Supplement for:

**SNAP Participation and Healthcare Use in Older Adults: A Cohort Study**

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**Technical Supplemental Materials**

Confounding results from a common cause between exposure (in this case, SNAP participation) and outcome. Different analytic approaches can help account for confounding, but make different assumptions in doing so. All types of analyses rely on assumptions, some of which may be untestable. In general, we can have more confidence in results if different analytical approaches that make different assumptions arrive at similar conclusions, as it is generally unlikely that different types of errors would all converge on the same effect estimates. In this study, we used four different analytic approaches, which each make different assumptions. This technical appendix is meant to provide more details about each of the approaches, and present results from testing various assumptions. We organize the appendix by analytic approach.

*Outcome Regression Analyses*

As our primary analytic approach, outcome regression analyses are described in detail in the main text. We conducted a modified Park test which resulted in the selection of a gamma distribution for cost outcomes.(1) Hypothesis testing and p-values for the outcome regression analyses was based on the regression coefficient for the SNAP term in the regression model. We adjusted for race/ethnicity variables in outcome regression analyses because these variables may indicate the experience of racism, which worsens health and may affect healthcare use and cost.

To formally test the sensitivity of the outcome regression analyses to unmeasured confounding, we used the EValue approach to quantify the strength of association an unmeasured confounder would need to have with both SNAP enrollment and the outcome for a given analysis in order to render the observed association null.(2) The specific implementation of the EValue approach that we used was based on the relative risk, defined in this study as the exponentiated regression coefficient for the SNAP term in the outcome regression model.

*Entropy Balancing Analyses*

The next set of analyses used a weighting based approach called entropy balancing.(3–6) Entropy balancing is similar to inverse probability weighting or other propensity score based weighting methods in that it finds a set of weights that balance covariates between those who do and do not enroll in SNAP. Entropy balancing works by solving a convex optimization problem that finds a set of weights that exactly balance sample moments (e.g., the mean) for all included covariates, while deviating from 1 to the smallest extent possible.(3) We used a robust set of demographic, clinical, and area-based covariates to estimate the entropy balancing weights, targeting the ATE as the estimand (as in the outcome regression analyses). Specifically, the covariates used to estimate the weights were: index date, age, gender, race/ethnicity (for the same reason as in outcome regression analyses), whether an individual was a partial versus full Medicaid beneficiary, number of baseline observation days, baseline inpatient admissions, baseline emergency department visits, baseline long term care admissions, baseline outpatient visits, baseline total Medicaid costs, baseline allowed Medicaid costs, Gagne comorbidity score, indicators of coronary heart disease, chronic kidney disease, depression, diabetes mellitus, hypertension, proportion of study participants who enrolled in SNAP at the HSA level, hospital discharges per 1000 Medicare enrollees at both the HSA and HRR level in 2015, percent mortality of Medicare beneficiaries in 2017 at both the HSA and HRR level, and mean Medicare reimbursement in 2017 at both the HSA and HRR level. We estimated the entropy balancing weights using the WeightIt package in R.(7)

After estimating the balancing weights, we then estimated the association between SNAP and the study outcomes in weighted regression models (negative binomial models for count outcomes and log-gamma models for expenditure outcomes). These models did not include covariates as the entropy balancing weights provide adjustment for confounding. We again used the regression coefficient for hypothesis testing (using robust standard errors given this was a weighted model(8)), and predictive margins to yield estimates of marginal means and the ATE.

To formally test the sensitivity of the entropy balancing analyses to unmeasured confounding, we again used the EValue approach based on the relative risk, defined in this study as the exponentiated regression coefficient for the SNAP term in the weighted regression model.

*Matching Analyses*

A key concern in the matching analyses was not only to try to account for individual-level confounding factors, but also to account for HSA-level. To do this, we followed an approach for matching in a hierarchical data structure described by Page et al.(9) This approach seeks to balance individual-level factors while matching within a given cluster (in our case, HSA). By ensuring that matching between treated and untreated units occurs within a given cluster, this should account for both measured and unmeasured cluster-level confounding factors. For this study, we implemented this approach by first estimating a propensity score (the probability of enrolling in SNAP), using the following variables: index date, age, gender, race/ethnicity (for the same reason as in outcome regression analyses), whether an individual was a partial versus full Medicaid beneficiary, number of baseline observation days, baseline inpatient admissions, baseline emergency department visits, baseline long term care admissions, baseline outpatient visits, baseline total Medicaid costs, baseline allowed Medicaid costs, Gagne comorbidity score, indicators of coronary heart disease, chronic kidney disease, depression, diabetes mellitus, hypertension, proportion of study participants who enrolled in SNAP at the HSA level, hospital discharges per 1000 Medicare enrollees at the HSA level in 2015, percent mortality of Medicare beneficiaries in 2017 at the HSA level, and mean Medicare reimbursement in 2017 at the HSA level. We then conducted a match, in a 10:1 ratio, based on this propensity score, while additionally requiring that participants be matched exactly by HSA (meaning a participant who enrolled in SNAP could only be matched to participants who did not enroll in SNAP from within their same HSA, based on their address as of the index date). Matching was done using the MatchIt package within R.(10) We inspected the balance achieved by this matching process by examining the standardized mean differences (SMD) of measured covariates in the matched sample. We considered an SMD of < 0.10 to indicate adequate balance.

After creating the matched subset, we then conducted regression analyses identical to those used in the outcome regression approach. However, it is important to note that whereas the outcome regression approach produces an estimate of the ATE, in the matched analysis the estimand is the average treatment effect in the matched sample, sometimes called the ATM.

To formally test the sensitivity of the matched analyses to unmeasured confounding, we again used the EValue approach based on the relative risk, defined in this study as the exponentiated regression coefficient for the SNAP term in the weighted regression model.

*Instrumental Variable Analyses*

The association between receipt of SNAP benefits and healthcare use and cost could be confounded by factors that are not measured in claims data, such as interest in receiving government assistance. To avoid bias caused by this confounding, we took advantage of a unique feature of the BDT dataset. Because of the large number of potentially SNAP eligible individuals to contact, not all individuals could receive outreach at the same time. To ensure a fair chance to receive outreach that did not rely on characteristics of the participants, each individual was assigned an outreach group at random (using a random number generator in Microsoft Excel). The groups received outreach at different times. During the study period, approximately 80% of individuals, received outreach, and 20% had not yet received outreach. Thus, although enrolling in SNAP may be correlated with study outcomes, receipt of outreach was not.

*Two-Stage Residual Inclusion versus Two-Stage Least Squares Instrumental Variable Analysis*

For the instrumental variable analyses, we did not use the two-stage least squares approach, because healthcare utilization and cost are not well modeled by linear regression, which uses ordinary least squares regression in both stages of the model.(11) Instead, we used the two-stage residual inclusion (2SRI, also called the ‘control function’) approach.(12–14) A generalization of two-stage least squares to non-linear models is called two-stage predictor substitution (or in other words, two-stage least squares is a special case of two-stage predictor substitution). However, while two-stage least squares is consistent, two-stage predictor substitution may not be consistent when using non-linear models.(12)

In the 2SRI approach, a first stage model using the instrumental variable and other covariates is used to estimate the probability of SNAP enrollment. Then, one fits a second-stage model that estimates study outcomes and includes an indicator of SNAP receipt, the residual (difference between the observed and predicted outcome) from the first-stage model, and other covariates. Though it was designed for scenarios, such as the one in this study, where outcomes are better suited for nonlinear models, simulation studies have shown that 2SRI can be biased in settings with particular types of non-linear models, specifically ones for binary outcomes.(15) However, the work of Wan et al.(14) clarifies that for 2SRI approaches to be unbiased without strong assumptions, collapsible second stage models must be used (common examples of non-collapsible second stage models that should not be used are logistic and Cox proportional hazards regression). Thus one explanation for bias in 2SRI analyses is use of non-collapsible second stage models. In this study we used collapsible second stage models for all analyses. For utilization outcomes, we used negative binomial second stage regression models. For expenditure outcomes, which often have a large point mass at zero and skewed right tails (i.e., a few individuals with very high expenditures), second stage models used a generalized linear model with a gamma error distribution and a log link function.(16) This was selected after conducting a modified Park test.(1) We used logistic regression for the first stage models as non-collapsibility in the first stage does not lead to bias.

