NBER WORKING PAPER SERIES

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Working Paper 35005
http://www.nber.org/papers/w35005

NATIONAL BUREAU OF ECONOMIC RESEARCH
1050 Massachusetts Avenue
Cambridge, MA 02138
March 2026

This research was conducted using the UK Biobank Resource under application number 58599. Data were made available under a material transfer agreement between UK Biobank with RAND, the University of Southern California, the University of California, Berkeley, and the University of Chicago. The data were provided by patients and collected by the National Health Service as part of their care and support. The authors are grateful to Dr. Liang Bai for valuable comments and assistance. The authors acknowledge financial support from the National Institute on Aging of the National Institutes of Health under grants R01AG065482, P30AG012815, P30AG012839, and T32AG000243. The views expressed herein are those of the authors and do not necessarily reflect the views of the National Institutes of Health or the National Bureau of Economic Research. The authors declare that they have no financial or material interests in the results.

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NBER Working Paper No. 35005
March 2026
JEL No. I1

ABSTRACT

Genetics confer 2–3-fold higher obesity risk through inherited mechanisms affecting appetite and metabolism, with pathways particularly modifiable during the first 1,000 days of life. We leverage the end of UK sugar rationing in September 1953, a sharp discontinuity in early-life sugar exposure by conception date, to examine whether sugar restriction mitigates genetically determined obesity risk using UK Biobank data linking an obesity polygenic index with adiposity phenotypes. Without rationing, high genetic risk individuals had triple the obesity prevalence of low-risk counterparts. Restriction through age two narrowed this disparity by 40%, operating through visceral rather than general adiposity, and was concentrated among high-risk adults with above-median adiposity levels. Early nutritional environments can alter inherited obesity trajectories, pointing to targeted early-life interventions to reduce genetically determined health inequalities.

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1. Introduction

Genetics account for up to 70% of obesity risk, with high genetic risk individuals facing obesity rates 2-3 fold higher than their low genetic risk counterparts.[1,2,3,4] One approach to mitigate these gaps is improved diet, particularly reduced intake of added sugars, given their strong links to obesity and interactions with inherited pathways governing appetite, reward, and metabolic function.[5,6] These same pathways are highly malleable during the first 1,000 days, when taste preferences, neural reward circuits, and metabolic programming are established.[7,8] Thus, early sugar restriction could counteract predetermined genetic disadvantages by narrowing genetic gaps in obesity, yet this remains empirically underexplored.

A major barrier to identifying causal gene-environment (G×E) interactions in adult obesity is that early-life diet is endogenous rather than randomly assigned. Existing studies compare outcomes between high versus low sugar intake across genetic risk groups, but this approach relies on strong confounder control assumptions that are challenging to meet. Early-life diet is influenced by difficult-to-measure factors such as family socioeconomic status, parental health literacy, and childhood food environments.[9,10,11,12] Statistical power poses an additional challenge, as G×E effects are typically smaller than main dietary effects and require larger samples than most studies can provide.[13,14] These challenges are compounded by widespread reliance on body mass index (BMI), a relatively crude measure as it cannot distinguish fat from lean mass or characterize fat distribution, often leading to misclassifications of metabolic risk.[15,16,17,18] Thus, while animal studies demonstrate that genetic variants affecting insulin signaling, fat storage, food choice, and reward pathways increase susceptibility to weight gain under high-sugar diets,[19,20,21,22] human evidence remains observational, correlational, and BMI-focused.

To causally examine whether early-life sugar restrictions can narrow the genetic gap in adult obesity, we leverage the UK's termination of sugar and sweets rationing in September 1953, first used in Gracner et al. (2024).[23] This event created quasi-experimental variation in early-life sugar exposure, determined by the individual's date of conception: those conceived or born during rationing experienced restricted sugar during critical developmental periods (in utero and early postnatal life), while those conceived afterward had unrestricted exposure to sugar from birth. We combined UK Biobank data with obesity polygenic indexes in an event study framework, comparing adults conceived before versus after rationing cessation across multiple adiposity measures: BMI, waist-to-hip ratio, body fat percentage, and trunk fat percentage. By stratifying effects by polygenic risk profiles, we examined whether genetic obesity risk was modified by early-life sugar restriction. By combining these data with a natural experiment, we balance confounders in expectation across comparison groups, avoiding confounding more credibly than existing GxE obesity studies, and contribute by examining measures beyond BMI. We hypothesize that early-life exposure to sugar rationing lowered the risk of adult adiposity, with greater benefits among individuals genetically predisposed to obesity.

2. Methods

a. Study data.

We used the UK Biobank (UKB, application 58599), which contains detailed genetic, health, and sociodemographic data on over 500,000 participants recruited between 2006 and 2010. Our study population consisted of all adults born between October 1951 and March 1956 who were aged between 52 and 56 at their baseline survey to ensure age overlap between rationed and non-rationed adults. We excluded individuals born outside the UK, those who were part of a multiple birth or adopted, who withdrew their data from UK Biobank, who were pregnant at the time of the survey, or who were missing covariates, genetic data, or adiposity measures, yielding a final sample of 46,914 adults (Figure A1). Distribution of births over time within our study period is presented in Table A1.

b. Study design and exposure to early-life sugar restrictions

In September 1953, the United Kingdom ended the rationing of sugar and sweets that had been in place since the beginning of World War II. Under rationing, sugar intake was limited—approximately 40 grams per day for adults and 15 grams for children, with young children under age two assumed to consume little to no added sugar. As documented previously,[23] these restrictions triggered an immediate surge in consumption, nearly doubling sugar intake in adults and sales of sweets (see Figure A2). No similar changes in intake of other foods among adults were observed following rationing cessation. Direct dietary data from the mid-1950s are unavailable for children; however, contemporaneous records document a post-1954 deterioration in children's dental health, prompting the UK Ministry of Health to launch the "Happy Smile" campaign,[24] consistent with broader evidence linking increased sugar intake to worse dental outcomes.[25,26,27]

In response, individuals conceived before September 1953 experienced sugar rationing during critical developmental periods (i.e., during the first 1000 days since conception), while those conceived after September 1953 had unrestricted sugar exposure from conception onward. Following Gracner et al.(2024) [23] we classified individuals into groups based on their duration of exposure to sugar rationing: never, in utero only, or in utero plus 6, 12, 18, or 24 months postnatally. To improve statistical power for some analyses, we also grouped exposure into three broader categories: in utero and up to age 1, in utero and up to age 2, or no exposure. Figure A2, panel B illustrates the timeline of rationing exposure.

c. Adiposity measures

Our primary outcomes were adiposity and obesity, defined using a multifactorial index of different adiposity measures of body fatness. These dimensions were objectively measured: body mass index (BMI; calculated as weight in kilograms divided by height in meters squared, fields 21001 and 23104), waist-to-hip ratio (WHR; the ratio of waist circumference to hip circumference, each measured in centimeters, fields 48 and 49), body fat percentage (% BF, field 23099) and trunk fat percentage (% TF, field 23127). Before constructing the index, each sub-measure was standardized individually, using the population never exposed to rationing as the reference group (i.e., individuals born after July 1954). To do this, used inverse-covariance weighting of standardized

outcome measures to create a domain-specific summary index, reducing dimensionality and accounting for correlation across outcomes.[28] We analyzed the adiposity index both as a continuous measure and created binary indicators for obesity, defined by index values equal or exceeding the 90th percentile of the never-rationed population distribution. We also separately analyzed general (BMI and body fat %) and visceral adiposity measures (WHR and trunk fat %).

d. Genetic risk assessment

We assessed heterogeneity in genetic risk for obesity using a standardized polygenic index for BMI. This measure, derived using GWAS summary statistics, represents a weighted sum of single-nucleotide polymorphism (SNP) genotypes, serving as an individual-level genetic predictor of traits associated with obesity. See Barcellos et al. (2018; return code 3586, application 1142)[14] and Supplementary materials for more details.

We divided participants into terciles based on the distribution of BMI polygenic index, representing high, medium, and low genetic obesity risk. To increase statistical power in main analyses, we combined the top two genetic risk terciles — whose similar patterns justified pooling — into a single group, creating a binary indicator for individuals with high genetic risk of obesity, defined as those above the bottom tercile, compared to low genetic risk of obesity, defined as those in the lowest tercile.

e. Covariates

We constructed indicator variables for age in year increments (with age 52 as the reference, field 21022), calendar birth month (January as the reference, field 52), male sex (vs. female, field 22001), country of birth (England as the reference vs. Wales and vs. Scotland, field 1647), each decile of a polygenic index for BMI (using the bottom decile as the reference), and each decile of north and east coordinates of birth location (fields 129 and 130). We also created indicators for self-reported parental history each of diabetes or cardiovascular disease (father/mother was ever diagnosed with diabetes, stroke, hypertension or heart disease, fields 20107 and 20110, respectively) along with an indicator for whether information on parental health history was missing.

f. Statistical analysis

To test whether early-life experiences aside from sugar rationing were similar across cohorts, we compared means and standard deviations (SD) of early-life or time-invariant characteristics between rationing-exposed and unexposed adults using t-test. Characteristics included sex, race, parental health history, place of birth, and genetics. For a subample with available data, we also compared childhood characteristics including whether individuals were abused, felt loved, received regular medical care, or took antibiotics during childhood or adolescence. We compared standardized BMI polygenic index distributions and means between adults exposed and unexposed to sugar rationing using the Kolmogorov-Smirnov (K-S) test. To examine whether the BMI polygenic index predicts adult adiposity, we compared its distribution across adiposity status groups (i.e., ≥90th percentile vs. below) using the K-S test and estimated the R^2 from linear

regressions to quantify the share of variation in adiposity index explained by the BMI polygenic index.

To empirically compare adiposity outcomes in adulthood between sugar rationing-exposued vs unexposed individuals, we first estimated the homogenous-model equation:

$$y_i = \sum_{k=-4,k\neq-1}^{4} \beta_k * (Cohort_k) + \theta' X_i + \epsilon_i \quad (1)$$

The outcome y_i represents an adiposity measure for individual *i*, specified as either a continuous adiposity index or a binary indicator for obesity. All regressions were estimated using ordinary least squares regression, under a linear model for the continuous adiposity measure and a linear probability model for binary obesity outcomes. To estimate the relationship between rationing exposure and adiposity outcomes, we classified individuals into two primary groups: those exposed to sugar and sweets rationing in early life ("rationed") and those who were never exposed ("non-rationed"). Within these two broad categories, we further divided individuals into subgroups ($Cohort_k$) based on the timing and duration of their exposure.

