Appendix Table 1. Prevalence and Prevalence Ratio (95% CI) of Maternal Hepatitis C Virus (HCV) Infection by Selected Maternal Characteristics: U.S. Birth Certificate Data, 2010–2018

Characteristics	Total[a]	Mean prevalence of HCV infection (per 1,000 births)	Prevalence ratio (95% CI)	Mean prevalence of HCV infection (per 1,000 births) among 34 areas reporting as of 2010[b]
All	32,382,561	3.5	NA	3.5
Maternal age at birth, years				
<20	2,135,244	1.3	0.43 (0.41, 0.45)	1.2
20–24	7,045,163	3.5	1.22 (1.20, 1.25)	3.5
25–29	9,336,207	4.4	1.53 (1.50, 1.56)	4.3
30–34	8,676,649	3.4	1.16 (1.14, 1.19)	3.2
35–39	4,205,696	2.9	1.00	2.8
≥40	983,602	2.7	0.94 (0.90, 0.98)	2.6
Maternal race/ethnicity				
Hispanic	7,667,524	1.3	1.00	1.3
Non-Hispanic White	17,088,090	5.2	3.84 (3.76, 3.92)	5.1
Non-Hispanic Black	4,649,433	1.4	1.03 (1.00, 1.06)	1.5
Other[c]	2,977,514	2.7	1.98 (1.92, 2.04)	2.5
Marital status				
Not married, no paternity acknowledgement	3,851,351	10.0	6.55 (6.45, 6.65)	10.0
Not married, paternity acknowledgement	8,854,163	5.1	3.32 (3.28, 3.37)	4.9
Married	18,750,733	1.5	1.00	1.5
Missing	926,314	1.1	0.69 (0.65, 0.74)	1.1
Maternal educational attainment				
No high school diploma or GED	4,945,859	5.9	9.80 (9.53, 10.08)	5.6

High school diploma or GED	8,089,644	5.5	9.08 (8.84, 9.34)	5.2
Some college	9,255,206	3.5	5.82 (5.66, 5.98)	3.4
Bachelor’s degree or higher	9,697,805	0.6	1.00 (NA)	0.6
Missing	394,047	4.4	7.29 (6.91, 7.69)	3.9
Expected source of payment for delivery				
Medicaid	13,950,384	6.2	5.74 (5.65, 5.84)	6.0
Private	15,382,822	1.1	1.00	1.0
Self-pay	1,322,241	2.4	2.19 (2.11, 2.28)	2.2
Other	1,402,604	3.5	3.19 (3.09, 3.29)	3.3
Missing	324,510	4.7	4.33 (4.11, 4.56)	4.6
WIC use during pregnancy				
Yes	13,614,251	5.1	2.24 (2.22, 2.27)	4.9
No	18,215,480	2.3	1.00	2.2
Missing	552,830	4.7	2.08 (2.00, 2.17)	5.0
Pre-pregnancy BMI				
Underweight	1,142,457	5.1	1.96 (1.90, 2.02)	4.9
Normal	14,176,191	3.9	1.52 (1.49, 1.54)	3.8
Overweight	8,069,854	3.3	1.30 (1.27, 1.32)	3.2
Obese	7,896,348	2.6	1.00	2.5
Missing	1,097,657	4.2	1.61 (1.56, 1.67)	4.1
Pregnancy smoking status[d]				
No	28,713,944	1.5	1.00	1.5
Yes	2,467,103	26.7	17.48 (17.27, 17.69)	26.4
Unknown/not stated	1,201,514	2.7	1.78 (1.71, 1.84)	2.5
First trimester prenatal care initiation				
No	7,577,614	6.6	2.70 (2.67, 2.73)	6.3

