ONLINE APPENDIX: "GENES, EDUCATION AND LABOR MARKET OUTCOMES: EVIDENCE FROM THE HEALTH AND RETIREMENT STUDY"

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Appendix A provides additional details on construction of the EA score. Appendix B discusses additional results and robustness checks discussed throughout the main text. Appendix C provides a model of measurement error that helps to guide our interpretation of estimates. In Appendix D, we relate the EA score to a cognitive test score available for HRS respondents. Appendix E describes how we weight observations due to possible sample selection issues along with our approach to correcting standard errors due to multiple hypothesis testing.

Appendix A: Additional Details on GWAS and Construction of the EA Score

In this appendix, we provide a brief introduction to molecular genetics and the kinds of genetic data that we use in this study. We repeat some portions of Section 2 so that this appendix can provide a self-contained introduction to GWAS and the EA score used in our analysis. First, we describe some basic features of the human genome. Next, we discuss how statistical gene-discovery projects can produce scores that are useful for the prediction of economic outcomes such as educational attainment. We highlight how recent advances permit credible and replicable inference.

The human genome consists of approximately 3 billion nucleotide pairs spread out over 23 chromosomes.[1] A DNA molecule is often thought of as double-helix ladder, with the nucleotide base pairs forming the "rungs" of the ladder. Each rung can either be an adenine-thymine pair, or a guanine-cytosine pair. If the DNA strand can be thought of as a ladder with nucleotide-pair rungs, then the rails or sides of the ladder are formed by phosphate and sugar molecules. These rails can be distinguished as either the positive (+) or negative (−) strands. At a particular location, it will matter which nucleotide molecule is attached to which strand. For example, if there is an

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1. Most of the background information presented here on the human genome follows Beauchamp et al. (2011) and Benjamin et al. (2012)

adenine-thymine pair in a particular position where the adenine molecule is attached to the positive strand, this would be denoted by an A. However, if instead the thymine molecule were attached to the positive strand, this would be denoted by a T. This means that four possible variants could exist at a given address: A, T, G or C, depending on which nucleotide pair is present, and the position of that pair relative to the positive strand. However, most SNPs are biallelic, meaning that there are only two observed alleles at a particular location. The human genome can therefore be thought of as a series of 3 billion genetic addresses, each of which contains a particular base pair molecule in a particular position.

At the vast majority of such locations (about 99%), there is no variation in the observed nucleotide pair. A single-nucleotide polymorphism (SNP) exists when there are differences in the nucleotide pair present at a particular location on the genome. A particular SNP can be referred to by a name (e.g., rs7937), which indicates its position in the genome. An allele refers to one of the variants that may be present at a particular SNP. If T (an adenine-thymine pair with the thymine attached to the positive strand) is more commonly found at a particular SNP, it is referred to as the major allele, and the other observed allele is referred to as the minor allele.[2]

A traditional approach to the discovery of gene-behavior associations rests on examining *candidate genes*. Under this paradigm, researchers use some knowledge of the relevant biological processes to suggest places in the genome that might contain SNPs associated with a particular outcome. Unfortunately, this approach to identifying gene-economic outcomes has also generated a large number of reported associations that have failed to replicate outside of their discovery samples. This problem has been so widespread that an editorial statement from the journal *Behavior Genetics* stated that "[t]he literature on candidate gene associations is full of reports that have not stood up to rigorous replication," and that "it now seems likely that many of the published findings of the last decade are wrong or misleading and have not contributed to real advances in knowledge," (Hewitt 2012). This pattern has emerged, in part, because traditional candidate gene studies have been severely underpowered to detect real genetic effects. Sample sizes in general have been too small relative to the true effect sizes of individual SNPs, making it likely that statistically significant associations are the result of chance. This problem is exacerbated when studies search over many candidate genes, creating a multiple hypothesis testing problem that increases the likelihood of finding false positive results (Benjamin et al. 2012).

An alternative to candidate genes is an approach called a genome-wide association study (GWAS). Under the GWAS methodology, researchers scan the entire genome for SNPs that are associated with a particular phenotype (trait or outcome), but adopt strong measures to deal with multiple hypothesis testing. For a particular outcome of interest, y_i, and for a set of observed SNPs, $\{SNP_{ij}\}_{j=1}^{N^J}$, a GWAS study proceeds by

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2.   In the case of SNPs that are not biallelic, there may be multiple minor alleles.

obtaining estimates of N^J separate regressions of the form:

$$y_i = \mu X_i' + \beta_j SNP_{ij} + \varepsilon_{ij} \tag{A.1}$$

Here SNP_{ij} measures the number of copies of a reference allele possessed by individual i for SNP j. For example, if the reference allele at SNP j is AT, then SNP_{ij} could take the values 0, 1, or 2. The maximum value of 2 reflects the fact that an individual can have at most two copies of the reference allele — one on each inherited chromatid. Additionally, X_i is a vector of controls, including principal components of the genetic variables $\{SNP_{ij}\}_{j=1}^{N^J}$. Principal components of the genetic data are added to control for population stratification. For example, it could be that SNP_{ij} is correlated with a particular ethnicity or ancestry group. Failure to control for the principal components could generate observed SNP-phenotype relationships that reflect the influence of broader ethnic differences rather than the influence of a particular genetic marker.

After obtaining estimates for all N^J versions of equation (A.1), those estimated coefficients $\widehat{\beta}_j$ with sufficiently small p-values are said to reflect relationships that are genome-wide significant. Given the huge number of regressions run under this methodology, the significance thresholds in modern GWAS are typically very strict. A conventional threshold is 5×10^{-8}. This approach has become popular and, as a consequence of its stringency requirements, has led to the discovery of a number of credible genetic associations. For example, the well-known FTO gene for obesity was discovered through a GWAS, despite the lack of any existing biology that would have suggested it as a candidate gene (Benjamin et al. 2012).

Existing work has demonstrated the importance of credibly identified SNPs for several economic outcomes. These SNPs either directly emerged from a GWAS, or were candidate genes that were validated by later GWAS results. An established literature documents a number of credible genetic associations with smoking behaviors (Bierut 2010; Thorgeirsson et al. 2010). Fletcher (2012) demonstrates that a SNP associated with smoking intensity also appears to moderate the effect of tobacco taxes. More closely related to our work, another set of studies suggests indirect linkages between genetic variants and human capital. For example, Fletcher and Lehrer (2011) use a set of SNPs associated with health outcomes to provide exogenous within-family variation to estimate a causal relationship between health and education. Finally, Thompson (2014) shows that a variant associated with the MAOA gene appears to moderate the relationship between income and education.

Recent work using GWAS has discovered some of the first direct associations between specific SNPs and education. Rietveld et al. (2013) identified three SNPs (rs9320913, rs11584700, rs4851266) attaining genome-wide significance in a GWAS for educational attainment. Follow-up work by the same team (the Social Science and Genetics Association Consortium) has recently extended the Rietveld et al. (2013) study to perform an educational attainment GWAS with a sample size of 293,723. This follow-up study, Okbay et al. (2016), has discovered 74 SNPs that attain genome-wide significance. In a second follow-up using a sample size of over 1.1 million, Lee et al. (2018) reports over 1,000 genome-wide significant SNPs and generates the

most predictive EA score to date. We build our analysis here on the gene-education associations found in this follow-up study.

One common technique adopted in the GWAS literature is to take observed SNPs and the estimated GWAS coefficients (the $\widehat{\beta}_j$) and aggregate them into a polygenic score that can be used for prediction. Typically these scores take the following form:

$$PGS_i = \sum_j \widetilde{\beta}_j SNP_{ij} \tag{A.2}$$

where $\widetilde{\beta}_j$ is some transformation of the underlying GWAS coefficients. The $\widehat{\beta}_j$ estimates are typically corrected to account for correlation between SNPs and prevent over or under prediction. In our study, we use SNP weights $\widehat{\beta}_j$ that have been adjusted using the Bayesian LDpred technique developed by Vilhjálmsson et al. (2015), and applied to the genetic data in the HRS.[3] We refer to the polygenic score created using these weights as the *EA score*, to indicate that this is a score developed to predict "Educational Attainment".

Appendix B: Additional Results and Robustness Checks

This appendix contains a series of additional analyses and robustness checks. In Appendix B.1 we address the relationship between the EA score and fixed effects in an earnings regression. Appendix B.2 provides suggestive evidence on mechanisms explaining the gene-SES interactions we estimate. In Appendix B.3, we present coefficient estimates for interaction terms between the EA score and childhood SES in regressions predicting degree outcomes. In Appendix B.4, we replicate results on SES and education for men and women separately (and pooling genders, but with a male interaction term). In Appendix B.5, we show results using alternative EA scores. Appendix B.6 provides additional information and results on income. Appendix B.7 discusses the EA score and labor supply. Finally, Appendix B.8 investigates the joint distribution of father's income, the EA score, and earnings.

B.1. The EA Score and Fixed Effects

Fixed-effects models are often estimated to control for time-invariant characteristics, including genetic factors, in models of earnings and other outcomes over the life-cycle. Here we examine the relationship between the EA score and estimated fixed effects from our SSA earnings sample. We first estimate a regression of log earnings on year dummies, age dummies, and individual fixed effects for our earnings panel. We next

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3.   We would like to especially thank Aysu Okbay, a member of the Social Science and Genetics Consortium, for graciously generating and sharing some of the scores that are not otherwise publicly available. We note as well that the polygenic score that we use in this study combines all SNPs analyzed in Lee et al. (2018), not just those reaching genome-wide significance.

extract estimates of the fixed effects from this regression and examine their relationship with the EA score. Figure B.1 plots the non-parametric relationship between the EA score and the fixed effects. There is a strong, positive, and approximately linear relationship between the EA score and the fixed effects. The correlation between these two variables is $\rho = 0.177$, and in a bivariate regression of the fixed effects on the EA score, the incremental R^2 associated with the EA score is 0.0313. The strong relationship between the fixed effects and the EA score is unsurprising, since the fixed effects absorb the substantial relationship between education and earnings, and the EA score is highly correlated with educational attainment.
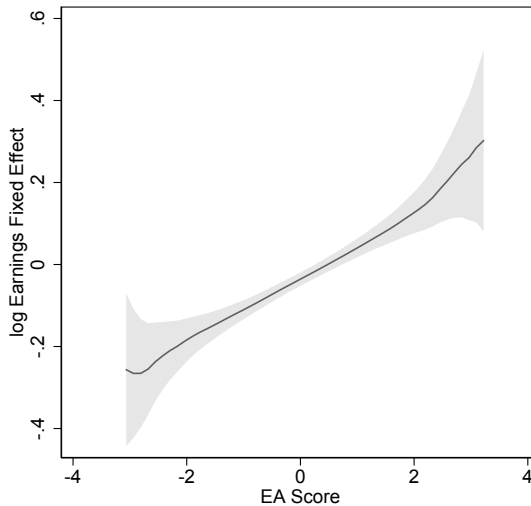
FIGURE B.1. The EA Score and Log Earnings Fixed Effect. Non-parametric (local polynomial) estimation relating the EA score and the estimated fixed effect for earnings. Shaded areas depict 95% confidence intervals.

