A1 Quality control procedures of genetic data

In Lifelines, Study participants were genotyped using blood samples drawn during the first assessment visit. Lifelines genotyped data was released for two subsamples. The first is the GWAS CytoSNP cohort which consists of 15,400 unrelated respondents that were 18 years or older. The second is the UGLI cohort which consists of 64,589 respondents aged 8 or older.

Genotypes of the CytoSNP cohort were measured using the Illumina CytoSNP-12v2 array, measuring $\sim$ 300,000 SNPs. Genotypes of the UGLI cohort were measured using the Infinium Global Screening Array®(GSA) MultiEthnic Disease Version, measuring 691,072 SNPs. Both genetic data cohorts were subject to strict quality control procedures prior to release.[35] Further, missing SNPs not measured by the genotyping arrays were imputed using the dense reference panels Genome of the Netherlands and 1000 Genomes. As a result, $\sim$40,000,000 loci are assessed in both subcohorts.[36]

To construct well-estimated PGIs, we performed various quality control (QC) procedures: ensuring only well-estimated SNPs and respondents with reliable genetic data were included. Most of these are recommended by Marees et al. 2018. We only use data on the first 22 chromosomes, ignoring the sex chromosome, which is the smallest. Restricting to the first 22 chromosomes ensures that the EA PGI will not be artificially higher in any of the sexes.

First, we treated the CytoSNP and UGLI cohorts as separate cohorts. Within each cohort, we dropped multiallelic SNPs and loci with a minor allele frequency of $< 1\%$ ($\sim$33.5 million in CytoSNP, $\sim$27.2 million in UGLI). We further dropped SNPs with low imputation quality, as determined by an info score of < 0.8 (744,661 SNPs in CytoSNP in 333,409 in

[35] The quality control reports for CytoSNP and UGLI are available from `http://wiki.lifelines.nl/doku.php?id=gwas` and `http://wiki.lifelines.nl/lib/exe/fetch.php?media=qc_report_ugli_r1.pdf`, respectively.

[36] Reliable imputation is feasible because SNPs are inherited in chunks (called haplotype blocks). This implies that SNPs that are closely located to one another in the genome are highly correlated (R^2 values > 0.99 are not uncommon). To save costs, genotyping arrays are designed to only measure a subset of SNPs in a given genomic region, knowing that reliable imputation can be used to map out the non-measured nearby SNPs.

UGLI). Last, we dropped individuals with excess homozygosity rates (3 standard deviations above or below the average), removing 126 respondents in CytoSNP and 529 in UGLI.

Further, we dropped SNPs that were not in Hardy-Weinberg Equilibrium (with p-value threshold 10^{-6}) (1,163 SNPs in CytoSNP, 22,549 in UGLI)[37])

1,289 respondents in the CytoSNP cohort were also part of the UGLI cohort. We removed these respondents from the CytoSNP cohort to avoid double counting. After all QC steps, there were 6,789,250 SNPs present in CytoSNP, and 7,000,369 in UGLI. We restricted both data sets to the 6,408,251 SNPs that they both had in common, and combined them using the –bmerge command in PLINK.[38]

A2 Details on estimation of PGI weights

We calculated polygenic indices on the genetic data in the Lifelines as follows. First, we used MetaSubtract to correct the publicly available summary statistics in the most recent GWAS on years of education for the inclusion of the Lifelines CytoSNP cohort in GWAS discovery Nolte (2020); Okbay et al. (2022). To implement Metasubtract, we first replicated Okbay et al.'s 2022 GWAS on years of education in the CytoSNP cohort: we first residualized years of education in this cohort from the first 10 principal components of the genetic data, a cube in age, a sex dummy, and an interaction of this sex dummy with the cube in age. We next used plink2 to perform a GWAS on this residualized years of education variable. We verified the validity of this GWAS analysis by checking the genetic correlation between Okbay et al.'s GWAS summary statistics and our own summary statistics conducted within the Lifelines CytoSNP cohort, and found no significant difference from one, as expected.[39]

[37] In both data cohorts, the data providers already performed this quality check prior to releasing the data, but in CytoSNP, they used a more lenient threshold of $P < 0.0001$

[38] The QC report of the first release of the UGLI cohort includes 606 respondents that were also genotyped using the CytoSNP genotyping array. The UGLI Quality Control report assessed that the concordance within individuals of the genotypes assessed using both arrays was extremely high, being 99.82% in the respondent with lowest concordance

[39] Genetic correlations were calculated using LD-score regression Bulik-Sullivan et al. (2015): $r_g = 1.07$ ($s.e. = 0.10$).