Yes	23,759,502	2.4	1.00	2.4
Unknown/not stated	1,045,445	5.0	2.06 (2.00, 2.12)	5.2
Year of birth				
2010	3,023,725	2.0	1.00	2.0
2011	3,239,254	2.1	1.05 (1.02, 1.09)	2.2
2012	3,386,804	2.6	1.28 (1.24, 1.32)	2.6
2013	3,523,904	3.0	1.47 (1.42, 1.51)	3.0
2014	3,817,035	3.4	1.68 (1.63, 1.73)	3.4
2015	3,826,812	3.8	1.87 (1.81, 1.92)	3.7
2016	3,936,251	4.2	2.09 (2.03, 2.15)	4.1
2017	3,845,524	4.7	2.33 (2.26, 2.40)	4.6
2018	3,783,252	5.0	2.48 (2.41, 2.55)	4.9
Annual prevalence change[e] (mean, SE)		0.39 (0.01)		0.38 (0.01)
County-level characteristics				
County of residence (percentage below poverty threshold)[f]				
<10%	5,318,647	2.9	1.00	2.7
10%–19%	22,047,015	3.5	1.20 (1.18, 1.23)	3.3
20%–29%	4,479,807	3.9	1.35 (1.32, 1.38)	3.8
≥30%	537,075	8.3	2.91 (2.81, 3.01)	9.0
County overdose death rate per 100,000 population[g]				
Quartile 1	7,784,521	1.1	1.00	1.0
Quartile 2	7,913,249	2.0	1.88 (1.83, 1.93)	2.0
Quartile 3	8,249,377	3.1	2.94 (2.87, 3.01)	3.1
Quartile 4	8,435,414	7.6	7.21 (7.05, 7.38)	7.6
6-Level Urban–Rural County Classification Scheme[h]				
Large central metro	10,946,243	2.1	1.00	2.0

Large fringe metro	7,408,107	3.2	1.56 (1.53, 1.58)	3.0
Medium metro	6,759,400	3.9	1.88 (1.85, 1.91)	3.7
Small metro	2,877,218	4.4	2.14 (2.09, 2.18)	4.3
Micropolitan	2,676,536	6.2	3.00 (2.94, 3.06)	6.5
Non-core	1,715,057	6.9	3.35 (3.28, 3.42)	7.2

[a] Among states reporting maternal hepatitis C infection as ‘Y’ or “N’.

[b] Among states reporting maternal hepatitis C infection as ‘Y’ or “N’ using the 2003 revised birth certificate as of 2010 (n=26,913,980).

[c] Includes Asian or Pacific Islander; American Indian or Alaska Native; Other; and Hispanic origin unknown or not stated; and unknown.

[d] Smoking during any trimester of pregnancy.

[e] Estimated from linear model.

[f] Generated by merging restricted-use data files with Census Bureau data on families below the poverty threshold by county Federal Information Processing Standard Publication (FIPS) for mother’s county of residence at the time of birth.

[g] Generated by merging restricted-use data files with vital records published data on overdose death rates by county Federal Information Processing Standard Publication (FIPS) for mother’s county of residence at the time of birth.

[h] 2013 National Center for Health Statistics 6-Level Urban–Rural Classification Scheme.

GED, General Education Diploma; WIC, Special Supplemental Nutrition Program for Women, Infants, and Children.

Appendix Table 2. Predicted Median Prevalence and 95% Credibility Interval of Maternal Hepatitis C Virus Infection by County and Year, 2016–2018

Please see attached Microsoft Excel file.

Appendix Text. Hierarchical Bayesian Spatial Model Specification

Several alternative hierarchical Bayesian models were fit via Integrated Nested Laplace Approximation (INLA) in R (http://www.r-inla.org/). Alternative models included Poisson (conventional), zero-inflated Poisson, and zero-inflated negative binomial models, and including/excluding variables and random effects; however, none of these alternative models resulted in improvements in fit, as assessed using the Widely Applicable Information Criterion (WAIC).

Model	**WAIC**
Zero-inflated Poisson	30,612.79
Zero-inflated binomial	30,147.31
Poisson	30,049.69
Binomial	30,020.63
Binomial, final adjusted model[a]	29,992.79

[a] Adjusted for birth year, county NCHS 6-level urban–rural classification, county poverty rate (as a continuous variable), county-level drug overdose death rate (as a continuous variable), maternal age category, maternal educational attainment, pregnancy smoking status, maternal race/ethnicity, marital status, expected source of payment for delivery, WIC use during pregnancy, and pre-pregnancy BMI.

