sociological science

Supplement to:

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SUPPLEMENTARY INFORMATION

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

Taddess, Zhang, & Trejo 2026; *Sociological Science*

Contents

1 SUPPLEMENTARY FIGURES

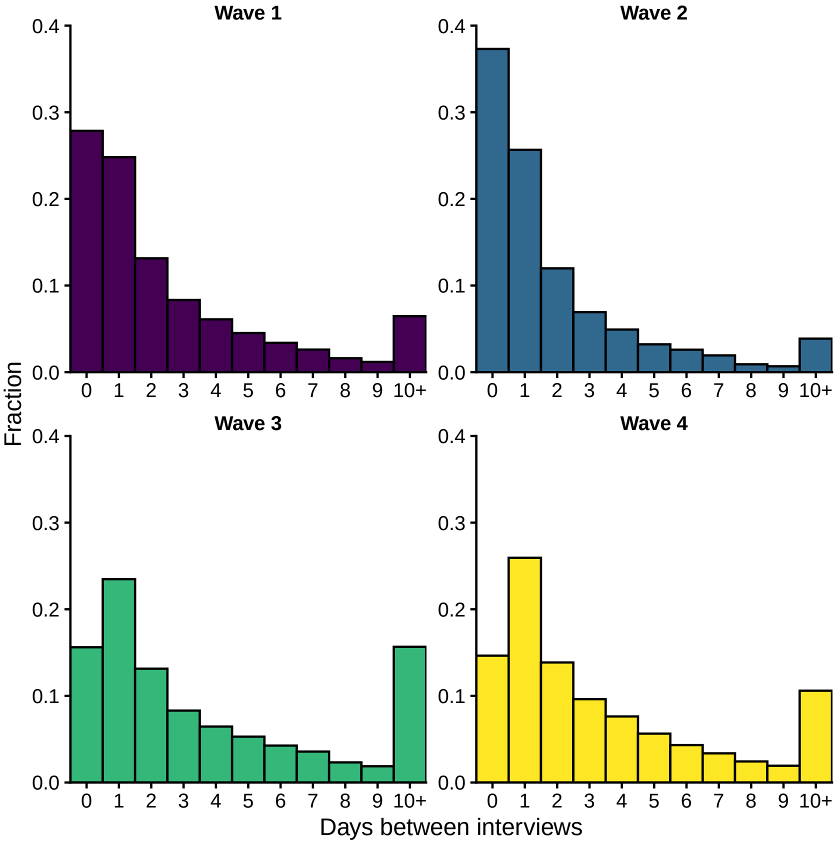

Figure S1: Distribution of Days between Interviews among Add Health Interviewers

This figure displays histograms of the number of days between respondent interviews conducted by the same interviewer across Waves I–IV of the Add Health study. Interviewers rarely conducted more than one interview within a single day, and sometimes more than a week passed between two interviews.

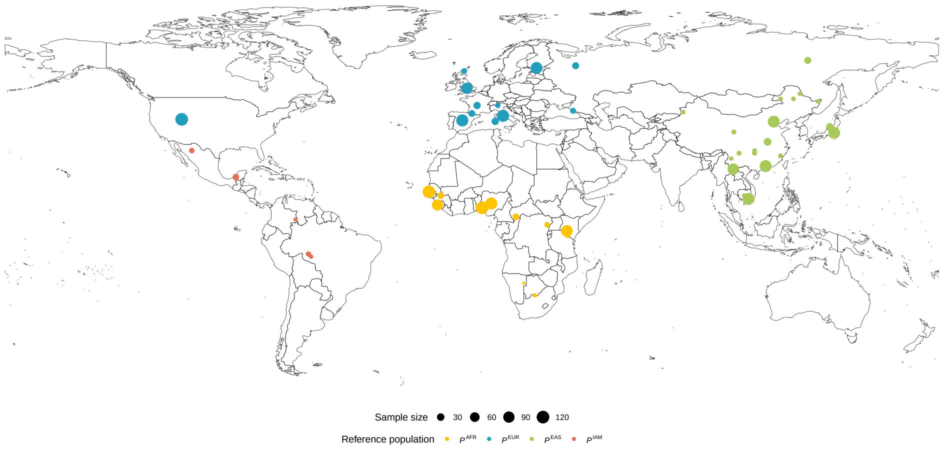

Figure S2: Geographic Location of Reference Panels for Supervised `ADMIXTURE` K $= 4$ Analysis

This map visualizes the geographic distribution of reference panels used to construct the Sub-Saharan African, European, East Asian, and Indigenous American genetic similarity proportions. The size of each dot or triangle indicates the sample size of the corresponding reference population. Coordinate information is extracted from `https://www.internationalgenome.org/data-portal/population`.

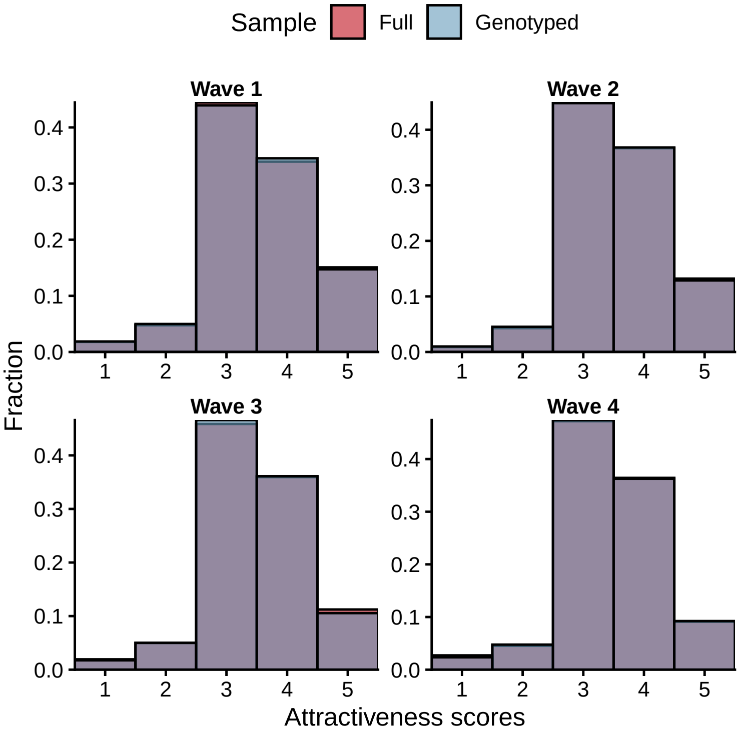

Figure S3: Distribution of Physical Attractiveness Ratings among Add Health Respondents

This figure displays histograms of the physical attractiveness ratings in Waves I–IV of the Add Health study. The blue bars represent the full Add Health sample, whereas the red bars represent the Add Health genotyped subsample. The close correspondence between the two distributions suggests that our analytic sample is largely representative of the overall Add Health population with respect to attractiveness ratings.

