sociological science

Leveraging Genomic Data to Document Within-Race Attractiveness Penalties Among Black Americans

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Abstract: In recent years, scholars of racial inequality have increasingly sought to move beyond simply quantifying *discrete* racial disparities and instead measure social stratification as a function of *continuous* racialized characteristics that vary both within and between racial groups. In this article, we draw on a sample of genotyped respondents from the Add Health study and construct genetic similarity proportions, individual-level measures that correlate with racialized physical features that vary across the expansive family tree of humanity (skin tone, facial structure, hair texture, etc.). We then investigate the relationship between these proportions and interviewer-rated physical attractiveness among self-identified Black Americans (N=2,087). Our findings highlight the existence of substantial attractiveness penalties related to having higher levels of Sub-Saharan African (as opposed to European) genetic similarity.

Keywords: racial inequality; social stratification; physical attractiveness; biodemography; genetic ancestry; human genomics

Reproducibility Package: All results needed to evaluate the conclusions in the article are present in the article and/or the Supplementary Materials. All syntax files needed to replicate our main text analyses are available at the following link: https://github.com/luyin-z/attractiveness_penalties. We utilized the restricted Add Health survey and genotype data, which can be accessed by researchers via application at https://data.cpc.unc.edu/projects/2/view.

Citation: Taddess, Beza, Luyin Zhang, and Sam Trejo. 2026. "Leveraging Genomic Data to Document Within-Race Attractiveness Penalties Among Black Americans" Sociological Science 13: 802-824.

Received: March 24, 2026

Accepted: May 13, 2026

Published: July 7, 2026

Editor(s): Ari Adut, Ellis Monk

DOI: 10.15195/v13.a31

A LARGE body of empirical research documents average disparities between White and Black Americans in a host of valued outcomes, ranging from childhood educational opportunity (Reardon, Kalogrides, and Shores 2019) to success in the dating market (Bruch and Newman 2018) to life expectancy (Wrigley-Field 2020). In recent years, however, scholars of racial inequality have increasingly sought to move beyond simply quantifying *discrete* disparities—for instance, the average difference in a variable of interest between two racial groups (e.g., the Black–White achievement gap)—to instead measure social stratification as a function of *continuous* racialized characteristics (Monk 2022; Sen and Wasow 2016),[1] which vary both within and between racial groups (e.g., skin tone; Santana 2024). An overemphasis on discrete racial categories can serve to obscure meaningful within-race inequalities, whereas shifting the focus to various racialized characteristics highlights that there exists variation in how individuals with the same racial identity experience race and its consequences. Though this line of inquiry offers much promise, studies of racialized characteristics have, thus far, faced two key methodological challenges: (i) it is difficult to know *a priori* which specific individual-level physical and social characteristics have become imbued with racial meaning and stigma and (ii) a relatively limited number of racialized characteristics (often measured with substantial error) are currently available in existing

nationally representative data sources.[2] To address these challenges, and in light of the increased availability of molecular genetic data, we propose a new tool for the empirical exploration of racial stratification: genetic similarity proportions (GSPs).

GSPs (National Academies of Sciences, Engineering, and Medicine 2023), also known as genetic ancestry proportions, have a wide range of applications in human genomics, including in the study of gene–ancestry interaction effects (Patel et al. 2022; Wojcik et al. 2019) and in the analysis of historical human admixture events (Haak et al. 2015). (Genetic admixture refers to genomic mixing of previously isolated populations.) However, recent social scientific research has demonstrated that GSPs may also be used to index variation in racialized physical features in the United States today (Trejo and Thompson 2025; Zhang and Trejo 2025, 2026). GSPs, which are readily constructed from genotype and/or sequence data, provide estimates of the fraction of a person's DNA that is categorized into various (often geographically defined) genomic reference populations (Browning, Waples, and Browning 2023; Tan and Atkinson 2023). Notably, GSPs vary continuously among admixed populations (such as Black and Hispanic Americans), are fixed at birth, and are estimated with little measurement error.[3] Moreover, the use of GSPs does not require researchers to prespecify which specific racialized characteristics might be relevant to a given social process; because racial ideologies are socially constructed using physical features that vary across the expansive family tree of humanity (Mathieson and Scally 2020; Trejo and Martschenko 2026), variation in GSPs will tend to capture phenotypic variation in these characteristics.[4]

Note, although race and ancestry are often conflated, they are nonetheless conceptually distinct. Race refers to a dynamic social process through which discrete identity groups are constructed and enforced across time, often to maintain social hierarchies. Ancestry, on the other hand, encompasses our genealogical and genomic link to others—the single family tree shared by all of humanity. We view efforts to leverage the empirical distribution of genetic variation to challenge or deny the social construction of race as an intellectual dead end.[5] Instead, in this article, we ask whether it is possible to leverage DNA to better measure and understand the consequences of racial construction in contemporary America.

In particular, we use GSPs to explore social stratification in externally rated physical attractiveness. Historically, sex-specific selection on attractiveness may have played an important role in the evolution of humans (Perrett et al. 1998), and, in the modern era, there are significant social advantages to being viewed as physically attractive (Maestripieri, Henry, and Nickels 2017; Mulford et al. 1998). Individuals perceived to be attractive tend to marry earlier (Jæger 2011), earn more (Abascal and Garcia 2022; Fletcher 2009; Hamermesh and Biddle 1994; Monk, Esposito, and Lee 2021; Scholz and Sicinski 2015; Wong and Penner 2016), live longer (Sheehan and Hamermesh 2024), and report higher subjective well-being than their less attractive counterparts (Hamermesh and Abrevaya 2013). Notably, exactly which physical features are viewed as attractive is subjective and culturally dependent, with past work documenting the existence of variation in preferences across the globe (Zhan et al. 2021). A recent analysis of dating app data found that Black Americans were the only racial group where both men and women were systematically viewed as less desirable than their White counterparts (Bruch and Newman 2018).

Past work on racialization and attractiveness has largely relied on interviewer-reported measures of physical features. However, such measures are inherently relational—reflecting one person's perception at a single point in time—and are therefore impacted by rater heterogeneity, contextual factors, and measurement error (Garcia and Abascal 2016; Hannon and DeFina 2016). Thus, while interviewer-reported measures may capture how respondents are seen by a specific interviewer at the time of the interview, they do not necessarily reflect how respondents are typically perceived by the broader social world. In contrast, an individual's genome—and, so too, any prespecified transformation of the genome—is stable across the life-course. In this way, GSPs provide a reference point which allows us to identify individuals who share a racial/ethnic identity but nonetheless differ in ancestral background (and, likely, physical appearance).