In traditional fixed effects models, including the one we estimate here, an individual fixed effect shifts the mean of the outcome variable by the same amount in every period. However, as demonstrated in Panel B of Figure 9, the relationship between the EA score and log-earnings appears to grow over the life-cycle. This pattern is obscured in the fixed effects results, and in subsequent analyses relating the EA score to the estimated fixed effects.

B.2. *Specific Investments: Books in the Household, Preschool, and Household Size*

The results in Section 3.4 suggest that childhood SES can moderate the relationship between the EA score and educational attainment. However, the mechanisms that give rise to this relationship remain unclear. For example, higher father's income

might relax credit constraints that prevent high-score children from pursuing a college degree, increasing the relationship between the EA score and possessing a college degree. Alternately father's income might also be associated with early life investments like preschool that could differentially affect later-life outcomes depending on an individual's genetic endowments. The policy implications of these results depend on which mechanisms gives rise to the moderation found in Section 3.4.

The literature on early childhood skill formation has examined the impact of preschool (Heckman et al. 2013) and books in the household (Cunha et al. 2010) on subsequent human capital formation. Moreover, the literature on the quantity-quality tradeoff in fertility suggests that households with fewer resources might choose to have more children and make lower human capital investments in these children (Becker 1960; Hotz et al. 1997). The two waves of the *Life History Mail Survey* from the HRS provide an opportunity to examine the role of these specific features of the environment. Specifically, the *Life History Mail Survey* contains items that ask the respondent whether they attended a preschool program before starting elementary school, how many non-school books were present in their home at age 10, and how many people were living in the household when the respondent was 10. The books question allows the following categorical responses: (i) None or very few (0-10 books); (ii) enough to fill one shelf (11-25 books); (iii) enough to fill one book case (26-100 books); (iv) enough to fill two book cases (101-200 books); and (v) enough to fill more than two bookcases (more than 200 books). We create a binary variable indicating a high number of books in the household if the respondent says there were at least enough books to fill one book case (26 or more books). For the household size question, we create a binary indicating the presence of more than five people in the house.

The first three columns of Table B.1 regress educational outcomes on our standard controls (including parental education), the EA score, and the variables measuring preschool attendance, books in the household, and household size. We examine years of schooling and indicators for completing at least a high school degree and at least a (four year) college degree as outcomes. We find that a high number of books in the household predicts higher educational attainment for all of these educational outcomes, while having more people in the house is negatively associated with all educational outcomes. These associations are substantial in size. For example, having at least one book case full of books is associated with a 13 percentage point increase in the probability of earning a college degree. We find more mixed associations for the preschool variable. Preschool attendance positively predicts earning a college degree (p-value<0.01), as well as years of schooling (p-value<0.05). We also unexpectedly find a negative association between preschool status and earning at least a high school degree.

Columns (4)-(6) of Table B.1 regress the high books, preschool, and household size indicators on our standard controls, the EA score, and the four family SES variables from Section 3.4. We find that all four SES variables significantly predict having a high number of books in the house. We note, however, that the association between the "father never unemployed" measure and the indicator for many books in the household is only marginally significant (p-value<0.10). High father's income exhibits a positive

and significant association with preschool attendance. High father's income and the "Family Well Off" measures are both significant negative predictors of household size. Taken together, the results in Table B.1 indicate that the number of books in the household is strongly associated with completed educational outcomes, and that the high family SES variables used earlier tend to predict higher propensities for making these investments. We also find fairly strong evidence linking household size to the at least two of the SES measures. The associations between preschool, education, and SES are weaker and less consistent. This provides suggestive evidence that early childhood investments like books could be among the mechanisms through which high SES operates to influence educational achievement and moderate the relationship between the EA score and education.

TABLE B.1. Family SES Measures and Specific Human Capital Measures

Dep Var.	(1) Educ	(2) At least High School	(3) At least College	(4) High Books	(5) Preschool	(6) > 5 in House
EA Score	0.570***	0.052***	0.115***	0.036***	0.026***	0.010
	(0.039)	(0.007)	(0.008)	(0.011)	(0.009)	(0.012)
High Num. of Books	0.838***	0.067***	0.130***			
	(0.096)	(0.015)	(0.017)			
Pre-School	0.312**	-0.051**	0.134***			
	(0.132)	(0.023)	(0.030)			
> 5 in House	-0.515***	-0.055***	-0.047***			
	(0.082)	(0.015)	(0.016)			
High Father's Inc.				0.059**	0.049***	-0.067**
				(0.023)	(0.018)	(0.027)
Family Well Off				0.095***	0.033*	-0.135***
				(0.031)	(0.020)	(0.032)
Never Move or Ask Help				0.093***	0.008	0.017
				(0.029)	(0.023)	(0.031)
Father Not Unemp.				0.048*	0.018	0.037
				(0.029)	(0.022)	(0.033)
Obs.	3981	3966	3966	3184	3163	3212
R^2	0.336	0.192	0.284	0.292	0.176	0.113

All regressions include the first 10 principle components of the full matrix of genetic data as controls, a full set of birth year dummies, a male dummy, interactions between the birth year and male dummies, and controls for parental education.

B.3. Regression Estimates for Interactions between SES and the EA Score

Here we present the coefficient estimates for the specifications that regress dummy variables for completed degree levels on the EA score, family SES measures, and interactions between the EA score and family SES. Each panel of Table B.2 presents estimates of Equation 1 for a different binary SES measure. The estimates for the interaction terms, along with the associated 95% confidence intervals, are plotted in Figure 6 of the main text.

TABLE B.2. Polygenic Score and Interactions with SES

Dep Var: At Least	(1) H.S. Equiv	(2) High School	(3) Two Yr.	(4) College	(5) Grad
Panel A: SES Measure - Father Occ. Income					
EA Score	0.056***	0.066***	0.079***	0.083***	0.037***
	(0.011)	(0.012)	(0.013)	(0.012)	(0.009)
High SES	0.062***	0.063***	0.103***	0.090***	0.021**
	(0.013)	(0.015)	(0.014)	(0.012)	(0.009)
EA Score × High SES	-0.028**	-0.026**	0.043***	0.054***	0.018*
	(0.011)	(0.012)	(0.014)	(0.012)	(0.009)
Obs.	6750	6750	6750	6750	6750
R^2	0.283	0.269	0.255	0.262	0.136
Panel B: SES Measure - Family Well Off					
EA Score	0.062***	0.087***	0.055***	0.064***	0.024***
	(0.013)	(0.014)	(0.014)	(0.012)	(0.009)
High SES	0.052***	0.080***	0.039***	0.031***	0.005
	(0.013)	(0.015)	(0.014)	(0.012)	(0.008)
EA Score × High SES	-0.018	-0.038***	0.057***	0.061***	0.029***
	(0.012)	(0.013)	(0.013)	(0.011)	(0.008)
Obs.	8387	8387	8387	8387	8387
R^2	0.259	0.253	0.228	0.241	0.132
Panel C: SES Measure - Move or Asked for Help					
EA Score	0.048***	0.077***	0.093***	0.107***	0.038***
	(0.012)	(0.014)	(0.016)	(0.013)	(0.010)
High SES	0.028**	0.048***	0.022	0.025**	0.002
	(0.014)	(0.016)	(0.015)	(0.012)	(0.008)
EA Score × High SES	-0.002	-0.028**	0.008	0.005	0.013
	(0.012)	(0.013)	(0.014)	(0.012)	(0.009)
Obs.	8362	8362	8362	8362	8362
R^2	0.258	0.248	0.224	0.238	0.130
Panel D: SES Measure - Father Unemployed					
EA Score	0.061***	0.080***	0.071***	0.090***	0.036***
	(0.012)	(0.013)	(0.016)	(0.013)	(0.010)
High SES	0.012	0.028*	0.029**	0.029**	0.009
	(0.014)	(0.015)	(0.014)	(0.012)	(0.008)
EA Score × High SES	-0.019*	-0.030**	0.035**	0.027**	0.015*
	(0.012)	(0.013)	(0.014)	(0.012)	(0.009)
Obs.	8402	8402	8402	8402	8402
R^2	0.255	0.246	0.223	0.237	0.129

Regressions relating educational attainment categories to the EA score and childhood SES along with interactions between the EA score and high SES. Regressions also include a full set of dummy variables for birth year, a male dummy and a full set of interactions between the birth year and gender dummies. Additionally, every specification includes the first 10 principle components of the full matrix of genetic data, a cubic in the EA score, and controls for parental education (years of paternal and maternal education and dummies indicating missing values for each).

B.4. Additional Results on Gender Differences

Analyses in Section 3 on education and childhood SES examine males and females together while our analyses in Section 4 limit attention to males. In choosing these analytic samples, the aim is to keep the largest sample possible unless there is a

compelling reason to do otherwise. Given selection into the labor market among females, especially those in the older HRS cohorts, there is good reason to focus on males when studying earnings. In this section, we assess whether results from Section 3 on education and SES change if we consider males and females separately. Tables B.3-B.4 replicate the specifications for years of education in Table 2 separately for men and women, respectively. Table B.5 again estimates these specifications using the pooled sample of men and women, but now adds an interaction term between the EA score and a dummy for male respondents. The results in these tables suggest that the EA score strongly predicts years of schooling for both men and women conditional on a rich set of controls. The interaction results in Table B.5 provide evidence that the association between the EA score and years of schooling is larger for men. This gender difference merits exploration in future research. Tables B.6 and B.7 replicate the degree specifications in Table 3 for males and females, respectively. We find that the EA score tends to predict college completion more strongly for men than for women.

Finally, we present estimates of the specifications with interactions between SES and the EA score separately by gender. Tables B.8-B.9 provide estimates of the interaction specifications in Equation 1 for men and women, respectively. The results for these specifications with our main pooled sample are found in Figure 6 and Table B.2. The results in Tables B.8-B.9 are largely consistent with our baseline results from the pooled sample. We find evidence of interactions between SES and the EA score in both males and females, although the coefficients are less precisely estimated. This could arise because of the smaller sample sizes generated by splitting the sample.

TABLE B.3. Polygenic Score and Educational Attainment for Males

	(1)	(2)	(3)	(4)	(5)
EA Score	0.889***	0.651***	0.642***	0.616***	0.666***
	(0.073)	(0.071)	(0.070)	(0.066)	(0.048)
Father Educ		0.162***	0.160***	0.099***	0.118***
		(0.023)	(0.023)	(0.025)	(0.021)
Mother Educ		0.135***	0.132***	0.098***	0.118***
		(0.028)	(0.028)	(0.026)	(0.025)
Child Health: Very Good			-0.308	-0.295	-0.307***
			(0.237)	(0.206)	(0.113)
Child Health: Good			-0.435**	-0.390**	-0.738***
			(0.216)	(0.198)	(0.145)
Child Health: Fair			-0.006	-0.061	-0.543**
			(0.321)	(0.293)	(0.250)
Child Health: Poor			0.202	0.361	-0.221
			(0.689)	(0.650)	(0.611)
Child Health: Missing			2.351***	2.494	4.366**
			(0.655)	(1.687)	(2.047)
Obs.	3560	3560	3560	3560	3560
R^2	0.272	0.394	0.397	0.436	0.599
Child SES Measures	N	N	N	Y	Y
Child Region	N	N	N	N	Y
Religion	N	N	N	N	Y

Regressions relating educational attainment (years) to the EA score for males. All regressions include a full set of dummy variables for birth year. All specifications include the first 10 principle components of the full matrix of genetic data as controls. Some specifications include controls for parental education, childhood health, childhood SES measures, region during childhood and religion, as indicated.