*How Does Two-Stage Residual Inclusion Analysis Work?*

Conceptually, the idea behind 2SRI analyses is as follows (throughout this explanation we assume all of the instrumental variable assumptions are met).(12) In the setting of confounding, it is difficult to get an unbiased estimate of the effect of a treatment on an outcome. This is because the correlation between the treatment and the outcome comes from two sources: the effect of the treatment on the outcome, and a correlation induced by the confounding (confounders are by definition causes of both the treatment and the outcome [or at least on the causal path between both]). To estimate the effect of a treatment on an outcome in the presence of confounding, we could fit a regression model that estimates the outcome as a function of the treatment and all confounders. The regression coefficient for the treatment variable in such a model would be an unbiased estimate of the effect of the treatment on the outcome, because all the confounding has been adjusted for (that is, loaded onto the regression coefficients for the confounding factors, and removed from the regression coefficient for the treatment). Unfortunately, while we can measure and adjust for some of the confounders, we cannot do that for all confounders—perhaps because we do not know what they are, or we do know what they are but do not have the data available to us. In this setting, to get an unbiased estimate of the effect of treatment on the outcome it is necessary to get some estimate of the unmeasured confounding, so we can then adjust for it.

To get this estimate of unmeasured confounding, we need an estimator of the vector of unmeasured confounders—that is, a way to estimate the unmeasured confounding. 2SRI provides this estimator by making use of the following idea. As noted above, the association between a treatment and outcome, in the presence of confounding, contains two parts—a part from the treatment itself, and a part from confounding. We would like to break this up, or partition this correlation into its two parts. We do this by using an instrumental variable—a variable that is correlated with the treatment, but is not correlated with the outcome except through the treatment. Thus, any correlation between the instrument and the outcome is not due to confounding. In the first stage model of 2SRI analysis, using the instrumental variable, we create a prediction of the treatment. This prediction will be based solely on information contained in the instrumental variable (and any measured confounders also included in the model). Crucially, this prediction will not be correlated with the outcome through confounding, only through any effect the treatment might have on the outcome. However, the prediction will not match up with the observed treatment exactly, because treatment is determined by an additional factor—unmeasured confounding (because a confounder has to cause both the treatment and the outcome). So because we do not have these unmeasured factors in the first stage model, the first stage model will not be perfectly accurate in predicting treatment. With our partially accurate prediction, we then calculate the residual by subtracting the prediction from the observed value of treatment (So, for example, if the person did receive treatment, then their observed value is one, and if their predicted probability of treatment is 0.9, then one type of residual might be calculated as 1- 0.9 = 0.1). This residual is now an estimate of the unmeasured causes of treatment—the factors that caused treatment but were not represented in the first stage model predicting treatment. Because confounders cause both the treatment and the outcome, this estimate of the unmeasured causes of treatment is also an estimate of unmeasured confounding. Now that we have this estimate of unmeasured confounding, we can adjust for it as a variable in the second stage model, which also includes a variable for the treatment. So in other words, having a prediction of treatment that is not associated with the outcome through confounding lets us split up the total association between the treatment and the outcome into its two parts: the part that is caused by the treatment, and the part that comes from unmeasured confounding. This is exactly what we do in the second stage model.

Now, by including the estimate of the confounding in the second stage model, the association between the treatment and outcome that comes from unmeasured confounding will be loaded onto the regression coefficient for the residual. The part of the association between the treatment and the outcome that is due to the treatment, and not due to the confounding, will be loaded onto the regression coefficient for the treatment term. If the regression coefficient for the treatment term is significantly different from zero, this indicates that the treatment has an effect on the outcome that is not due to confounding.

*Testing Instrumental Variable Assumptions*

Instrumental variable analyses rely on five assumptions for validity as discussed in Baiocchi et al. (17): 1) that the instrumental variable is positively correlated with the treatment, 2) that the instrumental variable is independent of unmeasured confounders (possibly conditional on covariates), 3) that the instrument only affects the outcomes through receipt of the treatment (also known as the exclusion restriction), 4)that there is only one version of the treatment and that one person receiving the treatment does not interfere with others receiving the treatment (also known as the Stable Unit Treatment Value Assumption, or SUTVA), and 5) that the instrument can increase the probability of receiving the treatment or have no effect, but cannot decrease the probability of receiving the treatment (monotonicity). We discuss the reasons for believing that these assumptions are met in the case of this study in the table below. For the first two assumptions, statistical tests are available, and we discuss those in greater detail here and in the tables below. Ultimately, however, we acknowledge that instrumental variable analysis is based on some assumptions that are untestable.(17–19) First, we examined the strength of the association between receipt of SNAP outreach and enrolling in SNAP using the partial F-statistic in a linear probability model(20), the Cragg-Donald statistic(21) (here we use critical values from Stock and Yogo(22) based on an allowable bias threshold, relative to ordinary least squares, of 5% of less), a chi-squared statistic and relative risk comparing proportions of those who did and did not enroll in SNAP after receiving or not receiving outreach, and by examining the distribution of measured covariates among those who enrolled SNAP after receiving versus not receiving outreach. 92,902 (80.2%) of participants received outreach. Though SNAP enrollment was low overall, outreach was strongly associated with SNAP enrollment. Of individuals who received outreach, 5.3% enrolled in SNAP, compared with 0.7% of those who did not receive outreach (p < .001).

Second, if the candidate instrumental variable does not share common causes with the study outcome, then categorizing study participants by whether they received outreach or not should serve to balance measured confounders (such as demographics and comorbidities) between groups, akin to how categorization by study arm assignment balances confounders in a randomized clinical trial. Therefore, we compared balance when categorizing study participants by SNAP enrollment status, and when categorizing participants by receipt of outreach. We expected that there would be imbalance when categorized by SNAP enrollment, but balance when comparing by receipt of outreach. As measures of balance we used the standardized mean difference. We considered a standardized mean difference of < 0.10 to indicate adequate balance. Participants who did versus did not receive outreach were well balanced on observed characteristics, with standardized mean differences less than 0.02 for all variables (see **Appendix Table 1**).

To test balance more formally, we also employed two permutation-based falsification tests, developed by Branson and Keele(23), that examine, using the sum of absolute bias and Mahalanobis distance of observed characteristics, whether categorization by the instrumental variable produces balance that would have been observed under randomization.(23)