The best-fitting binomial model is described below, for $i = 1, \ldots, m$ counties and $t = 1, \ldots, T$ years:

$$\text{logit}\,(p_{it}) = \alpha_0 + \boldsymbol{X_{it}}'\boldsymbol{\beta} + u_i + v_i + \varphi_{1t} + \psi_{it}$$

This model includes:

1. An outcome that is the county-level number of HCV+ births, with the total number of births as the denominator.

2. A logit link function log $(p_{it}/(1-p_{it}))$; where, p_{it} is the probability of HCV in county *i* and time *t*.

3. An overall intercept term α_0. The intercept, α_0 was assigned a flat prior: $\mathrm{P}(\alpha_0) \propto \text{constant}$, (where P indicates probability).

4. A set of fixed effects, $\boldsymbol{X_{it}}'\boldsymbol{\beta}$, where $\boldsymbol{X_{it}}$: is the *i* th row and *t* th column of the covariates matrix $\boldsymbol{X}$ and $\boldsymbol{\beta}$ is a vector of regression parameters. The $\boldsymbol{\beta}$ for fixed effects ($\boldsymbol{X_{it}}'\boldsymbol{\beta}$) were assigned Normal priors. $\boldsymbol{\beta} \sim N(0,100)$ Fixed covariates included dummy variables for urban–rural classification, drug overdose death rates, and year.

5. A Besag–York–Mollie (BYM) spatial random effect, u_i, to account for county-level spatial dependence (e.g., clustering). This term was modeled using conditionally autoregressive priors (CAR) where weights were assigned to each county according to adjacency; neighboring counties receive a weight of one while non-neighboring counties receive a weight of zero. This term also includes a non-spatial random effect, v_i, to account for residual county-level variation that is not spatially dependent. These random effects are not identifiable, but the BYM models are commonly used in disease mapping and we were not interested in interpreting the parameters separately.