TABLE B.4. Polygenic Score and Educational Attainment for Females

	(1)	(2)	(3)	(4)	(5)
EA Score	0.809***	0.586***	0.588***	0.574***	0.530***
	(0.058)	(0.049)	(0.050)	(0.056)	(0.040)
Father Educ		0.135***	0.132***	0.113***	0.098***
		(0.015)	(0.014)	(0.019)	(0.016)
Mother Educ		0.201***	0.198***	0.190***	0.181***
		(0.017)	(0.017)	(0.018)	(0.017)
Child Health: Very Good			-0.009	0.033	0.005
			(0.103)	(0.094)	(0.088)
Child Health: Good			-0.158	-0.115	-0.159
			(0.126)	(0.116)	(0.105)
Child Health: Fair			-0.283	-0.259	-0.318*
			(0.177)	(0.176)	(0.176)
Child Health: Poor			-1.190	-1.102	-1.191
			(0.801)	(0.742)	(0.754)
Child Health: Missing			-	-	-
			-	-	-
Obs.	4977	4977	4977	4977	4977
R^2	0.231	0.342	0.346	0.355	0.417
Child SES Measures	N	N	N	Y	Y
Child Region	N	N	N	N	Y
Religion	N	N	N	N	Y

Regressions relating educational attainment (years) to the EA score for females. All regressions include a full set of dummy variables for birth year. All specifications include the first 10 principle components of the full matrix of genetic data as controls. Some specifications include controls for parental education, childhood health, childhood SES measures, region during childhood and religion, as indicated.

TABLE B.5. Polygenic Score and Educational Attainment - EA Score x Male

	(1)	(2)	(3)	(4)	(5)
EA Score	0.809***	0.566***	0.562***	0.540***	0.505***
	(0.058)	(0.051)	(0.051)	(0.056)	(0.041)
EA Score x Male	0.080	0.107	0.108	0.110	0.186***
	(0.093)	(0.083)	(0.083)	(0.084)	(0.061)
Father Educ		0.147***	0.144***	0.107***	0.110***
		(0.013)	(0.013)	(0.016)	(0.013)
Mother Educ		0.173***	0.170***	0.149***	0.150***
		(0.016)	(0.016)	(0.016)	(0.015)
Child Health: Very Good			-0.144	-0.103	-0.126*
			(0.123)	(0.114)	(0.070)
Child Health: Good			-0.266**	-0.198*	-0.423***
			(0.123)	(0.120)	(0.089)
Child Health: Fair			-0.204	-0.120	-0.392***
			(0.165)	(0.171)	(0.145)
Child Health: Poor			-0.658	-0.554	-0.860
			(0.575)	(0.570)	(0.570)
Child Health: Missing			1.526***	1.066	1.982
			(0.408)	(1.173)	(1.269)
Obs.	8537	8537	8537	8537	8537
R^2	0.256	0.363	0.364	0.382	0.516
Child SES Measures	N	N	N	Y	Y
Child Region	N	N	N	N	Y
Religion	N	N	N	N	Y

Regressions relating educational attainment (years) to the EA score for males and females including a dummy variable for male interacted with the EA score. All regressions include a full set of dummy variables for birth year. All specifications include the first 10 principle components of the full matrix of genetic data as controls. Some specifications include controls for parental education, childhood health, childhood SES measures, region during childhood and religion, as indicated.

TABLE B.6. Polygenic Score and Categorical Education Outcomes for Males

Dep Var.	(1) No Degree	(2) Two-Year Coll.	(3) College	(4) College Plus	(5) Redo Grade
Panel A:					
EA Score	-0.066***	-0.003	0.065***	0.081***	-0.052***
	(0.008)	(0.005)	(0.008)	(0.007)	(0.008)
Obs.	3551	3551	3551	3551	3398
R^2	0.192	0.060	0.067	0.105	0.073
Panel B:					
EA Score	-0.046***	-0.004	0.049***	0.067***	-0.042***
	(0.007)	(0.005)	(0.007)	(0.006)	(0.009)
Father Educ	-0.012***	0.001	0.012***	0.014***	-0.012***
	(0.003)	(0.002)	(0.003)	(0.003)	(0.004)
Mother Educ	-0.009***	0.002	0.013***	0.008***	-0.004
	(0.003)	(0.003)	(0.003)	(0.003)	(0.004)
Obs.	3551	3551	3551	3551	3398
R^2	0.271	0.066	0.105	0.138	0.084

Regressions relating educational attainment categories or the probability of repeating a grade to the EA score for males. Specifications in Panel A do not include parental education. Specifications in Panel B include parental education. All regressions include a full set of dummy variables for birth year. Additionally, every specification includes the first 10 principle components of the full matrix of genetic data.

TABLE B.7. Polygenic Score and Categorical Education Outcomes for Females

Dep Var.	(1) No Degree	(2) Two-Year Coll.	(3) College	(4) College Plus	(5) Redo Grade
Panel A:					
EA Score	-0.070***	-0.012**	0.071***	0.048***	-0.032***
	(0.007)	(0.006)	(0.007)	(0.005)	(0.005)
Obs.	4961	4961	4961	4961	4768
R^2	0.213	0.042	0.095	0.067	0.043
Panel B:					
EA Score	-0.053***	-0.016***	0.053***	0.037***	-0.021***
	(0.007)	(0.006)	(0.007)	(0.005)	(0.005)
Father Educ	-0.005**	-0.001	0.014***	0.009***	-0.004*
	(0.002)	(0.002)	(0.002)	(0.002)	(0.002)
Mother Educ	-0.021***	0.006***	0.014***	0.008***	-0.012***
	(0.003)	(0.002)	(0.003)	(0.002)	(0.003)
Obs.	4961	4961	4961	4961	4768
R^2	0.250	0.048	0.135	0.092	0.064

Regressions relating educational attainment categories or the probability of repeating a grade to the EA score for females. Specifications in Panel A do not include parental education. Specifications in Panel B include parental education. All regressions include a full set of dummy variables for birth year. Additionally, every specification includes the first 10 principle components of the full matrix of genetic data.

TABLE B.8. Polygenic Score and Interactions with SES for Males

Dep Var: At Least	(1) H.S. Equiv	(2) High School	(3) Two Yr.	(4) College	(5) Grad
Panel A: SES Measure - Father Occ. Income					
EA Score	0.035**	0.041**	0.112***	0.096***	0.040***
	(0.017)	(0.018)	(0.019)	(0.017)	(0.014)
High SES	0.085***	0.086***	0.129***	0.113***	0.044***
	(0.018)	(0.022)	(0.020)	(0.019)	(0.015)
EA Score × High SES	-0.015	0.001	0.017	0.039**	0.023
	(0.016)	(0.018)	(0.020)	(0.019)	(0.015)
Obs.	2828	2828	2828	2828	2828
R^2	0.332	0.312	0.269	0.262	0.167
Panel B: SES Measure - Family Well Off					
EA Score	0.058***	0.074***	0.073***	0.078***	0.019
	(0.019)	(0.021)	(0.019)	(0.018)	(0.013)
High SES	0.070***	0.106***	0.042**	0.037*	0.018
	(0.020)	(0.022)	(0.020)	(0.019)	(0.013)
EA Score × High SES	-0.026	-0.032*	0.067***	0.062***	0.049***
	(0.019)	(0.019)	(0.019)	(0.018)	(0.012)
Obs.	3503	3503	3503	3503	3503
R^2	0.289	0.280	0.241	0.241	0.156
Panel C: SES Measure - Move or Asked for Help					
EA Score	0.043**	0.067***	0.121***	0.124***	0.041***
	(0.018)	(0.022)	(0.021)	(0.019)	(0.015)
High SES	0.051**	0.082***	0.015	0.019	-0.003
	(0.021)	(0.023)	(0.021)	(0.019)	(0.014)
EA Score × High SES	-0.007	-0.031	0.004	0.003	0.022
	(0.017)	(0.019)	(0.019)	(0.017)	(0.013)
Obs.	3475	3475	3475	3475	3475
R^2	0.290	0.277	0.235	0.235	0.149
Panel D: SES Measure - Father Unemployed					
EA Score	0.058***	0.070***	0.105***	0.115***	0.052***
	(0.018)	(0.020)	(0.021)	(0.020)	(0.016)
HighSES	-0.010	0.013	0.026	0.020	0.010
	(0.020)	(0.022)	(0.020)	(0.020)	(0.015)
EA3ScorexHighSES	-0.033*	-0.035*	0.020	0.013	0.004
	(0.018)	(0.018)	(0.019)	(0.018)	(0.015)
Obs.	3505	3505	3505	3505	3505
R^2	0.279	0.261	0.235	0.233	0.145

Regressions relating male educational attainment categories to the EA score and childhood SES along with interactions between the EA score and high SES. Regressions also include a full set of dummy variables for birth year. Additionally, every specification includes the first 10 principle components of the full matrix of genetic data and controls for parental education (years of paternal and maternal education and dummies indicating missing values for each).

TABLE B.9. Polygenic Score and Interactions with SES for Females

Dep Var: At Least	(1) H.S. Equiv	(2) High School	(3) Two Yr.	(4) College	(5) Grad
Panel A: SES Measure - Father Occ. Income					
EA Score	0.074***	0.086***	0.052***	0.069***	0.027***
	(0.013)	(0.015)	(0.016)	(0.014)	(0.009)
High SES	0.043**	0.043**	0.087***	0.076***	0.008
	(0.018)	(0.020)	(0.019)	(0.015)	(0.010)
EA Score × High SES	-0.036**	-0.045***	0.070***	0.075***	0.022**
	(0.014)	(0.016)	(0.018)	(0.015)	(0.011)
Obs.	3922	3922	3922	3922	3922
R^2	0.261	0.247	0.256	0.267	0.098
Panel B: SES Measure - Family Well Off					
EA Score	0.063***	0.097***	0.040**	0.053***	0.027**
	(0.016)	(0.018)	(0.018)	(0.016)	(0.011)
High SES	0.038**	0.059***	0.036**	0.023	-0.009
	(0.016)	(0.019)	(0.017)	(0.014)	(0.009)
EA Score × High SES	-0.012	-0.044**	0.051***	0.061***	0.012
	(0.016)	(0.017)	(0.017)	(0.014)	(0.011)
Obs.	4884	4884	4884	4884	4884
R^2	0.257	0.249	0.220	0.236	0.101
Panel C: SES Measure - Move or Asked for Help					
EA Score	0.055***	0.086***	0.073***	0.095***	0.033**
	(0.015)	(0.018)	(0.022)	(0.017)	(0.013)
High SES	0.012	0.022	0.026	0.026*	0.002
	(0.017)	(0.019)	(0.019)	(0.015)	(0.010)
EA Score × High SES	-0.002	-0.028	0.012	0.007	0.006
	(0.015)	(0.017)	(0.020)	(0.016)	(0.013)
Obs.	4887	4887	4887	4887	4887
R^2	0.253	0.240	0.215	0.234	0.101
Panel D: SES Measure - Father Unemployed					
EA Score	0.059***	0.084***	0.044**	0.071***	0.019*
	(0.015)	(0.017)	(0.022)	(0.017)	(0.010)
HighSES	0.031*	0.044**	0.030	0.035**	0.008
	(0.018)	(0.019)	(0.019)	(0.014)	(0.009)
EA3ScorexHighSES	-0.003	-0.022	0.048**	0.039**	0.024**
	(0.015)	(0.017)	(0.020)	(0.015)	(0.010)
Obs.	4897	4897	4897	4897	4897
R^2	0.257	0.249	0.218	0.235	0.101

Regressions relating female educational attainment categories to the EA score and childhood SES along with interactions between the EA score and high SES. Regressions also include a full set of dummy variables for birth year. Additionally, every specification includes the first 10 principle components of the full matrix of genetic data and controls for parental education (years of paternal and maternal education and dummies indicating missing values for each).