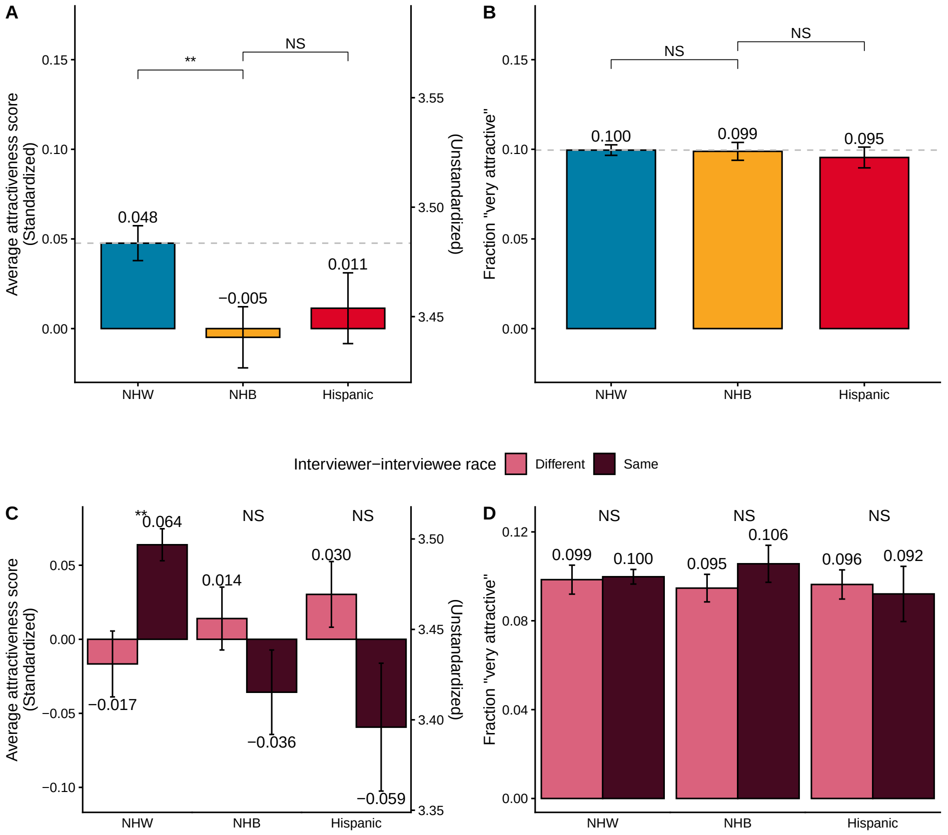

Figure S4: Attractiveness Ratings by Race and Respondent-Interviewer Racial Concordance

This figure displays bar graphs created using data on genotyped respondents of the Add Health study; only Waves III and IV contain information on the race of each interviewer, and therefore only attractiveness ratings from these two Add Health waves are displayed. Self-identified race is collected at Wave III, when the respondents were 18-26 years old; racial categories are mutually exclusive. Panels A and C display average Likert attractiveness score (1-5), which is standardized using the weighted mean and standard deviation of the full Add Health sample. Panels B and D display the fraction of respondents rated in the very highest attractiveness category ('very attractive'). Panels A and B show the average attractiveness ratings for each of three mutually exclusive self-identified racial groups: Non-Hispanic White Americans, Non-Hispanic Black Americans, and Hispanic Americans. Panels C and D further break these outcomes out by whether the respondent and interviewer are of the same race. White respondents receive slightly higher attractiveness scores (but not 'very attractive' ratings) from White interviewers than from interviewers of other races; in contrast, there is no statistically significant difference in ratings between same-race and different-race interviewers for Black and Hispanic respondents. Error bars display 95% confidence intervals. Asterisks indicate statistical significance: *$p<0.05$, **$p<0.01$, ***$p<0.001$, NS = not significant.

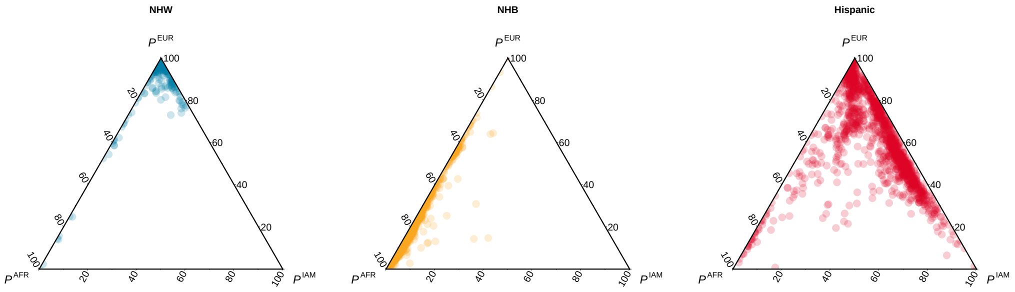

Figure S5: Ternary Plots of Genetic Similarity Proportions by Racial Identity

This figure displays ternary plots of genetic similarity proportion separately for members of three mutually exclusive self-identified racial groups: Non-Hispanic White Americans, Non-Hispanic Black Americans, and Hispanic Americans. Each dot represents an individual, with their position in the ternary plot reflecting their levels of Sub-Saharan African, European, and Indigenous American genetic similarity proportions. The top, bottom left, and bottom right corners of each plot correspond to 100% European, Sub-Saharan African, and Indigenous American genetic similarity, respectively. Note, 78 White respondents, 29 Black respondents, and 77 Hispanic respondents with values of East Asian genetic similarity (P^{EAS}) greater than 5% are not displayed. White Americans exhibit little evidence of admixture, with individuals generally having very low levels of both Sub-Saharan African and Indigenous American genetic similarity. Black Americans exhibit evidence of two-way admixture, with substantial variation on the axis between Sub-Saharan African and European genetic similarity and very few individuals having meaningful amounts of Indigenous American genetic similarity. Finally, Hispanic Americans exhibit evidence of three-way admixture, perhaps reflecting the complex demographic history of Latin America.