We draw on a sample of genotyped Americans from the National Longitudinal Study of Adolescent to Adult Health (Add Health) and construct GSPs linked to present-day populations from four global geographic regions (Auton et al. 2015; Byrska-Bishop et al. 2022; Bergström et al. 2020): Sub-Saharan Africa (P^{AFR}), Europe (P^{EUR}), East Asia (P^{EAS}), and Indigenous America (P^{IAM}). Then, we empirically test whether—among members of a single self-identified racial group—individuals with certain GSPs are systematically viewed as more attractive than others. While the bulk of our analyses focus on within-race variation in GSPs among Black Americans, the empirical results we present nonetheless inform understandings of average between-race disparities.

Our analysis sits in close conversation with prior work on racialization and perceived physical attractiveness. In particular, Monk, Esposito, and Lee (2021) document positive returns to physical attractiveness on earnings, with the strongest gradient observed among Black men and women. Our study builds on these results by investigating the factors that structure variation in attractiveness ratings among Black Americans—that is, why certain Black individuals are perceived as more attractive than others. We place Monk, Esposito, and Lee's (2021) observation that attractiveness ratings vary by skin tone within racial groups at the center of our analysis and explore the extent to which racialized physical features beyond skin tone—captured by GSPs—also shape perceptions of attractiveness.

Building on this engagement with prior work, our study makes multiple important contributions. First, we provide robust empirical evidence of racialized stratification in attractiveness among Black Americans, with individuals with higher amounts of Sub-Saharan African (as opposed to European) genetic similarity receiving the lowest ratings; this result implies that racial attractiveness disparities arise—not merely due to stigmatization of individuals based on their perceived race—but also due to a broader societal stigmatization of the physical features associated with Blackness. Second, our results point to methodological issues with survey-based physical attractiveness ratings and suggest such measures likely substantially understate the true magnitude of Black–White attractiveness disparities. Third, we demonstrate that GSPs represent a new tool for social scientists interested in studying racial inequality. Finally, our results have important implications for the interpretation of genome-wide association study results for complex traits, particularly among admixed populations.

Data and Methods

Add Health

The National Longitudinal Study of Adolescent to Adult Health (Add Health) is a longitudinal survey of a nationally representative sample of 20,745 middle and high school students in the United States (Harris et al. 2019). The initial wave was fielded in the 1994–1995 school year (wave I), followed by four additional waves of in-home interviews in 1996 (wave II), 2001–2002 (wave III), 2008 (wave IV), and 2016–2018 (wave V). At each wave, a rich set of sociodemographic, behavioral, psychosocial, familial, and contextual information was collected. Interviewers each surveyed an average of 25 respondents at each wave, and there was an average of approximately 4 days between each interview (see Fig. S1 in the online supplement). Approximately 80 percent of the respondents who participated in wave IV provided saliva samples and were genotyped using two Illumina platforms—Illumina Human Omni1-Quad BeadChip and Illumina Human Omni-2.5 Quad BeadChip. Rigorous quality control procedures were applied by the Add Health staff at both the SNP-level and the individual-level; in particular, SNPs with call rates $<$ 90 percent, minor allele frequency $<$ 0.5 percent, and deviations from Hardy–Weinberg equilibrium ($p < 5 \times 10^{-5}$) were removed, and individuals with call rates $<$ 90 percent and genetic sex discordance were removed. The final genotype data cover 609,130 SNPs for 9,974 individuals. Table S1 in the online supplement provides detailed descriptive statistics for our Add Health analytic sample, and Table S2 in the online supplement provides descriptive statistics of the Add Health interviewers. The Add Health interviewers of Black respondents tend to be highly educated (36 percent some college; 52 percent B.A. or above), and the majority identify as either White (56 percent) or Black (38 percent).

Genetic Similarity Proportions

We use supervised ADMIXTURE (Alexander and Lange 2011; Shringarpure et al. 2016) with $K = 4$ to estimate global GSPs for each genotyped Add Health respondent. Our four reference panels are, in order: 634 individuals from 12 populations in Sub-Saharan Africa ("AFR"), 680 individuals from 13 populations in Europe ("EUR"), 729 individuals from 23 populations in East Asia ("EAS"), and 61 individuals from 5 populations indigenous to the Americas ("IAM"). These reference panels consist of unrelated individuals retrieved from the 1000 Genomes Project (Auton et al. 2015; Byrska-Bishop et al. 2022; Sub-Saharan Africa, Europe, and East Asia) and the Human Genome Diversity Project (Bergström et al. 2020; Sub-Saharan Africa, Europe, East Asia, and Indigenous America). The geographic location of each reference panel is visually displayed in Figure S2 in the online supplement. We restrict to autosomal SNPs that are present in both the Add Health genotype data and our reference panels. After implementing linkage disequilibrium pruning (with a window size of 200 kb, a step size of 25, and an R^2 of 0.4) in PLINK1.9 (Chang et al. 2015), we retain 275,794 SNPs. Because the Add Health data contain siblings and half-siblings, we remove a random respondent from each pair to create a subsample of 9,166 unrelated respondents; all estimates were then projected for the remaining 808 genotyped respondents. Note that P^{AFR}, P^{EUR}, P^{EAS}, and P^{IAM} mechanically

sum to one for each individual. Unsupervised ADMIXTURE analysis recovers almost identical GSPs as our supervised ADMIXTURE estimates (see Fig. S3 from Zhang and Trejo 2026). Moreover, results from local genetic similarity estimation software, when summed across the genome, are highly comparable to those from ADMIXTURE (see Fig. S10 from Zhang and Trejo 2026). Finally, past research using highly similar methods has shown that, in U.S. samples, the resulting GSPs closely correspond to the global information provided by popular genetic ancestry tests (see Fig. S14 from Bryc et al. 2015 for a comparison with 23andMe). We focus our main text and supplementary analyses on Black Americans and Hispanic Americans due to the fact that these two racial groups—in contrast to White Americans—exhibit substantial within-group variation in GSPs. In addition, our sample size of Asian Americans is simply too small for rigorous subgroup analysis.

Survey Measures

Physical attractiveness: At wave I (age 12–21), wave II (age 13–22), wave III (age 18–26), and wave IV (age 24–32), Add Health interviewers were asked to rate the physical attractiveness of each respondent using a Likert scale with five categories (1 = "very unattractive," 2 = "unattractive," 3 = "about average," 4 = "attractive," and 5 = "very attractive"). To aid in the interpretation of our attractiveness score variable, we standardize it using the weighted mean and standard deviation (SD) ($\mu = 3.44,\ \sigma = 0.82$) of the full Add Health sample.

