# **Supplementary Materials**

### **Early Medicaid Expansion and Cancer Mortality**

#### **SUPPLEMENTARY METHODS**

#### *Covariates*

Covariates were selected a priori due to associations with cancer mortality and/or access to care. When available, we obtained county-level covariates corresponding to the beginning and end of the study period (2007 for the pre-early expansion period, and 2016 for the post-early expansion period). Intercensal estimates from the United States Census Bureau were obtained for county-level age (% elderly), race (% nonwhite, % black), ethnicity (% Hispanic), and sex (% female) data in 2007 and 2016.<sup>1,2</sup> County-level poverty (% of individuals living in poverty based on the federal poverty level definition) in 2007 and 2016 were obtained using US Census Bureau Small Area Income and Poverty Estimates.<sup>3</sup> U.S. Department of Agriculture Economic Research Service (USDA ERS) databases were utilized to obtain county-level education (% without at least a high school education) based on 2000 (pre-early expansion) and the 2013-17 average (post-early expansion) data.<sup>4</sup> Finally, metropolitan residence status (metropolitan or nonmetropolitan, based on rural-urban continuum codes) for 2003 and 2013 were also derived from USDA ERS databases.<sup>4</sup>

We obtained the variables % black and % Hispanic for the purpose of comparing county characteristics. The variable % Black was excluded from our regression models because of high collinearity with % nonwhite. The variable % Hispanic was excluded from our regression models due to a complex interplay between ethnicity and cancer outcomes; Hispanics have a lower cancer mortality rate than non-Hispanic whites, but Hispanics are more likely to experience

socioeconomic deprivation and thereby experience barriers to healthcare and subsequently poorer outcomes.<sup>5</sup> However, a sensitivity analysis including % Hispanic gave nearly identical results (data not shown).

#### *Unadjusted Analyses*

The DID estimate is defined as

 $DID = (Rate_{Early \ expansion, 2012-16} - Rate_{Early \ expansion, 2007-09})$ 

 $-(Rate<sub>Non-expansion</sub>, 2012-16 - Rate<sub>Non-expansion</sub>, 2007-09).$ 

To account for the variance of the age-adjusted mortality rates (which are based on the rate and population size) and correlation between observations from the same state group, variances of the estimates were calculated based on the statistical property of random variables X and Y that Variance(X-Y) = Variance(X) + Variance(Y) – 2 \* Covariance(X,Y). Specifically, variances for the different estimates were as follows:

 $V1 = Variance(Rate<sub>Early</sub> expansion, 2012-16 - Rate<sub>Early</sub> expansion, 2007-09) = Variance(Rate<sub>Early</sub> system)$ expansion,2012-16) + Variance(Rate $_{\text{Early expansion},2007-09}$ ) - 2 \* Covariance(Rate $_{\text{Early expansion},2012-16}$ , RateEarly expansion,2007-09)

 $V2 = \text{Variance}(Rate_{\text{Non-expansion}, 2012-16 - Rate_{\text{Non-expansion}, 2007-09}) = \text{Variance}(Rate_{\text{Non-pispansion}, 2007-09})$ expansion,2012-16) + Variance(Rate<sub>Non-expansion,2007-09</sub>) - 2 \* Covariance(Rate<sub>Non-expansion,2012-16,</sub> Rate<sub>Non-expansion,2007-09</sub>)

Variance(DID) =  $V1 + V2 - 0$ 

The covariance between mortality rates from expansion and non-expansion states was defined to be 0 (i.e. we assumed that observations from different state groups were independent). However, we assumed that observations from the same state group would be correlated.

The covariance between mortality rates over time from state group  $k \in (early Medicine)$ expansion, non-expansion) was derived from approximations of correlation (Rate  $_{\text{state group }k}$ , 2007-09, Rate<sub>State group *k*, 2012-16). This correlation was approximated by simulation study, calculating the</sub> correlation between vectors **Rate**<sub>pre, state group  $_k$  and **Rate**<sub>post, state group  $_k$ , with element Rate<sub>pre, state</sub></sub></sub> group *k,i* and Ratepost, state group *k,i* equal to two randomly selected single-year rates from state group *k*  (with replacement), defining the earlier year as the "pre-" year and the later year as the "post-" year, for  $i \in (1,2,...,500)$ . The resultant variances were used to derive standard errors, which were then used for confidence interval creation (estimate +/- 1.959964\* SE(estimate)) and for calculating Z statistics (estimate / SE(estimate)), which were used to obtain P-values.