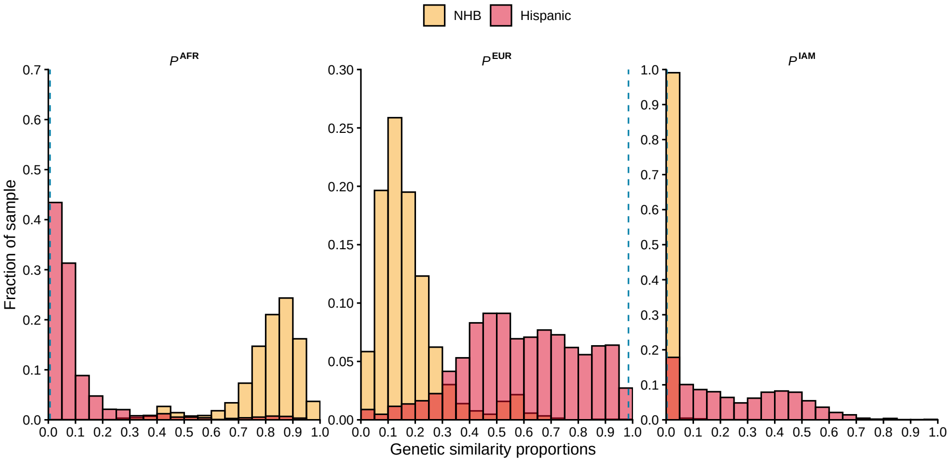

Figure S6: Distribution of Genetic Similarity Proportions among Black and Hispanic Americans

This figure displays histograms of Sub-Saharan African (left panel), European (middle panel), and Indigenous American (right panel) genetic similarity among genotyped respondents of the Add Health study. Histograms of two self-identified racial groups – Non-Hispanic Black Americans in yellow, and Hispanic Americans in red – are displayed separately. The blue dashed line in each panel indicates the average level of the respective genetic similarity proportion among self-identified non-Hispanic White Americans. Self-identified race is collected at Wave III, when the respondents were 18-26 years old; racial categories are mutually exclusive.

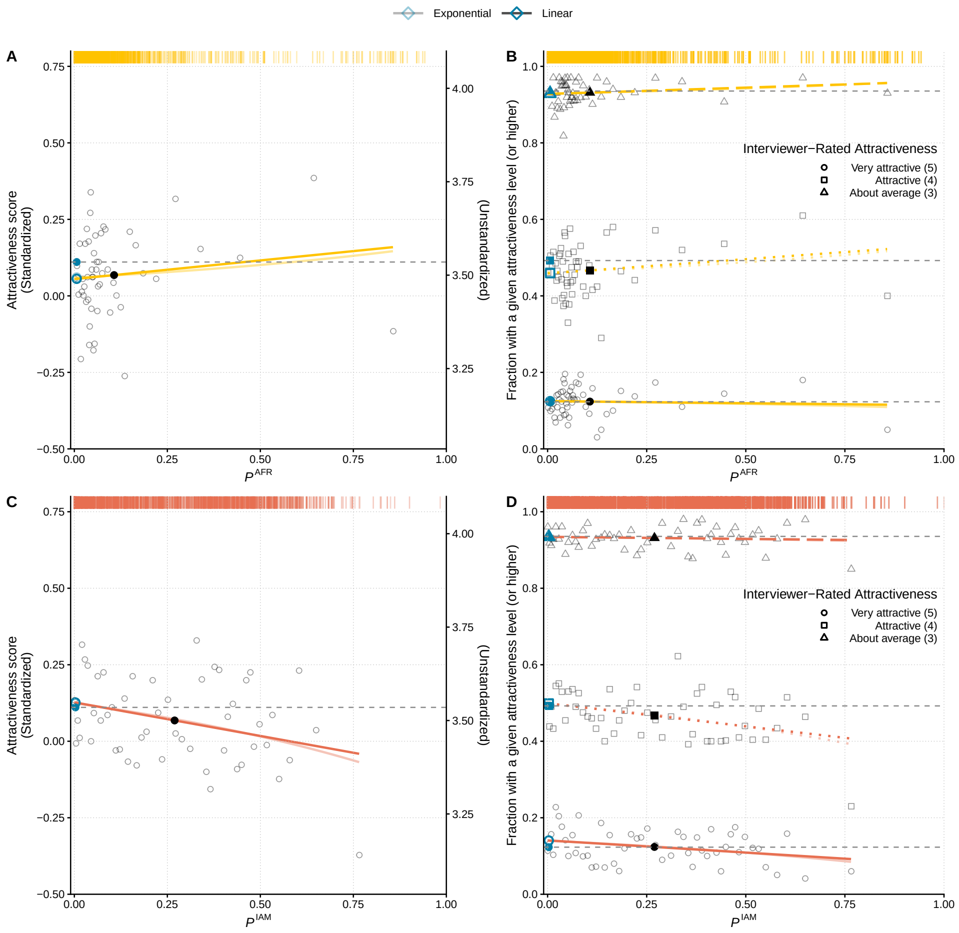

Figure S7: Relationship between P^{AFR} and P^{IAM} and Attractiveness Among Hispanic Americans

This figure displays binned scatter plots and linear/exponential regression fit lines using data from Waves I-IV on $1,469$ genotyped Hispanic respondents of the Add Health study. In Panels A and B, Sub-Saharan African genetic similarity is plotted on the X-axis, whereas in Panels C and D, Indigenous American genetic similarity is plotted on the X-axis. In all panels, interviewer-rated attractiveness is plotted on the Y-axis; while the attractiveness variable used in Panels A and C is the average Likert score (1-5), the attractiveness variable used in Panels B and D 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). The large, solid black markers display the average attractiveness and genetic similarity of Hispanic Americans. While Panels C and D suggest that, among Hispanic Americans, Indigenous American genetic similarity is negatively associated with attractiveness ratings, this relationship is considerably weaker than the relationship between Sub-Saharan African and attractiveness ratings observed among Black Americans.