Racial identity: We construct a categorical variable of the single racial identity that best describes a respondent's racial background using information collected in wave III. (In the rare event that an individual's wave III racial identity information is missing, we supplement with racial identity information collected at waves I and V.) The wave III Add Health self-reported race measure includes four categories: White, Black, Native American, and Asian/Pacific Islander. We intersect categorical responses from the racial identity question with binary responses to a Hispanicity question to create the following five mutually exclusive racial categories: non-Hispanic White (NHW), non-Hispanic Black (NHB), non-Hispanic Native American, non-Hispanic Asian/Pacific Islander (AAPI), and Hispanic American. Thus, when we refer to "Black Americans" and "White Americans," we are describing the group of individuals who self-identify as Black or White and who do *not* also self-identify as Hispanic. Due to the group's limited sample size (N = 68), we do not present results regarding self-identified non-Hispanic Native Americans.

Physical features: We rely on interviewer-reported measures from wave III to create categorical measures of physical features, including skin tone (black, dark brown, medium brown, light brown, and white), hair color (no hair, black, brown, blond, red, gray, and other), and eye color (black, brown, hazel, blue, green, and other).

Racial classification: Interviewer's racial classification of the respondent, coded based on their observation alone, was collected in waves I, III, and IV and contains the following five categories: White, Black, Native American, Asian/Pacific Islander, and others.

Socioeconomic variables: For our childhood socioeconomic status variable, we use the first principal component of wave I parental education, parental occupation, household income, and household receipt of public assistance (constructed by Belsky et al. 2018). For our neighborhood socioeconomic disadvantage variable, individuals are matched to the American Community Survey data of the census tract of their wave I home address; deciles of five tract-level variables—proportions of female-headed households, individuals living below the poverty threshold, individuals receiving public assistance, adults with less than a high school education, and adults who were unemployed—were totaled for each tract and then standardized within-sample (see Belsky et al. 2019 for more details).

Regression Analysis

We use multivariate regression analysis to assess the relationship between an individual's GSPs and their attractiveness rating. First, we treat attractiveness as a continuous variable and fit the following linear regression model for individual i observed at age j by interviewer k:

$$\begin{aligned} attractiveness_{ijk} = \delta_j + \gamma_k + \sum_{n=1}^{4}\left(\alpha_n race_{ijk}^n\right) \\ + \sum_{n=1}^{4}\sum_{m=1}^{3}\left(\beta_{n,m} race_{ijk}^n \times P_{ijk}^m\right) + \sum_{n=1}^{4}\left(race_{ijk}^n \times \mathbf{W}_{ijk}\mathbf{\Phi}\right) + \varepsilon_{ijk}, \end{aligned} \tag{1}$$

where $attractiveness_{ijk}$ represents the interviewer-rated attractiveness score of individual i at age j by interviewer k, δ_j denotes age fixed effects, γ_k denotes interviewer fixed effects, $race_{ijk}^n$ represents a binary variable for whether individual i self-identifies as race n, P_{ijk}^m represents the mth GSP of individual i, and $\mathbf{W}_{ijk}$ is a vector of covariates. P^{EUR} is the omitted GSP. The $\beta_{n,m}$ estimates are our coefficient of interest and capture the relationship between a given GSP m and attractiveness among individuals who self-identify as race n.

We also fit analogous logistic regression models, except with the outcome variable instead being $very - attractive_{ijk}$, a dichotomous variable for whether the interviewer rated the respondent as the highest attractiveness category ("very attractive"):

$$\begin{aligned} \ln\left(\frac{\mathbb{P}\left(very - attractive_{ijk} = 1\right)}{1 - \mathbb{P}(very - attractive_{ijk} = 1)}\right) = \delta_j + \gamma_k + \sum_{n=1}^{4}\left(\alpha_n race_{ijk}^n\right) \\ + \sum_{n=1}^{4}\sum_{m=1}^{3}\left(\beta_{n,m} race_{ijk}^n \times P_{ijk}^m\right) \\ + \sum_{n=1}^{4}\left(race_{ijk}^n \times \mathbf{W}_{ijk}\mathbf{\Phi}\right). \end{aligned} \tag{2}$$

For logistic regression models, we report the average marginal effects (AMEs) and estimate their standard errors using fractional weighted bootstrapping (implemented via the *inferences* function in the *marginaleffects* R package).

Importantly, our linear and logistic regression specifications contain no constant term, but we nonetheless utilize omitted categories in both vectors of fixed effects; this allows for the inclusion of dummy variables for all four racial groups—White, Black, Asian/Pacific Islander, and Hispanic—into the regression without introducing multicollinearity. While each interviewer rated an average of 25 total respondents, they interviewed an average of just 5 and 4 Black and Hispanic respondents, respectively; for this reason, we pool fixed effect estimates across races, thereby boosting statistical power and increasing precision. Interviewer identifiers are constructed to be mechanically nested within waves, meaning there is no need to explicitly control for wave fixed effects.

Finally, we decompose the $\beta_{n,m}$ estimates from Equations (1) and (2) by interacting our coefficient of interest with a vector of S mutually exclusive subgroup variables, which we call sub^{o}_{ijk}:

$$attractiveness_{ijk} = \delta_j + \gamma_k + \sum_{n=1}^{4} (\alpha_n race^{n}_{ijk}) + \sum_{n=1}^{4}\sum_{m=1}^{3}\sum_{o=1}^{S} \left(\beta_{n,m,o} race^{n}_{ijk} \times P^{m}_{ijk} \times sub^{o}_{ijk}\right) + \varepsilon_{ijk}, \tag{3}$$

$$\ln\left(\frac{\mathbb{P}\left(very-attractive_{ijk}=1\right)}{1-\mathbb{P}(very-attractive_{ijk}=1)}\right) = \delta_j+\gamma_k+\sum_{n=1}^{4}\left(\alpha_n race^{n}_{ijk}\right) + \sum_{n=1}^{4}\sum_{m=1}^{3}\sum_{o=1}^{S}\left(\beta_{n,m,o} race^{n}_{ijk} \times P^{m}_{ijk} \times sub^{o}_{ijk}\right). \tag{4}$$

The subgroup variables include interviewer race (White, Black, or others), interviewer gender, interviewer age (under 55 vs. 55 and above), respondent gender, respondent age (i.e., the average age at each Add Health wave, combining waves I and II), and respondent census region (West, Midwest, South, or Northeast). We focus on decompositions of our unconditional models (i.e., models with no covariates) to maximize statistical power. For each of our six dimensions, we utilize an omnibus F-test to determine whether all of the subgroup-specific coefficients are statistically identical. To address concerns regarding multiple hypothesis testing, we implement a 5 percent Benjamini–Hochberg false discovery rate correction (Benjamini and Hochberg 1995).