The unadjusted triple differences (DDD) estimates were according to:

 $DDD<sub>Black</sub> = DID<sub>Black</sub> - DID<sub>White</sub>$ 

 $DDD<sub>Other</sub> = DID<sub>Other</sub> - DID<sub>White</sub>$ 

where the DID for a given race was calculated using the DID formulation described above, the variance for the estimates was again calculated based on the properties of variance  $(X-Y)$ , and the resultant variances were used to create confidence intervals and calculate Z statistics.

### *Testing of the parallel trends assumption*

The parallel trends assumption of difference-in-differences analyses requires that the trends in the outcome (mortality rates, in this case) would have been parallel between the comparison groups (early Medicaid expansion vs. non-expansion states, in this case) in the

absence of the exposure (in this case, early Medicaid expansion). While this cannot be fully established, one can examine trends in the mortality rate prior to the Medicaid expansions; if the trends are parallel prior to the expansions, it may be reasonable to conclude that the trends would have continued to remain parallel in the absence of the expansions. Our tests of the parallel trends assumption have two components: visual inspection and formal hypothesis testing.

Yearly cancer mortality rate data for the early Medicaid expansion and non-expansion states were collected. Note that more granular mortality data (i.e. monthly, quarterly, etc.) were not available for download. First, we visually inspected the trajectories of the yearly mortality rates in early Medicaid expansion and non-expansion states to examine for diverging trends prior to 2010 (see **Figures 1 and 3** and **Supplementary Figures 3 and 4**). For the visual assessment, in order to detect potentially diverging trends over time, we evaluated mortality rates from 2002 to 2009 (or, for the analyses of the 2014 Medicaid expansions, 2005 to 2013). Second, we formally tested year-to-year changes in mortality rates in the expansion vs. non-expansion states using the same methodology utilized in the unadjusted DID analyses. For these formal tests, we focused on the pre-expansion period from the DID analyses, 2007 to 2009 (i.e. 2007 to 2008, 2008 to 2009). For example, the test of parallel trends from 2007 to 2008 was as follows:

Parallel trends<sub>2007-2008</sub> =  $(Rate_{\text{Early expansion},2008} - Rate_{\text{Early expansion},2007})$ 

#### $-$  (Rate<sub>Non-expansion,2008</sub> - Rate<sub>Non-expansion,2007</sub>).

The variance, confidence intervals, and p-values for this test were calculated with the same methodology used with the DID estimates. For the analyses of the 2014 Medicaid expansions, we conducted formal testing of the mortality rate trends in 2011 to 2012 and in 2012 to 2013. This flexible year-by-year approach for the formal testing was selected given that it is not subject to further assumptions that would be required in a single model/test (e.g. linear relationship

between mortality rate and time). The parallel trends assumption was considered satisfied if (1) there were no abnormal patterns visually that would imply non-parallel trends and (2) the Pvalues from both formal tests were greater than 0.05.

Note that this method of testing for parallel trends is statistically underpowered. Specifically, the formal tests compare only two years of mortality rates whereas a number of additional years are included in the DID analyses. In addition, the judgement of whether the year-to-year trends were parallel was based on a test of the null hypothesis that there was no significant difference in the mortality rate change between state groups.<sup> $6-8$ </sup> A more statistically rigorous approach could, for example, include tests of non-inferiority (see articles by Bilinski and Hatfield, Khan-Lang and Lang, and Roth for additional insights and discussion).<sup>7–9</sup> While we were able to identify some deviations from parallel trends in our visual assessments that were not detected in the formal tests, potentially overcoming some of the issues arising from limited statistical power, there may be other parallel trend violations that were missed. Finally, even if we find perfectly parallel trends in the pre-expansion period, pre-expansion parallel trends does not guarantee that the trends would have remained parallel afterwards, which is assumed though unobserved.<sup>9</sup>