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| Supplement Table A: Instrumental Variable Assumptions | | | |
| Assumption | Description of Assumption | Conceptual Argument for Meeting Assumption in this Study | Results of Statistical Test of Assumptions, if Available |
| IV is Positively Correlated with Treatment Assumption | Those exposed to the instrument are more likely to receive the treatment than those unexposed. | The outreach program offered by BDT has been proven in a prior randomized trial to increase SNAP enrollment.(24) | * First stage F-statistic: 912 * Cragg-Donald statistic: 334 (Stock and Yogo Critical Value for bias of 5% or less relative to ordinary least squares: 17) * Chi-squared statistic comparing proportion who did versus did not enroll in SNAP by receipt of outreach: 908 * Relative risk of SNAP enrollment comparing those who did versus did not receive outreach: 7.6 * Difference in measured covariates among those who enroll in SNAP with versus without outreach suggests that outreach is helping individuals enroll who would not otherwise (See Appendix Table 1) |
| IV is Independent of Unmeasured Confounders | Individuals should be exposed to the instrument effectively at random (possibly conditional on covariates) | The BDT process for assigning outreach group was known to be random | * Standardized mean differences for measured covariates < 0.10 when categorized by outreach group assignment * Permutation test of randomization using sum of absolute bias p-value: 0.98, which is consistent with outreach group assignment being random(23) * Permutation test of randomization using Mahalanobis distance p-value: 0.87, which is consistent with outreach group assignment being random(23) |
| Exclusion Restriction | The instrument effects the outcome only through receipt of treatment | Receipt of outreach for SNAP enrollment is unlikely to affect healthcare use and cost unless it results in SNAP enrollment | None available |
| Stable Unit Treatment Value Assumption | There is only one version of the treatment, and one person receiving the treatment does not interfere with another individuals’ chance of receiving the treatment | SNAP is federal program with clear and standardized administrative rules. Federal regulations provide that like cases are treated alike, so there are unlikely to be multiple ‘versions’ of SNAP received by different individuals. Because SNAP is a federal entitlement program, all eligible individuals who apply must be enrolled, and funding does not ‘run out’ as it can for non-entitlement programs such as WIC (Special Supplemental Nutrition Assistance Program for Women, Infants, and Children) or LIHEAP (Low Income Home Energy Assistance Program). Thus one person receiving SNAP does not prevent another eligible person from receiving SNAP. One possible SUTVA violation could occur if an individual was impacted by SNAP benefits received from someone else in their household. This could result in misclassification that biases estimates of treatment effect to the null (as people who benefitted from SNAP would be classified as not receiving SNAP). | None available |
| Monotonicity | Instrument may increase chance of receiving treatment or have no effect, but should not decrease chance of receiving treatment. | Conceptually, it is difficult to think of any reason why receiving outreach for SNAP enrollment would decrease SNAP enrollment (i.e., that someone would enroll in SNAP only if they do not receive outreach). Empirically, a previous randomized trial(24) of BDT’s outreach program observed increases, rather than decreases in enrollment in response to receiving outreach, suggesting that the monotonicity assumption is likely to hold. | None available |

*Variables for Adjustment, Standard Error Estimation, Statistical Inference, and Expression of Results for Instrumental Variable Analyses*

In instrumental variable analyses, it is important to adjust for factors that may confound the relationship between the instrumental variable and the outcome. Further, it can be important to adjust for other factors that may also influence interpretation of the results. In the case of this study, based on our knowledge of the random process of outreach group assignment, we did not expect there to be confounders of the relationship between outreach and study outcomes. However, there were other factors we needed to adjust for, as follows: the number of follow-up days (to account for differing risks of experiencing study outcomes), the index date (to account for secular trends regarding healthcare use and cost), and whether an individual was a partial versus full Medicaid beneficiary (which may reflect which healthcare claims were available in the Medicaid dataset). We included the same three covariates in both stages of the instrumental variable models.

We conducted statistical inference using the beta coefficient and standard error on the SNAP term in the second stage model. We did this because a prior simulation study by Palmer et al. has shown that this approach yields type 1 error rates and confidence bound coverage at approximately the nominal levels.(25) To estimate the standard error, we used the method proposed by Terza (12,25) that accounts for estimating both a first and second stage model. Hypothesis testing was based on whether the SNAP term in the second stage model was statistically significantly different from zero (which would indicate a difference in outcome between those who did and did not enroll in SNAP). For clarity, we have bolded this term in the tables that display the second stage models for the 2SRI analyses.

When communicating study results, simply reporting regression coefficients can be difficult to understand. Policymakers and clinicians think in terms of number of admissions and costs of care, not beta coefficients and standard errors. Thus, to aid understanding, we focus on expressing the results of our analyses in terms of number of events per 1000 person-years for count outcomes, and in terms of per person per year cost for expenditure outcomes. This represents an estimate of the local average treatment effect (LATE), the estimand for instrumental variable analyses. The LATE can be thought of as the treatment effect among those who enrolled in SNAP owing to the outreach program (and those whoe did not enroll in SNAP because they did not receive outreach—in other words, those for whom the instrument made the difference). The LATE estimated in these cases is the difference in marginal mean outcomes under the two counterfactual scenarios—one in which everyone had enrolled in SNAP owing to the outreach program, and one in which no one had. To quantify the uncertainty in these estimates, we used bootstrapping to produce 95% confidence intervals (using a percentile-based method with 1000 bootstrap replications of both stages of the modeling process, as we were unaware of any analytic approach to calculating standard errors for this case). As we used these predictive marginal means only to express results, and had already conducted hypothesis testing as above(25), we did not estimate standard errors for these predictions.

*Sensitivity Analyses for Instrumental Variables*

To examine the sensitivity of the findings to violations of instrumental variable assumptions, different modeling specifications, or unmeasured confounding, we conducted several sensitivity analyses.(2,17) Some evidence from simulation studies suggests that the type of residual used for 2SRI can affect the estimates.(15) Our main instrumental variable analyses used quantile residuals(26), so we re-ran our analyses of inpatient admission (primary outcome) using ‘raw’ residuals, ‘Pearson’ residuals, standardized residuals, ‘Student’ residuals, and Anscombe residuals, to determine if type of residual used affected the results.

**Supplement References**

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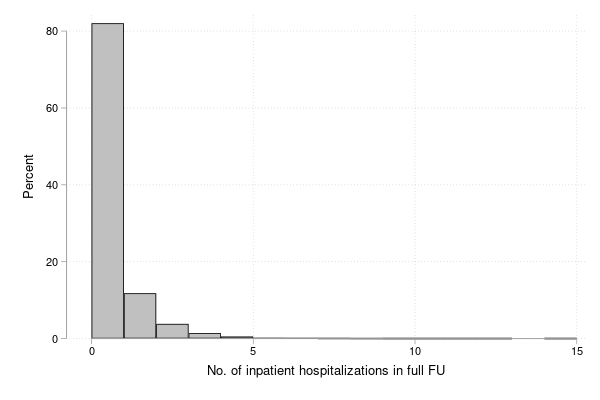
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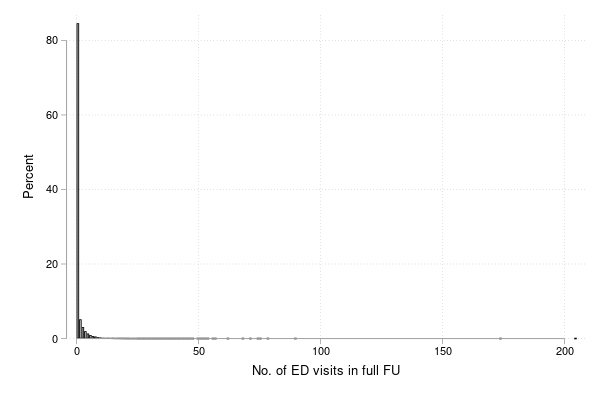
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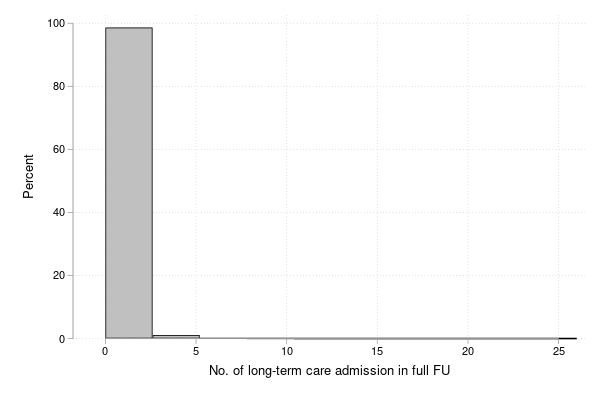
Supplement Figure 1: Histogram of Count of Inpatient Admissions During Follow-up Period