Results

We begin by examining racial disparities in interviewer-rated attractiveness using the Add Health data. Figure 1 contains four bar charts, each of which displays the average attractiveness ratings of four self-identified racial groups: White Americans,

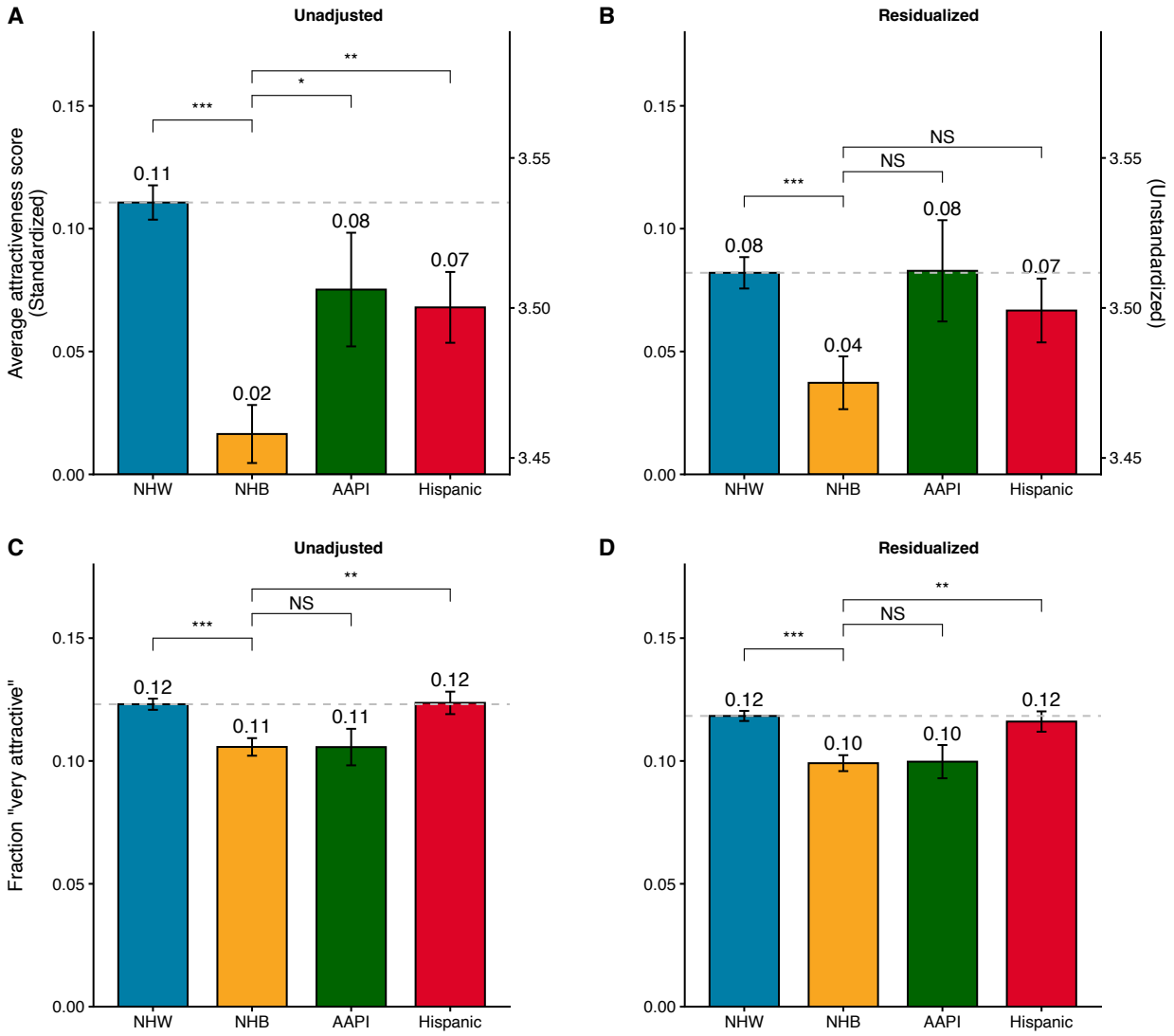

Figure 1: Racial disparities in interviewer-rated attractiveness. This figure displays bar graphs created using data from waves I to IV on 9,902 genotyped respondents of the Add Health study with valid information on racial identity and attractiveness. Self-identified race is collected at wave III, when the respondents were 18–26 years old. The four mutually exclusive racial categories are: Non-Hispanic White (NHW), Non-Hispanic Black (NHB), Non-Hispanic Asian/Pacific Islander (AAPI), and Hispanic. Panels (*A*) and (*B*) display the average Likert attractiveness score (1–5), which is standardized using the weighted mean and standard deviation of the full Add Health sample. Panels (*C*) and (*D*) display the fraction of respondents rated in the very highest attractiveness category ("very attractive"). Panels (*A*) and (*C*) ("Unadjusted") display unadjusted values, whereas panels (*B*) and (*D*) ("Residualized") display values that have been statistically adjusted for interviewer fixed effects. Error bars display 95 percent confidence intervals. Asterisks indicate statistical significance: $^{*}p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$, NS = not significant. See Figure S3 in the online supplement for histograms of the raw physical attractiveness ratings in waves I–IV and see Figure S4 in the online supplement for an analogous bar chart broken out by respondent-interviewer racial concordance.

Black Americans, Asian/Pacific Islander Americans, and Hispanic Americans. Figure 1A and B displays each race's average attractiveness score, whereas Figure 1C and D displays the fraction of respondents of a given race rated in the highest attractiveness category ("very attractive"). Figure 1A and C displays unadjusted values, whereas Figure 1B and D displays values that are residualized on interviewer fixed effects. Although White Americans tend to have the highest attractiveness ratings, we observe only small average differences across racial groups—in line with previous work using interviewer-reported survey measures. For instance, the unadjusted difference in the attractiveness score of White and Black Americans is just 0.094 SD, which aligns closely with the 0.08 SD Black–White gap reported by Monk, Esposito, and Lee (2021). These modest results stand in stark contrast to the substantial attractiveness disparities observed in the large-scale revealed preference analyses of dating app data (Bruch and Newman 2018)[6]; fortunately, the results from our subsequent GSP analysis offer some insight into this apparent empirical puzzle.