Finally, we used Metasubtract to process the summary statistics of Okbay et al. 2022 prior to PGI construction. Metasubtract analytically subtracts the GWAS summary statistics of CytoSNP from Okbay et al.'s 2022 summary statistics, using inverted versions of the formulas used to meta-analyze GWAS summary statistics. The resulting processed versions of Okbay et al.'s 2022 summary statistics are therefore independent from the CytoSNP cohort.

Using these processed EA GWAS summary statistics, we next constructed PGIs for EA in the Lifelines genetic data, using SbayesR Lloyd-Jones et al. (2019). This algorithm uses Bayesian regression to correct GWAS summary statistics for linkage disequilibrium, using a mixture of normal distributions as the prior. We use linkage disequilibrium scores included in the SBayesR software, estimated on respondents of the UK Biobank.

A3 Construction of inverse probability weights

Weights were calculated inversely proportional to the probability of inclusion in the same-generation sample (used to estimate the effects of the offspring PGI on their own SES). Frequency cells by sex, year of birth, and year of observation were first computed using the offspring generation in the main sample (the sample used to estimate next-generation genetic effects in Table 3). The same-generation sample was then constructed from all genotyped Lifelines respondents born between 1963 and 1992 for whom parental PGI sums could be imputed (see Appendix Table A1). Frequency cells were computed for this sample as well, and weights were assigned to each individual as the ratio of main-sample to same-generation frequencies, normalized to have mean one. To limit imprecision from sparse cells, weights were trimmed at the 1st and 99th percentiles.

A4 Additional Tables

Table A1: Overview of Subsamples Used in the Analysis

Sample	Genetic Data Requirements	Demographic Restrictions	Used In	Main Purpose It Is Used For	Sample Size
(1)	Reference and their parents (imputed)	Reference's offspring older than 30	All analyses except those listed below	Estimate the impact of reference's PGI on their own SES and on their offspring's SES	7,038 in reference generation / 14,117 in offspring
(2)	Individual and their biological parents	None	Figure 3	Show that the deviation of an individual's PGI from the average PGI of their parents is orthogonal to the latter	3,282
(3)	Individual and their parents (imputed)	Individuals born between 1963 and 1992—the birth years of the main sample's offspring generation	Equation (8) and Table 5	Estimate the impact of the offspring's PGI on their own SES	26,407
(4)	Reference, their partner, and their parents (imputed)	Reference and their partner older than 30	Equation (9) and Table 6	Investigate the relationship between exogenous variation in the reference's PGI and their partner's PGI	3,788
(5)	Reference, their offspring, and their parents (imputed)	None	Equation (10) and Figure 7	Investigate the relationship between exogenous variation in the reference's PGI and their offspring's PGI	3,852

Notes: This table summarizes the distinct subsamples employed across our analyses. Sample (1) serves as the main sample and is used in most of the primary analyses. With the exception of Sample (2), it is sufficient to have imputed genetic data for an individual's parents. In contrast, Sample (2) requires the observed genetic data of both biological parents. Sample (1) cannot be used to estimate how the offspring's PGI affects their own SES; for this purpose, we rely on Sample (3). Finally, while the estimates reported in Table 6 do not strictly require genetic data for the reference's parents, we restrict the analysis to the same sample used in equation (9) for consistency.

Table A2: Do Next-Generation Genetic Effects Vary with The Reference's Gender?

	$\mathbf{PGI^{2nd}} \times \mathbf{Male^{2nd}}$		$\mathbf{PGI^{2nd}}$		$\mathbf{Male^{2nd}}$	
	β	S.E.	β	S.E.	β	S.E.
Education						
Years of Schooling	-0.03	0.08	0.33	0.05	-0.05	0.05
College Graduate	0.003	0.018	0.068	0.01	-0.015	0.01
Income (percentiles)						
Individual Earnings	-0.25	0.93	1.81	0.51	-0.95	0.56
Individual Income	-0.31	0.92	1.97	0.50	-1.07	0.55
Household Income	-0.90	0.94	2.04	0.53	-0.36	0.46
Wealth (percentiles)						
Net Wealth	-0.38	0.93	1.47	0.56	-0.21	0.57
Assets	-1.18	0.91	1.95	0.53	0.58	0.55
Debt	-1.16	0.92	1.01	0.54	0.98	0.54
Real Estate	-1.10	1.03	1.49	0.60	0.78	0.61
Financial Assets	-0.48	0.93	2.17	0.55	0.17	0.58
Checkings & Savings	-0.48	0.93	2.10	0.55	0.30	0.57
Bonds & Stocks	-0.57	1.18	1.96	0.67	-1.39	0.70
1 if Has Bonds or Stocks	-0.005	0.013	0.022	0.007	-0.017	0.008
Mortgage (Own Home)	-1.14	1.03	0.78	0.61	0.61	0.62

Notes: This table examines whether the effects of a reference's genetics on their offspring's SES differ by the reference's gender. We regress the offspring's outcome on the reference's PGI, an indicator for whether the reference is male, and their interaction. Income and wealth are expressed in percentile ranks (except for the indicator for bond or stock ownership). We cannot reject the null hypothesis that the effect of the reference's PGI on offspring SES is the same for men and women. However, some point estimates are economically meaningful, and the lack of statistical significance may reflect limited statistical power.