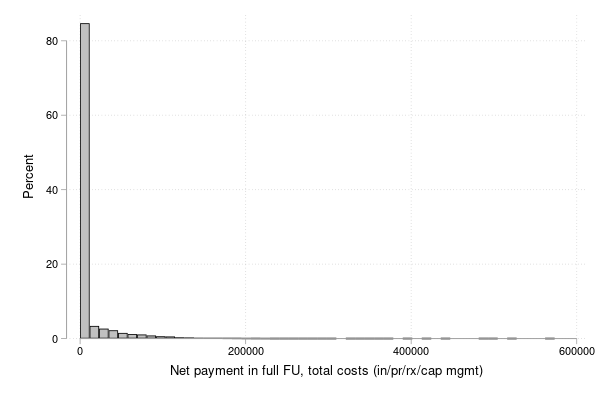
Supplement Figure 2: Histogram of Count of Emergency Department Visits During Follow-up Period



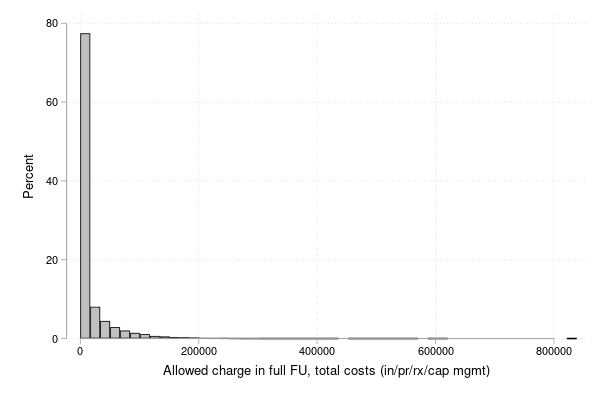
Supplement Figure 3: Histogram of Count of Long Term Care Admissions During Follow-up Period



Supplement Figure 4: Histogram of Actual Medicaid Spending During Follow-up Period



Supplement Figure 5: Histogram of Allowed Medicaid Spending During Follow-up Period



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| Supplement Table 1: Missingness of Variables | | | |
|  | Missing | Total | Percent Missing |
| SNAP Status | 0 | 115,868 | 0 |
| Days Follow-up | 0 | 115,868 | 0 |
| Index Date | 0 | 115,868 | 0 |
| Age, years | 0 | 115,868 | 0 |
| Female | 0 | 115,868 | 0 |
| Hispanic | 0 | 115,868 | 0 |
| Non-Hispanic Black | 0 | 115,868 | 0 |
| Non-Hispanic White | 0 | 115,868 | 0 |
| Other | 0 | 115,868 | 0 |
| Partially Dual-Eligible | 0 | 115,868 | 0 |
| Inpatient admissions per year during baseline period | 0 | 115,868 | 0 |
| Emergency department visits per year during baseline period | 0 | 115,868 | 0 |
| Long term care admissions per year during baseline period | 0 | 115,868 | 0 |
| Actual Medicaid costs per year during baseline period | 0 | 115,868 | 0 |
| Allowed Medicaid costs per year during baseline period | 0 | 115,868 | 0 |
| Comorbidity score\* | 0 | 115,868 | 0 |
| History of coronary heart disease | 0 | 115,868 | 0 |
| History of chronic kidney disease | 0 | 115,868 | 0 |
| History of depression | 0 | 115,868 | 0 |
| History of diabetes mellitus | 0 | 115,868 | 0 |
| History of hypertension | 0 | 115,868 | 0 |
| Days observed during baseline period | 0 | 115,868 | 0 |
| Proportion of study participants who enrolled in SNAP at HSA level | 16 | 115,868 | 0.01 |
| Discharges per 1000 Medicare enrollees at HSA level | 16 | 115,868 | 0.01 |
| Percent mortality of Medicare enrollees at HSA level | 16 | 115,868 | 0.01 |
| Mean Medicare reimbursement per enrollee at HSA level | 16 | 115,868 | 0.01 |
| Discharges per 1000 Medicare enrollees at HRR level | 16 | 115,868 | 0.01 |
| Percent mortality of Medicare enrollees at HRR level | 16 | 115,868 | 0.01 |
| Mean Medicare reimbursement per enrollee at HRR level | 16 | 115,868 | 0.01 |
| SNAP = Supplemental Nutrition Assistance Program  HSA = Hospital Service Area  HRR = Hospital Referral Region SMD = standardized mean difference  \*Comorbidity score ranges from -2 to 26 with higher scores indicating greater comorbidity | | | |

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| Supplement Table 2: Intraclass Correlation Coefficients for SNAP Enrollment and Study Outcomes by Different  Geographic Levels and Variation in SNAP Enrollment and Outcomes at HSA level | | | | | | |
| Geographic Level | Intraclass Correlation Coefficient for Variation in Each Factor | | | | | |
|  | SNAP | Inpatient  Admissions | Emergency  Department Visits | Long Term  Care  Admissions | Actual  Medicaid  Costs | Allowed  Medicaid  Costs |
| HSA | 0.002 | 0.005 | 0.009 | 0.001 | 0.008 | 0.008 |
| HRR | 0.001 | 0.005 | 0.004 | 0.001 | 0.006 | 0.006 |
| Zip Code | 0.002 | 0.005 | 0.009 | 0.002 | 0.014 | 0.013 |
|  | | | | | | |
| Variation in Each Factor at HSA Level | | | | | | |
|  | Mean | Min | 25th  Percentile | Median | 75th  Percentile | Max |
| Proportion of study  participants enrolled in SNAP | 0.04 | 0.01 | 0.04 | 0.04 | 0.05 | 0.07 |
| Inpatient  Admissions | 0.20 | 0 | 0 | 0 | 0.28 | 2.0 |
| Emergency  Department Visits | 0.56 | 0 | 0 | 0 | 0.89 | 6.0 |
| Long Term  Care  Admissions | 0.10 | 0 | 0 | 0 | 0.13 | 1.50 |
| Actual  Medicaid  Costs, $ | 6879 | 0 | 48 | 2675 | 9895 | 54608 |
| Allowed  Medicaid  Costs, $ | 11496 | 0 | 48 | 3563 | 16217 | 102904 |
| SNAP = Supplemental Nutrition Assistance Program  HSA = Hospital Service Area  HRR = Hospital Referral Region | | | | | | |

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| Supplement Table 3: Outcome Regression Model for Inpatient Admission Outcome | | | | | |
|  | Coefficient | Standard  Error | p | Lower 95%  Confidence Bound | Upper 95%  Confidence Bound |
| Enrolled in SNAP  (Ref: did not enroll) | -0.11 | 0.04 | 0.004 | -0.18 | -0.03 |
| Days follow up | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Index date | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Hispanic | -0.46 | 0.05 | <.001 | -0.55 | -0.37 |
| Non-Hispanic Black | -0.25 | 0.03 | <.001 | -0.31 | -0.20 |
| Non-Hispanic White | -0.08 | 0.03 | 0.002 | -0.14 | -0.03 |
| Other race/ethnicity | -0.25 | 0.04 | <.001 | -0.33 | -0.16 |
| Partially Medicaid eligible  (Ref: fully eligible) | 0.64 | 0.03 | <.001 | 0.58 | 0.70 |
| Age, years | 0.02 | 0.00 | <.001 | 0.01 | 0.02 |
| Female | -0.17 | 0.02 | <.001 | -0.20 | -0.14 |
| Days of baseline observation | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Gagne comorbidity score | 0.14 | 0.00 | <.001 | 0.13 | 0.14 |
| History of coronary heart disease | 0.21 | 0.02 | <.001 | 0.17 | 0.24 |
| History of chronic kidney disease | -0.07 | 0.02 | 0.001 | -0.11 | -0.03 |
| History of depression | 0.06 | 0.02 | 0.003 | 0.02 | 0.10 |
| History of diabetes mellitus | 0.16 | 0.02 | <.001 | 0.13 | 0.19 |
| History of hypertension | 0.95 | 0.02 | <.001 | 0.91 | 0.99 |
| Inpatient admissions during  baseline period | 0.21 | 0.02 | <.001 | 0.18 | 0.24 |
| Discharges per 1000 Medicare enrollees at HSA level | 0.00 | 0.00 | 0.002 | 0.00 | 0.00 |
| Percent mortality of Medicare enrollees at HSA level | -0.02 | 0.04 | 0.611 | -0.09 | 0.05 |
| Mean Medicare reimbursement per enrollee at HSA level | 0.00 | 0.00 | 0.846 | 0.00 | 0.00 |
| Proportion of study participants who enrolled in SNAP at HSA level | 0.59 | 0.79 | 0.453 | -0.95 | 2.13 |
| Results from a mixed effects negative binomial model with dependent variable of inpatient admissions, with observations clustered within HSA (random intercept)  A negative beta coefficient indicates fewer inpatient admissions  HSA = hospital service area | | | | | |