#### *Adjusted Analyses: Bayesian Hierarchical Model*

For our adjusted analyses, we wanted a regression model that would (1) enable adjusted difference-in-differences analyses, which are typically done with a class of multivariable linear regression models, (2) be capable of handling "repeated measures" given that the observational unit was the mortality rate of a county in a given time period (2007-2009 or 2012-2016), (3) account for correlation between observations in the same state, and (4) be able to explicitly

model the variability of the mortality rates, which differs from county to county based on population size and the number of observed events. The model that seemed most appropriate based on these criteria was a hierarchical (multilevel) Bayesian regression model. Note a fully Bayesian framework in the setting of this study is also advantageous given its ability to simultaneously impute missing (or, in this case, suppressed) values. The model was defined as follows:

With observed mortality rate  $y_{it}$  and its associated estimated variance  $s_{it}^2$  for county *i* within state *j* and for year group *t*, mortality rate average for the national population of interest *m,* and covariates *k*=1, …, K, we developed a hierarchical model such that:

 $y_{it} \sim N(\mu + X_{it} * \beta + \delta_i + \gamma_j, s_{it}^2) T[0, *),$  $\mu \sim N(m, a=100)$  $\beta \sim N(0, \Sigma_K)$ ,  $\Sigma_K = \text{diag}(\sigma_1^2, \ldots, \sigma_K^2)$  $\sigma_k$ ~ Cauchy(0, 2.5) T(0, Infinity)  $\delta_i \sim N(0, \rho)$  $\rho \sim$  Cauchy(0, 2.5) T(0, Infinity)  $\gamma_i \sim N(0, \tau)$  $\tau \sim$  Cauchy(0, 2.5) T(0, Infinity)

\* T[0,\*) denotes that the distribution of *yit* was truncated. A lower bound of 0 was used. An upper bound of infinity was used except in the case of suppressed data, where the distribution for the imputed value was constrained by an upper limit of 9 divided by the population size of county *i* (note that, by definition, data are suppressed when the number of events in the county is less than 10).

Mortality rates were assumed to follow a normal distribution by the central limit theorem, as the rate can be viewed as a mean.<sup>10</sup> However, the variance for the mortality rates were not be equal across counties given the vast differences in population and number of observed events (where in other regressions it may be reasonable to assume the same variance for all observations). For the case of the variance for suppressed mortality rates, we estimated the variance of a proportion *p,*  where *var* =  $(p*(1-p)/N)$ , both for  $p = 1$  / Population and for  $p = m/100,000$ , and selected the larger variance*.* A prior was not placed and imputation was not performed for these values given that the estimated variance is simply a function of other values. The prior for  $\mu$  was selected to be centered roughly around the corresponding cancer mortality rate for the nation over the study period, however with much greater variance. For mortality due to all cancers, we set *m*=100; for breast and lung cancer, we set *m*=20; for colorectal, cervix, liver, prostate, and pancreas cancer, we set *m*=5; for whites, we set *m*=80; for Blacks, we set *m*=110; for other races, we set *m*=50. The variance for the prior for  $\mu$  was set to  $a=100$  (corresponding to standard deviation of 10) for all analyses. The prior for  $\beta$  is typical for regression analyses. The prior for  $\sigma_k$  was a half Cauchy distribution, as recommended by Gelman et al.,  $^{11}$  given its precision with standard deviations closer to 0 and its ability to accommodate much larger standard deviations should the need arise. Note that the prior distribution for the  $\beta_k$  (assuming the null, as specified incorporating the  $\sigma_k$ ) has ~75% of its density between -5 and 5, over 10% of its density with values more extreme than 10 (or -10), and still over 1% of its density for values more extreme than 100 (or -100), which was deemed appropriate for the effect sizes expected with the present data. The rationale for the selection of priors for random effects was similar. Bayesian regression models resembling mixed models are frequently applied in spatiotemporal modeling of mortality rates and as such often include random effects for space and time.<sup>10,12,13</sup> Given that the primary purpose of this study

was to examine changes by state Medicaid expansion status, which was primarily political rather than based on geographic location, we created a simpler and more parsimonious Bayesian model by only including county and state random effects rather than a full spatiotemporal parameterization. The effect for county *i* was denoted by  $\delta_i$ , and the effect for state *j* was denoted by  $\gamma_i$ .

To facilitate modeling and avoid unstable parameter estimates, the covariates (including % unemployed, % high school education, % poverty, % non-White, % elderly, and % female) were scaled to have a mean of 0 and a standard deviation of 1. As a sensitivity analysis, these covariates were transformed into categorical variables based on quartiles. Results with this less parsimonious model parameterization were extremely similar to those presented in the main manuscript (data not shown).