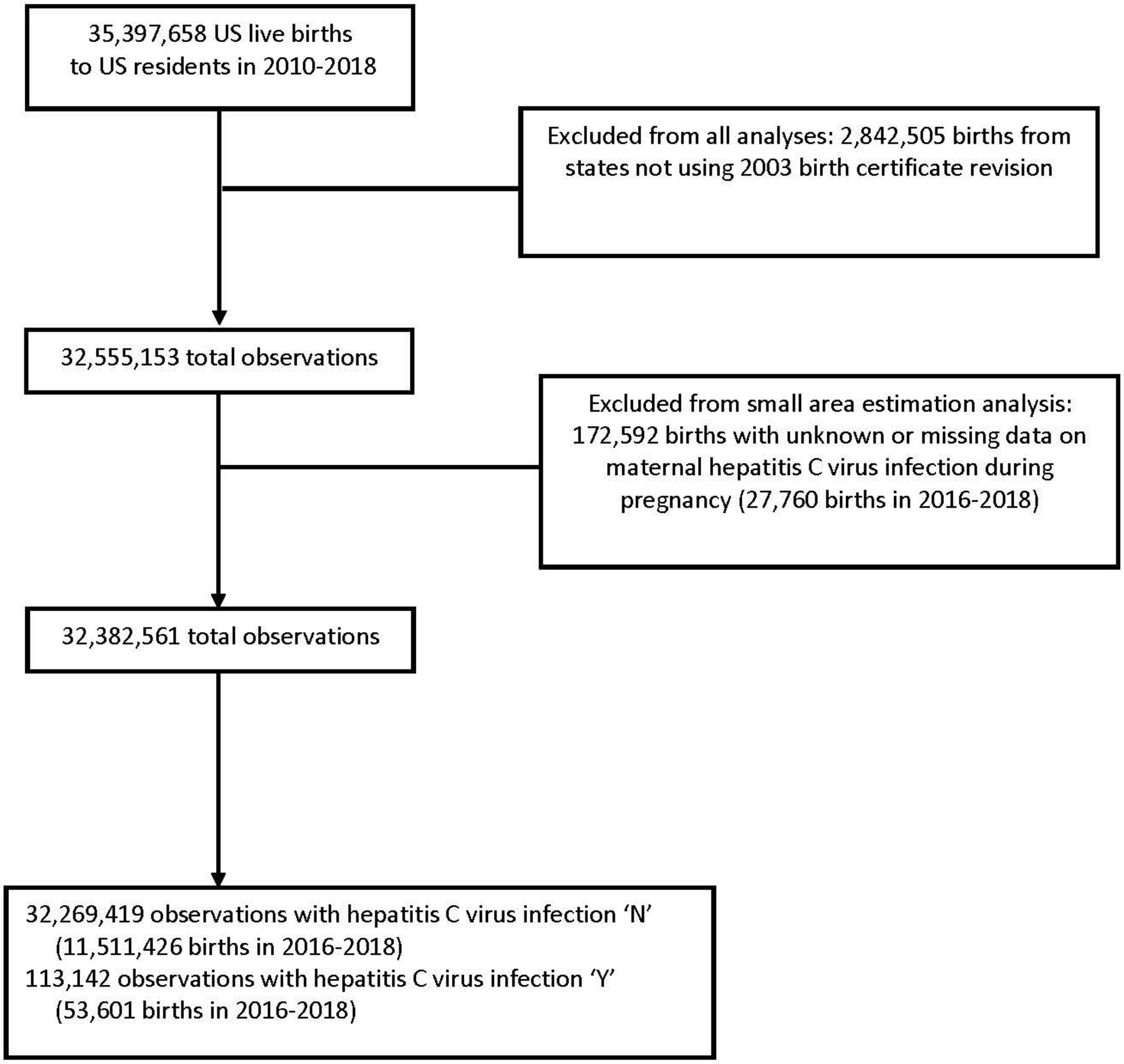
Counties were considered neighbors based on Delaunay triangulation, which generates Voronoi triangles from county centroids, where nodes connected by a triangle edge are considered neighbors. This spatial weighting scheme ensures that each county has at least one neighbor. The conditional precision of the spatial random effect was assigned $\tau_u \sim$ Gamma (1, 0.001) prior.

6. A temporal random effect, φ_{1t} , to account for temporal autocorrelation. Since there were only three years of data included, this term was assumed to be independently and identically

distributed $\varphi_{1t} \sim N(\varphi_{1t}, \frac{1}{\tau_{\varphi 1}})$. The conditional precision of the random effect was assigned $\tau_{\varphi 1} \sim$ Gamma (1, 0.001) prior.

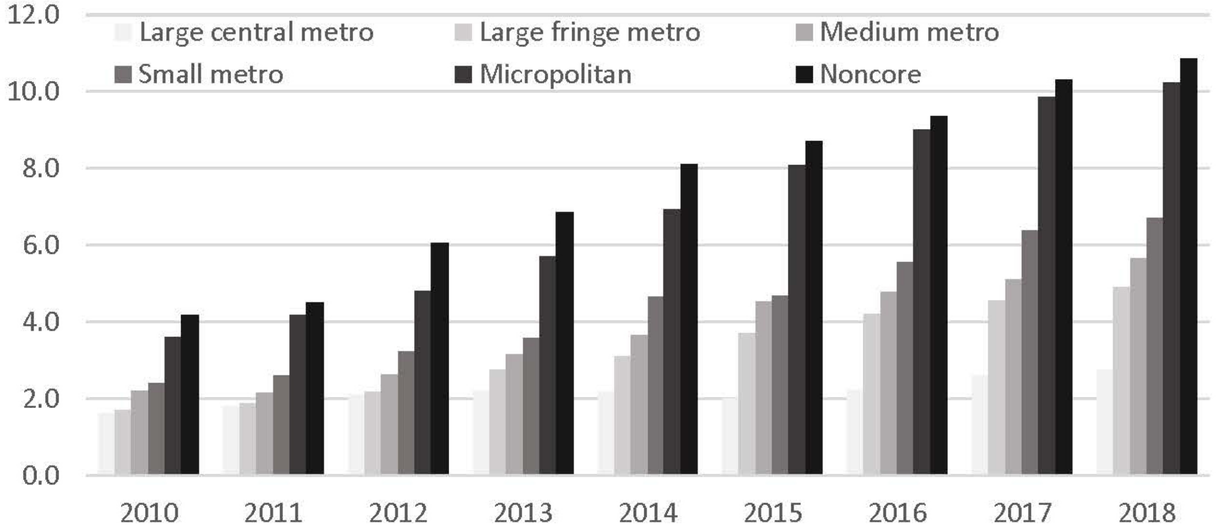
7. A space–time interaction term, ψ_{it}, which is a county- and year- specific random effect included to account for any residual spatiotemporal variation that was not captured by the spatial or temporal main effects. This term was assumed to be independently and identically distributed, $\psi_{it} \sim N(0, \frac{1}{\tau_{\psi}})$. The conditional precision of the random effect was assigned $\tau_{\psi} \sim$ Gamma (1, 0.001) prior.