We then formally tested differences in outcomes between genetic risk groups across exposure categories within a unified framework, while efficiently leveraging the full sample and improving statistical power by pooling birth cohorts into broader groups. We estimated the following model (2):

$$y_i = \gamma_k \mathbb{I}(Rationed_k) + \sum_{l=2,l\neq1}^{3} \sum_{k=1,\, k\neq0}^{3} \beta_{lk} * \mathbb{I}(PGI_l) * \mathbb{I}(Rationed_k) + \sum_{l=2,l\neq1}^{3} \delta_l \mathbb{I}(PGI_l) + \sum_{l=2,l\neq1}^{3} \theta_l' X_i * \mathbb{I}(PGI_l) + \varepsilon_i \quad (2)$$

PGI_l denotes genetic risk for obesity: low (*l*=1; bottom BMI polygenic index tercile [reference]), high (*l*=2, 3; top two BMI polygenic index terciles). $Rationed_k$ captures exposure categories: never-rationed (individuals born after July 1954, $k = 0$); in utero ($k = 1$); in utero and up to age 1 ($k = 2$); and in utero and up to age 2 ($k = 3$). The reference group was never-rationed individuals at the lowest genetic risk. Our key parameters of interest, β_{lk}, capture the difference in adiposity outcomes for each genetic–exposure subgroup relative to this reference. The control variables follow those included in model (1). We re-estimated these regressions by sex.

To examine whether the effects of early-life sugar restriction differed at various points in the adiposity distribution, we employed quantile regression. We estimated effects at the 10th through 90th percentiles in 10-percentile increments, comparing individuals exposed to sugar rationing in utero only versus in utero and postnatally relative to never-rationed individuals, using bootstrap quantile regression with 100 replications for low and high-risk adults. All models were adjusted for the covariates listed above.

Finally, we calculated the share of the genetic gap reduction due to sugar rationing for each exposure group using average marginal effects. For each exposure group, we estimated the average marginal effect of high versus low genetic risk (i.e., the genetic disparity in the probability of obesity or difference in adiposity score) while holding all other covariates at their mean values. We then expressed each group's genetic disparity as a ratio relative to the baseline genetic disparity among never-rationed adults. This ratio equals 1 for never-rationed participants by construction.

The percentage reduction in the genetic gap, calculated as one minus this ratio, represents the proportion of the original genetic disparity that was eliminated by sugar rationing. Using the Delta method, we tested whether the ratio of genetic effects differed significantly from 1. Values lower than 1 indicate that early-life sugar rationing reduced genetic disparities in adiposity outcomes; 0 implies that the gap was eliminated.

We presented 95% confidence intervals and p-values. where +, *, **, *** indicates significance at p value smaller than 0.1/0.05/0.01/0.001, respectively. We used Huber-White robust standard errors clustered by year-birth month. Analyses were conducted using the Stata SE software, version 18.0.

g. Sensitivity analyses

We assessed balance between rationed and never-rationed individuals by examining baseline characteristics across birth dates around the September 1953 cutoff, which revealed no discontinuities. Second, to examine distributional effects and test the sensitivity of our obesity results to threshold choices, we re-estimated our main regression models using quantile regressions. Third, to evaluate our genetic risk categorization approach and to justify combining the two highest genetic risk terciles, we present results for all three genetic risk terciles separately, rather than comparing only the top and bottom terciles. Fourth, to probe potential unobserved confounding, we repeated our analyses using polygenic indexes for traits unlikely to influence adiposity: genetic predisposition to nearsightedness and migraine. Finally, results were robust to the exclusion of covariates or limiting analyses on place of birth (e.g., England vs Scotland or Wales).

3. Results

a. Study population characteristics

Table 1 summarizes the balance of time-invariant characteristics between sugar rationed and never-rationed cohorts. Cohorts do not differ significantly by sex, self-reported family history of diabetes or cardiovascular disease. Additionally, several childhood characteristics (i.e., abused/felt loved/taken to the doctor regularly as a child, took antibiotics as a child or teenager), though available only for a subsample of survey respondents, also show balance between the cohorts. Rationed cohorts are slightly older at baseline (by 1.6 years; by design) and more likely born in England (vs Scotland or Wales). We control for baseline age and region of birth in all regressions, though results are robust to excluding individual regions from either the sample or the control set. Mean BMI polygenic index z-scores are not significantly different across cohorts, nor are their distributions (see Figure 1, panel A, K-S test with p=0.768). We also observe no evidence of discontinuities at the threshold in time-invariant characteristics (see Figure A3).

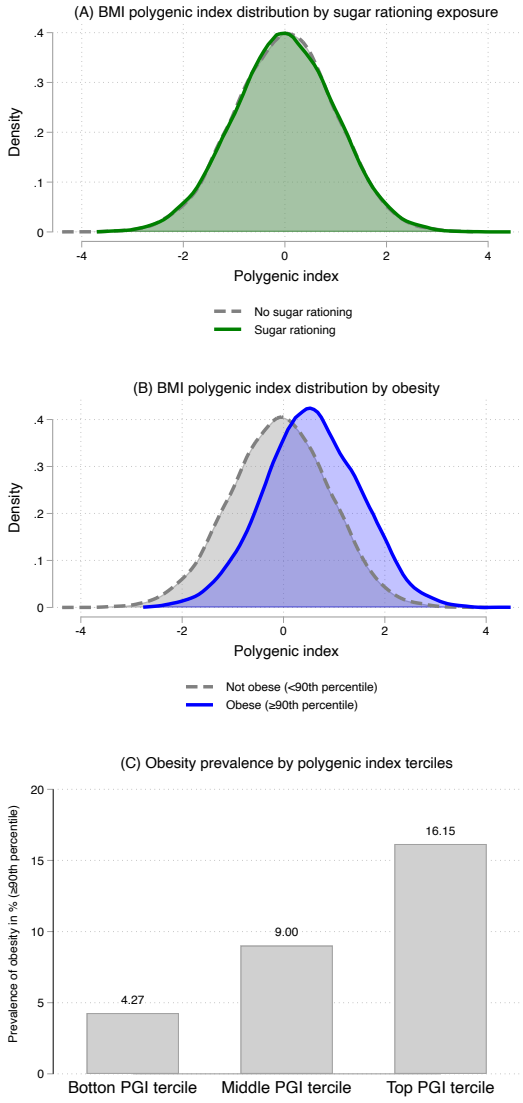
Table 1: Summary statistics on survey participants' time-invariant characteristics.

	Rationed %	Never-rationed %	Difference (percentage points)
Mean age at first survey (SD)	55.31 (SD 0.76)	53.72 (SD 0.10)	1.59*** (years)
Male	44.11	43.57	0.53
High risk (polygenic index, top 2 vs 1st tercile)	66.50	66.67	-0.00
Born in England	81.93	85.11	-3.18***
Non-white	6.80	6.86	-0.06
Family history: diabetes	17.04	18.03	-1.00
Family history: CVD	63.31	63.23	0.08
Often/very often felt loved as a child	77.16	76.81	0.34
Never sexually molested as a child	89.78	89.59	0.19
Had someone take me to a dr as a child	84.75	85.26	-0.52
Long-term antibiotic therapy as a child	15.08	15.97	-0.89
Observations	25,323	21,591	46,914

Notes: Sample sizes are 25,323 for rationed adults and 21,591 for never-rationed adults for most variables. Family history variables have slightly smaller samples (23,469 vs. 19,957) due to missing data; these are imputed and controlled for in all regressions. Childhood-related variables such as feeling loved, being taken to the doctor, and experiences of sexual molestation are based on smaller samples (9,269 and 8,109, respectively) as these questions were asked of a subset of respondents. Reported means are unadjusted. Statistical significance tests adjust for whether each parent was alive at the time of survey, as rationed individuals are older and thus more likely to have parents who were diagnosed with or died from age-related conditions. Differences between rationed and never-rationed groups are presented in percentage points (except for age presented in years), with statistical significance indicated at * $p<0.05$, ** $p<0.01$, or *** $p<0.001$.

Figure 1B presents the distribution of BMI polygenic index within our overall study population, by obesity status (90th percentile of the adiposity index or above). A K-S test confirms the distributions are significantly different by obesity status ($p<0.001$), which suggests that the BMI polygenic index is predictive of obesity in our sample. The BMI polygenic index explains 7.9% of the variation in adiposity ($R^2=0.079$); consistent with previous work showing that the BMI polygenic index typically accounts for 5-10% of BMI variance.[29,30,14,31] Figure 1C further illustrates the predictive value of the BMI polygenic index by showing the share of never-rationed adults with obesity across the bottom, middle, and top terciles of the BMI polygenic index distribution: 4.3% of individuals in the bottom tercile had obesity in adulthood, compared to 16.2% in the top tercile—a three-fold difference in prevalence.

Figure 1: Association of BMI polygenic index with sugar rationing and obesity

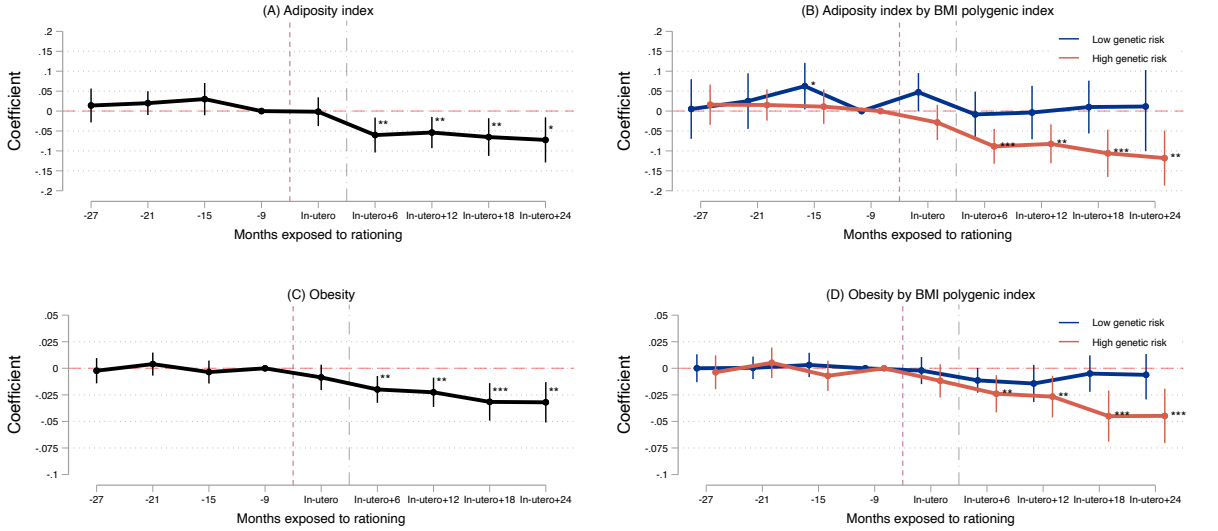


Notes: Obesity is defined as adiposity index at or above the 90th percentile of never rationed population. (A) shows BMI polygenic index distribution by sugar rationing exposure. (B) shows differences in obesity distribution by BMI polygenic index. (C) shows the share of study participants in the bottom, middle, and top terciles of the BMI polygenic index distribution by BMI polygenic index terciles.

b. Early-life sugar restriction and adiposity

We found that both the adiposity index and the share of adults with obesity decreased significantly with exposure to sugar rationing (Figure 2, panels A and B, Table A2). While in-utero exposure to sugar rationing alone did not significantly reduce adult adiposity or obesity, adults exposed both in utero and postnatally up to age two had lower adiposity index by 0.073 standard deviation (95% CI: –0.112 to –0.018) and were 3.2 percentage points (95% CI: –5.1 to –1.3 pp), or about 30%, less likely to have obesity compared to those never exposed.