B.5. Results Using Alternative Versions of the EA Score

In this section, we examine the robustness of our main results to the use of alternate polygenic scores for educational attainment. Specifically, we replicate eight key results: (i) the relationship between years of school and the EA score controlling for parental education (Column (2) in Table 2); (ii-v) the interactions between the EA score and the High Father's Income and Family Well Off binaries in predicting having at least a high school degree and at least a college degree (Columns (2) and (4) in Panels A and B of Table B.2; (vi) the relationship between log earnings and the EA score controlling for education (Column (2) in Panel A of Table 5); (vii) the interaction between the EA score and having at least a college degree in predicting earnings (Column (3) in Panel A of Table 5); and (viii) the interaction between the EA score and an indicator for years after 1980 in predicting log earnings (Column (2) in Panel b of Table 5).

The various panels of Table B.10 present these results for seven different scores. The scores differ in terms of the sample size of the underlying GWAS discovery sample used to estimate the coefficients applied to the SNPs in each score. The scores also differ in terms of the method used to construct the score. For ease of comparison, Panel A presents the baseline results from this paper, which use the score based on the GWAS results from Lee et al. (2018) ($N > 1.1$ million). This score is constructed using the LDpred method described in Vilhjálmsson et al. (2015), which is a Bayesian method that adjusts the coefficient estimates assuming a reasonable distribution of effect sizes (given the known heritability of education), and corrects for correlations between SNPs that are close to one another in the genome. Panel B presents results using a score based on the Lee et al. (2018) GWAS that does not use LDpred, but instead sums up all SNPs weighted by their unadjusted GWAS coefficients. This is the score that is available in the most recent public release of polygenic scores by the Health and Retirement Study. Even though this all SNPs score is available for more individuals, in Panel B we restrict the sample so that it is directly comparable to the results using the LDpred score that we use in our main results. Panel C uses the same score as in Panel B, but now includes individuals from all four waves of genotyping (2006, 2008, 2010, and 2012). Comparing results from Panels A-C demonstrates the effect of the LDpred method, and the effect of changing sample size and composition as more waves of genotyped individuals are included. To ensure comparability, all specifications in Table B.10 use the principal components distributed in the most recent version of the HRS Polygenic Score Data (PGS) file (V 3.0). These differ slightly from the principal components used in all other analyses in the paper, which are those released with the SSGAC's distribution of the LDpred polygenic score based on the Lee et al. (2018) GWAS, but only constructed for individuals genotyped in 2006 and 2008. As described in Appendix E, we construct sampling weights based on the inverse probability of participation in the collection of genetic data in 2006 and 2008. Note that when larger samples are used (e.g. in Panel C), we modify these weights so they are based on the inverse probability of being included in any of the waves of genotypic data, not just 2008 and 2006.

Panels D and E present results using an all SNPs score built on GWAS results from Okbay et al. (2016) with a smaller discovery sample size of $N = 293,723$. This is the score that has been made publicly available by the HRS for individuals who were genotyped in the 2006, 2008, 2010, and 2012 waves. This earlier-generation score is less predictive of educational attainment, but is available for more genotyped individuals than the LDpred version of the Lee et al. (2018) score, which only publicly available for individuals genotyped in 2006 and 2008. Panel D presents results using the all-SNPs Okbay et al. (2016) score restricted to the main analysis sample used in this paper. Panel E presents results using this score for all available individuals, increasing the sample size. Panel F presents results using an LDpred score based on the GWAS results from Rietveld et al. (2013) with a discovery sample of size $N = 126,559$. Panel G presents results using an all-SNPs score and unadjusted GWAS coefficients from Rietveld et al. (2013).

Comparing results across the panels of Table B.10, several patterns emerge. First, as expected, the predictive power of the polygenic score grows as the sample size of the underlying GWAS discovery sample grows. This is most apparent looking at the basic association with years of school (conditional on parental education) in Column (1). The interactions between the EA score and family SES in predicting a college degree (Columns 4-5) are robustly found with all scores. The interactions in predicting having at least a high school degree (Columns 2-3) are less robust, and are only consistently found to be statistically significant when using scores based on the largest GWAS (Panels A-C). We robustly find an association between the EA score and log earnings, except for the first generation scores from Rietveld et al. (2013). We fail to estimate a significant interaction between the EA score and having a college degree in any of the specifications predicting earnings. We find significant interactions between the EA score and a post-1980 indicator for all scores. A comparison of Panels B and C, as well as Panels D and E suggests that the changing composition of the genetic sample does little to alter our main results.

TABLE B.10. Results Using Alternate Polygenic Scores

Dep Var:	(1) Years of Educ.	(2) At Least H.S.	(3) At Least H.S.	(4) At Least Coll.	(5) At Least Coll.	(6) log Earn.	(7) log Earn.	(8) log Earn.
Panel A: LD Pred Score from Lee et al. (2018), $N > 1.1$ million								
EA Score	0.620***	0.064***	0.088***	0.083***	0.065***	0.030***	0.026***	0.009
	(0.042)	(0.012)	(0.014)	(0.012)	(0.012)	(0.009)	(0.010)	(0.007)
High Father's Inc.		0.061***		0.083***				
		(0.018)		(0.014)				
Score × High Fath. Inc.		-0.023*		0.051***				
		(0.012)		(0.012)				
Family Well Off			0.073***		0.030**			
			(0.017)		(0.015)			
Score × Fam. Well Off			-0.038***		0.060***			
			(0.013)		(0.011)			
Score × At Least Coll.							0.016	
							(0.020)	
Score × Post 1980								0.036***
								(0.013)
Obs.	8537	6750	8387	6750	8387	96721	96510	96510
R^2	0.360	0.266	0.255	0.262	0.240	0.190	0.195	0.205
Panel B: All SNPs Score from Lee et al. (2018), $N > 1.1$ million								
EA Score	0.475***	0.042***	0.044***	0.059***	0.052***	0.023**	0.021**	0.002
	(0.045)	(0.012)	(0.015)	(0.011)	(0.012)	(0.009)	(0.010)	(0.007)
High Father's Inc.		0.062***		0.086***				
		(0.018)		(0.014)				
Score × High Fath. Inc.		-0.023*		0.044***				
		(0.012)		(0.013)				
Family Well Off			0.071***		0.027*			
			(0.018)		(0.015)			
Score × Fam. Well Off			-0.013		0.041***			
			(0.014)		(0.012)			
Score × At Least Coll.							0.010	
							(0.022)	
Score × Post 1980								0.036***
								(0.013)
Obs.	8537	6750	8387	6750	8387	96721	96510	96510
R^2	0.343	0.256	0.245	0.240	0.216	0.189	0.194	0.204
Panel C: All SNPs Score from Lee et al. (2018), $N > 1.1$ million								
Sample: 2006, 2008, 2010, and 2012 Waves of HRS Genetics Sample								
EA Score	0.467***	0.057***	0.068***	0.056***	0.054***	0.025***	0.022**	0.004
	(0.033)	(0.010)	(0.012)	(0.010)	(0.010)	(0.008)	(0.009)	(0.006)
High Father's Inc.		0.068***		0.086***				
		(0.011)		(0.011)				
Score × High Fath. Inc.		-0.021**		0.056***				
		(0.009)		(0.011)				
Family Well Off			0.095***		0.030***			
			(0.012)		(0.010)			
Score × Fam. Well Off			-0.035***		0.043***			
			(0.011)		(0.010)			
Score × At Least Coll.							0.009	
							(0.017)	
Score × Post 1980								0.035***
								(0.011)
Obs.	11930	9252	11720	9252	11720	125346	125124	125124
R^2	0.322	0.235	0.232	0.226	0.208	0.190	0.193	0.205

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Regressions relating different versions of the EA score to various educational and labor outcomes examined in the main text. Regressions also include a full set of dummy variables for birth year, a male dummy and a full set of interactions between the birth year and gender dummies. Additionally, every specification includes the first 10 principle components of the full matrix of genetic data and controls for parental education (years of paternal and maternal education and dummies indicating missing values for each). Some regressions include measures of childhood SES and controls for own education, as indicated.

TABLE B.10. Results Using Alternate Polygenic Scores (Continued from Previous Page)

Dep Var:	(1) Years of Educ.	(2) At Least H.S.	(3) At Least H.S.	(4) At Least Coll.	(5) At Least Coll.	(6) log Earn.	(7) log Earn.	(8) log Earn.
Panel D: All SNPs Score from Okbay et al. (2018), N = 293,723								
Sample: 2006 and 2008 Waves of HRS Genetics Sample								
EA Score	0.346***	0.026**	0.027*	0.038***	0.033***	0.028***	0.023**	0.004
	(0.050)	(0.013)	(0.016)	(0.011)	(0.012)	(0.009)	(0.010)	(0.007)
High Father's Inc.		0.063***		0.085***				
		(0.018)		(0.014)				
Score × High Fath. Inc.		-0.009		0.052***				
		(0.013)		(0.013)				
Family Well Off			0.072***		0.028*			
			(0.018)		(0.015)			
Score × Fam. Well Off			0.002		0.050***			
			(0.015)		(0.012)			
Score × At Least Coll.							0.025	
							(0.021)	
Score × Post 1980								0.042***
								(0.013)
Obs.	8537	6750	8387	6750	8387	96721	96510	96510
R^2	0.333	0.249	0.238	0.233	0.208	0.190	0.195	0.205
Panel E: All SNPs Score from Okbay et al. (2018), N = 293,723								
Sample: 2006, 2008, 2010, and 2012 Waves of HRS Genetics Sample								
EA Score	0.375***	0.055***	0.054***	0.049***	0.043***	0.022***	0.016*	0.001
	(0.040)	(0.009)	(0.012)	(0.010)	(0.010)	(0.008)	(0.009)	(0.006)
High Father's Inc.		0.068***		0.085***				
		(0.011)		(0.011)				
Score × High Fath. Inc.		-0.018*		0.055***				
		(0.010)		(0.011)				
Family Well Off			0.097***		0.029***			
			(0.012)		(0.010)			
Score × Fam. Well Off			-0.017		0.043***			
			(0.012)		(0.010)			
Score × At Least Coll.							0.022	
							(0.017)	
Score × Post 1980								0.034***
								(0.011)
Obs.	11930	9252	11720	9252	11720	125346	125124	125124
R^2	0.313	0.231	0.226	0.220	0.200	0.189	0.193	0.205

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Regressions relating different versions of the EA score to various educational and labor outcomes examined in the main text. Regressions also include a full set of dummy variables for birth year, a male dummy and a full set of interactions between the birth year and gender dummies. Additionally, every specification includes the first 10 principle components of the full matrix of genetic data and controls for parental education (years of paternal and maternal education and dummies indicating missing values for each). Some regressions include measures of childhood SES and controls for own education, as indicated.