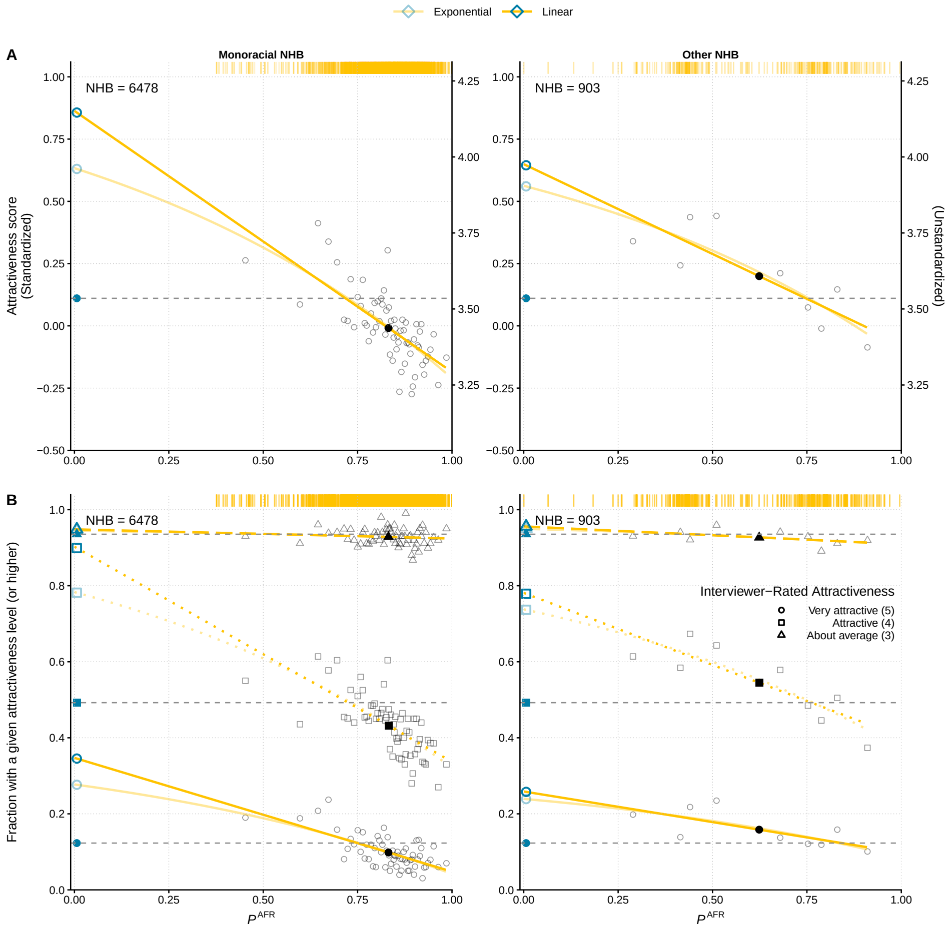

Figure S8: Relationship between P^{AFR} and Attractiveness (Monoracial vs. Multiracial Black)

This figure displays binned scatter plots and linear/exponential regression fit lines using data on genotyped non-Hispanic Black respondents of the Add Health study; only Waves III and IV contain information on the race of each interviewer, and therefore only attractiveness ratings from these two Add Health waves are displayed. This figure, unlike Figure 2, displays the relationship between Sub-Saharan African genetic similarity (X-axis) and interviewer-rated attractiveness (Y-axis) separately for Black respondents who identify exclusively as Black (i.e., monoracial) and for Black respondents who identify as Black and an additional race/ethnicity (multiracial). The attractiveness variable used in Panel A is the average Likert score (1-5), whereas the attractiveness variable used in Panel B is the fraction of respondents rated in a given attractiveness category or a higher category. Each bin contains approximately 100 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). The large, solid black markers display the average attractiveness and genetic similarity of non-Hispanic Black Americans. The negative association between Sub-Saharan African genetic similarity and attractiveness is similar for monoracial and multiracial Black Americans. This indicates that observed attractiveness penalties are not merely artifacts of ambiguity in racial identification/classification but rather likely reflect consistent stigmatization of physical features associated with Sub-Saharan African genetic similarity.

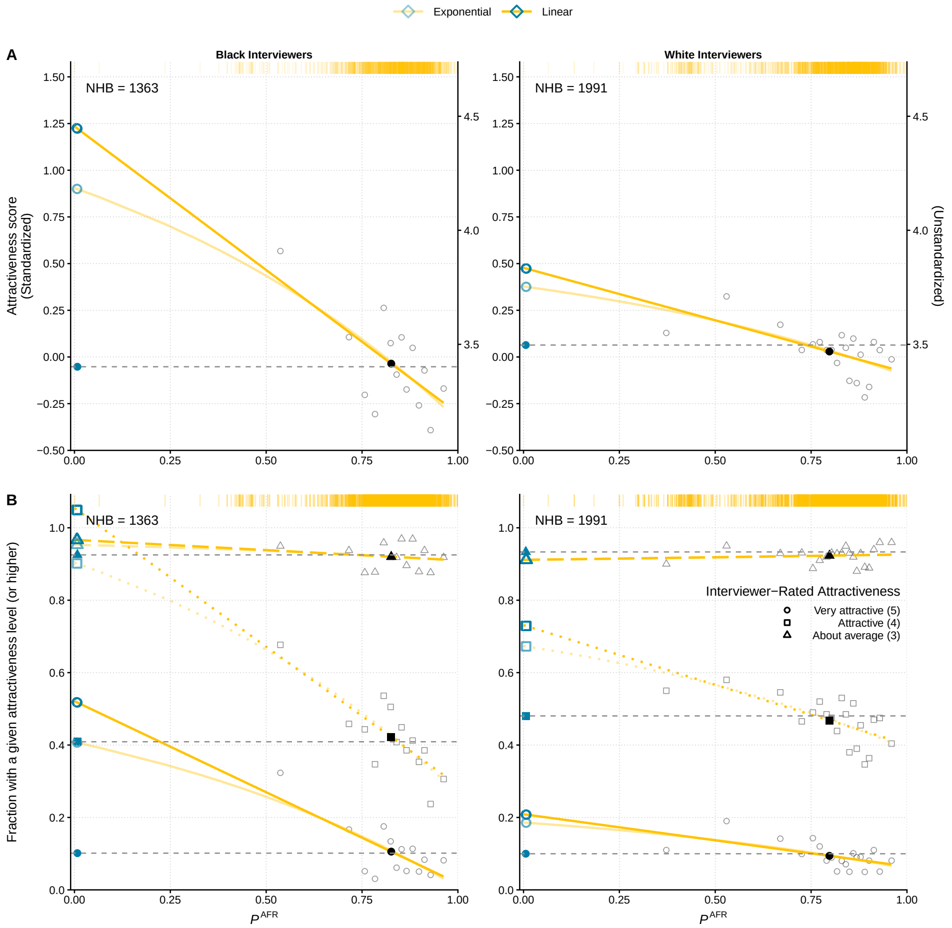

Figure S9: Relationship between P^{AFR} and Attractiveness by Interviewer Race

This figure displays binned scatter plots and linear/exponential regression fit lines using data on genotyped non-Hispanic Black respondents of the Add Health study; only Waves III and IV contain information on the race of each interviewer, and therefore only attractiveness ratings from these two Add Health waves are displayed. This figure, unlike Figure 2, displays the relationship between Sub-Saharan African genetic similarity (X-axis) and interviewer-rated attractiveness (Y-axis) separately for non-Hispanic Black interviewers and non-Hispanic White interviewers. The attractiveness variable used in Panel A is the average Likert score (1-5), whereas the attractiveness variable used in Panel B is the fraction of respondents rated in a given attractiveness category or a higher category. Each bin contains approximately 100 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). The large, solid black markers display the average attractiveness and genetic similarity of non-Hispanic Black Americans. While the attractiveness penalties associated with Sub-Saharan African genetic similarity are largest for Black interviewers, they are nonetheless also present for White interviewers; importantly, the larger slope estimates among Black interviewers appear to, at least in part, result 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’.