Figure 2: Effect of early-life sugar restrictions on adiposity outcomes overall and by genetic risk.



Notes: Coefficients represent differences in outcomes relative to the reference group (born July-December 1954, marked as -9 on the graph). Sample: N=46,914 adults (Panels A,C); N=15,884 low genetic risk (33%), N=31,768 high genetic risk (67%) based on BMI polygenic index tertiles (Panels B,D). Adiposity index is a summary measure of BMI, body fat percentage, trunk fat, and waist-to-hip ratio, standardized within sex to never-rationed adults. Models control for sex, age indicators, calendar birth month, birth location (Wales, Scotland, England as reference, and geo-coordinates), parental health history (diabetes, heart disease/hypertension/stroke), BMI polygenic index decile, and age indicators. Standard errors are clustered at month-year of birth. Joint tests of pre-trends among never-rationed adults show no significant differences for (A) adiposity index overall (p=0.253); (B) low- (p=0.101) and high-risk (p=0.872); (C) obesity overall (p=0.641); and (D) low- (p=0.918) or high-risk adults (p=0.400). Error bars show 95% confidence intervals. Stars indicate significant difference from 1.0: * p<0.10, ** p<0.05, *** p<0.001.

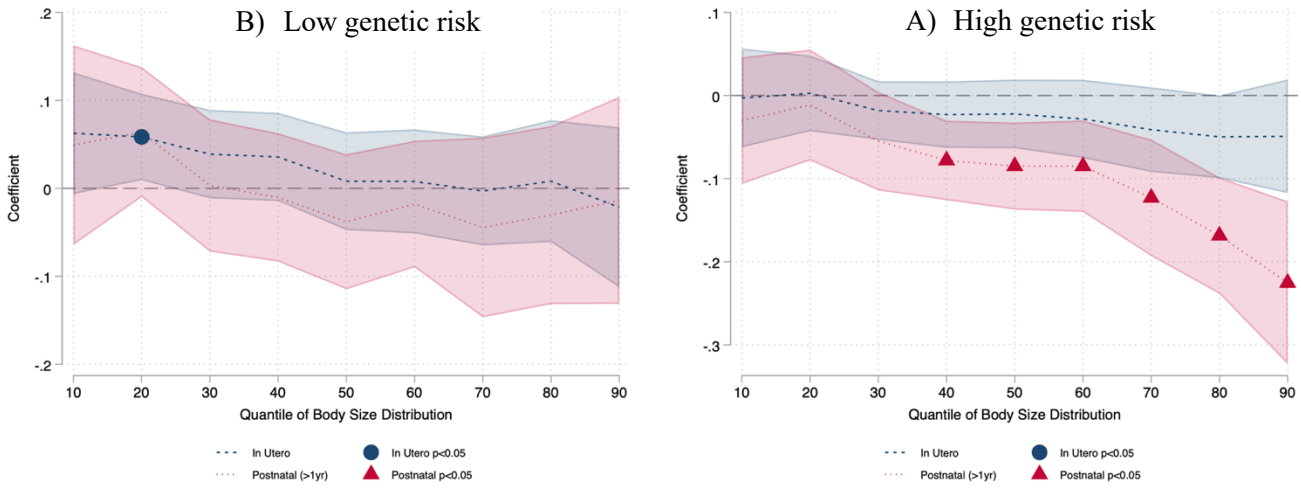
The health benefits of early-life rationing were not uniform across genetic risk groups. We found no significant impacts of sugar rationing on the adiposity index or in obesity among adults with low genetic risk, regardless of the duration or timing of their exposure to rationing. In contrast, individuals with high genetic risk for obesity experienced consistent protective effects that strengthened with longer exposure to sugar rationing. Specifically, for them, exposure to sugar rationing in-utero and through age 1 reduced adiposity by 0.082 standard deviations (95% CI: –0.131 to –0.033), with the effect increasing to 0.117 standard deviations (95% CI: –0.186 to –0.048) when exposure continued beyond the first year. A similar pattern emerged for obesity: there was no effect of rationing among low-risk individuals, while high-risk individuals experienced a 2.7 percentage point lower probability of adult obesity with exposure through the first year (95% CI: –0.046 to –0.007), and a 4.5 percentage point reduction with exposure up to age 2 (95% CI: –0.070 to –0.019) (Figure 2, panels C-D, Table A2). Patterns are similar by sex (Figure A5).

The protective effects of early-life sugar rationing detected in our composite adiposity measure were driven by visceral fat measures (trunk fat percentage and waist-to-hip ratio), especially among high genetic risk individuals (Figure A6). We detected no benefits of sugar rationing on obesity defined using BMI or total body fat percentage alone in either genetic risk group.

Figure 3 shows quantile regression estimates of early-life sugar rationing effects across the adiposity distribution, stratified by genetic risk. Among low-risk individuals, coefficients remain near zero across all quantiles. For high-risk individuals, effects are heterogeneous: nearly zero at

lower quantiles but increasingly negative at the upper tail especially from the median onward, reaching over -0.2 standard deviations at the 90th percentile ($p<0.05$). This demonstrates that early-life sugar restrictions primarily reduced adiposity at the upper end of the distribution (i.e., above median) rather than shifting the entire distribution uniformly. These larger effects at the 90th percentile compared to binary obesity indicators reflect additional adiposity reductions among those already in the upper tail, not merely threshold-crossing effects.

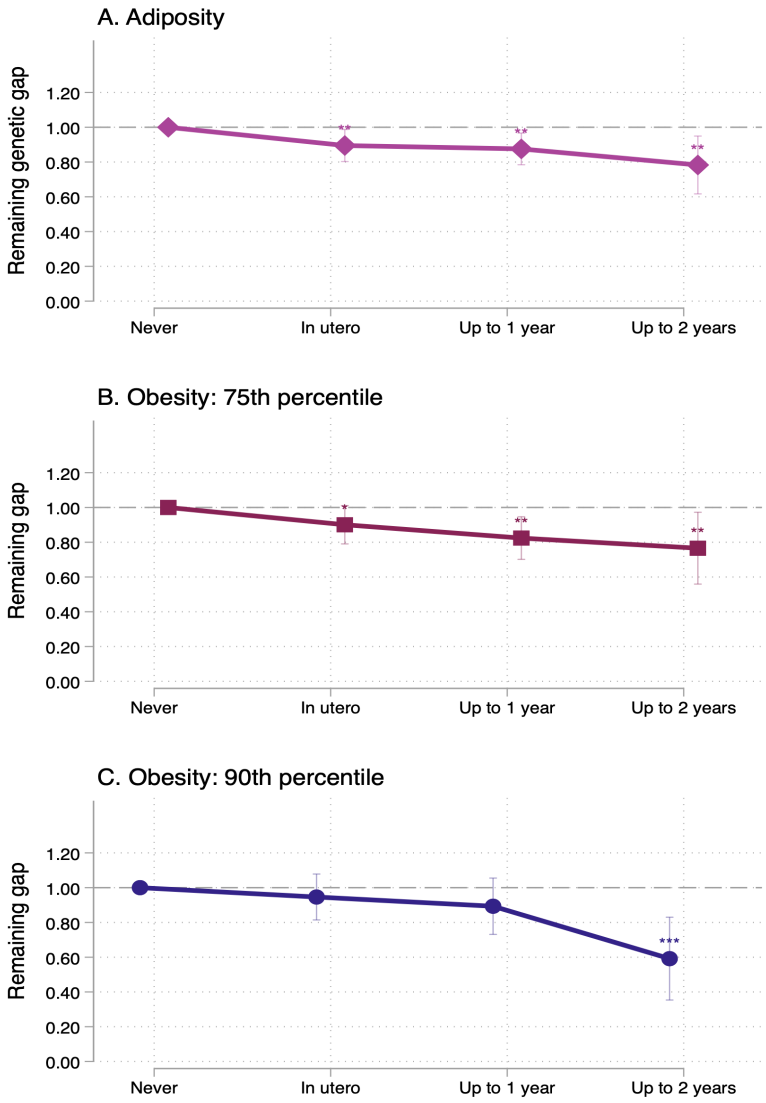
Figure 3: Distributional effects of sugar rationing on adult adiposity.



Notes: Quantile regression was used separately for A) low-risk (bottom polygenic index tercile) and B) high (top two polygenic index terciles) adults to estimate these effects on adiposity index as an outcome measure. Shaded areas represent 95% confidence intervals. Filled markers indicate $p<0.05$. Bootstrap standard errors are based on 100 replications.

Figure 4 (corresponding results in Table A4) demonstrate that sugar rationing progressively narrowed the difference in adiposity and obesity outcomes between high- and low-risk individuals, with larger effects for longer exposure durations. Among never-rationed adults, high genetic risk individuals had substantially worse outcomes than low-risk individuals: 0.42 SD higher adiposity (95% CI: 0.20 to 0.65), 16.3 percentage points more likely to exceed the 75th percentile for body size (95% CI: 6.6 to 26.0), and 6.0 percentage points more likely to exceed the 90th percentile (95% CI: 0.1 to 11.9). In-utero exposure alone modestly reduced the adiposity gap by 10.5% (ratio: 0.895; 95% CI: 0.803 to 0.988), with minimal effects on obesity prevalence. Rationing extending through the first year of life reduced the adiposity gap by 12.4% (ratio: 0.876; 95% CI: 0.785 to 0.966) and obesity difference at 75th and 90th percentile by 17.6% (ratio: 0.824; 95% CI: 0.702 to 0.946) and 11% (ratio: 0.893; 95% CI: 0.731 to 1.055), respectively. The largest effects occurred with rationing through age two, reducing the adiposity gap by 21.7% (ratio: 0.783; 95% CI: 0.617 to 0.949), the 75th percentile obesity difference by 23.4% (ratio: 0.766; 95% CI: 0.559 to 0.972), and the 90th percentile difference by 40.8% (ratio: 0.592; 95% CI: 0.354 to 0.830).