Next, we turn to our within-race analysis of Black Americans. Figure S5 in the online supplement displays ternary plots of respondent GSPs by racial group; consistent with prior work (Zhang and Trejo 2026), the genomes of most Black Americans in our sample are a mix of Sub-Saharan African ($\overline{P}^{\text{AFR}} = 0.81$) and European genetic similarity ($\overline{P}^{\text{EUR}} = 0.18$).[7] Table 1 presents results from linear and logistic regressions of a respondent's rated attractiveness on their GSPs. Among Black Americans, a 10 percentage point (pp) increase in Sub-Saharan African genetic similarity is associated with a 0.11 SD ($p < 0.001$) decrease in attractiveness score and a 3.5 pp (25 percent; $p < 0.001$) decrease in the probability of being rated as "very attractive." The magnitude of these associations slightly attenuates after controlling for various physical features (skin tone, hair color, and eye color), racial classification, and family and neighborhood socioeconomic status but remains highly statistically significant.[8] According to the estimates from model 1, the difference in average attractiveness score between an individual at the 5th and 95th percentiles, respectively, of the Black distribution of Sub-Saharan African genetic similarity ($P^{\text{AFR}} = 0.46$; $P^{\text{AFR}} = 0.94$) is equal to -0.52 SD; notably, this number is over five times as large as the average Black–White attractiveness disparity presented in Figure 1, and it is also roughly two and a half times as large as the within-Black light-vs-dark skin tone disparity reported by Monk, Esposito, and Lee (2021, Table A6).

Figure 2 presents a pair of binned scatterplots that graphically display the relationship between Sub-Saharan African genetic similarity and attractiveness among Black Americans; the Y axis in Figure 2A displays attractiveness scores, whereas the Y axis in Figure 2B displays the fraction of respondents who are rated as *at least* a given attractiveness category (i.e., "about average," "attractive," and "very attractive"). Note, these plots contain both the observed average attractiveness ratings of White Americans (solid blue markers) and the predicted average attractiveness scores of White Americans (hollow blue markers); the predicted values are useful for gaining a sense of how attractive we would expect White Americans to be on average, given the positive relationship between European (rather than African) genetic similarity observed among Black Americans. In Figure 2A, it can

Table 1: Regression of attractiveness ratings on Sub-Saharan African genetic similarity among Black Americans.

	Attractiveness Score				Pr ("Very Attractive")			
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
P^{AFR} (10 pp)	-0.109^{***}	-0.113^{***}	-0.081^{***}	-0.072^{***}	-0.035^{***}	-0.035^{***}	-0.028^{***}	-0.025^{***}
	(0.014)	(0.015)	(0.016)	(0.016)	(0.004)	(0.004)	(0.005)	(0.005)
Age FEs and interviewer FEs	X	X	X	X	X	X	X	X
Basic controls	X	X	X	X	X	X	X	X
Racial classification controls		X	X	X		X	X	X
Physical feature controls			X	X			X	X
Socioeconomic controls				X				X
N observations in the subgroup	4,628	4,628	4,628	4,628	3,434	3,434	3,434	3,434
N individuals in the subgroup	1,557	1,557	1,557	1,557	1,526	1,526	1,526	1,526
N interviewers	760	760	760	760	494	494	494	494

Notes: This table displays results from regressions of interviewer-rated attractiveness on the Sub-Saharan African genetic similarity proportion among sample of non-Hispanic Black Americans. Models 1−4 show beta coefficients from linear regression models with continuous attractiveness score (1−5) as the outcome variable, whereas models 5−8 show average marginal effects from logistic models with dichotomous "very attractive" (0,1) as the outcome variable. Note, models 5−8 have a smaller sample size because interviewers who rated no respondents as "very attractive" are mechanically dropped from the regression. The Likert attractiveness score variable is standardized using the weighted mean and standard deviation of the full Add Health sample. P^{EUR} is the omitted genetic similarity category (to eliminate multicollinearity). Among non-Hispanic Black Americans, the standard deviation of P^{AFR} is 0.13. See Table S3 in the online supplement for an analogous set of results among Hispanic Americans and Table S4 in the online supplement for an unstratified version of these results (i.e., pooled across races). $^{*}p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$.