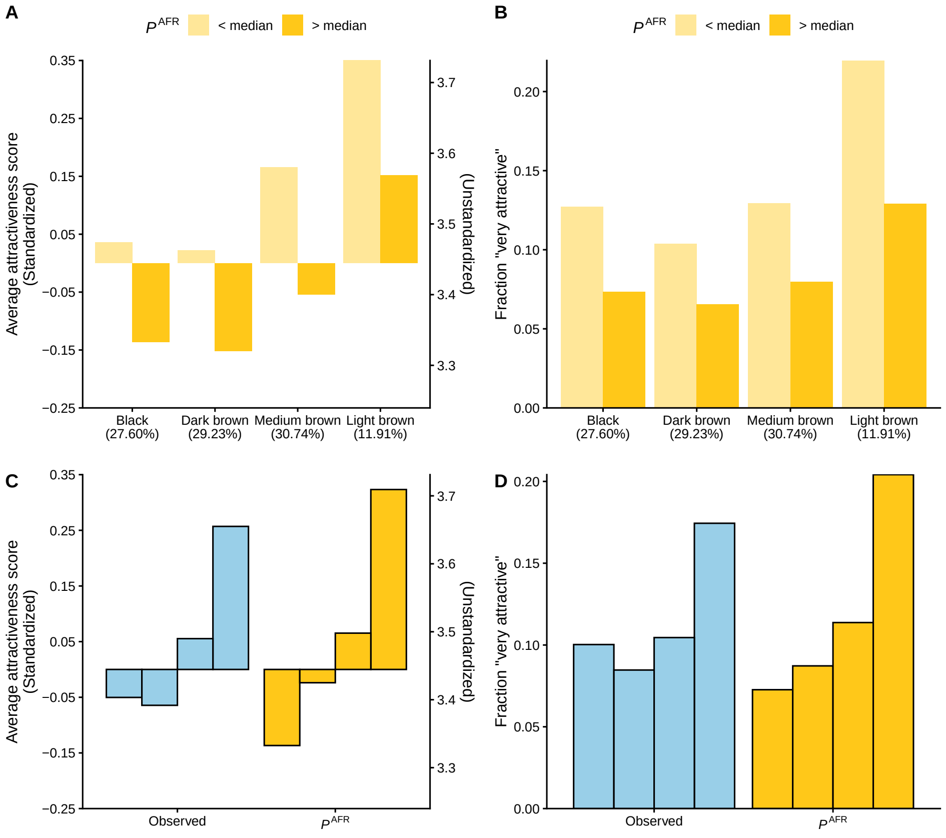

Figure S10: Comparing Attractiveness Penalties by Skin Tone and by P^{AFR} among Black Americans

This figure displays data on genotyped non-Hispanic Black respondents from Waves I-IV of the Add Health Study. Panels A and B show the average attractiveness ratings by interviewer-rated skin tone. Within each skin tone category, respondents are further divided into two equally sized subgroups at the median value of Sub-Saharan African genetic similarity in a given skin tone category. Panels C and D compare the skin tone attractiveness gradient to Sub-Saharan African genetic similarity attractiveness gradient; four groups of Sub-Saharan African genetic similarity are constructed by ranking the respondents in ascending order of P^{AFR} and dividing them into four groups using the same quantiles that separate each successive category in the observed distribution of skin tone. Panels A and C display average Likert attractiveness score (1-5), whereas Panels B and D display the fraction of respondents rated in the very highest attractiveness category ('very attractive'). Black respondents rated as white-skinned ($N = 9$) are excluded from the figure. Even among Black Americans with the same interviewer-rated skin tone, those with higher Sub-Saharan African genetic similarity proportions receive lower attractiveness ratings. In addition, skin tone groups display a weaker attractiveness gradient than equally sized groups based on Sub-Saharan African genetic similarity.

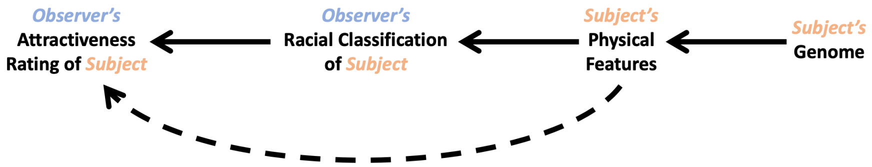

Figure S11: Directed Acyclic Graph

This directed acyclic graph (DAG) illustrates theoretical causal pathways linking genetic information to attractiveness ratings. The DAG depicts four key nodes: a subject's genome, a subject's physical features, an observer's racial classification of the subject, and an observer's attractiveness rating of the subject. A person's genome influences their eventual physical features via biological development. In turn, a person's physical features may influence their perceived attractiveness [i] indirectly via their racial classification by others and [ii] directly (if those features are culturally and/or aesthetically valued). Our study, by exploring within-group attractiveness variation among a population with little variation in racial classification, highlights the existence of a direct relationship between genetically influenced racialized physical features and perceived attractiveness (indicated by the dashed arrow above).