TABLE B.10. Results Using Alternate Polygenic Scores (Continued from Previous Page)

Dep Var:	(1) Years of Educ.	(2) At Least H.S.	(3) At Least H.S.	(4) At Least Coll.	(5) At Least Coll.	(6) log Earn.	(7) log Earn.	(8) log Earn.
Panel F: LD Pred Score from Reitveld et al. (2013), N = 126,559								
Sample: 2006 and 2008 Waves of HRS Genetics Sample								
EA Score	0.297***	0.020	0.022	0.015	0.017	0.014	0.012	-0.004
	(0.038)	(0.013)	(0.014)	(0.010)	(0.012)	(0.009)	(0.010)	(0.006)
High Father's Inc.		0.063***		0.082***				
		(0.018)		(0.014)				
Score × High Fath. Inc.		-0.008		0.041***				
		(0.012)		(0.012)				
Family Well Off			0.072***		0.023			
			(0.018)		(0.015)			
Score × Fam. Well Off			-0.014		0.030**			
			(0.014)		(0.012)			
Score × At Least Coll.							0.019	
							(0.020)	
Score × Post 1980								0.033***
								(0.013)
Obs.	8537	6750	8387	6750	8387	96721	96510	96510
R^2	0.330	0.246	0.234	0.220	0.196	0.189	0.193	0.204
Panel G: All SNPs Score from Reitveld et al. (2013), N = 126,559								
Sample: 2006 and 2008 Waves of HRS Genetics Sample								
EA Score	0.287***	0.022*	0.025*	0.018*	0.023*	0.012	0.009	-0.005
	(0.038)	(0.013)	(0.014)	(0.010)	(0.013)	(0.009)	(0.010)	(0.006)
High Father's Inc.		0.063***		0.083***				
		(0.018)		(0.014)				
Score × High Fath. Inc.		-0.008		0.042***				
		(0.012)		(0.012)				
Family Well Off			0.073***		0.023			
			(0.018)		(0.015)			
Score × Fam. Well Off			-0.013		0.027**			
			(0.014)		(0.012)			
Score × At Least Coll.							0.020	
							(0.020)	
Score × Post 1980								0.028**
								(0.013)
Obs.	8537	6750	8387	6750	8387	96721	96510	96510
R^2	0.330	0.246	0.234	0.220	0.196	0.188	0.193	0.203

Regressions relating different versions of the EA score to various educational and labor outcomes examined in the main text. Regressions also include a full set of dummy variables for birth year, a male dummy and a full set of interactions between the birth year and gender dummies. Additionally, every specification includes the first 10 principle components of the full matrix of genetic data and controls for parental education (years of paternal and maternal education and dummies indicating missing values for each). Some regressions include measures of childhood SES and controls for own education, as indicated.

B.6. Further Details on Top-Coding and Alternative Income Measures

One limitation of the SSA earnings data is that they are subject to fairly heavy rates of top-coding, and the severity of the top coding has changed over time. The maximum amount of earnings subject to social security taxes dictates the level of top-coding in the SSA earnings data, and this has changed with reforms to the social security system. For example, while the taxable maximum stood at $3,000 in 1950 ($27,144 in 2010 dollars), it grew to $7,800 ($43,836) in 1970, $51,300 ($85,587) in 1990, and $106,800 in 2010 (Whitman and Shoffner 2011). Panel A of Figure B.2 plots the evolution of the fraction of individuals who report incomes that are subject to the top code, both using the SSA earnings data for our sample, and using data from the March Current Population Survey. Top Coding rates were quite severe in earlier decades and exceeded 60% for most years before 1980. The top coding rates plummeted with changes at the end of the 1970s. Starting at levels just over 20%, the top coding rate has declined slowly and steadily since 1980.

The pattern of top-coding observed in Panel A of Figure B.2 raises questions about how to interpret some of our findings linking the EA score and log earnings. Specifically, in Panel B of Table 5, we find that the relationship between the EA score and earnings grew after 1980. One interpretation of this result is that the economic environment shifted over this time period to increasingly reward the kinds of traits possessed by people with high values of the EA score. However, this pattern could also simply reflect changes in the top coding scheme in earnings, if the relationship between the EA score and earnings is primarily located in the upper half of the earnings distribution. To shed a bit more light on this, Panel B of Figure B.2 presents nonparametric local polynomial plots of the relationship between calendar year and log earnings residuals for each tercile of the EA score distribution. The residuals here arise from a regression of log earnings on our basic control set and controls for parental and own education. We find that residual earnings differences between EA terciles (especially the top and bottom tercile) tend to fan out continuously after 1980. This suggests that the changes in top coding do not offer a complete explanation for our results, since the fraction of the population subject to top coding declined quite slowly after 1980, while differences in earnings by EA tercile accelerated.

Another way of assessing the impact of top coding is to compare earnings results from the SSA data with self-reported earnings measures asked by the HRS. Table B.11 presents comparable specifications using both the HRS data and the SSA data. Column (1) regresses log earnings on the EA score and our basic controls, without controls for own or parental education. Column (2) regresses log earnings, our basic controls, and controls for own and parental education. Column (3) then adds an interaction between the EA score and an indicator for a college degree to the previous specification, along with interactions between the principal components and the college variable. Panel A examines the log of self-reported earned income in the HRS as the dependent variable and restricts the sample to men between the ages of 50-64 who work at least 20 hours per week. Panels B uses the log of SSA earnings as the dependent variable, but restricts the sample to men earning more than $10,000 (real 2010 dollars) during or after the

year 1992 (to match the HRS). The results across both specifications tend to be quite similar. The point estimates in Column (1) are nearly identical, and we find evidence of a return to the EA score above and beyond education in both samples. This suggests that the extent of top coding observed in the 1980s and beyond is unlike to substantially influence our results using the SSA data for that time period.

Another difference between the SSA data and self-reports in the HRS is that the SSA data reports earnings totals for the year, but not hours worked, and thus does not permit an analysis of wages. Questions on the number of hours worked per week in the HRS allow one to construct a measurement of the log wage for each worker. In Panel C of Table B.11, we repeat the specifications in Panel A, but now use the log wage instead of log income in the HRS. We find similar results whether using income or the wage in the HRS, suggesting that the patterns we observe are unlikely to be due to changes in labor supply. One difference is that we find a significant interaction between the EA score and the College indicator in the HRS sample for the log Wage (Column 3), while we do not find such an interaction in earnings using either data source.

TABLE B.11. Polygenic Score and Earnings in the HRS and SSA Data

	(1)	(2)	(3)
Panel A: log of Self-Reported Earnings in HRS			
EA Score	0.143***	0.043**	0.025
	(0.018)	(0.018)	(0.020)
EA Score x College			0.040
			(0.037)
Obs.	8479	8479	8443
R^2	0.067	0.156	0.160
Panel B: log of Earnings in SSA Data			
EA Score	0.142***	0.056***	0.036*
	(0.018)	(0.019)	(0.022)
EA Score x College			0.046
			(0.039)
Obs.	16208	16208	16148
R^2	0.082	0.170	0.173
Panel C: log of Self-Reported Wages in HRS			
EA Score	0.130***	0.029*	0.002
	(0.016)	(0.015)	(0.018)
EA3ScorexAtLstCollege			0.067**
			(0.032)
Obs.	7142	7142	7114
R^2	0.078	0.216	0.222

Regressions relating different measures of earnings to the EA score and completed education (college degree). The sample is limited to males. All regressions include a full set of dummy variables for birth year. Additionally, every specification includes the first 10 principle components of the full matrix of genetic data.

Panel A: Fraction of Earnings Observations Above SSA Top Codes
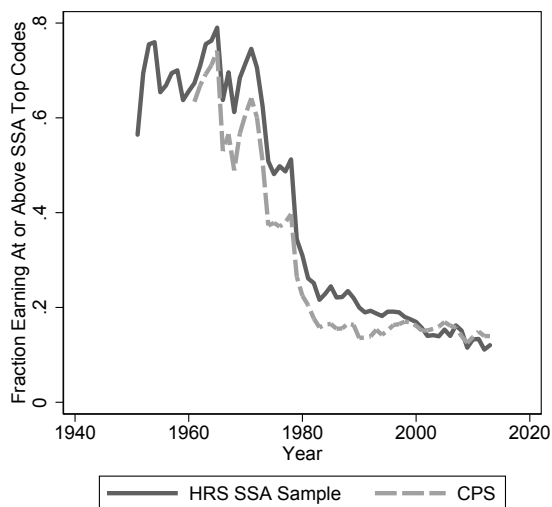
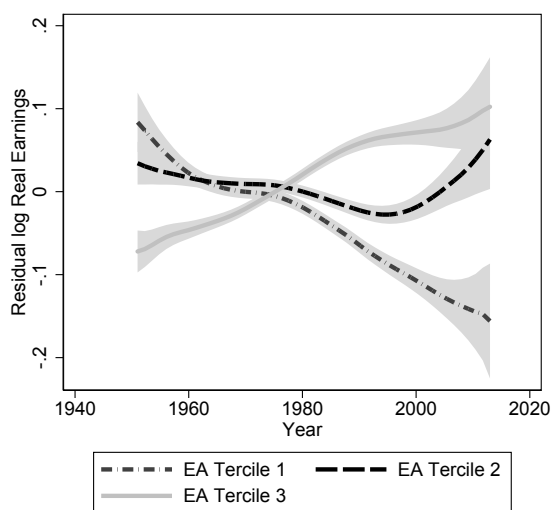Panel B: Residual Earnings Over Time by EA Tercile

FIGURE B.2. Top Coding and Residual Earnings by EA Tercile. Panel B presents non-parametric (local polynomial) estimation relating year and earnings separately for terciles of the EA score distribution. Shaded areas depict 95% confidence intervals.

B.7. *The EA Score and Labor Supply*

Panels A and B of Table B.12 provide estimated associations between the EA score and work status and retirement, respectively. As with wages, only men are included in these regressions because of the substantial amount of selection governing female labor force participation for these cohorts. Panel A investigates the relationship between the EA score and a binary variable indicating whether or not the respondent is working for pay. Column (1) reports results when the only controls are the principal components of the genetic data, a full set of dummy variables for age, dummy variables for each birth year, and dummy variables for each calendar year. For ease of exposition, we use a linear probability model. The coefficient in Column (1) of 0.056 suggests that a one standard deviation increase in the EA score is associated with a 5.6 percentage point increase in the probability of working. In Column (2), we add controls for own education (years of schooling and a complete set of degree dummies) as well as parental education. Adding these controls causes the coefficient on EA Score to fall to 0.036, though it remains statistically significant. In Column (3), we also allow for an interaction between EA score and a dummy for obtaining at least a college degree to allow for possible complementarities between schooling and genetic factors that promote education. We find no evidence of such complementarities for this measure of work.