Figure 4: Reduction in the genetic gap in adult adiposity by exposure to sugar rationing.



Notes: Sample includes 46,914 UK Biobank participants aged 52–56 at baseline. The adiposity index combines BMI, body fat percentage, trunk fat, and waist-to-hip ratio, standardized by sex to never-rationed adults. Obesity thresholds correspond to the 75th and 90th percentiles of the adiposity distribution among never-rationed adults. Each point shows the ratio of the genetic gap—defined as the difference in adiposity outcomes between high- and low-BMI polygenic index groups—within each rationing exposure group relative to never-rationed adults (ratio = 1 by construction). Ratios were estimated from fully interacted models of genetic risk and rationing exposure controlling for sex, birth timing, location, parental health, and age. Values < 1 indicate that early-life sugar rationing reduced genetic disparities in adiposity outcomes; 0 implies complete elimination of the gap. Differences from 1 were tested using the Delta method. Error bars show 95% CIs with standard errors clustered by month–year of birth. *p < 0.10, **p < 0.05, ***p < 0.001.

Collectively, these findings suggest that early-life sugar restrictions reduced adiposity primarily among genetically susceptible individuals, narrowing the gap between genetic risk groups. Effects were concentrated in visceral fat measures (waist-to-hip ratio and trunk fat percentage), were

strongest with exposure that lasted through early childhood, and operated mainly at the upper tail of the adiposity distribution. These patterns suggest that dietary interventions during critical periods may be most effective at preventing extreme adiposity outcomes among those at highest genetic risk.

c. Sensitivity analyses

Our results are robust to several sensitivity checks. First, results remain insensitive to the choice of obesity threshold and to the exclusion of control variables (Figures 4 and A7). Second, Table A3 support our decision to combine the top two BMI polygenic index terciles to improve power, as the effects for the second and third terciles were not significantly different across outcomes. Third, we found no differential long-term effects of early-life exposure to sugar restrictions by genetic predisposition to nearsightedness and migraine; polygenic indices for conditions likely unrelated to diet and/or adiposity (Figure A4).

4. Discussion

The UK's sugar rationing policy reduced adult adiposity and obesity overall, but its most consequential effect was the marked narrowing of genetic disparities. Individuals at high genetic risk benefited disproportionally: in-utero exposure reduced adiposity gaps by 11%, and sustained restriction through age two narrowed disparities in adiposity by 22% and in obesity by 40%. These patterns demonstrate that nutritional environments during critical developmental windows can meaningfully offset inherited vulnerabilities, whereas low-risk individuals showed little change.

Sugar restriction mattered most where risk was highest. Quantile regressions show that effects were concentrated in the upper tail of the adiposity distribution among genetically high-risk individuals, with near-zero impacts at lower quantiles or among low-risk adults. Importantly, the largest benefits at higher adiposity levels required sustained exposure: reduction in moderate adiposity improved with in-utero restriction, but reducing obesity at the 90th percentile—our most severe measure - required rationing through at least age one, reflecting the need to counter stronger genetic predispositions during developmental windows when adiposity trajectories remain malleable. In turn, these gene–environment interactions were equity-enhancing: rationing reduced adiposity among the most genetically vulnerable while leaving low-risk individuals largely unaffected, narrowing existing disparities. Together, the results illustrate gene–environment complementarity: early nutritional constraints can offset genetic susceptibility, but overcoming severe inherited risk requires sustained exposure during periods when adiposity trajectories are still modifiable.

Our finding that early-life sugar restriction acted primarily through reductions in visceral rather than general adiposity provides a clinically meaningful pathway linking early nutritional environment to long-term health. Fructose, a major component of added sugars, is rapidly metabolized in the liver and preferentially fuels visceral fat accumulation, initiating hepatic and systemic inflammation that elevates cardiometabolic risk.[32] Visceral and ectopic fat in organs such as the liver, heart, and skeletal muscle is a major source of insulin resistance and chronic inflammation and confers substantially greater diabetes and hypertension risk than peripheral subcutaneous fat.[33,34] The visceral adiposity effects provide a plausible pathway for chronic disease

reductions in rationed cohorts reported elsewhere and align with emerging clinical guidance emphasizing abdominal markers over BMI for metabolic risk assessment,[23,35,36,37] including the 2025 Lancet Commission on Clinical Obesity.[38,39] This perspective also underscores the importance of measurement. While the bioelectrical-impedance components of our composite adiposity index have limitations, integrating multiple correlated indicators reduces measurement error, minimizes multiple-testing concerns, and improves detection of clinically meaningful changes that BMI alone can miss, particularly when fat loss coincides with gains in lean mass.[40,41,34]

The question remains: why do those with higher genetic predisposition to obesity show larger adiposity benefits from early-life sugar restriction? One plausible explanation, supported by large genome-wide association studies, is that genetic risk for obesity is highly polygenic and it reflects multiple pathways that regulate appetite, reward processing, energy expenditure, and fat storage.[30,42,43] This diffuse, polygenic architecture, which we utilize here, suggests that individuals with higher polygenic indexes may face cumulative vulnerabilities across multiple biological systems rather than a single mechanism. Early-life sugar exposure may interact with these pathways at a time when metabolic set points and appetitive traits are being programmed:[44,45] individuals with variants that increase reward sensitivity to sugar or impair satiety signaling not only consume more sugar-rich foods but may also mount stronger inflammatory and metabolic responses to sugar exposure.[46,47,48] Behavioral imprinting may also play a role: sugar intake remained higher among never-rationed adults even fifty years later, though this was not assessed by genetic risk group.[37] Accordingly, restricting exposure during early developmental windows may yield disproportionately large benefits for genetically susceptible children by counteracting multiple metabolic pathways simultaneously. Whether effects operate primarily through metabolic reprogramming, behavioral conditioning, or other pathways requires further study.

These result may suggest a role for precision prevention strategies in metabolic health. Similar to proposed genetic-risk-stratified recommendations for early screening for breast cancer or cardiovascular disease,[49,50] providing additional dietary resources and support to parents of children with higher risk of obesity may optimize resource allocation and maximize preventive benefits.

a. Limitations

This study has limitations. First, UK Biobank participants are healthier and wealthier than the general population,[51] potentially limiting generalizability, particularly for our population-relative obesity thresholds. Second, obesity treatment following chronic disease diagnosis may reduce measured adiposity, suggesting our estimates may be conservative. Third, while the mechanisms underlying the BMI polygenic index are well-studied, the mechanisms underlying its interaction with sugar rationing my differ. Furthermore, the mechanisms that drive visceral obesity may also differ.[52,53] Last, as an observational study rather than a randomized trial, confounding remains a potential concern. However, multiple lines of evidence support a causal interpretation: we observed no pre-existing time trends in adiposity measures overall or by genetic risk group, confirmed similar genetic risk and early-life characteristics across the rationing cutoff using a narrow comparison window, and found that other early-life or time-invariant characteristics potentially linked to adult adiposity did not change discontinuously at rationing termination.

Results were also robust to using genetic traits unrelated to obesity as placebo tests and to the inclusion or exclusion of control variables. Our previous work demonstrated that diets in the 1950s, aside from sugar, were similar between cohorts, and that food affordability remained stable during and after rationing.[23,37]

b. Strengths

This study also has several strengths. First, the abrupt cessation of sugar rationing provides a natural experiment that eliminates the self-selection bias inherent in traditional gene-environment studies, strengthening the causal interpretation through exogenous variation in early-life sugar exposure. Second, our results proved robust across multiple adiposity definitions and genetic risk thresholds, demonstrating consistency rather than sensitivity to methodological choices. Third, the UK Biobank's large sample provided high statistical power which enabled the estimation of precise effects and subgroup analyses, even within a narrow window around the end of sugar rationing. Fourth, the availability of multiple adiposity phenotypes, including continuous measures, visceral adiposity indicators, body mass and body fatness measures, and quantile regression, enabled a comprehensive assessment of intervention effects across the entire adiposity distribution.

5. Conclusion

Early-life sugar restriction substantially reduces genetic disparities in adult obesity by disproportionately benefiting individuals with high genetic susceptibility, primarily through reductions in visceral adiposity. These findings support both early-life sugar reduction policies and precision medicine approaches targeting genetically at-risk populations during critical developmental windows.

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Supplementary Materials for

Early sugar restrictions reduce genetic disparities in adult obesity

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The file includes:

Materials and Methods

Data Source

Our study uses data from UK Biobank, a population-based cohort study launched by the UK National Health Service (NHS). Between 2006 and 2010, approximately 9.2 million NHS-registered adults aged 40-69 living within 25 miles of 22 assessment centers across the UK received study invitations. Of these, 503,325 individuals enrolled, yielding a 5.47% response rate.[1,2]

We restricted our analytic sample to participants born between October 1951 and March 1956 who were aged 52-56 at baseline, ensuring age overlap between rationed and never-rationed cohorts. We excluded individuals born outside the UK, those from multiple births or who were adopted, participants who withdrew consent, those pregnant at the time of the survey, and individuals with missing covariates, genetic information, or adiposity measures. Our final analytic sample comprises 46,914 adults (Figure A1). Baseline participants' time-invariant characteristics are presented in Table 1.

UK Biobank is not a nationally representative sample. It recruited only individuals living within 25 miles of one of the 22 assessment centers, all of which were in urban areas. Males, and those living in socioeconomically deprived areas and particular regions of the UK were less likely to accept the invitation to join the study.[3] UK Biobank participants also tend to be healthier than the general population. These sampling characteristics limit the external validity and generalizability of our results to broader populations, but do not compromise the internal validity of our estimates. There is no differential selection into the study between rationed and never-rationed cohorts; mortality rates at ages 52-56 are very low and equivalent across both cohorts (see Figure A8), ensuring balanced representation of both groups. These features mean that while the absolute levels of our outcomes may not generalize to the full UK population, the effect of early-life rationing that we estimate remains internally valid.

Adiposity measure

Assessment and Measurement

Study participants completed baseline assessments comprising touchscreen questionnaires, computer-assisted interviews, physical measurements, and collection of blood, urine, and saliva samples. Participants were also genotyped for genetic analysis.