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| Supplement Table 4: Outcome Regression Model for Emergency Department Visits Outcome | | | | | |
|  | Coefficient | Standard  Error | P | Lower 95%  Confidence Bound | Upper 95%  Confidence Bound |
|  |  |  |  |  |  |
| Enrolled in SNAP (Ref: did not enroll) | -0.32 | 0.04 | <.001 | -0.39 | -0.25 |
| Days follow up | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Index date | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Hispanic | -0.10 | 0.04 | 0.012 | -0.18 | -0.02 |
| Non-Hispanic Black | -0.31 | 0.03 | <.001 | -0.36 | -0.25 |
| Non-Hispanic White | -0.17 | 0.03 | <.001 | -0.23 | -0.12 |
| Other race/ethnicity | -0.21 | 0.04 | <.001 | -0.29 | -0.13 |
| Partially Medicaid eligible  (Ref: fully eligible) | 0.64 | 0.02 | <.001 | 0.60 | 0.69 |
| Age, years | 0.02 | 0.00 | <.001 | 0.02 | 0.02 |
| Female | -0.24 | 0.02 | <.001 | -0.27 | -0.21 |
| Days of baseline observation | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Gagne comorbidity score | 0.10 | 0.00 | <.001 | 0.10 | 0.11 |
| History of coronary heart disease | 0.09 | 0.02 | <.001 | 0.05 | 0.13 |
| History of chronic kidney disease | -0.10 | 0.02 | <.001 | -0.15 | -0.06 |
| History of depression | 0.18 | 0.02 | <.001 | 0.13 | 0.22 |
| History of diabetes mellitus | 0.17 | 0.02 | <.001 | 0.13 | 0.20 |
| History of hypertension | 0.98 | 0.02 | <.001 | 0.95 | 1.01 |
| Emergency department visits during baseline period | 0.34 | 0.01 | <.001 | 0.33 | 0.35 |
| Discharges per 1000 Medicare enrollees at HSA level | 0.00 | 0.00 | 0.001 | 0.00 | 0.00 |
| Percent mortality of Medicare enrollees at HSA level | 0.03 | 0.05 | 0.593 | -0.08 | 0.13 |
| Mean Medicare reimbursement per enrollee at HSA level | 0.00 | 0.00 | 0.033 | 0.00 | 0.00 |
| Proportion of study participants who enrolled in SNAP at HSA level | -1.06 | 0.93 | 0.250 | -2.88 | 0.75 |
| Results from a mixed effects negative binomial model with dependent variable of emergency department visits, with observations clustered within HSA (random intercept)  A negative beta coefficient indicates fewer emergency department visits HSA = hospital service area | | | | | |

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| Supplement Table 5: Outcome Regression Model for Long Term Care Admissions Outcome | | | | | |
|  | Coefficient | Standard Error | P | Lower 95%  Confidence Bound | Upper 95%  Confidence Bound |
| Enrolled in SNAP  (Ref: did not enroll) | -0.61 | 0.08 | <.001 | -0.76 | -0.46 |
| Days follow up | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Index date | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Hispanic | -0.65 | 0.10 | <.001 | -0.85 | -0.45 |
| Non-Hispanic Black | 0.31 | 0.06 | <.001 | 0.20 | 0.43 |
| Non-Hispanic White | 0.48 | 0.06 | <.001 | 0.37 | 0.59 |
| Other race/ethnicity | -0.12 | 0.09 | 0.161 | -0.29 | 0.05 |
| Partially Medicaid eligible  (Ref: fully eligible) | -0.08 | 0.04 | 0.036 | -0.15 | 0.00 |
| Age, years | 0.06 | 0.00 | <.001 | 0.06 | 0.07 |
| Female | -0.24 | 0.03 | <.001 | -0.30 | -0.19 |
| Days of baseline observation | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Gagne comorbidity score | 0.14 | 0.01 | <.001 | 0.13 | 0.15 |
| History of coronary heart disease | -0.02 | 0.04 | 0.617 | -0.09 | 0.06 |
| History of chronic kidney disease | -0.08 | 0.04 | 0.057 | -0.17 | 0.00 |
| History of depression | 0.10 | 0.04 | 0.020 | 0.02 | 0.19 |
| History of diabetes mellitus | 0.16 | 0.03 | <.001 | 0.09 | 0.23 |
| History of hypertension | 0.16 | 0.03 | <.001 | 0.09 | 0.22 |
| Long term admissions during  baseline period | 2.06 | 0.05 | <.001 | 1.96 | 2.16 |
| Discharges per 1000 Medicare enrollees at HSA level | 0.00 | 0.00 | 0.617 | 0.00 | 0.00 |
| Percent mortality of Medicare enrollees at HSA level | 0.04 | 0.05 | 0.393 | -0.06 | 0.14 |
| Mean Medicare reimbursement per enrollee at HSA level | 0.00 | 0.00 | 0.992 | 0.00 | 0.00 |
| Proportion of study participants who enrolled in SNAP at HSA level | 0.64 | 1.04 | 0.538 | -1.40 | 2.69 |
| Results from a mixed effects negative binomial model with dependent variable of long term care admissions, with observations clustered within HSA (random intercept)  A negative beta coefficient indicates fewer long term care admissions HSA = hospital service area | | | | | |

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| Supplement Table 6: Outcome Regression Model for Actual Medicaid Costs Outcome | | | | | |
|  | Coefficient | Standard Error | P | Lower 95%  Confidence Bound | Upper 95%  Confidence Bound |
| Enrolled in SNAP (Ref: did not enroll) | -0.52 | 0.04 | <.001 | -0.60 | -0.44 |
| Index date | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Hispanic | -0.29 | 0.05 | <.001 | -0.38 | -0.19 |
| Non-Hispanic Black | 0.40 | 0.04 | <.001 | 0.33 | 0.47 |
| Non-Hispanic White | 0.39 | 0.04 | <.001 | 0.32 | 0.46 |
| Other race/ethnicity | 0.03 | 0.05 | 0.600 | -0.07 | 0.12 |
| Partially Medicaid eligible (ref: fully eligible) | -0.18 | 0.02 | <.001 | -0.22 | -0.13 |
| Age, years | 0.07 | 0.00 | <.001 | 0.06 | 0.07 |
| Female | -0.07 | 0.02 | <.001 | -0.10 | -0.03 |
| Days of baseline observation | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Gagne comorbidity score | 0.13 | 0.00 | <.001 | 0.12 | 0.14 |
| History of coronary heart disease | -0.13 | 0.03 | <.001 | -0.18 | -0.07 |
| History of chronic kidney disease | -0.21 | 0.03 | <.001 | -0.27 | -0.14 |
| History of depression | 0.14 | 0.03 | <.001 | 0.08 | 0.20 |
| History of diabetes mellitus | 0.07 | 0.02 | 0.003 | 0.02 | 0.12 |
| History of hypertension | -0.28 | 0.03 | <.001 | -0.33 | -0.22 |
| Actual Medicaid expenditures during baseline period | 0.13 | 0.00 | <.001 | 0.13 | 0.13 |
| Discharges per 1000 Medicare enrollees at HSA level | 0.00 | 0.00 | 0.532 | 0.00 | 0.00 |
| Percent mortality of Medicare enrollees at HSA level | 0.01 | 0.04 | 0.858 | -0.07 | 0.08 |
| Mean Medicare reimbursement per enrollee at HSA level | 0.00 | 0.00 | 0.586 | 0.00 | 0.00 |
| Proportion of study participants who enrolled in SNAP at HSA level | 0.55 | 0.96 | 0.569 | -1.33 | 2.43 |
| Results from a mixed effects generalized linear model with log link and gamma error distribution, with observations clustered within HSA (random intercept)  A negative beta coefficient in the gamma regression model indicates lower estimated expenditures per year of follow-up HSA = hospital service area | | | | | |