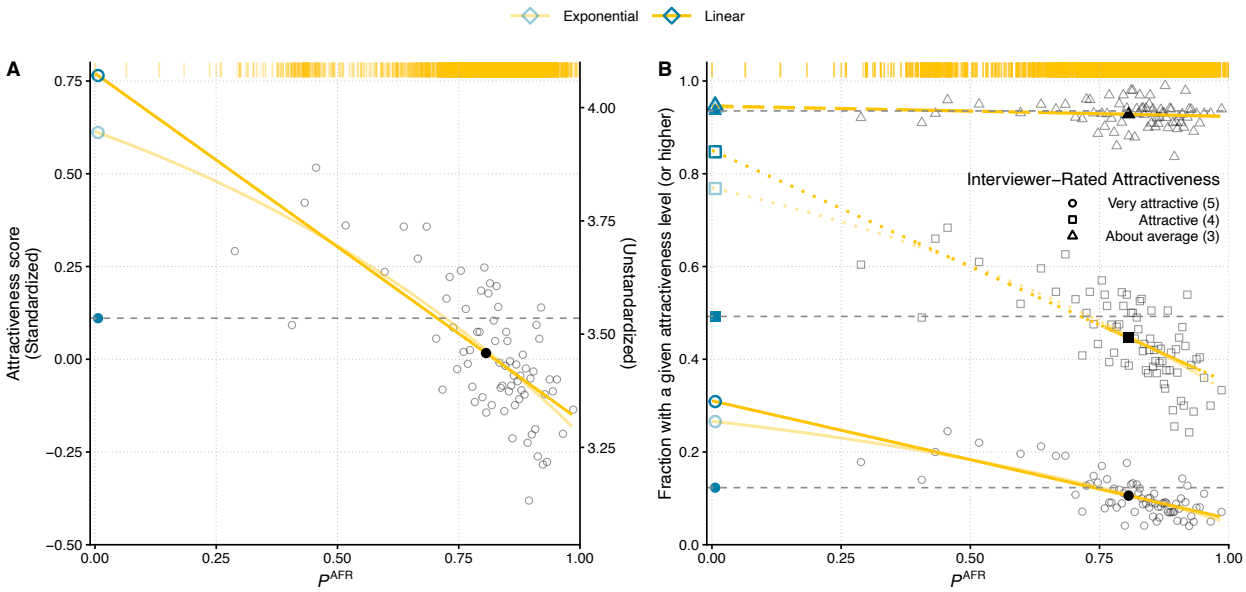

Figure 2: Black Americans with greater Sub-Saharan African genetic similarity are rated as less attractive. This figure displays binned scatter plots and linear/exponential bivariate regression fit lines using data from waves I to IV on 2,087 genotyped non-Hispanic Black respondents of the Add Health study; Sub-Saharan African genetic similarity is plotted on the *X* axis (with a marginal rug-plot displaying the individual-level distribution), and interviewer-rated attractiveness is plotted on the *Y* axis. In panel (*A*), the attractiveness variable used is the average Likert score (1–5), which is standardized using the weighted mean and standard deviation of the full Add Health sample. In panel (*B*), the attractiveness variable used is the fraction of respondents rated in a given attractiveness category (or a higher category). Each bin contains approximately 100 respondent-wave observations. The large, solid blue markers display the average attractiveness and genetic similarity of non-Hispanic White Americans, and the large, hollow blue markers display the predicted attractiveness of non-Hispanic White Americans (using their average genetic similarity and extrapolation from bivariate linear/exponential regression). The large, solid black markers display the average attractiveness and genetic similarity of non-Hispanic Black Americans. See Figure S8 in the online supplement for a similar figure that plots mono-racial and multi-racial Black Americans separately.

be plainly seen that there exist large average differences between the observed attractiveness scores of White Americans (solid blue marker) and the predicted attractiveness scores of White Americans (hollow blue marker); thus, while the observed Black–White disparity is only −0.094 SD, extrapolation of the relationship between GSP and attractiveness among Black Americans yields a predicted Black–White disparity that is far greater.[9] This, as we discuss later, casts some doubt on the extent to which interviewer-reported attractiveness ratings accurately measure underlying perceptions of attractiveness. See Table S3 in the online supplement and Figure S7 in the online supplement for an analogous set of results regarding the relationship between respondent GSPs and attractiveness among Hispanic Americans; in general, a far more limited set of associations exists in our Hispanic sample, all of which fall to statistical insignificance after the inclusion of physical and social covariates.

Importantly, there exists meaningful heterogeneity regarding exactly how intensely different Black respondents are penalized. In Figure 3A, we decompose our

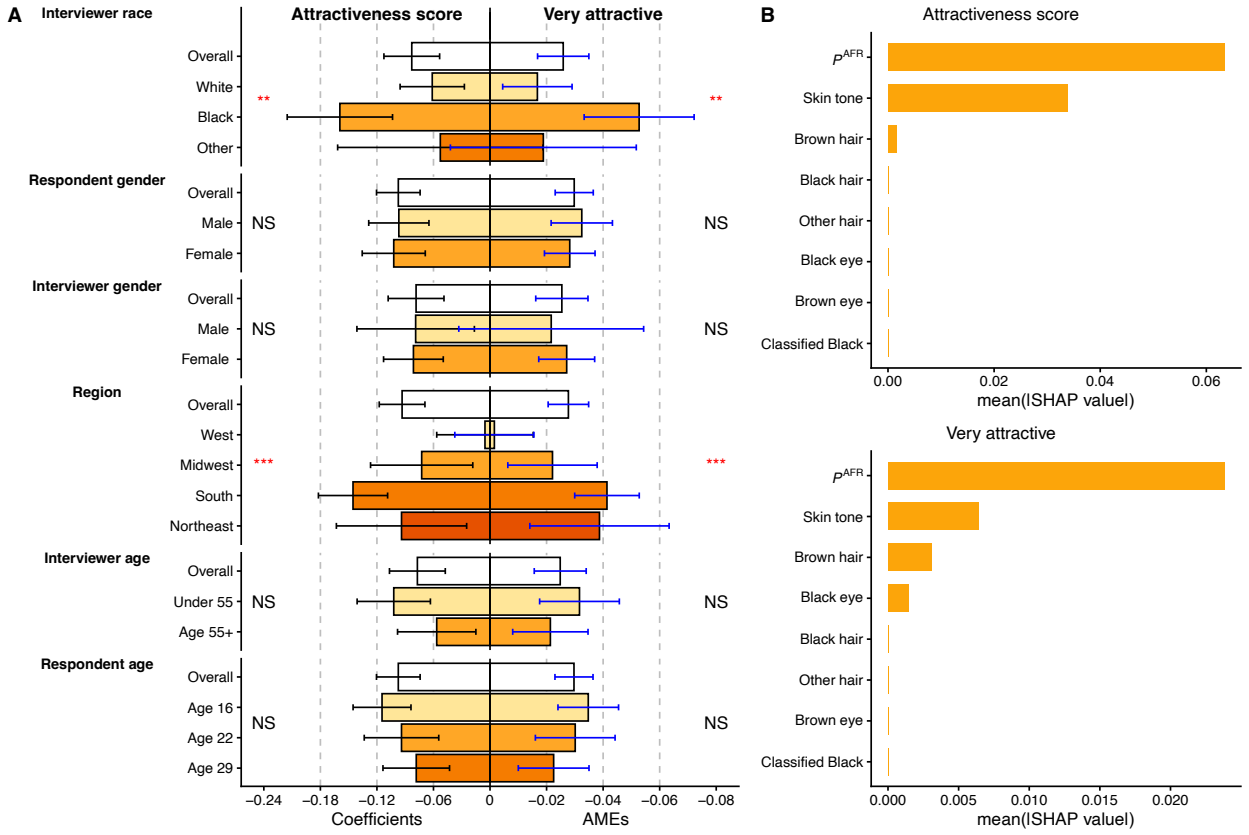

Figure 3: Decomposition and prediction analyses. Panel (*A*) displays results from a decomposition analysis on how the relationship between Sub-Saharan African genetic similarity (P^{AFR}) and attractiveness ratings among non-Hispanic Black respondents varies across six dimensions: interviewer race, gender, and age and respondent gender, age, and census region. Sample sizes vary across dimensions due to data availability. Beta coefficients for attractiveness score (left side) and average marginal effects for "very attractive" (AMEs; right side) from linear and logistic regression models, respectively, are displayed; see Equations (3) and (4). Statistical significance levels are denoted by asterisks ($^{*}p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$), with "NS" indicating non-significant results. See Tables S5–S10 in the online supplement for the full set of decomposition results. Panel (*B*) presents average absolute SHAP values from two elastic net regularized regression models with attractiveness score and "very attractive" as the target variables; SHAP values indicate the relative importance of different characteristics in predicting attractiveness ratings.