Our primary outcome is an adiposity index constructed from four anthropometric measures: body mass index (BMI), body fat percentage, trunk fat percentage, and waist-hip ratio. BMI was calculated as weight (kg) divided by height squared (m^2). Waist-hip ratio was calculated as the ratio between waist and hip circumference. All measurements were standardized across the 22 UK Biobank assessment centers and collected by trained healthcare practitioners. Weight, height, waist and hip circumferences were measured directly by trained staff. Body and trunk fat percentages were also assessed by a trained staff using bioelectrical impedance analysis (BIA) with the Tanita BC-418MA body composition analyzer. BIA measures electrical impedance through the body,

exploiting differential conductivity between tissues: fat tissue (minimal water content) exhibits higher resistance than lean tissue (approximately 70% water content). The device performs segmental analysis, partitioning the body into trunk, arms, and legs. Participants stood barefoot on the analyzer while holding handles, allowing calculation of regional fat percentages using proprietary algorithms that incorporate impedance values along with height, weight, age, and sex.[4,5]

Statistical analysis

The two authors who analyzed the data (T.G. and C.B.) have coded and reviewed all parts of the analysis. Occasional minor differences, resulting from different data coding choices, were resolved through discussion.

Adiposity Measures. We construct a summary index of adiposity as a weighted average of several individual measures. Each measure is first standardized separately by sex, using those born after July 1954 (i.e., never rationed) as the reference group. We then combine these standardized measures into indices following the procedure proposed by Anderson (2008), which assigns weights based on the variance-covariance matrix of the input measures. The indices are constructed so that higher values correspond to greater adiposity. Our primary outcome is an overall adiposity index constructed from all four measures: BMI, total body fat percentage, waist-hip ratio, and trunk fat percentage. To examine distinct dimensions of adiposity, we additionally construct two component indices: a visceral adiposity index (waist-hip ratio and trunk fat percentage) and a general adiposity index (BMI and total body fat percentage). We create binary indicators for excess adiposity based on the 75th and 90th percentiles and apply quantile regressions to assess distributional effects across the adiposity distribution.

While our composite adiposity measures have some limitations—for instance, bioelectrical impedance can be influenced by hydration and food intake—they offer substantial advantages over analyzing individual measures separately. First, they reduce the number of outcomes and mitigate multiple hypothesis testing concerns. Second, they decrease measurement error by averaging across multiple correlated indicators of the same underlying construct, thereby increasing statistical power. This approach aligns with recent clinical recommendations: the 2025 Lancet Commission on Clinical Obesity recommends moving beyond BMI as a sole diagnostic criterion, emphasizing that BMI can both underestimate and overestimate adiposity and fails to capture fat distribution. The Commission specifically recommends using waist circumference or waist-hip ratio in addition to BMI to more accurately assess excess adiposity and fat distribution.[6,7] Our indices align with these recommendations by incorporating visceral adiposity measures (waist-hip ratio and trunk fat percentage), which capture visceral fat distribution more effectively than BMI. These indicators are more strongly associated with cardiometabolic disease risk because visceral and ectopic fat accumulation, in organs such as the liver, heart, and skeletal muscle, poses substantially higher health risks than peripheral subcutaneous fat.[8,9] Finally, overall and central adiposity measures together better detect subtle changes in body composition, particularly when fat loss is offset by muscle gain—a scenario BMI alone would miss.[10,11,12] We treat the relationship between these indices as approximately monotonic over the observed range.

Polygenic Index (PGI). We use data on BMI PGI generated by Barcellos et al.[13] Their BMI polygenic score for individual i is calculated as a weighted sum of SNP genotypes:

$$S_i = \Sigma_j \, x_{ij} \times w_j$$

where $x_{ij} \in {}^{1}$ is the count of reference alleles for individual $_i$ at SNP $_j$, and w_j is the weight associated with SNP_j. The weights are derived from GWAS summary statistics for BMI and transformed using linkage disequilibrium (LD) prediction.[14,15] LDpred requires both the GWAS results and a reference sample to estimate the linkage disequilibrium (correlation) structure of the genetic data. The 1000 Genomes Project, a catalog of genetic variation from over 2,500 individuals across diverse populations was used as the reference sample. The GWAS itself consists of regressions of BMI on individual SNP genotypes, controlling for sex, age, and principal components of genetic ancestry. To avoid overfitting, samples independent from the prediction sample were used to estimate the weights. In our sample, the resulting BMI PGI explains approximately 7% of the variation in BMI, aligned with data estimates elsewhere.[16,17,18]

We use the BMI PGI as our primary genetic measure. To validate that observed heterogeneity is specific to obesity-related genetics rather than spurious stratification, we conduct placebo tests using PGI for migraine and myopia; traits unlikely related to obesity or diet. The absence of treatment effect heterogeneity by these unrelated genetic traits confirms the specificity of our findings.

APPENDIX TABLES

APPENDIX FIGURES

TABLES

Table A1: Distribution of births over time within our study period.

Month and year of birth	N	Percent (%)	Cumulative percent (%)	Exposure to rationing	
1951m10	221	0.47	0.47	up to 24 months + in-utero	Exposed to rationing
1951m11	236	0.5	0.97		
1951m12	315	0.67	1.65		
1952m1	341	0.73	2.37		
1952m2	405	0.86	3.24		
1952m3	509	1.08	4.32		
1952m4	482	1.03	5.35	up to 18 months + in-utero	
1952m5	555	1.18	6.53		
1952m6	543	1.16	7.69		
1952m7	583	1.24	8.93		
1952m8	539	1.15	10.08		
1952m9	652	1.39	11.47		
1952m10	689	1.47	12.94	up to 12 months + in-utero	
1952m11	609	1.3	14.24		
1952m12	689	1.47	15.71		
1953m1	770	1.64	17.35		
1953m2	815	1.74	19.08		
1953m3	896	1.91	20.99		
1953m4	969	2.07	23.06	up to 6 months + in-utero	
1953m5	1,046	2.23	25.29		
1953m6	999	2.13	27.42		
1953m7	956	2.04	29.46		
1953m8	977	2.08	31.54		
1953m9	973	2.07	33.61		
1953m10	945	2.01	35.63	In-utero	
1953m11	910	1.94	37.57		
1953m12	952	2.03	39.6		
1954m1	1,082	2.31	41.9		
1954m2	1,069	2.28	44.18		
1954m3	1,188	2.53	46.71		
1954m4	1,070	2.28	48.99		
1954m5	1,229	2.62	51.61		
1954m6	1,109	2.36	53.98		

1954m7	1,118	2.38	56.36	Conceived post-rationing / never-rationed	Not exposed to rationing
1954m8	1,101	2.35	58.71		
1954m9	1,010	2.15	60.86		
1954m10	1,028	2.19	63.05		
1954m11	950	2.02	65.08		
1954m12	1,000	2.13	67.21		
1955m1	1,018	2.17	69.38		
1955m2	985	2.1	71.48		
1955m3	1,123	2.39	73.87		
1955m4	1,055	2.25	76.12		
1955m5	1,155	2.46	78.58		
1955m6	1,088	2.32	80.9		
1955m7	1,070	2.28	83.18		
1955m8	944	2.01	85.19		
1955m9	950	2.02	87.22		
1955m10	989	2.11	89.33		
1955m11	960	2.05	91.37		
1955m12	996	2.12	93.5		
1956m1	984	2.1	95.59		
1956m2	935	1.99	97.59		
1956m3	1,132	2.41	100		
Total	46,914	100			

Table A2: Effect of early sugar restrictions on adult adiposity by high vs low genetic risk (supporting Figure 2).

VARIABLES	(1) **Adiposity index Overall**	(2) **Adiposity index Low genetic risk**	(3) **Adiposity index High genetic risk**	(4) **Obese (90th pct) Overall**	(5) **Obese (90th pct) Low genetic risk**	(6) **Obese (90th pct) High genetic risk**
27 months before rationing ended	0.014	0.005	0.016	-0.002	0.000	-0.004
SE	(0.021)	(0.037)	(0.025)	(0.006)	(0.007)	(0.008)
95% CI	-0.028 - 0.056	-0.070 - 0.080	-0.034 - 0.067	-0.014 - 0.010	-0.013 - 0.013	-0.020 - 0.012
p-value	(0.512)	(0.890)	(0.526)	(0.700)	(0.992)	(0.645)
21 months before rationing ended	0.020	0.025	0.015	0.004	0.000	0.005
SE	(0.015)	(0.035)	(0.020)	(0.005)	(0.005)	(0.007)
95% CI	-0.010 - 0.050	-0.045 - 0.095	-0.024 - 0.054	-0.007 - 0.015	-0.010 - 0.011	-0.009 - 0.020
p-value	(0.188)	(0.476)	(0.441)	(0.467)	(0.934)	(0.476)
15 months before rationing ended	0.030	0.063*	0.011	-0.004	0.003	-0.007
SE	(0.020)	(0.029)	(0.021)	(0.005)	(0.006)	(0.007)
95% CI	-0.010 - 0.070	0.004 - 0.121	-0.032 - 0.054	-0.014 - 0.007	-0.008 - 0.015	-0.021 - 0.007
p-value	(0.142)	(0.036)	(0.606)	(0.514)	(0.585)	(0.325)
In-utero	-0.002	0.047	-0.029	-0.009	-0.002	-0.012
SE	(0.018)	(0.024)	(0.022)	(0.006)	(0.006)	(0.008)
95% CI	-0.038 - 0.035	-0.001 - 0.095	-0.073 - 0.016	-0.020 - 0.003	-0.015 - 0.011	-0.027 - 0.004
p-value	(0.931)	(0.054)	(0.201)	(0.155)	(0.739)	(0.135)
In-utero + 6 months	-0.060**	-0.008	-0.089***	-0.020**	-0.011	-0.024**
SE	(0.022)	(0.028)	(0.022)	(0.006)	(0.006)	(0.009)
95% CI	-0.104 - -0.016	-0.065 - 0.049	-0.132 - -0.045	-0.032 - -0.007	-0.023 - 0.000	-0.041 - -0.006
p-value	(0.008)	(0.769)	(0.000)	(0.003)	(0.056)	(0.008)
In-utero + 12 months	-0.054**	-0.004	-0.082**	-0.023**	-0.014	-0.027**
SE	(0.020)	(0.033)	(0.024)	(0.007)	(0.009)	(0.010)
95% CI	-0.093 - -0.015	-0.071 - 0.063	-0.131 - -0.034	-0.036 - -0.009	-0.032 - 0.003	-0.046 - -0.007
p-value	(0.008)	(0.913)	(0.001)	(0.002)	(0.107)	(0.009)
In-utero + 18 months	-0.065**	0.010	-0.106***	-0.032***	-0.005	-0.045***
SE	(0.024)	(0.033)	(0.029)	(0.009)	(0.009)	(0.012)
95% CI	-0.112 - -0.018	-0.056 - 0.076	-0.165 - -0.047	-0.049 - -0.014	-0.022 - 0.012	-0.069 - -0.021
p-value	(0.008)	(0.761)	(0.001)	(0.001)	(0.564)	(0.000)
In-utero + 24 months	-0.072*	0.011	-0.118**	-0.032**	-0.006	-0.045***
SE	(0.028)	(0.056)	(0.034)	(0.009)	(0.012)	(0.013)
95% CI	-0.129 - -0.016	-0.101 - 0.124	-0.187 - -0.049	-0.051 - -0.013	-0.029 - 0.017	-0.070 - -0.019
p-value	(0.013)	(0.838)	(0.001)	(0.001)	(0.598)	(0.001)
Observations	46,914	15,680	31,234	46,914	15,680	31,234
Mean Y among non-rationed	0	-0.313	0.157	0.100	0.0425	0.129

Note: Obese defined as >=90th percentile of adiposity index. Low genetic risk = bottom tercile of BMI PGS. High genetic risk = top tercile of BMI PGS. Standard errors are clustered by month-year of birth. Sample includes 46,914 UK Biobank participants aged 52-56 at baseline. Adiposity index combines BMI, body fat percentage, trunk fat, and waist-to-hip ratio, standardized by sex to never-rationed adults. Obesity threshold is defined at 90th percentile of adiposity distribution of never-rationed adults. Stars indicate significant difference at * p<0.10, ** p<0.05, *** p<0.001.