Table A3: Do Next-Generation Genetic Effects Vary with The Offspring's Age?

	Reference PGI × Offspring Age		**Reference PGI**		**Offspring Age**	
	β	S.E.	β	S.E.	β	S.E.
Education						
Years of Schooling	0.01	0.01	0.32	0.04	-0.05	0.01
College Graduate	0.00	0.001	0.07	0.01	-0.01	0.001
Income						
Individual Earnings	-0.01	0.06	1.67	0.42	-0.33	0.07
Individual Income	0.00	0.05	1.80	0.42	-0.34	0.07
Household Income	0.03	0.06	1.70	0.43	-0.29	0.07
Wealth						
Net Wealth	0.10	0.06	1.29	0.45	-0.27	0.07
Total Assets	0.14	0.06	1.50	0.43	-0.41	0.07
Total Debt	0.06	0.06	0.59	0.44	-0.31	0.07
Housing Assets	0.19	0.07	1.14	0.48	-0.02	0.07
Financial Assets	0.03	0.06	1.89	0.44	-0.47	0.07
Checkings & Savings	0.03	0.06	1.81	0.44	-0.59	0.07
Bonds & Stocks	-0.05	0.09	1.81	0.54	0.03	0.08
1 if Has Bonds or Stocks	0.00	0.00	0.02	0.01	0.00	0.00
Mortgage Debt	0.12	0.07	0.45	0.49	0.18	0.08

Notes: This table examines whether the effects of a reference's genetics on their offspring's SES vary with the offspring's age. We regress the offspring's outcome on the reference's PGI, the offspring's age, and their interaction. Income and wealth are expressed in percentile ranks (except for the indicator for bond or stock ownership). The results show that the effect of the reference's PGI on offspring housing assets rises sharply with age. A similar pattern emerges for broader wealth measures that include housing, such as total assets and net wealth.

Table A4: Intergenerational Transmission of SES: Associations of Parental Wealth and Income with Offspring Outcomes

	Effect on Offspring of Moving Reference 10 Percentiles Up in the Distribution			
	. . . of Net Wealth		**. . . of Hhld. Income**	
	Estimate	S.E.	Estimate	S.E.
Education				
Years of Schooling	0.23	0.01	0.24	0.01
College Graduate	0.047	0.003	0.049	0.003
Income (in Percentile Ranks)				
Individual Earnings	1.89	0.11	2.04	0.12
Individual Income	1.79	0.11	2.04	0.12
Household Income	1.86	0.11	2.17	0.12
Wealth (in Percentile Ranks)				
Net Wealth	3.54	0.10	0.81	0.12
Total Assets	3.20	0.99	1.64	0.12
Financial Assets	3.55	0.98	1.56	0.12
Housing Assets	2.65	0.12	1.53	0.13

Notes: This table summarizes the degree of intergenerational SES transmission observed in our data. Columns 1-2 present the changes in offspring outcomes associated with moving the reference 10 percentiles higher in the net wealth distribution, while Columns 3-4 present the changes in offspring outcomes associated with moving the reference 10 percentiles higher in the household income distribution. Odd columns report post estimates, even columns robust standard errors.

Table A5: Gene-by-Environment: Do Same-Generation Genetic Effects Depend on Previous Generation's SES?