While "observation weights" are an abstract notion in the Bayesian paradigm, we conducted a sensitivity analysis where the estimates were weighted by county population. Prior to modeling, each trio  $(y_{it}, s_{it}, \text{and } \mathbf{X}_{it})$  was replicated by a factor of the population of county *i* divided by 35,000, rounded up to the next integer (correlation with actual population number > 0.9999). To maintain the variance estimates associated with each county-year group unit, the variance was also increased by the same factor. Results with this model parameterization were similar to non-weighted estimates (data not shown).

Draws from the posterior distribution were obtained with Gibbs sampling via R2jags. We obtained 30,000 draws and discarded the first 2,000 as burn in. Convergence of the draws were assessed visually and with the Geweke, Raftery and Lewis, and Heidelberger and Welch diagnostics. Additional draws were discarded as burn in if necessary based on chain diagnostic criteria. A summary of those tests for the posterior distribution of the DID estimator (the

interaction between time period and early Medicaid expansion status) are given in

**Supplementary Table 2** and **Supplementary Figure 1**. Note that the halfwidth mean test, where the ratio of the halfwidth (half of the width of a 95% CI about the chain mean) to the chain mean is supposed to be less than a specified value (0.1 in this case) has little meaning when the chain mean (or DID estimate in this case) is essentially 0, especially in comparison to a relatively large variance. After these considerations, there were no chains with concerning convergence statistics. However, some analyses required additional iterations of the MCMC algorithm, and a few analyses required priors that were more non-informative (the half Cauchy hyperprior for the standard deviation parameters was modified to have scale 25 instead of 2.5). Note that a sensitivity analysis using these minimally informative half Cauchy(0, 25) priors resulted in extremely similar estimates (and did not affect convergence diagnostics for other analyses). Chain diagnostics for the sensitivity analyses were also satisfactory (data not shown).

#### *Estimating Number of Cancer Deaths Averted*

The number of deaths averted was calculated by multiplying the DID estimates  $(1.38 / 100000)$ unadjusted, or 3.07 / 100000 adjusted) by the at risk population (ie the denominator used in estimating the cancer mortality rate of the time period), given in the table below.



In this case, the number of cancer deaths averted in EEXP states from 2012-16 was calculated as DID estimate  $*$  194,609,695 = 2,686. Due to a slightly different population in the adjusted,

county-level analyses (limited to 25-64 rather than 20-64), the number was calculated as DID estimate \* 171,849,340 = 5,276.

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## **SUPPLEMENTARY TABLES**



Supplementary Table 1: Formal tests of the parallel trends assumption, early Medicaid expansion<sup>a</sup>

<sup>a</sup> Please refer to **Figure 1** and **Supplementary Figure 3** for depictions of the year-by-year trends in cancer mortality. Visually, the trends in mortality rates were largely similar between early Medicaid expansion and nonexpansion states, with the exception of liver cancer mortality, where the rates increased more rapidly in nonexpansion states than in expansion states during the pre-expansion period.

bEstimates shown are the difference-in-differences estimators for the changes in mortality rates between early and not early Medicaid expansion states over the (pre-expansion) time period given.

 $cP = two$ -tailed p-value from Z test of the null hypothesis that the difference-in-differences estimate is equal to 0. See **Supplementary Methods** for details.

<sup>d</sup>The parallel trends assumption was violated due to diverging trends in our formal testing from 2007-2009.