Table A3: Early sugar restrictions and adult adiposity by genetic risk terciles.

VARIABLES	(1) **Adiposity Index**	(2) **Obese (90th pct)**
Middle tercile BMI PGI	0.238*	-0.001
SE	(0.112)	(0.035)
95% CI	0.013 - 0.464	-0.072 - 0.069
p-value	(0.039)	(0.970)
Top tercile BMI PGI	0.635***	0.127**
SE	(0.137)	(0.037)
95% CI	0.360 - 0.910	0.052 - 0.202
p-value	(0.000)	(0.001)
Years exposed to rationing =In-utero	0.016	-0.003
SE	(0.018)	(0.005)
95% CI	-0.020 - 0.052	-0.013 - 0.006
p-value	(0.384)	(0.459)
Years exposed to rationing = In-utero + up to 1 year	-0.036	-0.014**
SE	(0.023)	(0.005)
95% CI	-0.082 - 0.010	-0.024 - -0.004
p-value	(0.125)	(0.008)
Years exposed to rationing = In-utero + up to 2 years	-0.013	-0.006
SE	(0.033)	(0.007)
95% CI	-0.079 - 0.052	-0.021 - 0.009
p-value	(0.685)	(0.402)
Middle tercile BMI PGI * In-utero	-0.055*	-0.003
SE	(0.027)	(0.007)
95% CI	-0.109 - -0.000	-0.017 - 0.010
p-value	(0.048)	(0.616)
Middle tercile BMI PGI * In-utero + up to 1 year	-0.065*	-0.006
SE	(0.027)	(0.008)
95% CI	-0.118 - -0.011	-0.022 - 0.009
p-value	(0.019)	(0.397)
Middle tercile BMI PGI * In-utero + up to 2 years	-0.109*	-0.031*
SE	(0.046)	(0.012)
95% CI	-0.200 - -0.017	-0.056 - -0.007
p-value	(0.021)	(0.013)
Top tercile BMI PGI * In-utero	-0.052	-0.008
SE	(0.027)	(0.008)
95% CI	-0.106 - 0.001	-0.024 - 0.009
p-value	(0.055)	(0.351)
Top tercile BMI PGI * In-utero + up to 1 year	-0.057	-0.013
SE	(0.029)	(0.012)
95% CI	-0.115 - 0.001	-0.037 - 0.011
p-value	(0.056)	(0.280)
Top tercile BMI PGI * In-utero + up to 2 years	-0.099*	-0.042**
SE	(0.045)	(0.015)
95% CI	-0.189 - -0.008	-0.072 - -0.011
p-value	(0.033)	(0.008)
Observations	46,914	46,914
R-squared	0.075	0.034
Mean Y among non-rationed	0	0.100

Note: Sample includes 46,914 UK Biobank participants aged 52-56 at baseline. Adiposity index combines BMI, body fat percentage, trunk fat, and waist-to-hip ratio, standardized by sex to never-rationed adults. Obese defined as >=90th percentile of adiposity index of never-rationed adults. Low/middle/top genetic risk = bottom/middle/top tercile of BMI PGS. Reference group is the bottom tercile of BMI PGI (lowest genetic risk). Rationing effects are not significantly different between 2nd and 3rd PGI BMI tercile in any of the regressions. Stars indicate significant difference at * p<0.10, ** p<0.01, *** p<0.001.

Table A4: Reduction in genetic gap (supporting Figure 4).

Exposure Period	**Body Size Index**			**Obesity: 75th percentile**			**Obesity: 90th percentile**		
	Ratio	95% CI	P-value	Ratio	95% CI	P-value	Ratio	95% CI	P-value
Never (Reference)	1	/	/	1	/	/	1	/	/
In utero	0.895**	[0.803, 0.988]	0.026	0.901*	[0.790, 1.011]	0.078	0.946	[0.814, 1.078]	0.425
Up to 1 year	0.876**	[0.785, 0.966]	0.007	0.824**	[0.702, 0.946]	0.005	0.893	[0.731, 1.055]	0.196
Up to 2 years	0.783**	[0.617, 0.949]	0.011	0.766**	[0.559, 0.972]	0.026	0.592***	[0.354, 0.830]	0.001

Note: Standard errors calculated using Delta Method. *p<0.05, **p<0.01, ***p<0.001.

FIGURES

Figure A1: Analytical sample construction.

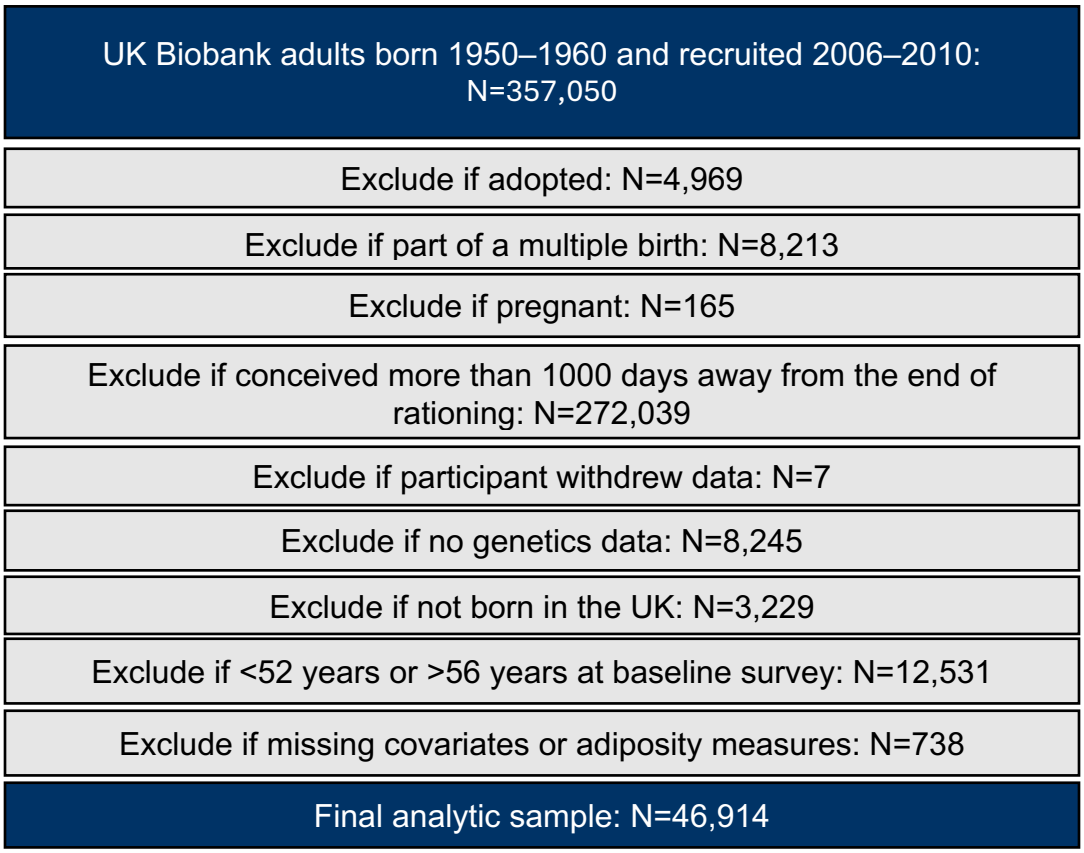
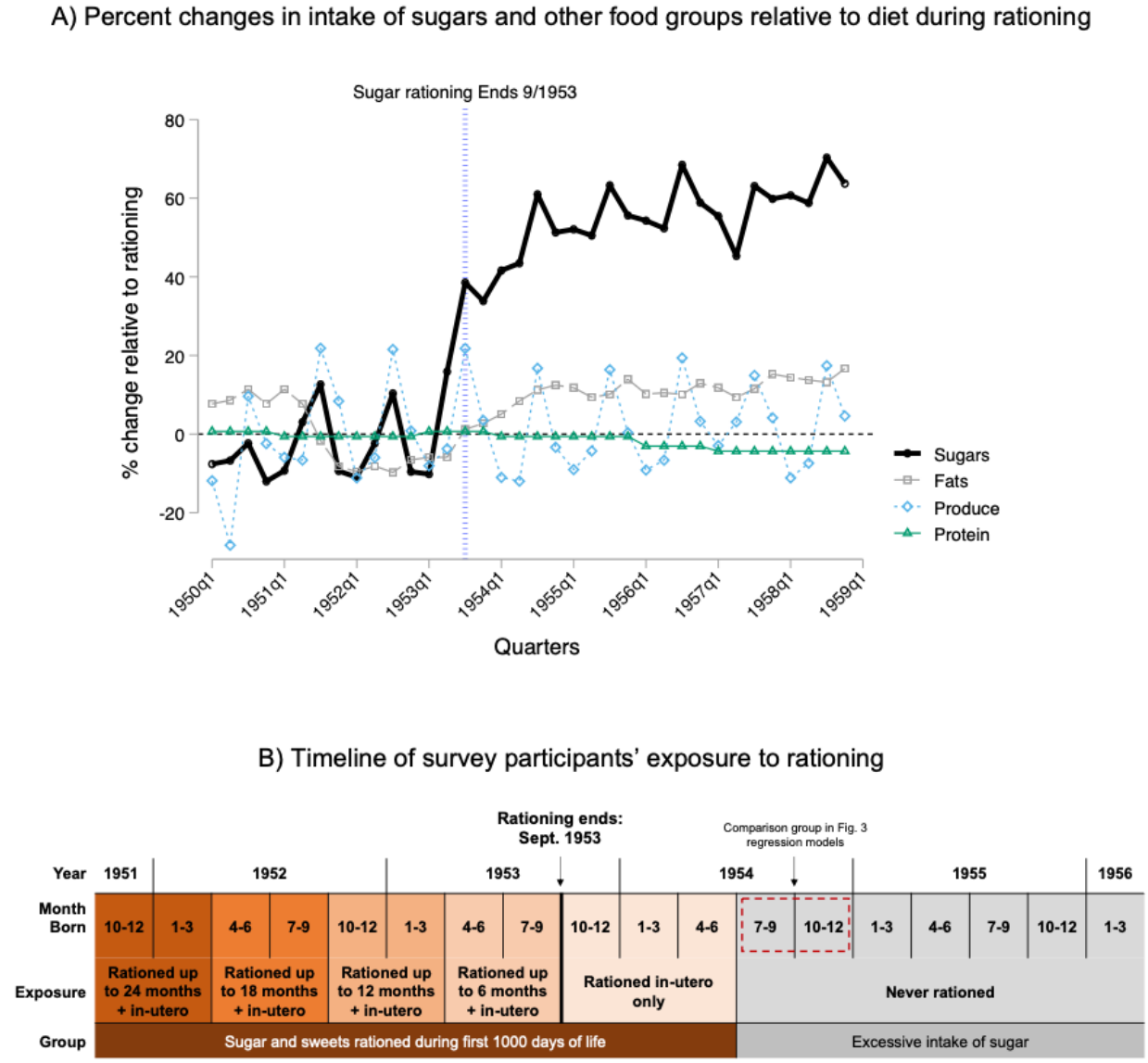
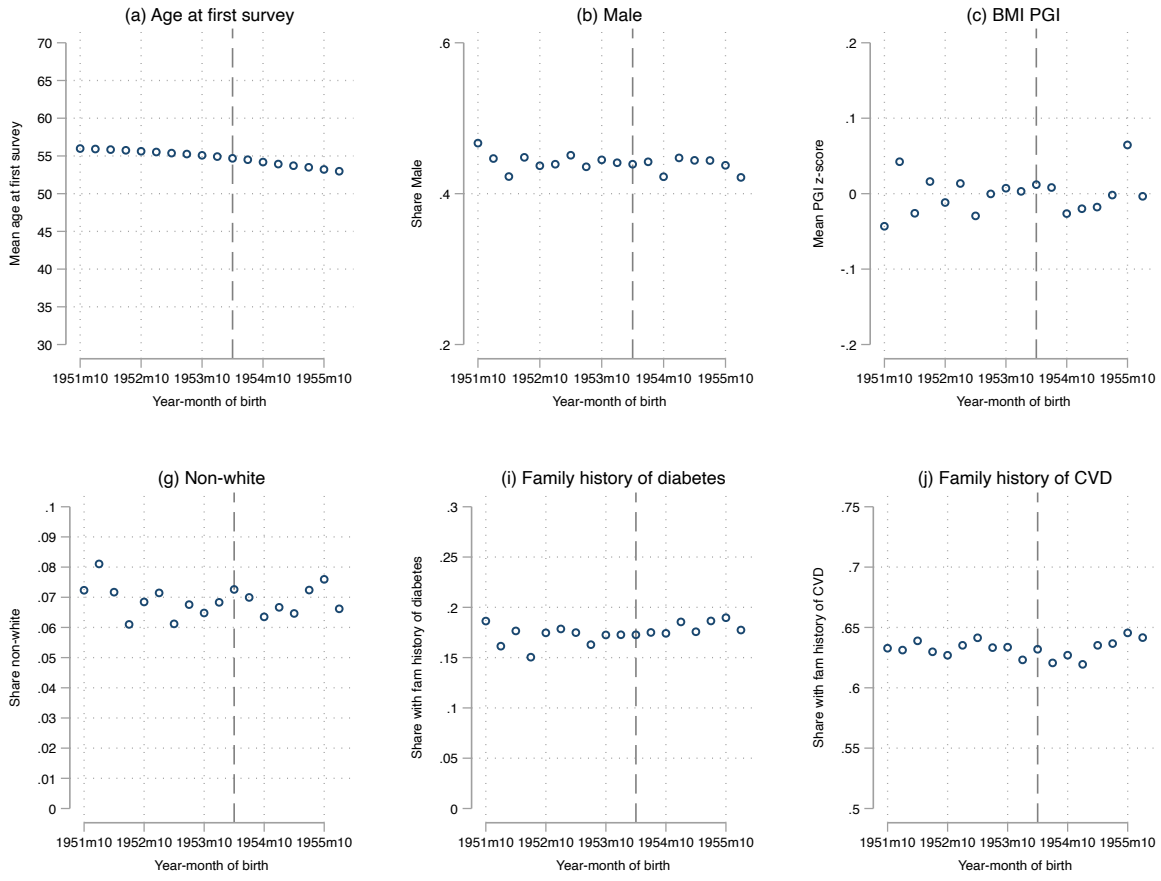