	Individual's PGI × SES of Individual's Parents		**Individual's PGI**		**SES of Individual's Parents**	
	β	S.E.	β	S.E.	β	S.E.
Panel A						
Education						
Years of Schooling	0.03	0.04	0.36	0.04	0.52	0.03
College Graduate	0.01	0.01	0.07	0.01	0.10	0.01
Income						
Individual Earnings	-0.34	0.47	3.03	0.35	3.14	0.28
Individual Income	-0.21	0.47	3.07	0.35	2.95	0.28
Household Income	0.11	0.49	1.92	0.37	3.80	0.32
Wealth						
Net Wealth	-0.31	0.51	0.79	0.39	12.12	0.30
Total Assets	-0.61	0.47	1.70	0.35	9.90	0.27
Total Debt	-0.76	0.46	1.53	0.37	3.02	0.29
Housing Assets	-0.97	0.52	1.55	0.39	7.42	0.36
Financial Assets	-0.36	0.48	2.15	0.37	11.38	0.32
Checkings & Savings	-0.26	0.48	1.93	0.37	11.09	0.28
Bonds & Stocks	0.36	0.69	1.63	0.49	7.78	0.49
1 if Has Bonds or Stocks	0.00	0.01	0.02	0.01	0.09	0.01
Mortgage Debt	-0.73	0.54	1.59	0.41	0.58	0.32
Panel B						
Education						
Years of Schooling	0.001	0.001	0.38	0.02	0.014	0.001
College Graduate	0.0003	0.0002	0.08	0.01	0.0026	0.0001
Income (percentiles)						
Individual Earnings	-0.006	0.010	2.80	0.23	0.086	0.006
Individual Income	-0.004	0.010	2.93	0.24	0.081	0.006
Household Income	-0.006	0.010	1.94	0.24	0.108	0.006
Wealth (percentiles)						
Net Wealth	-0.016	0.010	0.61	0.25	0.336	0.006
Total Assets	-0.026	0.010	1.32	0.23	0.281	0.006
Total Debt	-0.026	0.011	1.14	0.25	0.002	0.006
Housing Assets	-0.034	0.011	0.96	0.25	0.198	0.006
Financial Assets	-0.014	0.010	1.94	0.23	0.368	0.006
Checkings & Savings	-0.012	0.010	1.76	0.23	0.297	0.006
Bonds & Stocks	0.010	0.015	1.86	0.35	0.227	0.009
1 if Has Bonds or Stocks	0.0001	0.0002	0.021	0.004	0.0025	0.0001
Mortgage Debt	-0.030	0.012	1.14	0.27	0.002	0.007

Notes: This table investigates whether the effect of an individual's PGI on their own SES varies with the SES of the individual's parents. Each outcome is regressed on the individual's PGI, a measure of the SES of the individual's parents, and their interaction, controlling also for the sum of the PGIs of the individual's parents and its interaction with the parents' SES. In Panel A, parental SES is measured by an indicator for whether the father's net wealth was above the median; in Panel B, it is the father's net wealth percentile rank (demeaned). For both Panels A and B, if the father's net wealth was unavailable, we used the mother's net wealth rank instead. The number of observations are: For income and wealth outcomes, $Nindividuals = 25,892$ and $Nobservations = 335,439$; for educational attainment $Nobservations = 25,727$.

Table A6: Summary statistics of the same-generation sample, before and after weighting

	Which Effect is the Sample Used to Estimate?		
	Next-Generation Genetic Effect	Same-Generation Genetic Effect	
		Unweighted	*Weighted*
Demographics			
Male	0.51	0.39	0.46
	(0.50)	(0.49)	(0.50)
Birth Year	1983.5	1976.1	1982.9
	(6.90)	(8.44)	(6.84)
N	14,117	26,407	
Education			
Years of Schooling	14.5	14.6	14.8
	(2.20)	(2.17)	(2.00)
College Graduate	0.53	0.55	0.56
	(0.50)	(0.50)	(0.49)
N	12,625	20,306	
Income			
Individual Earnings	€46,157	€44,648	€47,259
	(29,490)	(28,735)	(27,424)
Individual Income	€48,435	€46,398	€48,731
	(28,307)	(28,030)	(26,654)
N	121,575	343,655	
Wealth			
Net Wealth	€109,772	€160,047	€122,249
	(235,884)	(275,806)	(244,539)
Total Assets	€289,241	€335,965	€302,372
	(293,217)	(312,110)	(283,388)
Total Debt	€178,193	€173,368	€178,428
	(139,317)	(137,622)	(129,719)
Housing Assets	€213,944	€242,050	€216,249
	(183,233)	(179,994)	(176,692)
Financial Assets	€34,491	€44,338	€37,208
	(56,335)	(66,874)	(56,057)
Checkings & Savings	€29,492	€37,067	€32,166
	(42,743)	(50,211)	(43,352)
Bonds & Stocks	€4,147	€6,148	€4,281
	(18,262)	(22,891)	(18,245)
Mortgage Debt	€165,452	€162,547	€167,522
	(132,927)	(121,853)	(120,021)
N	120,366	343,655	

Notes: When quantifying the relative contribution of the genetic transmission channel in Table 5, we use two different samples: the same-generation sample (used to estimate the effects of the offspring PGI on their own SES) and the next-generation sample (used to estimate the next-generation genetic effects in Table 3). To improve comparability, we re-weight the same-generation sample to match the year-of-birth-by-gender distribution in the next-generation sample. Column 1 reports averages for the next-generation sample, while Columns 2 and 3 report averages for the same-generation sample before and after reweighting, respectively. Standard deviations in parentheses. Both samples are restricted to individuals born between 1963 and 1992. See Appendix Table A1 for details on the eligibility criteria of the two samples: the next-generation sample corresponds to Sample (1), and the same-generation sample corresponds to Sample (3).