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| Supplement Table 7: Outcome Regression Model for Allowed Medicaid Costs Outcome | | | | | |
|  | Coefficient | Standard Error | P | Lower 95%  Confidence Bound | Upper 95%  Confidence Bound |
| Enrolled in SNAP (Ref: did not enroll) | -0.49 | 0.04 | <.001 | -0.57 | -0.41 |
| Index date | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Hispanic | -0.37 | 0.05 | <.001 | -0.47 | -0.27 |
| Non-Hispanic Black | 0.19 | 0.04 | <.001 | 0.12 | 0.26 |
| Non-Hispanic White | 0.26 | 0.04 | <.001 | 0.19 | 0.33 |
| Other race/ethnicity | -0.11 | 0.05 | 0.023 | -0.21 | -0.02 |
| Partially Medicaid eligible (ref: fully eligible) | -0.06 | 0.02 | 0.014 | -0.10 | -0.01 |
| Age, years | 0.05 | 0.00 | <.001 | 0.05 | 0.06 |
| Female | -0.16 | 0.02 | <.001 | -0.20 | -0.13 |
| Days of baseline observation | 0.00 | 0.00 | <.001 | 0.00 | 0.00 |
| Gagne comorbidity score | 0.15 | 0.00 | <.001 | 0.14 | 0.16 |
| History of coronary heart disease | -0.03 | 0.03 | 0.232 | -0.09 | 0.02 |
| History of chronic kidney disease | -0.19 | 0.03 | 0.000 | -0.26 | -0.12 |
| History of depression | 0.07 | 0.03 | 0.018 | 0.01 | 0.14 |
| History of diabetes mellitus | 0.06 | 0.02 | 0.015 | 0.01 | 0.11 |
| History of hypertension | -0.08 | 0.03 | 0.002 | -0.13 | -0.03 |
| Allowed Medicaid expenditures during baseline period | 0.12 | 0.00 | <.001 | 0.12 | 0.12 |
| Discharges per 1000 Medicare enrollees at HSA level | 0.00 | 0.00 | 0.217 | 0.00 | 0.00 |
| Percent mortality of Medicare enrollees at HSA level | -0.01 | 0.04 | 0.710 | -0.08 | 0.06 |
| Mean Medicare reimbursement per enrollee at HSA level | 0.00 | 0.00 | 0.511 | 0.00 | 0.00 |
| Proportion of study participants who enrolled in SNAP at HSA level | -0.38 | 0.83 | 0.647 | -2.02 | 1.25 |
| Results from a mixed effects generalized linear model with log link and gamma error distribution, with observations clustered within HSA (random intercept)  A negative beta coefficient in the gamma regression model indicates lower estimated expenditures per year of follow-up HSA = hospital service area | | | | | |

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| Supplement Table 8: Healthcare Utilization and Cost Outcomes Amongst Subset of Sample that is Fully Dual Eligible | | | | |
| Outcome Regression Analyses | | | | |
|  | Estimated annual utilization or cost if everyone had received SNAP  (95% CI) | Estimated annual utilization or cost if no one had received SNAP  (95% CI) | Difference (ATE)  (95% CI) | P |
| Inpatient admissions, per 1000 person years | 39.1  (24.1 to 54.1) | 75.8  (65.7 to 85.9) | -36.7  (-52.2 to -21.1) | <.001 |
| Emergency department visits, per 1000 person years | 159.0  (88.0 to 230.1) | 295.7  (202.7 to 388.7) | -136.7  (-204.1 to -69.2) | <.001 |
| Long term care admissions, per 1000 person years | 43.3  (26.0 to 60.7) | 108.4  (91.2 to 125.6) | -65.1  (-84.6 to -45.6) | <.001 |
| Actual Medicaid costs, $ per person per year | 3931  (2685 to 5177) | 7114  (5693 to 8534) | -3183  (-4292 to -2074) | <.001 |
| Allowed Medicaid costs, $ per person per year | 5283  (3701 to 6866) | 9308  (7682 to 10934) | -4024  (-5444 to -2604) | <.001 |
| Two Stage Residual Inclusion Instrumental Variable Analyses | | | | |
|  | Estimated annual utilization or cost if everyone had received SNAP due to outreach  (95% CI) | Estimated annual utilization or cost if no one had received SNAP due to outreach  (95% CI) | Difference (LATE)  (95% CI) | P |
| Inpatient admissions, per 1000 person years | 30.0  (16.7 to 42.9) | 70.3  (64.2 to 76.4) | -40.3  (-55.8 to -26.4) | <.001 |
| Emergency department visits, per 1000 person years | 73.6  (43.4 to 123.7) | 185.0  (160.4 to 210.7) | -111.5  (-147.9 to -61.1) | <.001 |
| Long term care admissions, per 1000 person years | 25.9  (15.4 to 42.0) | 97.8  (88.6 to 106.4) | -72.0  (-85.7 to -53.3) | <.001 |
| Actual Medicaid costs, $ per person per year | 893  (695 to 1332) | 3395  (3193 to 3584) | -2502  (-2714 to -2028) | <.001 |
| Allowed Medicaid costs, $ per person per year | 1367  (1018 to 1771) | 4886  (4627 to 5126) | -3520  (-3954 to -3085) | <.001 |
| SNAP = Supplemental Nutrition Assistance Program  LATE = Local Average Treatment Effect  Estimates and confidence bounds are from predictive margins.  Two stage residual inclusion analyses adjust for index date, follow-up time, and whether an individual was a partial versus full Medicaid beneficiary.  Utilization is expressed per 1000 person-years, and cost is expressed as per person per year  P-values from beta coefficient for SNAP term in second stage model for two stage residual inclusion analyses, following the method proposed by Terza.  Count outcomes used negative binomial models and cost outcomes used log-gamma models. | | | | |

