;

where EDV = **1**;

title 'Emergency Dept: DX1 Kidney - Group 1';

**run**;

/\*Group 1 DX1DX2 Comparison Code\*/

ods select parameterestimates oddsratios;

**proc** **logistic** data=hcup;

class studyG1 (desc);

model died (event='1') = studyG1 AHRF\_Primary\_Care AHRF\_Health\_Insurance BRFSS\_Smoking2017 Age MedianHHIncome Education;

where DX1DX2\_Kidney = **1**;

title 'Death: DX1DX2 Kidney - Group 1';

**run**;

ods select parameterestimates oddsratios;

**proc** **logistic** data=hcup;

class studyG1 (desc);

model DX1DX2\_Kidney (event='1') = studyG1 AHRF\_Primary\_Care AHRF\_Health\_Insurance BRFSS\_Smoking2017 Age MedianHHIncome Education;

where Hospital = **1**;

title 'Hospitalizations: DX1DX2 Kidney - Group 1';

**run**;

ods select parameterestimates oddsratios;

**proc** **logistic** data=hcup;

class studyG1 (desc);

model DX1DX2\_Kidney (event='1') = studyG1 AHRF\_Primary\_Care AHRF\_Health\_Insurance BRFSS\_Smoking2017 Age MedianHHIncome Education;

where EDV = **1**;

title 'Emergency Dept: DX1DX2 Kidney - Group 1';

**run**;