	Geweke Diagnostic	Heidelberger-Welch Diagnostic		Raftery-Lewis Diagnostic	
Subgroup	Z score	Stationary Start, p	Halfwidth Test, mean (halfwidth)	N <sub>chain</sub> (Dependence Factor)	
All Malignancies	0.14	0.64	$-3.066(0.022)$	26140 (6.98)	
Breast <sup>a,b</sup>	$-1.61$	0.33	$-0.185(0.0093)$	28164 (7.52)	
Cervix <sup>b</sup>	1.05	0.14	$-0.314(0.0098)$	26799 (7.15)	
Colorectal	1.72	0.24	$0.013(0.0059)$ <sup>c</sup>	19476 (5.20)	
Liver	$-0.09$	0.94	$-0.465(0.0065)$	24198 (6.46)	
Lung <sup>a,b</sup>	0.65	0.12	$-0.364(0.014)$	23856 (6.37)	
Pancreas	$-1.35$	0.49	$-0.465(0.0056)$	20343 (5.43)	
Prostate	$-1.21$	0.63	$-0.162(0.010)$	27204 (7.26)	
Whiteb	0.99	0.12	$-3.81(0.024)$	26605(7.10)	
<b>Black</b> <sup>b</sup>	1.93	0.46	$-0.58(0.0363)$	27480 (7.34)	
Other <sup>a,b</sup>	$-0.01$	0.25	$-0.474(0.031)$	56772 (15.20)	
Black relative to Whiteb	0.88	0.93	$0.188(0.054)$ <sup>c</sup>	11076 (2.96)	
Other relative to White <sup>b</sup>	$-1.28$	0.14	$0.1043(0.0256)^{\circ}$	16860 (4.50)	

Supplementary Table 2: MCMC diagnostics for hierarchical Bayesian model

<sup>a</sup>The dependence factor from the Raftery-Lewis diagnostic for these chains was high enough that  $>$ 30,000 draws were needed. For these analyses, 40,000 (60,000, Other) draws were obtained.

<sup>b</sup>The initial chains were unsatisfactory. Analyses were repeated with more noninformative priors (scale of the Cauchy hyperprior for the standard deviation parameters was set to 25 instead of 2.5) with satisfactory results, as seen above.

c Indicates the chain failed the given test based on the standard criteria. Note that failing the halfwidth Heidelberger-Welch test when the estimated mean is near 0 has little meaning; all failures above occurred when the effect size was small (especially relative to the variance of the estimate).

<b>State</b>	Medicaid Coverage Rate		
Early Expansion States <sup>d</sup> : Median (range)	$0.08(0.06-0.17)$		
Not early expansion states: Median (range)	$0.07(0.03-0.16)$		
United States, Total	0.08		
Alabama	0.07		
Alaska	0.05		
Arizona	0.1		
Arkansas	0.08		
California <sup>d</sup>	0.09		
Colorado	0.05		
Connecticut <sup>d</sup>	0.08		
Delaware	0.1		
District of Columbia <sup>d</sup>	0.17		
Florida	0.05		
Georgia	0.05		
Hawaii	0.07		
Idaho	0.04		
Illinois	0.08		
Indiana	0.07		
Iowa	0.07		
Kansas	0.04		
Kentucky	0.09		
Louisiana	0.08		
Maine	0.16		
Maryland	0.05		
Massachusetts	0.13		
Michigan	0.1		
Minnesota <sup>d</sup>	0.08		
Mississippi	0.09		
Missouri	0.07		
Montana	0.05		
Nebraska	0.05		
Nevada	0.03		
New Hampshire	0.04		
New Jersey <sup>d</sup>	0.06		
New Mexico	0.09		
New York	0.13		
North Carolina	$0.07\,$		

Supplementary Table 3: Medicaid<sup>a</sup> coverage rates for adults ages 19-64 years by state, 2008<sup>b,c</sup>



<sup>a</sup>Medicaid in this table includes those covered by Medicaid, Medical Assistance, Children's Health Insurance Plan (CHIP) or any kind of government-assistance plan for those with low incomes or a disability, as well as those who have both Medicaid and another type of coverage, such as dual eligibles who are also covered by Medicare. Rate is the proportion of the population or subpopulation with Medicaid.

<sup>b</sup>The data are Kaiser Family Foundation estimates based on the Census Bureau's American Community Survey (ACS), 2008-2018. See KFF website:<https://www.kff.org/medicaid/state-indicator/rate-by-age-3/>

ACS includes a 1% sample of the US population and allows for precise state-level estimates. The ACS asks respondents about their health insurance coverage at the time of the survey. Respondents may report having more than one type of coverage; however, individuals are sorted into only one category of insurance coverage. A person reporting having Medicaid coverage and another type of coverage would be categorized as having Medicaid coverage in this analysis.