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| Supplement Table 9: Characteristics of study participants before and after entropy balance weights | | | | | | | |
|  | Overall | Before Weighting | | | After Weighting | | |
|  |  | Did not receive SNAP | Received SNAP | SMD | Did not receive outreach | Received outreach | SMD |
|  | N=  115868 | N=  110775 | N=  5093 |  | N=  110775 | N=  5093 |  |
|  | Mean (SD) or N (%) | Mean (SD) or N (%) | Mean (SD) or N (%) |  | Mean (SD) or Weighted N (%) | Mean (SD) or WeightedN (%) |  |
| Age, years | 74.23 (7.61) | 74.24 (7.63) | 74.00 (7.28) | 0.033 | 74.23 (7.62) | 74.23 (7.56) | <0.001 |
| Female | 78124 (67.4) | 74512 (67.3) | 3612 (70.9) | 0.079 | 74683.1 (67.4) | 3433.8 (67.4) | <0.001 |
| Hispanic | 5571 (4.8) | 5478 (4.9) | 93 (1.8) | 0.173 | 5308.9 (4.8) | 245.0 (4.8) | 0.001 |
| Non-Hispanic Black | 39963 (34.5) | 38027 (34.3) | 1936 (38.0) | 0.077 | 38199.6 (34.5) | 1756.6 (34.5) | <0.001 |
| Non-Hispanic White | 56880 (49.1) | 54198 (48.9) | 2682 (52.7) | 0.075 | 54360.0 (49.1) | 2500.1 (49.1) | <0.001 |
| Other | 6074 (5.2) | 5827 (5.3) | 247 (4.8) | 0.019 | 5810.2 (5.2) | 266.9 (5.2) | <0.001 |
| Partially Dual-Eligible | 95047 (82.0) | 91111 (82.2) | 3936 (77.3) | 0.124 | 90860.7 (82.0) | 4177.7 (82.0) | <0.001 |
| Inpatient admissions per year during baseline period | 0.15 (0.50) | 0.15 (0.50) | 0.11 (0.41) | 0.090 | 0.15 (0.50) | 0.15 (0.47) | <0.001 |
| Emergency department visits per year during baseline period | 0.49 (1.63) | 0.50 (1.65) | 0.31 (1.08) | 0.137 | 0.49 (1.62) | 0.49 (1.52) | <0.001 |
| Long term care admissions per year during baseline period | 0.05 (0.37) | 0.05 (0.38) | 0.02 (0.20) | 0.11 | 0.05 (0.37) | 0.05 (0.38) | <0.001 |
| Actual Medicaid costs per year during baseline period | 3421.09 (8917.83) | 3480.73 (9020.35) | 2124.06 (6146.29) | 0.176 | 3421.14 (8848.19) | 3421.56 (8519.00) | <0.001 |
| Allowed Medicaid costs per year during baseline period | 6328.72 (13280.07) | 6427.90 (13388.99) | 4171.59 (10408.43) | 0.188 | 6329.16 (13202.03) | 6329.83 (13290.77) | <0.001 |
| Comorbidity score\* | 1.27 (2.51) | 1.29 (2.52) | 0.90 (2.09) | 0.165 | 1.27 (2.51) | 1.27 (2.50) | <0.001 |
| History of coronary heart disease | 14898 (12.9) | 14379 (13.0) | 519 (10.2) | 0.087 | 14241.4 (12.9) | 654.7 (12.9) | <0.001 |
| History of chronic kidney disease | 12130 (10.5) | 11687 (10.6) | 443 (8.7) | 0.063 | 11603.4 (10.5) | 533.6 (10.5) | <0.001 |
| History of depression | 10061 (8.7) | 9679 (8.7) | 382 (7.5) | 0.045 | 9623.7 (8.7) | 442.6 (8.7) | <0.001 |
| History of diabetes mellitus | 26002 (22.4) | 25087 (22.6) | 915 (18.0) | 0.117 | 24851.9 (22.4) | 1143.1 (22.4) | <0.001 |
| History of hypertension | 50798 (43.8) | 48995 (44.2) | 1803 (35.4) | 0.181 | 48551.3 (43.8) | 2233.3 (43.8) | <0.001 |
| Days observed during baseline period | 335.95 (74.74) | 336.02 (74.77) | 334.44 (74.14) | 0.021 | 335.95 (74.85) | 335.95 (72.19) | <0.001 |
| Proportion of study participants who enrolled in SNAP at HSA level | 0.04 (0.01) | 0.04 (0.01) | 0.05 (0.03) | 0.174 | 0.04 (0.01) | 0.04 (0.01) | <0.001 |
| Discharges per 1000 Medicare enrollees at HSA level | 260.57 (43.51) | 260.46 (43.41) | 262.85 (45.62) | 0.054 | 260.56 (43.50) | 260.57 (43.90) | <0.001 |
| Percent mortality of Medicare enrollees at HSA level | 4.55 (0.49) | 4.55 (0.49) | 4.58 (0.49) | 0.062 | 4.55 (0.49) | 4.55 (0.49) | <0.001 |
| Mean Medicare reimbursement per enrollee at HSA level | 9271.77 (719.61) | 9269.25 (719.22) | 9326.56 (725.91) | 0.079 | 9271.75 (719.50) | 9271.74 (708.67) | <0.001 |
| Discharges per 1000 Medicare enrollees at HRR level | 253.05 (15.13) | 253.01 (15.13) | 253.75 (14.95) | 0.049 | 253.05 (15.13) | 253.05 (14.87) | <0.001 |
| Percent mortality of Medicare enrollees at HRR level | 4.46 (0.19) | 4.46 (0.19) | 4.46 (0.19) | 0.026 | 4.46 (0.19) | 4.46 (0.18) | <0.001 |
| Mean Medicare reimbursement per enrollee at HRR level | 9194.79 (402.18) | 9194.08 (403.60) | 9210.27 (369.56) | 0.042 | 9194.78 (402.02) | 9194.79 (387.83) | <0.001 |
| SNAP = Supplemental Nutrition Assistance Program  HSA = Hospital Service Area  HRR = Hospital Referral Region SMD = standardized mean difference  \*Comorbidity score ranges from -2 to 26 with higher scores indicating greater comorbidity | | | | | | | |

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| Supplement Table 10: Characteristics of matched cohort participants | | | |
|  | Did not receive SNAP | Received SNAP | SMD |
|  | N=50887 | N=5090 |  |
|  | Mean (SD) or N (%) | Mean (SD) or N (%) |  |
| Age, years | 73.96 (7.44) | 74.00 (7.28) | 0.004 |
| Female | 35931 (70.6) | 3610 (70.9) | 0.007 |
| Hispanic | 951 (1.9) | 93 (1.8) | 0.003 |
| Non-Hispanic Black | 19240 (37.8) | 1935 (38.0) | 0.004 |
| Non-Hispanic White | 26739 (52.5) | 2680 (52.7) | 0.002 |
| Other | 2629 (5.2) | 247 (4.9) | 0.014 |
| Partially Dual-Eligible | 39731 (78.1) | 3933 (77.3) | 0.019 |
| Inpatient admissions per year during baseline period | 0.11 (0.43) | 0.11 (0.41) | <0.001 |
| Emergency department visits per year during baseline period | 0.32 (1.10) | 0.31 (1.08) | 0.008 |
| Long term care admissions per year during baseline period | 0.02 (0.18) | 0.02 (0.20) | 0.001 |
| Actual Medicaid costs per year during baseline period | 2130.67 (5758.87) | 2115.37 (6129.92) | 0.003 |
| Allowed Medicaid costs per year during baseline period | 4199.38 (9412.02) | 4162.13 (10396.52) | 0.004 |
| Comorbidity score\* | 0.92 (2.07) | 0.90 (2.09) | 0.007 |
| History of coronary heart disease | 5297 (10.4) | 518 (10.2) | 0.008 |
| History of chronic kidney disease | 4557 (9.0) | 443 (8.7) | 0.009 |
| History of depression | 3919 (7.7) | 381 (7.5) | 0.008 |
| History of diabetes mellitus | 9427 (18.5) | 915 (18.0) | 0.014 |
| History of hypertension | 18416 (36.2) | 1802 (35.4) | 0.016 |
| Days observed during baseline period | 334.92 (76.21) | 334.42 (74.16) | 0.007 |
| Proportion of study participants who enrolled in SNAP at HSA level | 0.05 (0.01) | 0.05 (0.01) | <0.001 |
| Discharges per 1000 Medicare enrollees at HSA level | 262.9 (45.6) | 262.9 (45.6) | <0.001 |
| Percent mortality of Medicare enrollees at HSA level | 4.58 (0.49) | 4.58 (0.49) | <0.001 |
| Mean Medicare reimbursement per enrollee at HSA level | 9326 (725) | 9326 (725) | <0.001 |
| SNAP = Supplemental Nutrition Assistance Program  HSA = Hospital Service Area SMD = standardized mean difference  \*Comorbidity score ranges from -2 to 26 with higher scores indicating greater comorbidity | | | |