Appendix Figure 1. Exclusion criteria for sample.

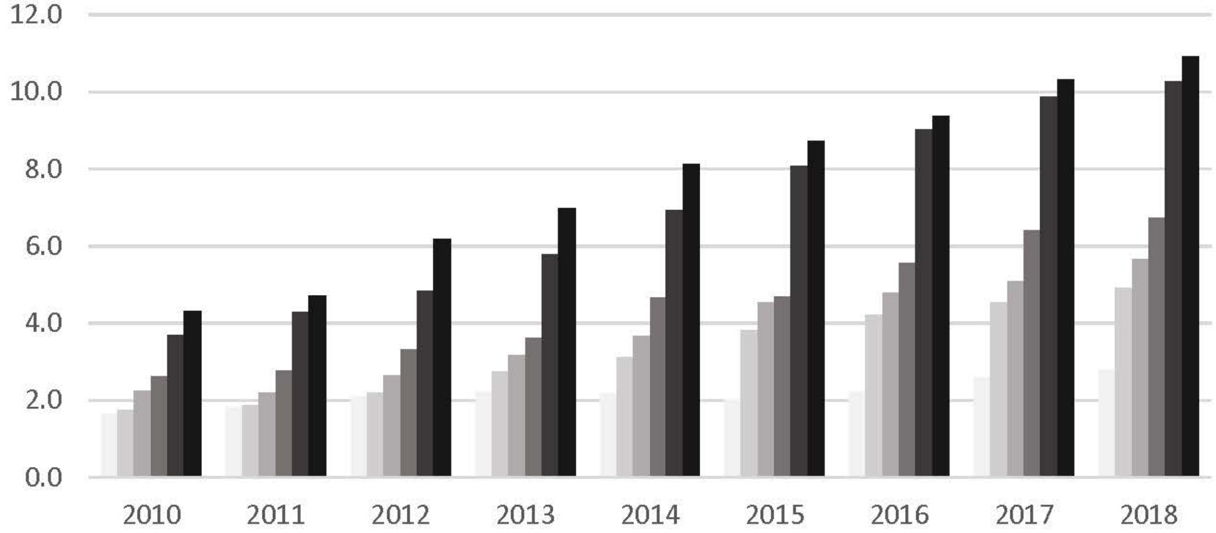


Appendix Figure 2. Prevalence of maternal hepatitis C virus infection (per 1,000 births) by 2013 National Center for Health Statistics' 6-Level Urban–Rural Classification Scheme for Counties: U.S. birth certificate data among 34 areas reporting as of 2010,[a] 2010–2018 (n=26,913,980).

Appendix Figure 2A. Prevalence (per 1,000 births).



Appendix Figure 2B. Prevalence (per 1,000 births), with missing prevalence of maternal hepatitis C infection data imputed.



[a] Among states reporting maternal hepatitis C infection as "Y" or "N" using the 2003 revised birth certificate as of 2010.

Appendix Figure 3. Prevalence of Bayesian modeled maternal hepatitis C virus infection per 1,000 live births, top decile counties (above 18.4 per 1,000 births).