Figure A2: UK's sugar rationing timeline in the mid 1950s.



Notes: This figure was originally prepared for and has been published in Gracner et al (2024).[19] See Supplementary Materials in Gracner et al (2024) for additional figures describing dietary patterns between 1950 and 1960s.[19]

Figure A3: Observable characteristics by cohorts.



Notes: Figure displays binned means of the share of participants with certain characteristics by month–year of birth. Each point represents the average outcome within bins of the running variable (birth month), with no fitted line shown. The vertical reference line indicates the last cohort that was exposed to sugar rationing.

Figure A4: Impact of early-life sugar restrictions on changes in adiposity, stratified by PGIs unrelated to obesity traits.

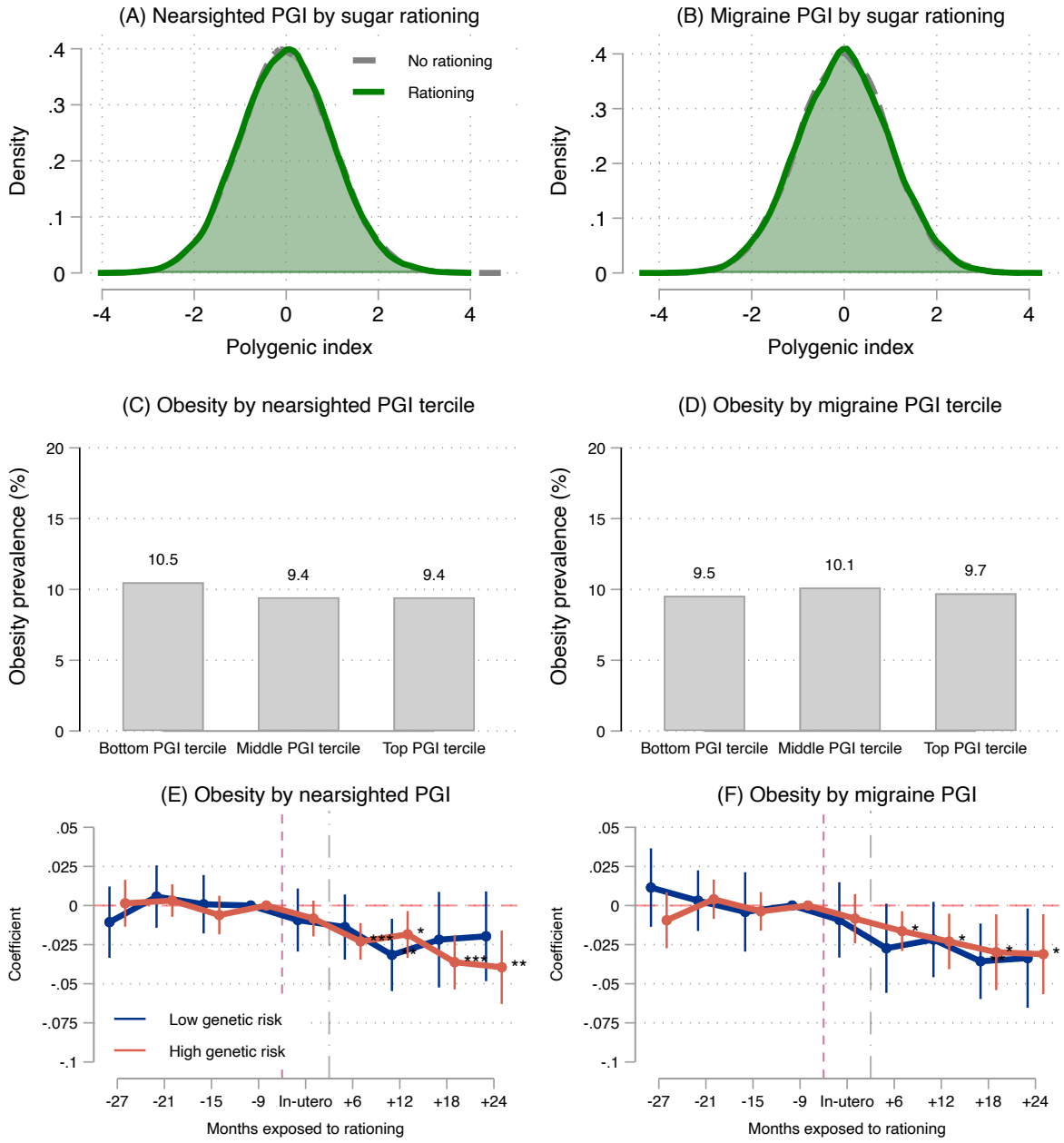
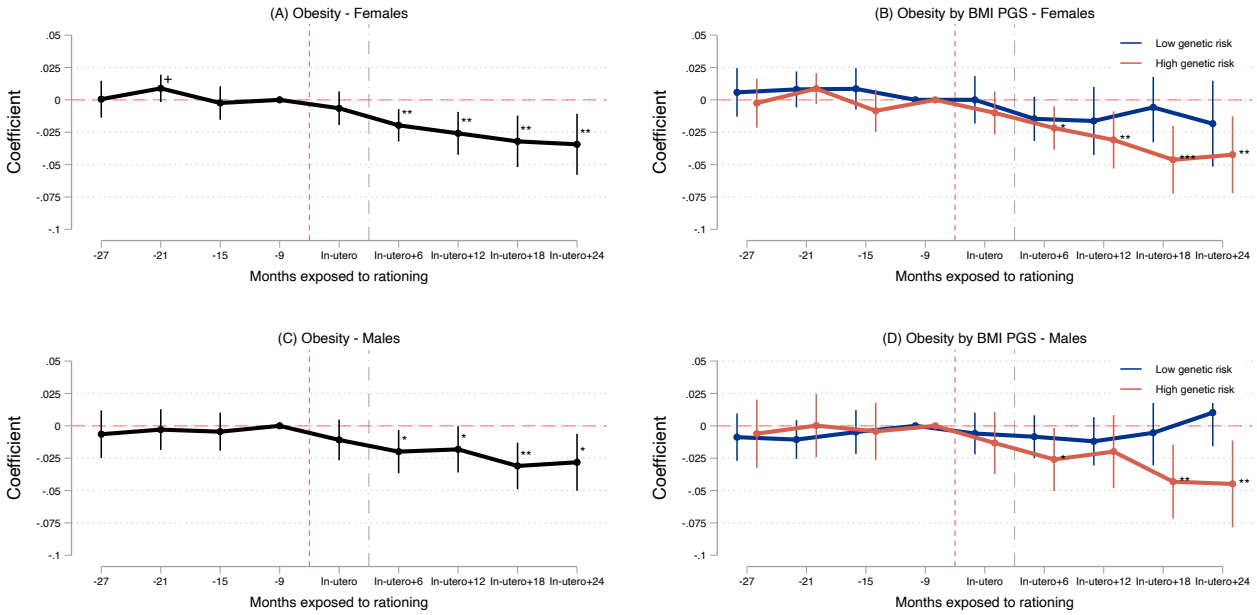
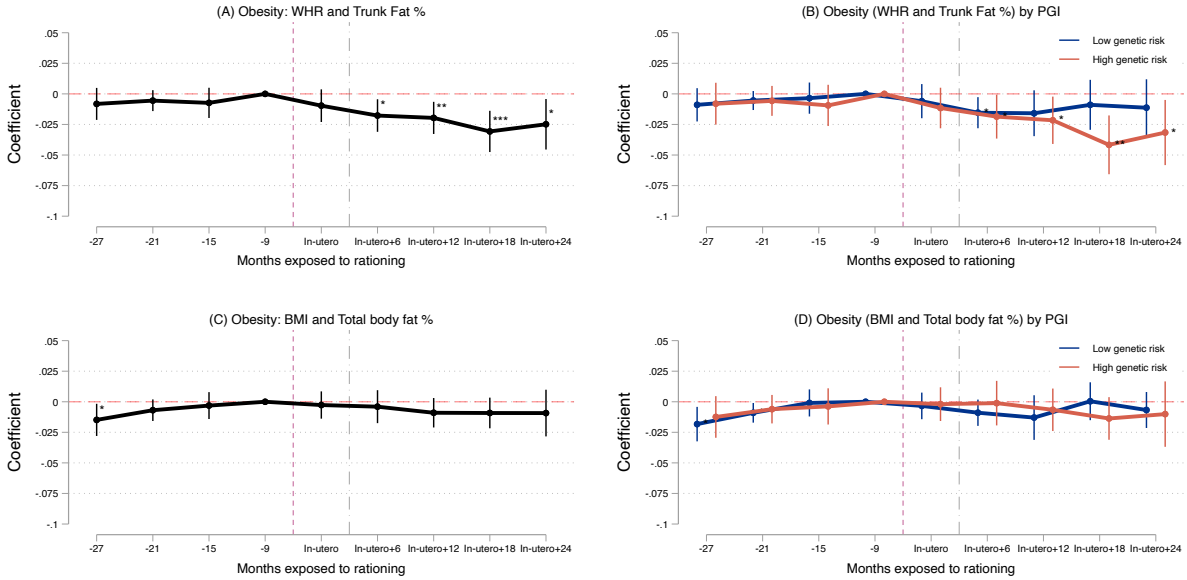