<sup>c</sup>Data may not sum to totals due to rounding.

d Indicates the early Medicaid expansion states



Supplementary Table 4: Sensitivity Analyses (adjusted difference-in-differences analyses)

<sup>a</sup>The analysis examining 2002-2007 to 2012-2016 included 20-64 year old patients at time of death, since we were able to utilize data from SEER\*Stat due to the year ranges of interest. Other analyses (based on CDC WONDER compressed mortality data) were limited to 25-64 year old patients at time of death due to differences in estimating age-adjusted mortality rates (the CDC compressed mortality data adjust for 15-24 year olds as a group). CrI = Credible Interval (Bayesian),

b2014-2016 expansion states included AK, AZ, AR, CO, DE, HI, IL, IN, IA, KY, LA, MA, MD, MI, MT, NV, NH, NM, NY, ND, OH, OR, PA, RI, VT, and WV.

<sup>c</sup> One-tailed probability of Bayesian estimate being null. As  $Pr$  is one-sided,  $Pr \le 0.025$  is required for statistical significance.

	2011-2012		2012-2013	
Subgroup	Estimate <sup>b</sup> (95% CI)	$P^{\rm c}$	Estimate <sup>b</sup> (95% CI)	$P^{\rm c}$
All Malignancies	$0.48(-0.34, 1.31)$	0.25	$0.05$ ( $-0.74$ , $0.85$ )	0.9
<b>Breast</b>	$0.1$ ( $-0.43$ , $0.63$ )	0.71	$0.22 (-0.31, 0.75)$	0.41
$Cervix^d$	$-0.28(-0.56, 0)$	0.048	$0.05(-0.24, 0.34)$	0.74
Colorectal <sup>d</sup>	0.34(0.02, 0.66)	0.036	$-0.08$ $(-0.39, 0.22)$	0.59
Liver <sup>e</sup>	$-0.05$ $(-0.24, 0.13)$	0.58	$-0.13(-0.32, 0.07)$	0.2
Lung <sup>f</sup>	$0.28(-0.09, 0.66)$	0.14	$-0.23$ $(-0.59, 0.14)$	0.23
Pancreas <sup>g</sup>	$-0.1$ $(-0.35, 0.15)$	0.44	$0.22(-0.02, 0.45)$	0.076
Prostateh	$-0.07$ $(-0.29, 0.16)$	0.56	$-0.17(-0.4, 0.06)$	0.15
White <sup>1</sup>	$0.67(-0.21, 1.55)$	0.13	$-0.13(-0.97, 0.71)$	0.76
Black <sup>j</sup>	$-1.9$ ( $-4.39$ , $0.59$ )	0.13	$1.47(-1.11, 4.06)$	0.26
Other	$0.72(-2.5, 3.93)$	0.66	$-1.62$ ( $-4.76$ , $1.52$ )	0.31

Supplementary Table 5: Formal tests of the parallel trends assumption, 2014 Medicaid expansion<sup>a</sup>

<sup>a</sup>Please refer to **Figure 3** and **Supplementary Figure 4** for depictions of the year-by-year trends in cancer mortality. <sup>b</sup>Estimates shown are the difference-in-differences estimators for the changes in mortality rates between Medicaid expansion and non-expansion states over the (pre-expansion) time period given.

See below for descriptions of visually diverging mortality rate trends.

 $c_{\text{P}}$  = two-tailed p-value from Z test of the null hypothesis that the difference-in-differences estimate is equal to 0. See **Supplementary Methods** for details.

<sup>d</sup>Analyses failed to satisfy the parallel trends assumption due to diverging trends in mortality rates between expansion and non-expansion states in formal testing during the pre-expansion period (2011-2013).

<sup>e</sup>While there were no statistically significant differences in our formal testing from 2011-2013, visual assessment suggested that mortality rates increased more rapidly in non-expansion states than in expansion states during the preexpansion period. Hence, the parallel trends assumption was violated. Note that this would be expected to lead to bias favoring expansion states.

<sup>f</sup>While there were no statistically significant differences in the trends in mortality rates in Medicaid expansion vs. non-expansion states in formal testing, on visual inspection, the mortality rate appeared to decline more rapidly in non-expansion states than expansion states over the study period. Hence, the parallel trends assumption was violated. Note that the more rapidly declining rates in non-expansion states will lead to bias favoring non-expansion states.

<sup>g</sup>While the analyses satisfied the parallel trends assumption per our definition, the slightly lower-than-expected mortality rates in non-expansion states from 2010-12 may lead to a slightly biased result, favoring Medicaid expansion states.