results regarding the relationship between Sub-Saharan African genetic similarity and attractiveness across six dimensions: interviewer race, gender, and age and respondent gender, age, and census region. After implementing a 5 percent Benjamini–Hochberg false discovery rate correction (Benjamini and Hochberg 1995), only two of these dimensions—interviewer race and respondent census region—capture statistically significant variation in the association between Sub-Saharan African genetic similarity and attractiveness ratings. Black interviewers impose stronger penalties on Black respondents than White interviewers do; while among Black interviewers, a 10 pp increase in Sub-Saharan African genetic similarity is associated with a 0.159 SD decrease in attractiveness score and a 5.3 pp decrease in

the probability of being rated as "very attractive," these relationships attenuate to 0.061 SD and 1.7 pp among White interviewers (but nonetheless remain statistically significant). Similarly, the magnitude of Sub-Saharan African genetic similarity attractiveness penalties is the largest in the South, smaller in the Northeast, and smaller still in the Midwest; in the West, there exists no statistically detectable attractiveness penalty.

Finally, we conduct a simple machine learning analysis to compare the predictive performance of Sub-Saharan African genetic similarity to a range of interviewer-reported survey measures related to race and appearance. In particular, we train prediction models using elastic net regularization, with attractiveness score and "very attractive" as the target variables. Figure 3B displays Shapley additive explanations (SHAP) values derived from these two penalized regression models (Lundberg and Lee 2017); SHAP values decompose a model's overall predictions into feature-level contributions, with higher average values indicating the most important features. Thus, this approach allows us to quantify the explanatory power of Sub-Saharan African genetic similarity compared to the other variables in our model (skin tone, racial classification, hair color, and eye color). For both the attractiveness score and "very attractive" prediction models, Sub-Saharan African genetic similarity yields the greatest SHAP values of all the features. These findings suggest that, among Black Americans, genetic ancestry captures a broader range of racialized features related to attractiveness evaluations than conventional survey-based measures.

Discussion

It is challenging to distinguish between two competing explanations of White–Black attractiveness disparities: do such gaps arise as a result of observers discretely classifying subjects (and then penalizing those they deem to be Black), or do they instead arise from a broader stigmatization of a constellation of physical features associated with Blackness?[10] Our empirical results provide robust evidence of the existence of substantial attractiveness stratification among Black Americans. Notably, interviewers did not have any direct knowledge of a respondent's GSPs—in fact, because the attractiveness ratings were collected between 1996 and 2008, interviewers had likely never even heard of a genetic ancestry test (Regalado 2018)—but they nonetheless systematically penalized those with higher levels of Sub-Saharan African genetic similarity. These results imply that, while discrete classification biases may well exist, the collective stigmatization of physical features associated with Blackness is a key part of the story. Importantly, our results do not imply that there is an objective or universal notion of attractiveness, or that a person's perceived attractiveness is an inevitable result of their biology. Instead, consistent with past work (Monk, Esposito, and Lee 2021), our findings indicate that contemporary American society has socially constructed a Eurocentric conceptualization of beauty that devalues physical features more common in individuals with higher amounts of Sub-Saharan African (rather than European) genetic similarity. And, although so-called "lookism" and colorism are closely related, our results show that inherited physical features beyond skin tone, such as hair texture and facial structure, likely also matter.

Why do we observe larger attractiveness penalties among Black interviewers and for respondents living in certain geographic regions? One potential explanation for these patterns is the varying degrees of social exposure to Black individuals. Most Black Americans live in the South (56 percent), followed by the Northeast (17 percent) and Midwest (17 percent), and finally the West (10 percent); notably, the South also contains every majority-Black U.S. county (Martinez and Passel 2025; Schaeffer 2019). And, due to segregated schools, neighborhoods, and social networks, Black Americans tend to—compared to individuals of other races—have a greater number of social interactions and relationships with Black people (Massey and Denton 1993). It may be that the racialized physical features correlated with Sub-Saharan African genetic similarity are especially stigmatized, net of racial classification, in social contexts with a sufficient number of Black individuals. Alternatively, individuals who are exposed to many Black social peers may simply become more accurate at either implicitly or explicitly distinguishing between Black individuals with varying amounts of Sub-Saharan African genetic similarity. In addition, it is worth noting that the more extreme slope estimates among Black interviewers appear to result, at least in part, from the fact that they are more likely than interviewers of other races to rate Black respondents with low Sub-Saharan African genetic similarity as "attractive" or "very attractive" (see Fig. S9 in the online supplement). Finally, the historical legacy of slavery in the South, as well as elevated levels of contemporary racial animus (Stephens-Davidowitz 2014), could also play an important role.

Our findings also help reconcile conflicting results regarding (small) Black–White attractiveness disparities from studies using survey-based attractiveness ratings, like those in Add Health, and the (large) disparities observed in studies using real-world behavior on dating apps. In particular, our within-race analysis revealed strong penalties of Sub-Saharan African genetic similarity, which, combined with the very large difference in Sub-Saharan African genetic similarity between Black and White Americans, would lead us to expect Black–White attractiveness disparities far larger in magnitude than we, in fact, observe. This suggests an important limitation of survey-based attractiveness measures: they may suffer from social desirability bias (Edwards 1958; Goffman 1959). That is, interviewers adjust their responses, either consciously or subconsciously, so as not to produce large average differences in attractiveness ratings across racial groups. Nonetheless, this correction appears to be relatively coarse; while interviewers are able to almost entirely eliminate unsavory average differences in attractiveness between racial groups, their responses nonetheless still show them penalizing Black Americans with high amounts of Sub-Saharan African genetic similarity. If survey-based measures suffer from this form of social desirability bias, then subsequent analyses will substantially understate the true magnitude of Black–White attractiveness disparities. In addition, these findings illustrate how discrete correction procedures fail to successfully mitigate stratification based on a continuous set of underlying dimensions.

Our results also have substantial methodological implications. The superior predictive power of GSPs compared to other measures of physical features (e.g., skin tone), as well as their desirable measurement properties, highlight their strength as a new tool for social scientists interested in measuring and studying processes

of racialization. Notably, we argue GSPs represent a complement to—and not a replacement of—existing survey strategies for quantifying the many continuous dimensions of race. In addition, many studies that lack measures of racialized physical features and racial classification (for instance, the Health and Retirement Study; Sonnega et al. 2014) nonetheless have collected genetic data, meaning the use of GSPs may aid the continuing expansion of scholarship on continuous (rather than discrete) racial stratification.