Table A7: Contribution of Genetic Transmission to Next-Generation Genetic Effects—No Weighting

	Total Effect		**Genetic Transmission**		**Ratio**	
	β_1	S.E.	$\lambda_1/2$	S.E.	$\lambda_1/2\beta_1$	95% CI
Education						
Years of Schooling	0.32	0.04	0.19	0.01	0.58	[0.49–0.82]
College Graduate	0.07	0.01	0.039	0.003	0.56	[0.47–0.82]
Income						
Individual Earnings	1.74	0.43	1.38	0.12	0.80	[0.52–1.67]
Individual Income	1.87	0.42	1.45	0.12	0.77	[0.52–1.49]
Household Income	1.75	0.44	0.95	0.12	0.54	[0.33–1.11]
Wealth						
Net Wealth	1.34	0.45	0.24	0.14	0.18	[-0.02–0.60]
Total Assets	1.58	0.43	0.61	0.12	0.38	[0.20–0.90]
Financial Assets	2.01	0.44	0.90	0.12	0.48	[0.28–0.82]
Housing Assets	1.13	0.49	0.44	0.13	0.39	[0.12–2.74]

Notes: Table 5 in the main text quantifies the contribution of the genetic transmission channel to the next-generation genetic effects. This table replicates the exercise without the re-weighting discussed in Section 6.1. The first two columns reproduce results from Table 3, estimating the total effect of the reference's PGI on their offspring's SES: Column 1 reports the point estimate, and Column 2 reports the corresponding standard errors. The two middle columns quantify the genetic transmission channel: Column 3 presents the estimated effect of the offspring's PGI on their own SES (i.e., the coefficient λ_1 from equation (8)), divided by 2, and Column 4 reports the corresponding standard errors. The final two columns assess the share of the next-generation genetic effects attributable to genetic transmission: Column 5 displays the ratio of Column 3 to Column 1, and Column 6 show bootstrapped 95% confidence level intervals for this proportion.

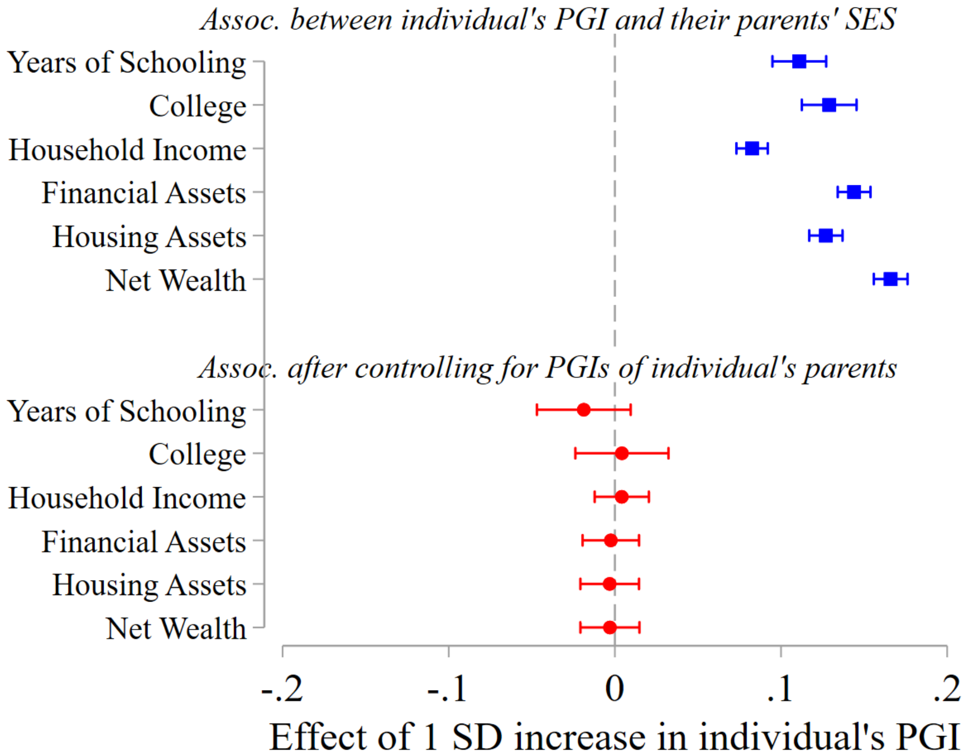
Table A8: Sensitivity of Results to Unequal Number of Observations per Reference

	Levels		**Percentile Rank**	
	β_1	S.E.	β_1	S.E.
Education				
Years of Schooling	0.32	0.04		
College Graduate	0.07	0.01		
Income				
Individual Earnings	€1,857	€399	1.77	0.41
Individual Income	€1,842	€373	1.87	0.40
Household Income	€2,163	€668	1.34	0.40
Wealth				
Net Wealth	€5,489	€3,021	0.87	0.41
Total Assets	€7,353	€3,953	0.92	0.39
Total Debt	€1,931	€1,927	0.32	0.40
Housing Assets	€4,627	€2,523	0.25	0.48
Financial Assets	€2,073	€702	1.67	0.41
Checking & Savings	€1,872	€557	1.63	0.41
Bonds & Stocks	€220	€200	1.51	0.51
1 if Has Bonds or Stocks	0.02	0.01		
Mortgage Debt	€761	€1,805	-0.25	0.51