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| Supplement Table 11: First Stage Model for Two Stage Residual Inclusion Analyses | | | |
|  | Beta Coefficient | Standard Error | p |
| Intercept | -7.83 | 1.94 | 0.001 |
| Received outreach | 2.01 | 0.08 | <.001 |
| Days follow-up | 0.00 | 0.00 | <.001 |
| Index date | 0.00 | 0.00 | 0.18 |
| Partially Medicaid eligible (ref: fully eligible) | -0.42 | 0.04 | <.001 |
| Results from a logistic regression model with dependent variable of SNAP enrollment | | | |

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| Supplement Table 12: Second Stage Model for Inpatient Admission Outcome in Two Stage Residual Inclusion Analyses | | | | | |
|  | Beta Coefficient | Standard Error\* | Lower Bound of 95% Confidence Interval | Upper Bound of 95% Confidence Interval | p |
| Intercept | 38.670 | 0.997 | 36.717 | 40.623 | <.001 |
| **Enrolled in SNAP (ref: did not enroll in SNAP)** | **-0.233** | **0.043** | **-0.317** | **-0.148** | **<.001** |
| Residual from first stage model | 0.006 | 0.008 | -0.011 | 0.022 | 0.50 |
| Days follow-up | 0.000 | 0.000 | 0.000 | 0.000 | <.001 |
| Index date | -0.002 | 0.000 | -0.002 | -0.002 | <.001 |
| Partially Medicaid eligible (ref: fully eligible) | 1.294 | 0.029 | 1.238 | 1.351 | <.001 |
| Results from a negative binomial model with dependent variable of inpatient admissions  A negative beta coefficient indicates fewer inpatient admissions  \*Standard error, confidence interval, and p-values calculated using method proposed by Terza to account for both stages of analyses  Bold text indicates the regression coefficient term used for hypothesis testing | | | | | |

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| Supplement Table 13: Second Stage Model for Emergency Department Visits Outcome in Two Stage Residual Inclusion Analyses | | | | | |
|  | Beta Coefficient | Standard Error\* | Lower Bound of 95% Confidence Interval | Upper Bound of 95% Confidence Interval | p |
| Intercept | 35.370 | 0.981 | 33.447 | 37.292 | <.001 |
| **Enrolled in SNAP (ref: did not enroll in SNAP)** | **-0.418** | **0.044** | **-0.504** | **-0.331** | **<.001** |
| Residual from first stage model | 0.001 | 0.009 | -0.016 | 0.018 | 0.92 |
| Days follow-up | 0.001 | 0.000 | 0.001 | 0.001 | <.001 |
| Index date | -0.002 | 0.000 | -0.002 | -0.002 | <.001 |
| Partially Medicaid eligible (ref: fully eligible) | 1.284 | 0.024 | 1.236 | 1.331 | <.001 |
| Results from a negative binomial model with dependent variable of emergency department visits  A negative beta coefficient indicates fewer emergency department visits  \*Standard error, confidence interval, and p-values calculated using method proposed by Terza to account for both stages of analyses  Bold text indicates the regression coefficient term used for hypothesis testing | | | | | |

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| Supplement Table 14: Second Stage Model for Long Term Care Admission Outcome in Two Stage Residual Inclusion Analyses | | | | | |
|  | Beta Coefficient | Standard Error\* | Lower Bound of 95% Confidence Interval | Upper Bound of 95% Confidence Interval | p |
| Intercept | 40.161 | 1.682 | 36.864 | 43.459 | <.001 |
| **Enrolled in SNAP (ref: did not enroll in SNAP)** | **-0.860** | **0.087** | **-1.030** | **-0.690** | **<.001** |
| Residual from first stage model | 0.009 | 0.015 | -0.021 | 0.039 | 0.55 |
| Days follow-up | 0.000 | 0.000 | 0.000 | 0.000 | <.001 |
| Index date | -0.002 | 0.000 | -0.002 | -0.002 | <.001 |
| Partially Medicaid eligible (ref: fully eligible) | 0.172 | 0.038 | 0.098 | 0.247 | <.001 |
| Results from a negative binomial model with dependent variable of long term care admissions  A negative beta coefficient indicates fewer long term care admissions  \*Standard error, confidence interval, and p-values calculated using method proposed by Terza to account for both stages of analyses Bold text indicates the regression coefficient term used for hypothesis testing | | | | | |

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| Supplement Table 15: Second Stage Model for Actual Medicaid Cost Outcome in Two Stage Residual Inclusion Analyses | | | | | |
|  | Beta Coefficient | Standard Error\* | Lower Bound of 95% Confidence Interval | Upper Bound of 95% Confidence Interval | p |
| Intercept | 6.259 | 0.858 | 4.578 | 7.940 | <.001 |
| **Enrolled in SNAP (ref: did not enroll in SNAP)** | **-0.573** | **0.040** | **-0.652** | **-0.494** | **<.001** |
| Residual from first stage model | 0.005 | 0.008 | -0.011 | 0.021 | 0.57 |
| Days follow-up | 0.002 | 0.000 | 0.002 | 0.002 | <.001 |
| Index date | 0.000 | 0.000 | 0.000 | 0.000 | 0.190 |
| Partially Medicaid eligible (ref: fully eligible) | 0.273 | 0.020 | 0.235 | 0.312 | <.001 |
| Results from a generalized linear model with log link and gamma error distribution  A negative beta coefficient in the gamma regression model indicates lower estimated expenditures  \*Standard error, confidence interval, and p-values calculated using method proposed by Terza to account for both stages of analyses  Bold text indicates the regression coefficient term used for hypothesis testing | | | | | |

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| Supplement Table 16: Second Stage Model for Allowed Medicaid Cost Outcome in Two Stage Residual Inclusion Analyses | | | | | |
|  | Beta Coefficient | Standard Error\* | Lower Bound of 95% Confidence Interval | Upper Bound of 95% Confidence Interval | p |
| Intercept | 19.548 | 0.746 | 18.087 | 21.010 | <.001 |
| **Enrolled in SNAP (ref: did not enroll in SNAP)** | **-0.492** | **0.035** | **-0.560** | **-0.423** | **<.001** |
| Residual from first stage model | 0.001 | 0.007 | -0.013 | 0.015 | 0.91 |
| Days follow-up | 0.002 | 0.000 | 0.002 | 0.002 | <.001 |
| Index date | -0.001 | 0.000 | -0.001 | 0.000 | <.001 |
| Partially Medicaid eligible (ref: fully eligible) | 0.529 | 0.017 | 0.496 | 0.562 | <.001 |
| Results from a generalized linear model with log link and gamma error distribution  A negative beta coefficient in the gamma regression model indicates lower estimated expenditures  \*Standard error, confidence interval, and p-values calculated using method proposed by Terza to account for both stages of analyses  Bold text indicates the regression coefficient term used for hypothesis testing | | | | | |

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| Supplement Table 17: Comparing SNAP Coefficient in Second Stage of Two Stage Residual Inclusion Models using Different Types of First Stage Residuals | | | | | |
| Type of Residual | Estimate | Standard  Error | Lower 95%  Confidence  Limit | Upper 95%  Confidence  Limit | P |
| Quantile (used in main analysis) | -0.233 | 0.043 | -0.317 | -0.148 | <.0001 |
| Raw | -0.806 | 0.240 | -1.276 | -0.337 | 0.0008 |
| Pearson | -0.678 | 0.116 | -0.904 | -0.451 | <.0001 |
| Standardized | -0.806 | 0.240 | -1.276 | -0.337 | 0.0008 |
| Anscombe | -0.786 | 0.192 | -1.162 | -0.409 | <.0001 |
| Student | -0.806 | 0.240 | -1.276 | -0.337 | 0.0008 |
| SNAP = Supplemental Nutrition Assistance Program | | | | | |