2 SUPPLEMENTARY TABLES

	Non-Hispanic Black			Hispanic			Other Races		
Characteristic	**N**	**Mean / %**	**SD**	**N**	**Mean / %**	**SD**	**N**	**Mean / %**	**SD**
P^{AFR}	2087	0.81	0.13	1469	0.11	0.16	6415	0.01	0.04
P^{EUR}	2087	0.18	0.12	1469	0.60	0.22	6415	0.91	0.25
P^{EAS}	2087	0.01	0.04	1469	0.03	0.11	6415	0.07	0.24
P^{IAM}	2087	0.01	0.01	1469	0.27	0.20	6415	0.01	0.05
Attractiveness score	7381	0.02	1.01	5176	0.07	1.04	22951	0.11	1.01
"Very attractive"	7381	10.57%		5176	12.36%		22951	12.12%	
Gender	2087			1469			6415		
Male		44.47%			50.99%			47.67%	
Female		55.53%			49.01%			52.33%	
Birth year	2087	1978.98	1.76	1469	1978.60	1.73	6415	1978.95	1.74
Educational attainment	2087			1469			6415		
Less than high school		10.97%			10.28%			7.19%	
High school		17.39%			21.10%			15.98%	
Some college		48.92%			48.26%			43.73%	
Bachelor's or above		22.71%			20.35%			33.11%	
Skin tone	1721			1201			5450		
Black		27.60%			1.00%			0.22%	
Dark brown		29.23%			2.66%			0.42%	
Medium brown		30.74%			11.32%			1.96%	
Light brown		11.91%			36.30%			6.97%	
White		0.52%			48.71%			90.42%	
Hair color	1721			1201			5450		
No hair		1.16%			1.50%			0.73%	
Black		79.78%			46.13%			13.93%	
Brown		16.27%			43.80%			53.60%	
Blond		0.35%			5.08%			26.11%	
Red		1.16%			1.58%			4.59%	
Grey		0.00%			0.00%			0.00%	
Other		1.28%			1.92%			1.05%	
Eye color	1721			1201			5450		
Black		16.91%			8.66%			2.42%	
Brown		79.90%			74.94%			40.99%	
Hazel		2.38%			8.33%			17.83%	
Blue		0.06%			3.50%			27.54%	
Green		0.41%			3.08%			7.49%	
Other		0.35%			1.50%			3.72%	
W1 social origins score	1907	-0.37	1.46	1347	-0.59	1.41	6157	0.29	1.17
W1 neighborhood disadvantage	2064	34.33	11.31	1459	29.27	10.49	6334	22.18	9.71

Table S1: Descriptive Statistics of Add Health Genotyped Sample by Racial Identity

Means, proportions, and standard deviations of genetic similarity proportions, attractiveness ratings, demographic characteristics, and physical features among genotyped members of the Add Health Study. Descriptive statistics are displayed separately for non-Hispanic Black Americans, Hispanic Americans, and Non-Hispanic Other Races. Sample sizes vary slightly across measures due to missing data. For the attractiveness score and 'very attractive', the reported N values reflect the total number of ratings across Waves I-IV. Genetic similarity proportions range from 0 to 1, with P^{AFR} indicating Sub-Saharan African genetic similarity, P^{EUR} indicating European genetic similarity, P^{EAS} indicating East Asian genetic similarity, and P^{IAM} indicating Indigenous American genetic similarity.

	N = 667	
	Mean (SD) / %	
Characteristic	**Unweighted**	**Weighted**
Number of interviewees	25 (20)	
Number of Non-Hispanic Black interviewees	5 (8)	
Interviewer's age	51 (11)	52 (11)
Female interviewer	83%	83%
Interviewer's race		
Non-Hispanic White	62%	56%
Non-Hispanic Black	26%	38%
Non-Hispanic Native American	1%	1%
Non-Hispanic Asian/Pacific Islander	1%	0%
Hispanic	9%	5%
Other	1%	1%
Interviewer's educational attainment		
High school or less	11%	12%
Some college	43%	36%
Bachelor's degree or above	47%	52%

Table S2: Descriptive Statistics of Add Health Interviewers

Means, proportions, and standard deviations of selected demographic characteristics of Add Health interviewers. Weighted column displays descriptive statistics where each interviewer is weighted by the number of Non-Hispanic Black respondents that they interviewed.

	Attractiveness Score				**Pr("Very Attractive")**			
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
P^{AFR} (10 pp)	0.016	0.002	0.008	0.010	-0.003	-0.009	-0.007	-0.007
	(0.013)	(0.016)	(0.016)	(0.016)	(0.005)	(0.007)	(0.007)	(0.007)
P^{IAM} (10 pp)	-0.028*	-0.028*	-0.023+	-0.011	-0.014**	-0.012**	-0.009+	-0.006
	(0.011)	(0.011)	(0.012)	(0.012)	(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 Subgroup	3,254	3,254	3,254	3,254	2,333	2,333	2,333	2,333
N Individuals in Subgroup	1,095	1,095	1,095	1,095	1,068	1,068	1,068	1,068
N Interviewers	727	727	727	727	487	487	487	487

Table S3: Regression Models of Attractiveness on GSPs (Hispanic Americans)

This table displays results from regressions of interviewer-rated attractiveness on Sub-Saharan African and Indigenous American genetic similarity proportions among Hispanic Americans. The top panel shows beta coefficients from linear regression models with Likert attractiveness score (1-5) as the outcome variable, whereas the bottom panel displays average marginal effects from logistic models with a ‘very attractive’ (0,1) as the outcome variable. The 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). Note, Among Hispanic Americans, the standard deviations of P^{AFR} and P^{IAM} are 0.16 and 0.20, respectively.

	Attractiveness Score				**Pr("Very Attractive")**			
	Model 1	Model 2	Model 3	Model 4	Model 1	Model 2	Model 3	Model 4
P^{AFR} (10 pp)	-0.010***	-0.043***	-0.035***	-0.022*	-0.005***	-0.015***	-0.016***	-0.013***
	(0.002)	(0.008)	(0.009)	(0.010)	(0.001)	(0.003)	(0.003)	(0.004)
P^{EAS} (10 pp)	-0.003	-0.001	-0.005	0.002	-0.004**	-0.003	-0.005	-0.004
	(0.003)	(0.008)	(0.009)	(0.009)	(0.001)	(0.003)	(0.003)	(0.003)
P^{IAM} (10 pp)	-0.018**	-0.015*	-0.023**	-0.001	-0.006**	-0.004	-0.007*	-0.001
	(0.006)	(0.006)	(0.008)	(0.008)	(0.002)	(0.003)	(0.003)	(0.003)
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
Num. Obs.	35,508	27,998	24,852	23,285	27,194	21,755	18,859	17,429
Num. Inds.	9,971	9,971	8,372	7,843	9,837	9,745	8,216	7,678
Num. Age	20	20	20	20	20	20	20	20
Num. Inter. × Waves	1,564	1,218	1,211	1,207	1,041	814	783	765
R^2	0.181	0.171	0.182	0.194	—	—	—	—
R^2 Within	0.009	0.010	0.016	0.026	—	—	—	—
Pseudo R^2	—	—	—	—	0.156	0.153	0.154	0.162

Table S4: Regression Models of Attractiveness on GSPs (All Races Pooled)

This table displays results from regressions of interviewer-rated attractiveness on genetic similarity proportions in the full sample of genotyped Add Health respondents. That is, in this set of models, the association between each genetic similarity proportion and attractive rating is *not* estimated separately for each self-identified racial group but instead pooled across groups. While Models 1-4 on the left show beta coefficients from linear regression models with Likert attractiveness score (1-5) as the outcome variable, Models 1-4 on the right show average marginal effects from logistic models with a 'very attractive' (0,1) as the outcome variable. The 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).