Notes: In our main specification (i.e., Table 3 and equation (6)), some references contribute more observations than others—either because a reference has multiple children or because offspring from earlier birth cohorts contribute more years of data. To test the sensitivity of our results to this uneven weighting, this table collapses the data to a single observation per reference. Specifically, we first average outcomes across the years observed for each offspring, and then average across all of a reference's children. We then re-estimate the causal effect of the reference's genetics on their offspring's average SES. The first two columns report results with outcomes measured in levels, while the last two columns present results with outcomes measured in percentile ranks. Odd-numbered columns show point estimates, while even-numbered columns report robust standard errors. All regressions control for the sum of the PGIs of the reference's parents, the reference's year of birth and gender, and the (average) gender of the reference's offspring. Only the coefficient on the reference's PGI is reported in the table. Percentile ranks are calculated within calendar year and year of birth (of the offspring). *N observations* = 6,831 for education and 7,038 for income and wealth.

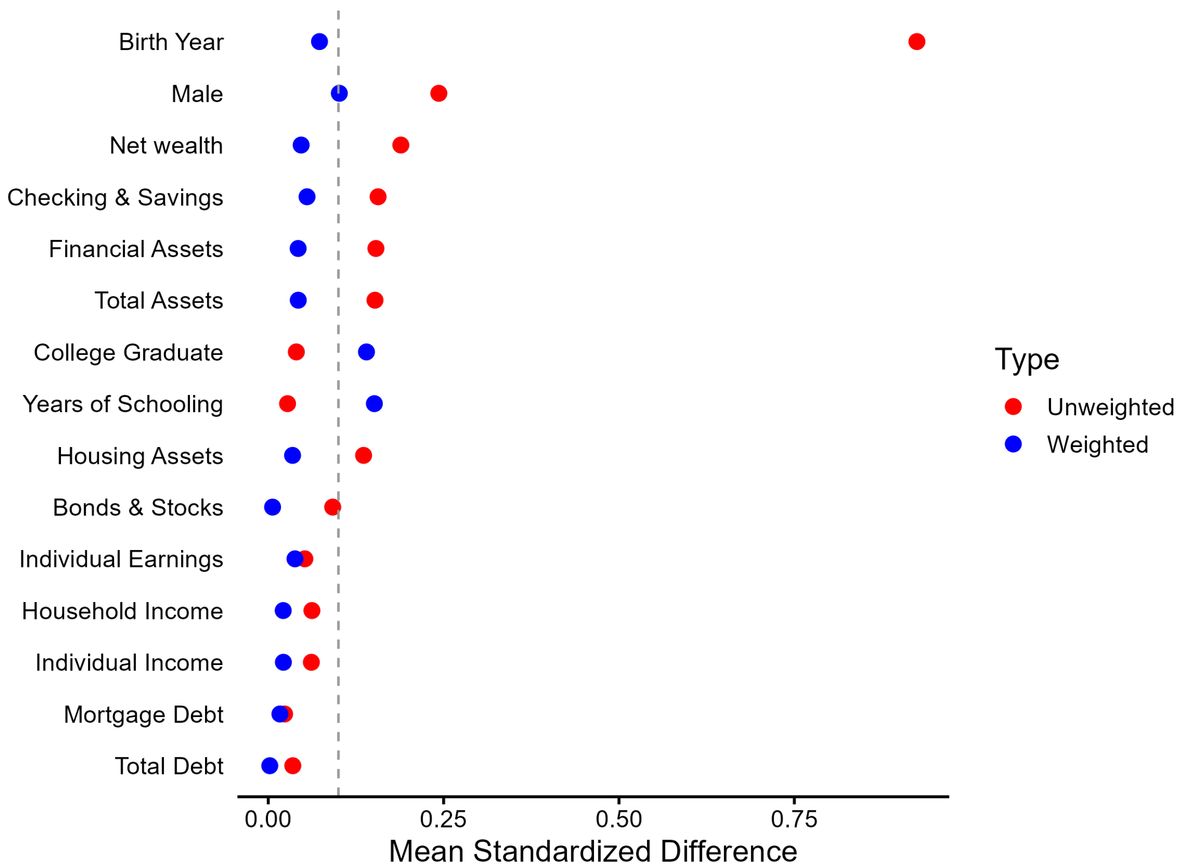
A5 Additional Figures

Figure A1: Balance Test—The Association between the Current Generation's PGI and the Previous Generation's SES