<sup>h</sup>While there was no statistical evidence of non-parallel trends from 2011-2013, visual inspection suggested that the mortality rate trends in expansion and non-expansion rates diverged from 2011-2014 (decrease in expansion states), with a return to baseline after 2015. Hence, the parallel trends assumption was violated. Note that due to the (incidentally) low mortality rates in 2011-13 in Medicaid expansion states in the pre-expansion period (and perhaps also an incidentally higher mortality rate in non-expansion states in 2013) leads to bias favoring non-expansion states.

<sup>i</sup>While there were no statistically significant differences in our formal testing from 2011-2013, visual assessment suggested that mortality rates decreased more rapidly in expansion states than in non-expansion states during the pre-expansion period. Hence, the parallel trends assumption was violated. Note that this would be expected to lead to bias favoring expansion states.

<sup>j</sup>Despite no statistical evidence of non-parallel trends, visual inspection suggested that the mortality rate in nonexpansion states declined more rapidly than in expansion states during the pre-expansion period (as well as in the post-expansion period). As such, the parallel trends assumption was violated. Note that the more rapidly declining rates in non-expansion states will lead to bias favoring non-expansion states.

	% of current smokers			
State group	1992-1993	2006-2007	Change	
Early Expansion <sup>b</sup>	23.07	16.29	$-6.78$	
$2014$ Expansion <sup>c</sup>	26.6	20.41	$-6.18$	
Non-expansion <sup>d</sup>	28.13	21.28	$-6.85$	

Supplementary Table 6: Changes in smoking rates by state Medicaid expansion status<sup>a</sup>

<sup>a</sup>Data were derived from state-level smoking rates reported by Jemal et al., which were based on data from the Tobacco Use Supplement to the Current Population Survey.<sup>14</sup>

<sup>b</sup>Early Medicaid expansion states include CA, CT, DC, MN, NJ, and WA.

<sup>c</sup>2014 expansion states included AZ, AR, CO, DE, HI, IL, IA, KY, MA, MD, MI, NV, NH, NM, NY, ND, OH, OR, RI, VT, and WV (note early expansion states were excluded from this group).

<sup>d</sup>Non-expansion states are those that had not implemented Medicaid expansion as of 12/31/2016; includes AL, FL, GA, ID, KS, ME, MS, MO, NE, NC, OK, SC, SD, TN, TX, UT, VA, WI, WY.

# **SUPPLEMENTAY FIGURES**

Supplementary Figure 1: Draws from the posterior distribution. The panels show the 28,000+ draws, excluding burn-in, from each of the marginal posterior distributions of the difference-in-differences estimates (A-K) or triple differences estimates (L-M) based on the MCMC algorithm. The parameter spaces are well-explored and the chains appear to have converged.



(M) Other vs. White (reference)

Supplementary Figure 2: CONSORT Diagram for county-level analyses



Note the odd numbers are due to changes in county definitions (i.e. consolidation or creation of new counties) occurring over the study period in VA and AK (affecting 6 counties in those states, 0.2% of total counties). Supplementary Figure 3: Temporal trends in cancer mortality rate for various subgroups by early Medicaid expansion status. Mortality rates shown are from breast (A), cervix (B), colorectal (C), liver (D), lung (E), and prostate (F) cancers, and by racial subgroups for White (G), Black (H), and Other (I) patients. The dashed line for "trend comparison," for easier visual comparison of temporal trends, is equal to the trends of the not early expansion states translated up or down such that the comparison mortality rates at the end of the pre-expansion study period (2007) are equal to the rate in the early expansion group. Mortality Rate is per 100,000 population.



Supplementary Figure 4: Temporal trends in cancer mortality rate for various subgroups by 2014 Medicaid expansion status. Mortality rates shown are from breast (A), cervix (B), colorectal (C), liver (D), lung (E), and prostate (F) cancers, and by racial subgroups for White (G), Black (H), and Other (I) patients. The dashed line for "trend comparison," for easier visual comparison of temporal trends, is equal to the trends of the non-expansion states translated up or down such that the comparison mortality rates at the end of the pre-expansion study period (2013) are equal to the rate in the expansion group. Mortality Rate is per 100,000 population.