	Non-Hispanic Black				**Hispanic**			
	White Int.	Black Int.	Other Int.	P-value	White Int.	Hisp. Int.	Other Int.	P-value
				Attractiveness Score				
P^{AFR} (10 pp)	-0.061***	-0.159***	-0.053	0.010	0.023	-0.054+	0.018	0.056
	(0.017)	(0.029)	(0.056)	(0.030)	(0.017)	(0.029)	(0.023)	(0.167)
P^{IAM} (10 pp)	-0.167	0.043	-0.009	0.804	-0.038*	-0.054*	-0.022	0.595
	(0.285)	(0.146)	(0.571)	(0.964)	(0.015)	(0.024)	(0.022)	(0.840)
N Respondents	1519	1143	227		1035	489	587	
N Interviewers	272	144	58		271	60	133	
N Observations	1991	1363	238		1357	543	667	
				Pr("Very Attractive")				
P^{AFR} (10 pp)	-0.017**	-0.053***	-0.019	0.001	0.000	-0.057	-0.013	0.150
	(0.006)	(0.010)	(0.017)	(0.004)	(0.008)	(0.046)	(0.015)	(0.225)
P^{IAM} (10 pp)	0.029	-0.037	0.071	0.539	-0.013+	-0.016	-0.017	0.936
	(0.075)	(0.066)	(0.484)	(0.964)	(0.007)	(0.012)	(0.010)	(0.938)
N Respondents	1312	901	175		877	364	395	
N Interviewers	195	82	37		200	33	80	
N Observations	1638	1015	180		1085	397	426	

Table S5: Regression Decomposition by Interviewer Race

This table displays results from stratified regressions of interviewer-rated attractiveness on Sub-Saharan African and Indigenous American genetic similarity proportions among samples of non-Hispanic Black Americans and Hispanic Americans. The top panel shows beta coefficients from linear regression models with Likert attractiveness score (1-5) as the outcome variable, whereas the bottom panel displays average marginal effects from logistic models with a 'very attractive' (0,1) as the outcome variable. The 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). Note, these regressions are estimated on only Waves III and IV, as Waves I and II did not collect information on the interviewer race. We utilize an omnibus F-test to determine whether all of the subgroup-specific coefficients are statistically identical. Raw p-values are displayed without parentheses above, and adjusted p-values (using a Benjamini-Hochberg false discovery rate correction) are displayed in parentheses below.

	Non-Hispanic Black			Hispanic		
	Male Resp.	Female Resp.	P-value	Male Resp.	Female Resp.	P-value
			Attractiveness Score			
P^{AFR} (10 pp)	-0.097***	-0.102***	0.814	0.033*	-0.020	0.010
	(0.016)	(0.017)	(0.888)	(0.015)	(0.014)	(0.121)
P^{IAM} (10 pp)	-0.012	-0.124	0.594	-0.041***	-0.020	0.201
	(0.098)	(0.186)	(0.964)	(0.012)	(0.013)	(0.840)
N Respondents	928	1159		749	720	
N Interviewers	816	865		772	758	
N Observations	3239	4142		2630	2546	
			Pr("Very Attractive")			
P^{AFR} (10 pp)	-0.032***	-0.028***	0.521	0.004	-0.012*	0.040
	(0.006)	(0.005)	(0.695)	(0.006)	(0.006)	(0.158)
P^{IAM} (10 pp)	-0.002	0.002	0.935	-0.020***	-0.011*	0.177
	(0.064)	(0.035)	(0.964)	(0.006)	(0.005)	(0.840)
N Respondents	915	1143		740	713	
N Interviewers	566	606		534	548	
N Observations	2378	3212		1902	1984	

Table S6: Regression Decomposition by Respondent Gender

This table displays results from stratified regressions of interviewer-rated attractiveness on Sub-Saharan African and Indigenous American genetic similarity proportions among samples of non-Hispanic Black Americans and Hispanic Americans. The top panel shows beta coefficients from linear regression models with Likert attractiveness score (1-5) as the outcome variable, whereas the bottom panel displays average marginal effects from logistic models with a ‘very attractive’ (0,1) as the outcome variable. The 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). We utilize an omnibus F-test to determine whether all of the subgroup-specific coefficients are statistically identical. Raw p-values are displayed without parentheses above, and adjusted p-values (using a Benjamini-Hochberg false discovery rate correction) are displayed in parentheses below.

	Non-Hispanic Black			**Hispanic**		
	Male Int.	Female Int.	P-value	Male Int.	Female Int.	P-value
			Attractiveness Score			
P^{AFR} (10 pp)	-0.079*	-0.081***	0.945	-0.041	0.015	0.074
	(0.032)	(0.016)	(0.945)	(0.028)	(0.015)	(0.177)
P^{IAM} (10 pp)	0.020	0.032	0.964	-0.051+	-0.036**	0.588
	(0.166)	(0.210)	(0.964)	(0.027)	(0.012)	(0.840)
N Respondents	542	1933		402	1376	
N Interviewers	82	397		79	389	
N Observations	608	3000		441	2152	
			Pr("Very Attractive")			
P^{AFR} (10 pp)	-0.022	-0.027***	0.700	-0.023	-0.009	0.331
	(0.017)	(0.005)	(0.840)	(0.024)	(0.007)	(0.395)
P^{IAM} (10 pp)	0.028	0.014	0.856	-0.010	-0.017**	0.498
	(0.226)	(0.050)	(0.964)	(0.012)	(0.006)	(0.840)
N Respondents	365	1756		233	1203	
N Interviewers	42	275		44	272	
N Observations	396	2446		244	1688	

Table S7: Regression Decomposition by Interviewer Gender

This table displays results from stratified regressions of interviewer-rated attractiveness on Sub-Saharan African and Indigenous American genetic similarity proportions among samples of non-Hispanic Black Americans and Hispanic Americans. The top panel shows beta coefficients from linear regression models with Likert attractiveness score (1-5) as the outcome variable, whereas the bottom panel displays average marginal effects from logistic models with a 'very attractive' (0,1) as the outcome variable. The 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). Note, these regressions are estimated on only Waves III and IV, as Waves I and II did not collect information on the interviewer gender. We utilize an omnibus F-test to determine whether all of the subgroup-specific coefficients are statistically identical. Raw p-values are displayed without parentheses above, and adjusted p-values (using a Benjamini-Hochberg false discovery rate correction) are displayed in parentheses below.