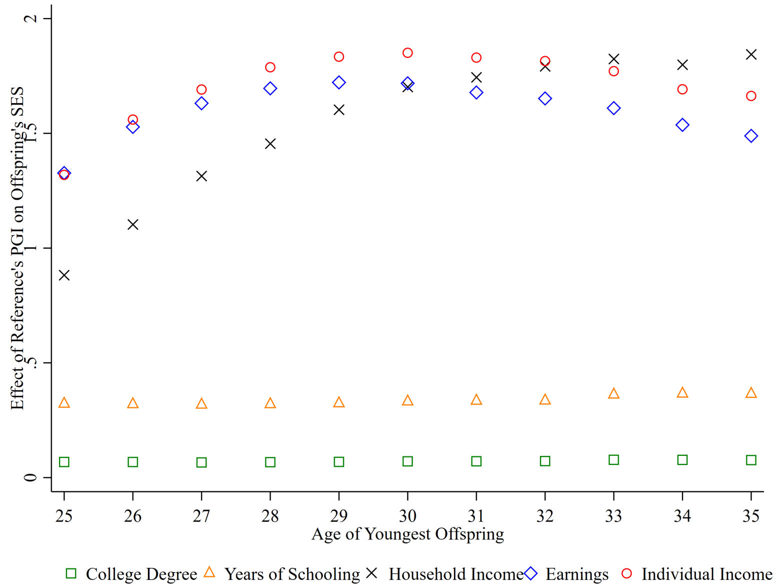
Notes: The analysis in Figure 4 is limited to the references for whom measures of their parents' SES are available. This figure repeats the same exercise in the largest sample for which we jointly observe an individual's PGI, the (imputed) sum of their parents' PGIs, and parental SES measures—see Figure 4 for details on construction. These results lead to the same conclusion. For household income N *individuals* = 32,195 and N *observations* = 586,580. For assets and wealth, N *individuals* = 31,461 and N *observations* = 484,843. For Years of Schooling and College, N *individuals* =N *observations* = 14,677, due to missingness in years of schooling in the administrative data for especially older generations.

Figure A2: Comparing The Two Samples Used for Estimating The Genetic Transmission Channel

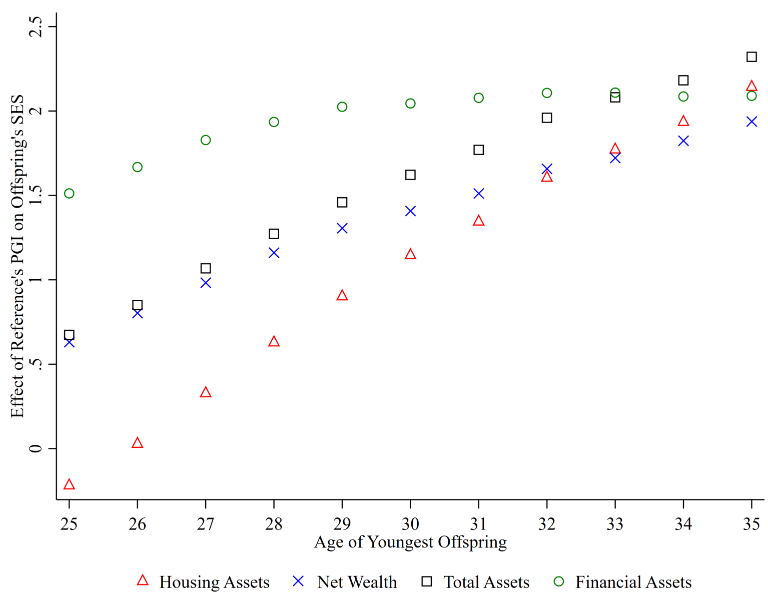


Notes: When quantifying the relative contribution of the genetic transmission channel in Table 5, we use a different sample to estimate the effects of the offspring PGI on their SES than the one used to estimate the next-generation genetic effects in Table 3. To make the former sample as comparable as possible to the latter, we re-weight it to match the year-of-birth-by-gender distribution in the offspring generation of our main sample. This figure compares these two samples before and after reweighting. The red circles plot the standardized mean differences prior to reweighting (the absolute difference in group means divided by the pooled standard deviation), while the blue circles show the same measure after applying the weights. Although both samples are restricted to the same birth-year range, their distributions differ before reweighting. The sample used to estimate the next-generation genetic effects is younger on average because, in addition to the PGI of one parent, we also require the (imputed) sum of the PGIs of that parent's parents—see Appendix Table A1.