In Panel B of Table B.12, we consider the discrete-time hazard of retiring given employment in the previous wave of the HRS. We restrict the sample to those who were not retired and who were working for pay in the previous HRS wave. We regress a binary outcome for whether or not an individual declares that they are currently retired onto the same sets of regressors used in the wage equations. The estimated coefficient on the EA score is -0.013 in the first two specifications and -0.015 in the third. The magnitude of this association is particularly striking. The probability of retirement in any year of our sample is about 11%. The estimated associations here suggest that a one standard deviation change in the EA score is associated with a roughly 1.3 percentage point reduction in retirement probability, even after controlling for own and parental education.[4] This represents an association that is more than 10% of the average retirement rate in our sample.

---

4.   An extension would look at retirement more carefully, taking into account that a discrete time hazard may overlook important non-linearities in retirement probability as individuals age.

TABLE B.12. Polygenic Score and Labor Supply Outcomes

Panel A: Dep. Var Work For Pay	(1)	(2)	(3)
EA Score	0.056***	0.036***	0.040***
	(0.008)	(0.008)	(0.011)
EA Score x College			-0.020
			(0.015)
Obs.	13744	13744	13695
R^2	0.093	0.115	0.119
Educ. Controls	N	Y	Y
Parent Controls	N	Y	Y

Panel B: Dep. Var Retired	(1)	(2)	(3)
EA Score	-0.013***	-0.013***	-0.015***
	(0.004)	(0.004)	(0.005)
EA Score x College			0.004
			(0.009)
Obs.	8218	8218	8188
R^2	0.095	0.100	0.101
Educ. Controls	N	Y	Y
Parent Controls	N	Y	Y

Regressions relating the EA score to labor market outcomes. In Panel A, the dependent variable is employment (working for pay). In Panel B, the dependent variable is retirement and conditions on not being retired in the previous period. All regressions include the first 10 principle components of the full matrix of genetic data along with a full set of dummy variables for birth year, calendar year and age. Because of collinearity a subset of these dummies is dropped. The specifications in Columns 2 and 3 include controls for parental education (years of paternal and maternal education and dummies indicating missing values for each) and own education (years of schooling and a full set of completed degree dummies). The specification in Column 3 includes as additional controls interactions between the principle components and an indicator for earning at least a college degree. The sample in Panel A is restricted to men between the ages of 50 and 64. The sample in Panel B is restricted to men between the ages of 50 and 64 who worked for pay in the last period and were not retired in the last period.

B.8. Father's Income, the EA Score and Earnings

Figure B.3 repeats the analysis conducted to generate Figure 5, but uses average real earnings as the outcome variable. This exercise is restricted to include only the men in the baseline earnings sample. Once again, we assign each individual to a quartile of the EA score distribution and a quartile of the father's income distribution, generating 16 possible combinations of SES and EA quartile groupings. Figure B.3 shows average annual earnings (ages 30-50) for each quartile combination. We find that average adult earnings generally rise in both the EA quartile and the father's income quartile. Within each EA score quartile, we can reject the null hypothesis that average earnings are equal for individuals in quartile 4 (Q4) and quartile 1 (Q2) of the father's income distribution (p-val<0.05 in all cases). We do not find consistent evidence that the average earnings gap between Q4 and Q1 of the father's income distribution rises as we move across EA quartiles. However, there does seem to be a pattern if we instead look at the difference in average earnings between Q4 and Q2 of the father's income distribution. For individuals in the lowest EA score quartile, we cannot reject the null hypothesis that average earnings are equal for individuals in Q4 and Q2 of the father's income distribution. However, in all of the higher EA score quartiles, we find a statistically significant difference in average earnings between Q4 and Q2 of the father's income distribution. The confidence intervals indicate that the relationships are noisier in general than in the case of the degree completion. Still, Figure B.3 suggests that the interactions between the EA score and father's income shape earnings outcomes, though perhaps in a more complicated way than for educational outcomes.
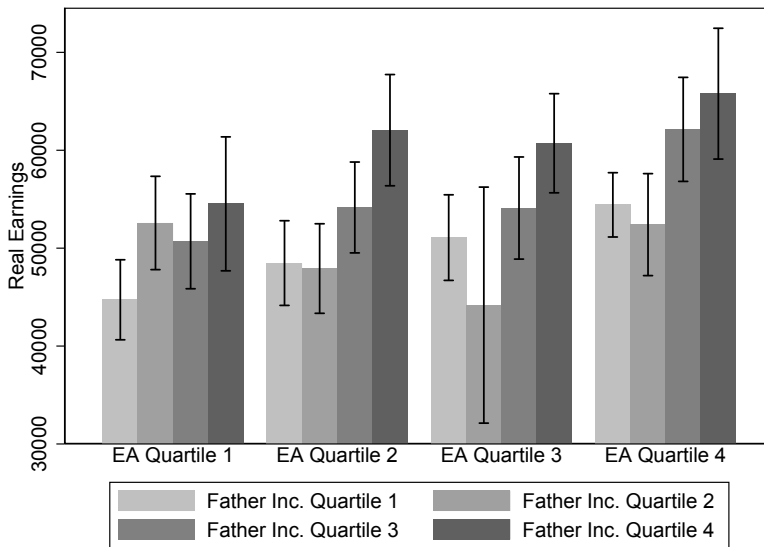

FIGURE B.3. Average Earnings (Age 30-50) by Father's Income and EA Score. Bars are plotted with 95% confidence intervals.

Appendix C: Bias in Estimated Coefficients

In this appendix, we discuss potential biases to parameter estimates. A key problem is that genetic endowments can affect returns to human capital investments, but also drive these investments. One reason is that parents who provide advantageous genetic material may also be more likely to invest in their children. Further problems arise since we do not measure human capital investments directly. Instead, we proxy for them using various measures of parent SES. These proxies may be systematically mis-measured. Here, we explore the consequences for parameter estimates.

First, suppose we want to relate a continuous economic outcome y_i to a polygenetic score and denoted G_i, and a continuous investment in human capital I_i

$$y_i = G_i \varphi_1 + I_i \varphi_2 + (G_i \times I_i)\varphi_3 + \varepsilon_i \tag{C.1}$$

In this equation, ε_i is an iid disturbance. φ_3 is of particular policy relevance as it captures whether genetic endowments and investments are complements ($\varphi_3 > 0$) or substitutes ($\varphi_3 < 0$).

There are two difficulties in estimating equation (C.1) which we emphasize. First, we proxy for investments using family SES, which we denote S_i. Investments may therefore be systematically mis-measured as follows:

$$I_i = S_i \rho_1 + G_i \rho_2 + G_i^P \rho_3 + v_i \tag{C.2}$$

The investment equation captures three features of our setting. First, family SES is an imperfect measurement of human capital investments. Second, the measurement error may be systematically related to genotype G_i. For example, if $\rho_2 > 0$, then parent SES systematically underestimates investments in children with high polygenic scores. Finally, parents with stronger genetic endowments, which we denote G_i^P, may also provide better environments for their children even after we have controlled for parent SES.

Another feature of our setting is that G_i reflects parent genetic endowments, which we denote G_i^P. We capture this with the following equation:

$$G_i = G_i^P \alpha + e_i \tag{C.3}$$

Notice that investments and SES, though they may be correlated with unobservable variables that affect outcomes, cannot influence an individual's polygenetic score. This will prove helpful for inference on how innate abilities interact with investments. In particular, we are interested in the structural relationship expressed in equation (C.1). We rewrite it, but substituting in the investment relationship from equation (C.2) to obtain an estimable expression:

$$
\begin{aligned}
y_i = {} & G_i \varphi_1 + \left[S_i \rho_1 + G_i \rho_2 + G_i^P \rho_3 + v_i \right] \varphi_2 \\
& + \left(G_i \times \left[S_i \rho_1 + G_i \rho_2 + G_i^P \rho_3 + v_i \right] \right) \varphi_3 + \varepsilon_i \\
= {} & G_i (\varphi_1 + \rho_2 \varphi_2) + S_i \rho_1 \varphi_2 + (G_i \times S_i)\rho_1 \varphi_3 \\
& + G_i^P \rho_3 \varphi_2 + G_i^2 \rho_2 \varphi_3 + G_i G_i^P \rho_3 \varphi_3 + v_i \varphi_2 + G_i v_i \varphi_3 + \varepsilon_i \tag{C.4}
\end{aligned}
$$

Next, recognize that $G_i^P = \frac{G_i - e_i}{\alpha}$. Thus, we can rewrite the outcome as:

$$
\begin{aligned}
y_i = {} & G_i(\varphi_1 + \rho_2\varphi_2) + S_i\rho_1\varphi_2 + (G_i \times S_i)\rho_1\varphi_3 \\
& + G_i\frac{\rho_3\varphi_2}{\alpha} + G_i^2\rho_2\varphi_3 + G_i^2\frac{\rho_3\varphi_3}{\alpha} + v_i\varphi_2 + G_iv_i\varphi_3 + \varepsilon_i \\
& - e_i\frac{\rho_3\varphi_2}{\alpha} - G_ie_i\frac{\rho_3\varphi_3}{\alpha}
\end{aligned}
\tag{C.5}
$$

Simplifying, leads us to the following estimable expression:

$$
\begin{aligned}
y_i &= G_i\kappa_1 + S_i\kappa_2 + (G_i \times S_i)\kappa_3 + G_i^2\kappa_4 + \xi_i \\
\kappa_1 &= \varphi_1 + \rho_2\varphi_2 + \frac{\rho_3\varphi_2}{\alpha} \\
\kappa_2 &= \rho_2\varphi_2 \\
\kappa_3 &= \rho_1\varphi_3 \\
\kappa_4 &= \rho_2\varphi_3 + \frac{\rho_3\varphi_3}{\alpha} \\
\xi_i &= v_i\varphi_2 - e_i\frac{\rho_3\varphi_2}{\alpha} + G_iv_i\varphi_3 - G_ie_i\frac{\rho_3\varphi_3}{\alpha} + \varepsilon_i
\end{aligned}
\tag{C.6}
$$

The final equation is similar to the type of equations we estimate. Estimated parameters are related to the parameters of interest in equation (C.1). To simplify the discussion, we assume that $\varphi_1 > 0$ (the impact of G_i on y_i is positive) and $\varphi_2 > 0$ (the impact of investments on y_i are positive). We also maintain the assumptions that $\rho_1 > 0$ (higher SES translates to higher investments) and $\rho_3 > 0$ (parents with more advantageous genetic endowments invest more in their children even after we have controlled for SES). Finally, we recognize that parent and child genetic endowments are positively correlated ($\alpha > 0$).

The following are true.