	Non-Hispanic Black					Hispanic				
	West	Midwest	South	Northeast	P-value	West	Midwest	South	Northeast	P-value
Attractiveness Score										
P^{AFR} (10 pp)	-0.005	-0.073**	-0.145***	-0.094**	0.000	0.014	0.069*	-0.015	0.012	0.089
	(0.026)	(0.028)	(0.019)	(0.035)	(0.001)	(0.031)	(0.030)	(0.015)	(0.025)	(0.177)
P^{IAM} (10 pp)	-0.318+	-0.100	0.052	0.663	0.099	-0.025	-0.011	-0.034*	-0.027	0.938
	(0.175)	(0.067)	(0.129)	(0.410)	(0.964)	(0.015)	(0.043)	(0.015)	(0.026)	(0.938)
N Respondents	282	367	1236	133		580	109	548	192	
N Interviewers	282	235	528	166		366	183	372	188	
N Observations	995	1304	4384	446		2034	379	1939	672	
Pr("Very Attractive")										
P^{AFR} (10 pp)	-0.002	-0.022**	-0.041***	-0.039**	0.000	0.005	0.015	-0.015*	-0.006	0.023
	(0.007)	(0.008)	(0.006)	(0.013)	(0.001)	(0.010)	(0.011)	(0.006)	(0.017)	(0.140)
P^{IAM} (10 pp)	-0.001	-0.021	-0.024	0.141	0.493	-0.007	-0.021	-0.019**	-0.005	0.377
	(0.093)	(0.072)	(0.050)	(0.316)	(0.964)	(0.006)	(0.018)	(0.006)	(0.014)	(0.840)
N Respondents	276	363	1224	126		576	108	545	184	
N Interviewers	190	176	371	98		248	135	274	115	
N Observations	730	1018	3339	273		1567	292	1460	411	

Table S8: Regression Decomposition by Census Region

This table displays results from stratified regressions of interviewer-rated attractiveness on Sub-Saharan African and Indigenous American genetic similarity proportions among samples of non-Hispanic Black Americans and Hispanic Americans. The top panel shows beta coefficients from linear regression models with Likert attractiveness score (1-5) as the outcome variable, whereas the bottom panel displays average marginal effects from logistic models with a ‘very attractive’ (0,1) as the outcome variable. The 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). We utilize an omnibus F-test to determine whether all of the subgroup-specific coefficients are statistically identical. Raw p-values are displayed without parentheses above, and adjusted p-values (using a Benjamini-Hochberg false discovery rate correction) are displayed in parentheses below.

	Non-Hispanic Black			**Hispanic**		
	Int. under 55	Int. aged 55+	P-value	Int. under 55	Int. aged 55+	P-value
			Attractiveness Score			
P^{AFR} (10 pp)	-0.102***	-0.057**	0.102	0.012	-0.011	0.362
	(0.020)	(0.021)	(0.244)	(0.016)	(0.020)	(0.395)
P^{IAM} (10 pp)	0.158	-0.111	0.353	-0.036*	-0.044**	0.681
	(0.163)	(0.224)	(0.964)	(0.015)	(0.016)	(0.840)
N Respondents	1535	1291		1020	987	
N Interviewers	281	194		262	197	
N Observations	2014	1549		1342	1209	
			Pr("Very Attractive")			
P^{AFR} (10 pp)	-0.032***	-0.021**	0.189	-0.017+	-0.004	0.233
	(0.007)	(0.007)	(0.352)	(0.010)	(0.009)	(0.310)
P^{IAM} (10 pp)	0.037	0.005	0.586	-0.018*	-0.014*	0.700
	(0.073)	(0.070)	(0.964)	(0.008)	(0.007)	(0.840)
N Respondents	1310	1061		829	795	
N Interviewers	186	132		180	133	
N Observations	1613	1227		994	935	

Table S9: Regression Decomposition by Interviewer Age

This table displays results from stratified regressions of interviewer-rated attractiveness on Sub-Saharan African and Indigenous American genetic similarity proportions among samples of non-Hispanic Black Americans and Hispanic Americans. The top panel shows beta coefficients from linear regression models with Likert attractiveness score (1-5) as the outcome variable, whereas the bottom panel displays average marginal effects from logistic models with a ‘very attractive’ (0,1) as the outcome variable. The 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). Note, these regressions are estimated on only Waves III and IV, as Waves I and II did not collect information on the interviewer age. We utilize an omnibus F-test to determine whether all of the subgroup-specific coefficients are statistically identical. Raw p-values are displayed without parentheses above, and adjusted p-values (using a Benjamini-Hochberg false discovery rate correction) are displayed in parentheses below.

	Non-Hispanic Black				**Hispanic**			
	Age 16	Age 22	Age 29	P-value	Age 16	Age 22	Age 29	P-value
				Attractiveness Score				
P^{AFR} (10 pp)	-0.115***	-0.094***	-0.078***	0.213	0.007	-0.008	0.013	0.693
	(0.016)	(0.020)	(0.018)	(0.352)	(0.016)	(0.019)	(0.016)	(0.693)
P^{IAM} (10 pp)	-0.133	0.009	-0.035	0.653	-0.021+	-0.037*	-0.042**	0.376
	(0.101)	(0.205)	(0.140)	(0.964)	(0.012)	(0.017)	(0.013)	(0.840)
N Respondents	2063	1718	2078		1449	1196	1466	
N Interviewers	555	267	229		517	250	231	
N Observations	3585	1718	2078		2514	1196	1466	
				Pr("Very Attractive")				
P^{AFR} (10 pp)	-0.035***	-0.030***	-0.023***	0.235	0.002	-0.017+	-0.006	0.127
	(0.005)	(0.007)	(0.006)	(0.352)	(0.006)	(0.009)	(0.010)	(0.218)
P^{IAM} (10 pp)	-0.016	0.048	-0.026	0.361	-0.011*	-0.016*	-0.018*	0.631
	(0.045)	(0.086)	(0.062)	(0.964)	(0.005)	(0.008)	(0.008)	(0.840)
N Respondents	1723	1328	1695		1256	960	1037	
N Interviewers	381	179	151		364	177	150	
N Observations	2567	1328	1695		1889	960	1037	

Table S10: Regression Decomposition by Respondent Age

This table displays results from stratified regressions of interviewer-rated attractiveness on Sub-Saharan African and Indigenous American genetic similarity proportions among samples of non-Hispanic Black Americans and Hispanic Americans. The top panel shows beta coefficients from linear regression models with Likert attractiveness score (1-5) as the outcome variable, whereas the bottom panel displays average marginal effects from logistic models with a 'very attractive' (0,1) as the outcome variable. The 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). We utilize an omnibus F-test to determine whether all of the subgroup-specific coefficients are statistically identical. Raw p-values are displayed without parentheses above, and adjusted p-values (using a Benjamini-Hochberg false discovery rate correction) are displayed in parentheses below.