Finally, our findings add important nuance to the interpretation of genome-wide association study results for complex traits. Consider, for instance, that a given genetic variant is found to have a statistically significant causal effect on a psychiatric trait, like anxiety or depression (Tan et al. 2024); while this genetic effect might operate strictly through biologically proximal processes within the body—for example, the regulation of neurotransmitters in the brain—it may also operate through biologically distal processes outside of the body: for instance, the social stigmatization of certain individuals based on their genetically influenced physical features (Trejo and Martschenko 2026). In a similar vein, our results highlight that many popular genomic methods that utilize GSPs to identify gene–gene interaction effects (Patel et al. 2022; Wojcik et al. 2019) may, in fact, simply be identifying genetic heterogeneity related to social experiences of racialization.

Funding

This work has been supported by a grant from the Princeton Data Driven Social Sciences Initiative.

Author Contributions

ST designed the research. BT, LZ, and ST analyzed the data. BT, LZ, and ST wrote the article. BT and LZ contributed equally to the work.

Competing Interests

The authors declare that they have no competing interests.

Notes

1 We use the term racial group to describe the intersection of traditional racial categories (e.g., Black, White, Native American, and Asian/Pacific Islander) and Hispanicity. Note, these racial/ethnic groups—henceforth simply "racial groups"—are constructed to be mutually exclusive (see *Data and Methods*). For the remainder of this article, when we use the terms "Black Americans" and "White Americans," we are describing the group of individuals who self-identify as Black or White, respectively, and who do *not* also self-identify as Hispanic.

2 Despite their wide use in the study of colorism, existing measures of skin tone contain a substantial amount of measurement error (Campbell et al. 2020; Hannon and DeFina 2020), which serves to attenuate estimates of within-race stratification towards zero.

3 In principal component analysis and related methods (including global GSP estimation), measurement error arises when the estimated SNP-level weights for a given component meaningfully vary across models fit on different finite samples of the same underlying population. Past work has shown that the amount of measurement error in the four genetic similarity proportions used in this study, which correspond to the first four axes of genetic variation in the Add Health data, is relatively small (Zhang and Trejo 2026). However, as the number of GSPs estimated (i.e., K) increases, so does the amount of measurement error (Privé et al. 2020). So, while our approach allows us to accurately distinguish between Sub-Saharan African and European genetic similarity, there is no guarantee that the same methods and data could accurately distinguish between Northern and Southern European genetic similarity (or even more granular ancestral differences).

4 Social scientists use the term racial formation to describe the process through which racial meanings extend to previously unclassified relationships, practices, or groups (Omi and Winant 2014). Through racial formation, physical and social characteristics are transformed into markers of racial group membership that influence social perceptions and experiences.

5 For further sociological and demographic discussion of DNA and the social construction of race, see Zhang and Trejo (2026)—forthcoming at *Demography*.

6 For instance, Monk, Esposito, and Lee (2021) use interviewer-rated attractiveness measures and find a Black–White disparity of just 0.08 SD. On the other hand, Bruch and Newman (2018) apply a link analysis algorithm to dating app data and find White Americans are, on average, ranked at the 53rd percentile of the attractiveness distribution, whereas Black Americans are ranked at the 40th percentile. While it is difficult to directly compare standard deviation units to percentiles, a shift of 13 percentiles from the mean of a standard normal distribution is equal to 0.33 SD. Results derived from dating app behavior, however, likely partly reflect sorting on dimensions of desirability other than physical attractiveness (like, for instance, educational attainment and socioeconomic status) and may also suffer from bias from differential selection into app usage across race.

7 The genomes of Hispanic Americans in our sample are, on the other hand, a combination of European ($\overline{P}^{\mathrm{EUR}} = 0.60$), Indigenous American ($\overline{P}^{\mathrm{IAM}} = 0.27$), and Sub-Saharan African genetic similarity ($\overline{P}^{\mathrm{AFR}} = 0.11$). See Figure S6 in the online supplement for histograms of Sub-Saharan African, European, and Indigenous American genetic similarity among Black and Hispanic Americans.

8 Note, while the GSPs are correlated with skin tone, hair color, and eye color, we include these three measures as covariates to test the extent to which the GSPs explain variation in attractiveness *net* of currently available physical feature measures. Figure S10 in the online supplement graphically illustrates the fact that P^{AFR} explains variation in attractiveness among Black Americans of the same interviewer-rated skin tone.

9 For instance, when using bivariate linear extrapolation, the predicted Black–White disparity in attractiveness score is about eight times as large as the measured Black–White disparity.

10 See Figure S11 in the online supplement for a directed acyclic graph depicting this theoretical process. A key challenge in answering this question is that the racial boundary that separates individuals as either Black or another race is generally quite clear; thus, there

is generally very little variation in the racial classification by others among self-identified Black individuals. In Add Health, for instance, Add Health interviewers classified more than 98 percent of self-identified Black respondents as Black. By exploring within-group attractiveness variation among a population with little variation in racial classification, our study highlights the existence of a direct relationship between genetically influenced (racialized) physical features and perceived attractiveness.

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Acknowledgments: We are grateful to Dalton Conley, Filiz Garip, Iain Mathieson, Ellis Monk, and Marissa Thompson for helpful comments. This research uses data from Add Health, funded by grant P01 HD31921 (Harris) from the Eunice Kennedy Shriver National Institute of Child Health and Human Development (NICHD), with cooperative funding from 23 other federal agencies and foundations. Add Health is currently directed by Robert A. Hummer and funded by the National Institute on Aging cooperative agreements U01 AG071448 (Hummer) and U01AG071450 (Hummer and Aiello) at the University of North Carolina at Chapel Hill. Add Health was designed by J. Richard Udry, Peter S. Bearman, and Kathleen Mullan Harris at the University of North Carolina at Chapel Hill. No direct support was received from grant P01 HD31921 for this analysis. Information on obtaining Add Health data is available on the project website. Send correspondence to Sam Trejo, samtrejo@princeton.edu.

Significance Statement: This study provides new evidence on how racialized physical features shape social experiences within a single self-identified racial group. By using genetic similarity proportions—genetic ancestry measures that correlate with physical traits such as skin tone and facial structure—the authors show that Black Americans with higher levels of Sub-Saharan African genetic similarity are systematically rated as less physically attractive. These results reveal a form of racialized disadvantage that operates within racial categories and is not captured by typical survey measures and help explain why traditional surveys report relatively small Black–White attractiveness gaps (whereas real-world behavior shows much larger differences). More broadly, the study offers genetic similarity proportions as a new tool for exploring processes of racialization in contemporary society.

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