1. We over-estimate the positive impact of G_i on y_i ($\kappa_1 > \varphi_1$) if $\rho_2\varphi_2 + \frac{\rho_3\varphi_2}{\alpha} > 0$. This holds if $\rho_2 \geq 0$. If $\rho_2 < 0$, the direction of bias cannot be signed.
2. We over-estimate φ_2 if $\rho_2 > 1$. If $\rho_2 < 1$, then we under-estimate it.
3. As long as SES predicts actual investments ($\rho_1 > 0$), the sign of κ_3 is the same as the sign of φ_3. In other words, we estimate the correct sign of φ_3, which governs whether the polygenic score and investments in human capital are complements or substitutes. This is important as we are particularly interested in understanding how heterogeneity in genetic endowments is mitigated human capital investments.
4. The estimating equations should control for a second-order polynomial in genetic score. This controls for how genetic score affects y_i both directly and through its impact on mis-measured investments.
5. Estimating equations should take account of heteroskedasticity since the variance of ξ_i is a function of G_i.

One of the key results of this exercise is to show that we can identify the correct sign of φ_3, which governs interactions between endowments and investments, which

are measured using child SES. We obtain the correct sign even though SES, genes and parent genes can all affect investments. Here, we show that our ability to identify the sign of φ_3 rests on the fact that the polygenic score is not affected by investments. Suppose instead that we use a traditional proxy for ability or cognition endowments, such as cognitive test scores, which are affected by investments. In this case, we can no longer identify the sign of φ_3. We illustrate this point with a simpler version of the model. Once again, our goal is to estimate the parameters in equation (C.1). We add two more equations to the system: a simplified version of the investment equation and an equation relating cognitive test scores (denoted C_i) to genes and investments. The investment equation is

$$I_i = S_i \gamma_1 + G_i \gamma_2 + v_i^I \tag{C.7}$$

Here, we have dropped parent genes G_i^P for ease of exposition. Cognitive test scores are explained by:

$$C_i = I_i \alpha_1 + G_i \alpha_2 + v_i^C \tag{C.8}$$

This means that a cognitive test score is a function of investments I_i and genes G_i. The next step is to solve for G_i and I_i as functions of observable variables S_i and C_i, which are then substituted into equation (C.1) to obtain an estimable expression. The estimable expression is similar to equation (C.1), but in place of G_i, we have C_i:

$$y_i = C_i \delta_1 + S_i \delta_2 + (C_i \times S_i)\delta_3 + v_i^Y \tag{C.9}$$

It can be shown that $sign(\delta_3) = sign(\varphi_3)$ if $\frac{\alpha_2}{\alpha_1} + \gamma_2 > 2\gamma_1$. The interpretation is that if factors other than genetics are important in explaining C_i, we are more likely to mis-estimate the sign of φ_3.

Appendix D: Cognitive Test Scores

A natural question to ask is how the polygenic score relates to more typical proxies for ability, such as cognitive test scores. Fortunately, we are able to compare cognitive test scores to the polygenic score. The HRS features a number of items related to cognition, including two memory tests, two simple math exercises, and eight general knowledge questions, which have been used in prior literature as a measure of cognition (McArdle et al. 2009).

Each memory test is scored out of ten, for a total of twenty possible points. Subjects' memory was tested using a list of ten common nouns. They were asked to recall as many of the nouns as possible both immediately after the list was read and after a predetermined set of survey questions (or about five minutes). The math exercises account for seven points: two awarded for correctly counting back from 20 to 10 on the first try (or one on a second try), and one each for 5 rounds of correctly subtracting 7 from 100. Eight points are scored by correctly naming the day of the week, date, month, and year, the objects "people usually use to cut paper" and the "kind of prickly plant that grows in the desert", and the sitting President and Vice President.

Our specific measure of cognitive functioning comes from the *Imputation of Cognitive Functioning Measures* file of the HRS. Specifically, we use the imputed "Total Cognition Summary Score" for each wave. This score aggregates the previously mentioned cognition measures and takes values between 0-35. To remove the effects of age and gender, we regress all observations of the total cognition score for genetic Europeans on a male dummy, a quartic in age, and an interaction between male and the quartic age terms. We then average the residuals for each individual and standardize this average so that it has zero mean and a standard deviation of one.

We plot the distribution of the cognition score in Figure D.1. Similar to the EA score (refer back to Figure 2), the cognition score is approximately normally distributed. The correlation between cognition score and EA score is positive but modest ($\rho = 0.23$). A scatter plot indicates this weak positive correlation (Figure D.2).

We next assess whether the EA score and the cognition score exhibit similar relationships with educational attainment. Table D.1 presents specifications that add the cognition score to our basic set of regressions explaining educational attainment from Table 2. Both the EA score and the cognition score exhibit a substantial, highly significant statistical relationship with educational attainment. Since the two scores are somewhat correlated, the coefficient on the EA score does drop somewhat when the cognition score is added. In the full specification with all SES controls, the coefficient on the EA score is 0.458 compared to 0.587 in the same specification without the cognition score (compare the coefficient attached to EA score in Column (5) of Table 2 from the main text with the analogous coefficient in Column (5) of Table D.1 in this appendix). The relationship between the cognition score and education is sizable, with a one standard deviation increase in the cognition score being associated with an increase of educational attainment of 0.702 years.

In Table D.2, we re-estimate our specifications that interact the EA score with SES measures in predicting a degree at or above five different thresholds. Here we also add the cognition score, and an interaction between the cognition score and the SES measure in each specification. Adding the cognition interactions does not change our conclusions about the pattern and significant of interactions between the EA score and childhood SES.

Finally, Table D.3 repeats some key earnings specifications while also controlling for the cognition score and interactions between the cognition score and other regressors. In particular, the EA score remains a significant predictor of earnings even after controlling for cognition and education. Interestingly, while we find evidence that the association between earnings and the EA score rose after 1980, we find no evidence of this interaction with the cognition score. This suggests that the two measures may reflect distinct bundles of traits or skills.

TABLE D.1. Polygenic Score, Cognition Score, and Educational Attainment

	(1)	(2)	(3)	(4)	(5)
EA Score	0.615***	0.478***	0.475***	0.458***	0.458***
	(0.045)	(0.043)	(0.042)	(0.044)	(0.031)
Cog. Score	0.914***	0.727***	0.726***	0.710***	0.702***
	(0.060)	(0.055)	(0.056)	(0.053)	(0.035)
Father Educ		0.126***	0.126***	0.090***	0.094***
		(0.013)	(0.013)	(0.015)	(0.012)
Mother Educ		0.136***	0.135***	0.117***	0.119***
		(0.015)	(0.015)	(0.015)	(0.014)
Obs.	8470	8470	8470	8470	8470
R^2	0.346	0.414	0.415	0.431	0.568
Child SES Measures	N	N	Y	Y	Y
Child Region	N	N	N	Y	Y
Religion	N	N	N	N	Y

Regressions relating educational attainment (years) to the EA score and the cognition score. All regressions include a full set of dummy variables for birth year, a male dummy and a full set of interactions between the birth year and gender dummies. All specifications include the first 10 principle components of the full matrix of genetic data as controls. Some specifications include controls for parental education, childhood health, childhood SES measures, region during childhood and religion, as indicated.
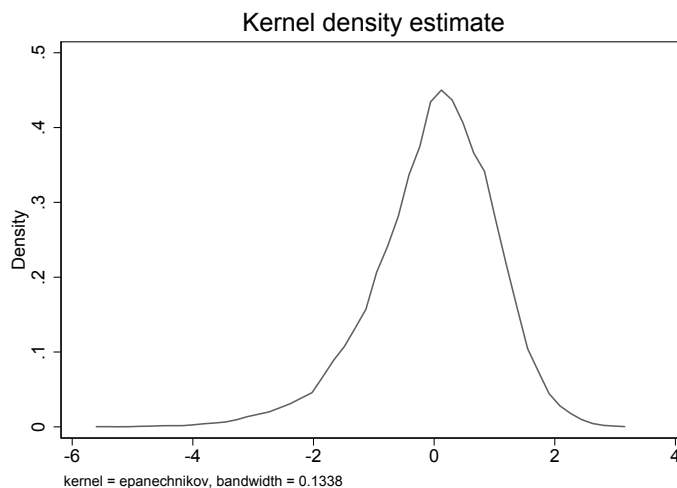

FIGURE D.1. Distribution of cognitive test scores (cognition score), which is the standardized individual-level average residual from a regression of cognition on age

TABLE D.2. Polygenic Score, Cognition Score, and Interactions with SES

Dep Var: At Least	(1) H.S. Equiv	(2) High School	(3) Two Yr.	(4) College	(5) Grad
Panel A: SES Measure - Father Occ. Income					
High SES	0.038***	0.048***	0.065***	0.072***	0.028***
	(0.010)	(0.011)	(0.013)	(0.012)	(0.008)
EA Score	0.041***	0.041***	0.088***	0.078***	0.017**
	(0.013)	(0.015)	(0.014)	(0.012)	(0.009)
EA Score × High SES	-0.014	-0.017	0.040***	0.053***	0.020**
	(0.011)	(0.013)	(0.013)	(0.012)	(0.009)
Obs.	6705	6705	6705	6705	6705
R^2	0.334	0.310	0.283	0.287	0.138
Panel B: SES Measure - Family Well Off					
High SES	0.038***	0.059***	0.044***	0.055***	0.018**
	(0.013)	(0.014)	(0.014)	(0.013)	(0.009)
EA Score	0.051***	0.080***	0.034**	0.031**	0.005
	(0.013)	(0.015)	(0.014)	(0.012)	(0.008)
EA Score × High SES	-0.005	-0.023*	0.049***	0.057***	0.028***
	(0.012)	(0.014)	(0.013)	(0.011)	(0.008)
Obs.	8321	8321	8321	8321	8321
R^2	0.312	0.300	0.259	0.271	0.137
Panel C: SES Measure - Move or Asked for Help					
High SES	0.029**	0.054***	0.085***	0.103***	0.034***
	(0.012)	(0.014)	(0.015)	(0.013)	(0.010)
EA Score	0.028**	0.050***	0.016	0.026**	0.003
	(0.014)	(0.015)	(0.014)	(0.012)	(0.008)
EA Score × High SES	0.005	-0.018	-0.003	-0.006	0.008
	(0.012)	(0.014)	(0.014)	(0.012)	(0.009)
Obs.	8298	8298	8298	8298	8298
R^2	0.309	0.294	0.256	0.268	0.136
Panel D: SES Measure - Father Unemployed					
High SES	0.043***	0.058***	0.059***	0.083***	0.030***
	(0.011)	(0.013)	(0.016)	(0.013)	(0.010)
EA Score	0.011	0.029**	0.023	0.030**	0.009
	(0.013)	(0.014)	(0.014)	(0.012)	(0.008)
EA Score × High SES	-0.014	-0.023*	0.029**	0.019	0.012
	(0.011)	(0.013)	(0.014)	(0.012)	(0.009)
Obs.	8336	8336	8336	8336	8336
R^2	0.306	0.291	0.254	0.266	0.134

Regressions relating educational attainment categories to the EA score, the cognition score and childhood SES along with interactions between the EA score and high SES. Regressions also include a full set of dummy variables for birth year, a male dummy and a full set of interactions between the birth year and gender dummies. Additionally, every specification includes the first 10 principle components of the full matrix of genetic data and controls for parental education (years of paternal and maternal education and dummies indicating missing values for each). Every specification includes the cognition score and an interaction between the cognition score and the High SES indicator.