Figure A5: Effect of early-life sugar restrictions on adult adiposity by sex.



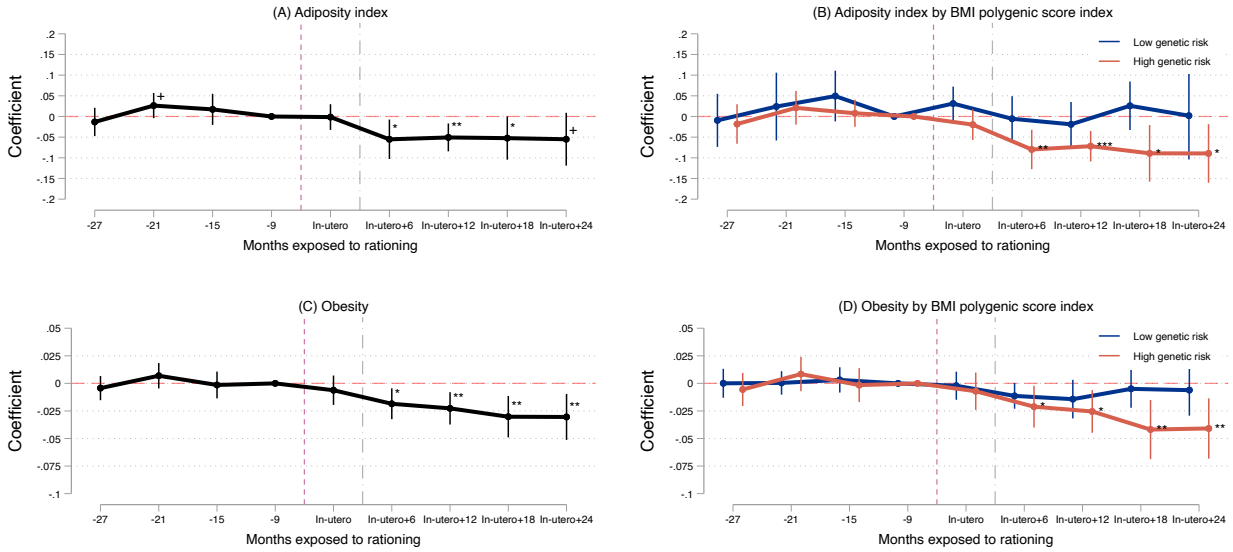
Notes: Panels A and B show the effects of early-life sugar restriction on adult obesity among women, and Panels C and D show the corresponding effects among men. Coefficients represent differences in outcomes relative to the reference group (born July-December 1954, marked as -9 on the graph). Sample: N=46,914 adults (Panels A,C); N=15,884 low genetic risk (33%), N=31,768 high genetic risk (67%) based on BMI polygenic index tertiles (Panels B, D). Error bars show 95% confidence intervals. Stars indicate significant difference from 1.0: * p<0.10, ** p<0.05, *** p<0.001. Adiposity index is a summary measure of BMI, body fat percentage, trunk fat, and waist-to-hip ratio, standardized within sex to never-rationed adults. Models control for sex, age indicators, calendar birth month, birth location (Wales, Scotland, England as reference, and geo-coordinates), parental health history (diabetes, heart disease/hypertension/stroke), BMI PGI decile, and age indicators. Standard errors are clustered at month-year of birth. Joint tests of pre-trends among never-rationed adults show no significant differences for (A) adiposity index overall (p=0.253); (B) low- (p=0.101) and high-risk (p=0.872); (C) obesity overall (p=0.641); and (D) low- (p=0.918) or high-risk adults (p=0.400).

Figure A6: Effect of early-life sugar restrictions on central (A, B) and general adiposity (C, D).



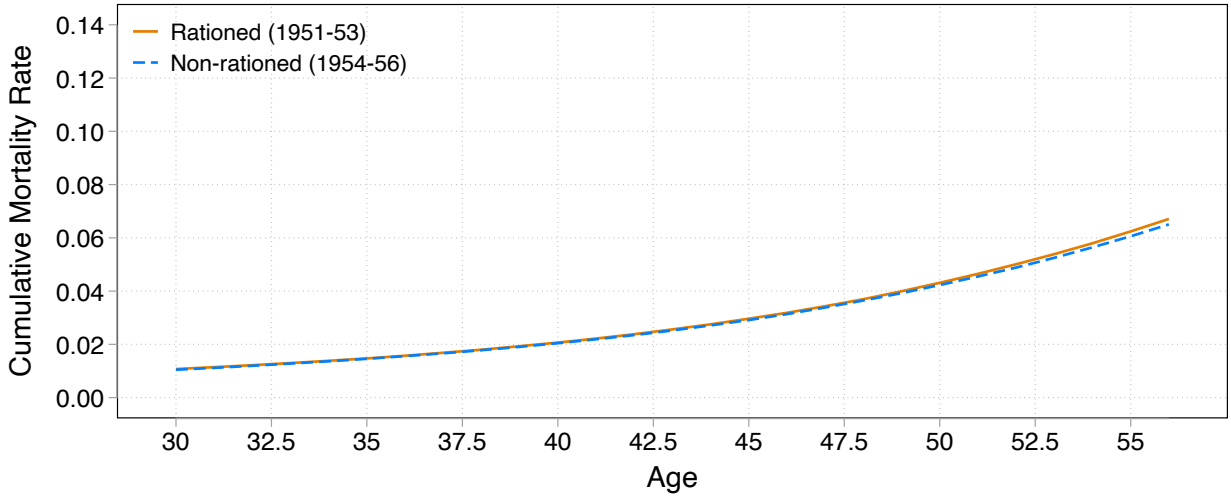
Notes: Coefficients represent differences in outcomes relative to the reference group (born July-December 1954, marked as -9 on the graph). Sample: N=46,914 adults (Panels A,C); N=15,884 low genetic risk (33%), N=31,768 high genetic risk (67%) based on BMI polygenic index tertiles (Panels B,D). Models control for sex, age indicators, calendar birth month, birth location (Wales, Scotland, England as reference, and geo-coordinates), parental health history (diabetes, heart disease/hypertension/stroke), BMI PGI decile, and age indicators. Error bars show 95% confidence intervals. Stars indicate significant difference from 1.0: * p<0.10, ** p<0.05, *** p<0.001.

Figure A7: Effect of early-life sugar restrictions and adult adiposity without controls.



Notes: Coefficients represent differences in outcomes relative to the reference group (born July-December 1954, marked as -9 on the graph). Sample: N=46,914 adults (Panels A,C); N=15,884 low genetic risk (33%), N=31,768 high genetic risk (67%) based on BMI polygenic index tertiles (Panels B,D). Adiposity index is a summary measure of BMI, body fat percentage, trunk fat, and waist-to-hip ratio, standardized within sex to never-rationed adults. Models control for age indicators only. Error bars show 95% confidence intervals. Stars indicate significant difference from 1.0: * p<0.10, ** p<0.05, *** p<0.001.

Figure A8: Mortality rates by age across cohorts.



Notes: Mortality rates were calculated as the number of deaths divided by the number of live births within each birth cohort. We used data on live births and cumulative deaths for cohorts born between 1950 and 1959, followed from 1965 through 2019, obtained from the Office for National Statistics. Mortality rates were calculated for England and Wales only; Scotland and Northern Ireland were excluded due to data constraints.

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