Figure A3: Next-Generation Genetic Effects: Sensitivity to Minimum Offspring Age



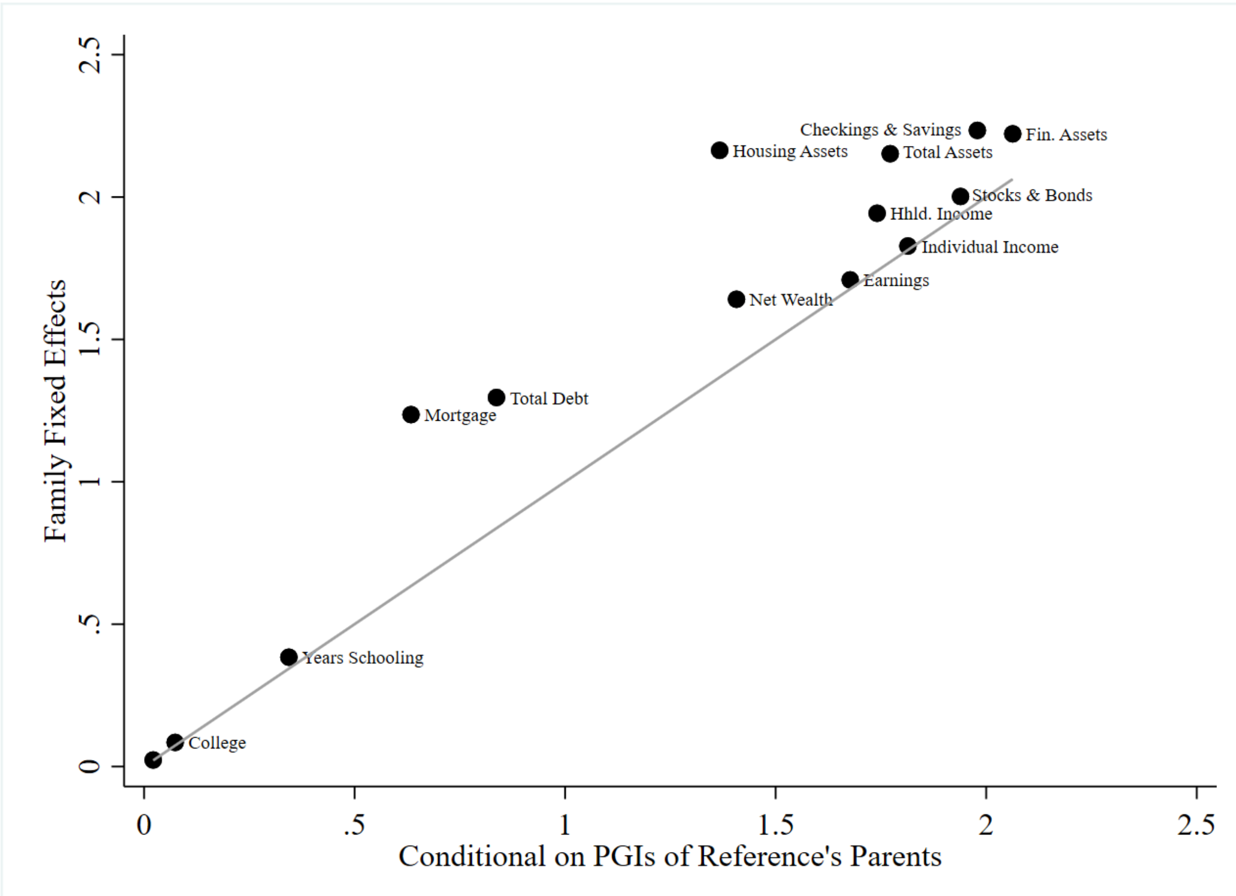
(a) Education and income-related outcomes



(b) Wealth-related outcomes

Notes: A potential concern with our design is that our age restriction (requiring offspring to be at least 30 years old) may induce selection on the reference's PGI. If the PGI affects the age at which individuals have their first child, then it could influence the likelihood that a reference and their offspring are included in our sample. This figure shows how the next-generation genetic effects in Table 3 change as we vary the minimum offspring age cutoff. The x-axis indicates the age of the youngest offspring included. For example, the first markers plotted at 25 correspond to estimates obtained when the sample includes offspring ages 25 and older. Each series of markers traces the estimated effect for a specific outcome across different age cutoffs.

Figure A4: Comparing Estimates of Next-Generation Genetic Effects from Two Alternative Specifications



Notes: This figure compares estimates of next-generation genetic effects obtained from two alternative specifications: one that controls for the sum of the PGIs of the reference's parents (i.e., equation (6), and another that includes a fixed effect for the reference and their full siblings (i.e., equation (7). Estimates from the former are plotted on the horizontal axis, and those from the latter on the vertical axis. Each marker represents the estimated effects for a specific outcome. For any given outcome, both specifications are estimated on the same set of observations. Sibling Fixed effects estimates are based on 4,897 families with at least two genotyped siblings who have children aged above 30, with outcomes available in the administrative data.