TABLE D.3. Polygenic Score, Cognitive Score, and Earnings

Dep Var.: log SSA Earnings Basic Specifications	(1)	(2)	(3)	(4)
EA Score	0.057***	0.029***	0.023**	0.007
	(0.009)	(0.009)	(0.010)	(0.007)
EA Score × College			0.011	
			(0.020)	
EA Score × Post 1980				0.039***
				(0.012)
Cog. Score	0.088***	0.042***	0.059***	0.031***
	(0.010)	(0.010)	(0.011)	(0.008)
Cog. Score × College			-0.060**	
			(0.025)	
Cog. Score × Post 1980				0.020
				(0.013)
College × Post 1980				0.249***
				(0.030)
Obs.	95945	95945	95734	95734
R^2	0.168	0.195	0.200	0.210
Age Group	25-64	25-64	25-64	25-64
Period	All Years	All Years	All Years	All Years
Educ. Controls	N	Y	Y	Y
Parent Controls	N	Y	Y	Y

Regressions relating the EA score and the cognition score to log earnings. In all specifications, we restrict the sample to earnings records for men between the ages of 25 and 64 over the years 1951-2013 in which the respondent earns more than $10,000 in real 2010 dollars. In Column (4), the sample is narrowed to cover person-years in which respondents are aged between 40 and 64. In Columns (5), the sample again includes all ages 25-64, but is now restricted to years 1980-2013. The dependent variable is the the log of real earnings. All regressions include the first 10 principle components of the full matrix of genetic data along with a full set of dummy variables for birth year, calendar year and age. As noted in the table, the specifications in Columns (2)-(4) include controls for parental education (years of paternal and maternal education and dummies indicating missing values for each) and own education (years of schooling and a full set of completed degree dummies). Standard errors in all specifications are clustered at the person level.
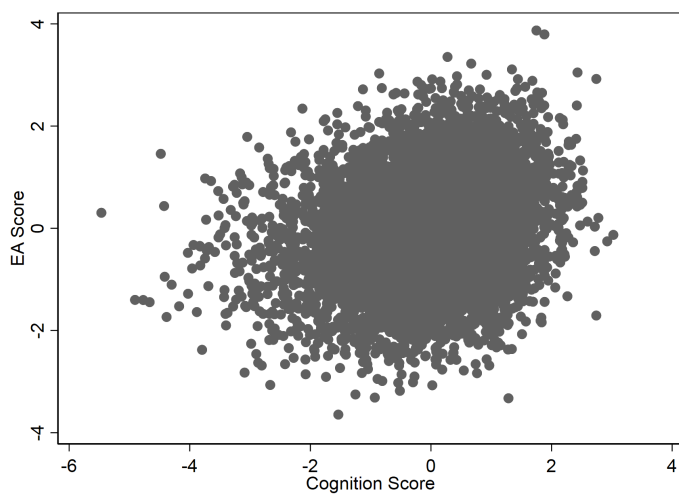
FIGURE D.2. Scatter Plot by Individual of EA Score and Cognition Score.

Appendix E: Construction of Weights and Multiple Hypothesis Testing

E.1. Inverse Probability Weights

To create weights, we first estimate a probit model predicting inclusion in the 2006 or 2008 genetic sample for all HRS respondents as a function of birth year dummies, region of birth dummies, completed degree dummies, years of schooling, father's education, mother's education, separate dummy variables for missing father's or mother's education, and a male dummy. We use the estimates of this model to generate a predicted probability of sample inclusion conditional on these observables:, $\widehat{\pi}_i = \widehat{P}(In\ Sample \mid X_i)$. Let ω_i represent the cross-sectional HRS sampling weight associated with individual i. We multiply these weights by the factor $(1/\widehat{\pi}_i)$ to adjust for non-random selection into the genotyped sample. That is, the sampling weights applied to our sample are $(\omega_i/\widehat{\pi}_i)$. The cross-sectional respondent-level weight generated by the HRS changes across waves as the sample is expanded or reweighted. A major change occurred in 2004, when the weights were post-stratified to match the American Community Survey instead of the smaller March CPS (Staff 2015). Given this change, we set ω_i equal to the first non-zero cross-sectional sampling weight provided in or after the 2004 wave. For a small number of individuals without any non-zero weight matching this criterion, we use the first non-missing household-level weight provided in or after the 2004 wave.

E.2. Multiple Hypothesis Testing

Given the fairly large number of hypotheses tested in this paper, we now consider formal corrections in the p-values of our results to address multiple comparisons. In particular, we split our results into two families of new hypotheses: (i) Interactions between the EA score and SES measures in predicting completed degrees; and (ii) Associations between the EA score and labor market outcomes above and beyond completed schooling. Figure 6 summarizes our results for Family 1, which consists of 20 hypothesis tests, based on the use of four distinct SES measures each interacted with the EA score in predicting five different degree outcomes. Family 2 consists of regression results on earnings as well as job tasks. Family 2 includes the regression on log earnings on the EA score after controlling for education, the regression of log earnings on the EA score and an interaction between the score and the college dummy variable, the regression of the log earnings on the EA score and an interaction between the score and a post-1980 indicator, and the regression of log earnings on the EA score and an interaction between the score and a post-1942 birth year indicator. In addition to these four earnings hypotheses, we also include ten hypotheses related to job tasks. In addition to the five hypotheses contained in Table 6, we also include five more

specifications analogous to those in 6, but using dummies for above median values of the job tasks as the dependent variable.[5]

We correct for multiple comparisons in two ways. First, we apply a Bonferroni correction by multiplying the p-values by the number of hypotheses tested. We do this both within the two families separately (20 hypotheses and 14 hypotheses, respectively), and for the combined family of all hypotheses (34 hypotheses). We also correct for multiple comparisons using the bootstrap procedure developed by Romano and Wolf (2005) and elaborated in Romano and Wolf (2016). We again apply this procedure separate to each family, and we also apply the procedure to the meta-family of all 34 hypotheses.

Table E.1 lists our 34 hypotheses and indicates the dependent variable and coefficient of interest involved in the test. We report the original p-values for each test, as well as the Bonferroni and Romano-Wolf corrected p-values. We find strong evidence for interactions between the EA score and at least two SES measures (Father's Income and Family Well Off) in predicting a college degree, even when applying the Bonferroni correction. The negative interaction between the EA score and the Family Well Off in predicting the high school outcome survives as marginally significant in the within-family corrections. The significance of the association between log earnings and the EA score (conditional on education) survives all corrections, and we find a significant p-value for the hypothesis on the interaction between the EA score and the post-1980 indicator in predicting earnings (p-value<0.10 in all corrections and p-value<0.05 in the within-family corrections). The result relating the EA score to the non-routine analytic task intensity (Task 1) survives as marginally significant in the omnibus corrections (p-value<0.10), and significant in the within-family corrections (p-value<0.05).

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5. In a previous version of the paper, we used the median-based measure, but switched to using standardized job tasks in this draft. We include all of these specifications in this family for the purpose of corrections for multiple comparisons.

TABLE E.1. Corrections for Multiple Hypothesis Testing

Hyp. Num.	Dep. Var.	Coeff.	Original p−value	Bonferroni All Hyp.	Bonferroni in Family	Romano-Wolf All Hyp.	Romano-Wolf in Family
Family 1: SES Interactions							
(1)	HS Equiv.	EA Score × Fam Well Off	0.139	1.000	1.000	0.823	0.522
(2)	HS	EA Score × Fam Well Off	0.005	0.166	0.098	0.160	0.101
(3)	Two Yr.	EA Score × Fam Well Off	1.2e-05	4.24e-04	2.49e-04	0.001	0.001
(4)	College	EA Score × Fam Well Off	7.9e-08	2.7e-06	1.6e-06	0.001	0.001
(5)	Grad	EA Score × Fam Well Off	2.95e-04	0.010	0.006	0.018	0.011
(6)	HS Equiv.	EA Score × High Fath. Inc	0.011	0.380	0.223	0.270	0.178
(7)	HS	EA Score × High Fath. Inc	0.036	1.000	0.713	0.508	0.332
(8)	Two Yr.	EA Score × High Fath. Inc	0.002	0.058	0.034	0.087	0.053
(9)	College	EA Score × High Fath. Inc	5.6e-06	1.91e-04	1.12e-04	0.001	0.001
(10)	Grad	EA Score × High Fath. Inc	0.056	1.000	1.000	0.616	0.426
(11)	HS Equiv.	EA Score × Nev. Move/Ask	0.864	1.000	1.000	0.999	0.904
(12)	HS	EA Score × Nev. Move/Ask	0.036	1.000	0.714	0.508	0.332
(13)	Two Yr.	EA Score × Nev. Move/Ask	0.570	1.000	1.000	0.998	0.904
(14)	College	EA Score × Nev. Move/Ask	0.667	1.000	1.000	0.999	0.904
(15)	Grad	EA Score × Nev. Move/Ask	0.169	1.000	1.000	0.852	0.522
(16)	HS Equiv.	EA Score × Nev. Unemp.	0.094	1.000	1.000	0.756	0.510
(17)	HS	EA Score × Nev. Unemp.	0.017	0.571	0.336	0.337	0.234
(18)	Two Yr.	EA Score × Nev. Unemp.	0.014	0.486	0.286	0.321	0.214
(19)	College	EA Score × Nev. Unemp.	0.025	0.845	0.497	0.432	0.285
(20)	Grad	EA Score × Nev. Unemp.	0.100	1.000	1.000	0.756	0.510
Family 2: Earnings and Tasks							
(21)	log. Earnings	EA Score	0.001	0.017	0.007	0.033	0.016
(22)	log. Earnings	EA Score × College	0.428	1.000	1.000	0.987	0.955
(23)	log. Earnings	EA Score × Post 1980	0.002	0.077	0.032	0.095	0.044
(24)	log. Earnings	EA Score × BY > 1942	0.650	1.000	1.000	0.999	0.988
(25)	> Med. Task 1	EA Score	0.001	0.023	0.010	0.040	0.020
(26)	> Med. Task 2	EA Score	0.006	0.221	0.091	0.192	0.080
(27)	> Med. Task 3	EA Score	0.634	1.000	1.000	0.999	0.988
(28)	> Med. Task 4	EA Score	0.653	1.000	1.000	0.999	0.988
(29)	> Med. Task 5	EA Score	0.958	1.000	1.000	0.999	0.988
(30)	Std. Task 1	EA Score	0.002	0.062	0.026	0.087	0.039
(31)	Std. Task 2	EA Score	0.015	0.503	0.207	0.325	0.144
(32)	Std. Task 3	EA Score	0.367	1.000	1.000	0.982	0.937
(33)	Std. Task 4	EA Score	0.675	1.000	1.000	0.999	0.988
(34)	Std. Task 5	EA Score	0.331	1.000	1.000	0.980	0.928

This table presents p-values using different methods to correct for multiple hypothesis testing.

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