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Genetic evidence of assortative mating in humans

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In human populations, assortative mating is almost universally positive, with similarities between partners for quantitative phenotypes[1–6], common disease risk[1,3,7–10], behaviour[6,11], social factors[12–14] and personality[4,5,11]. The causes and genetic consequences of assortative mating remain unresolved because partner similarity can arise from different mechanisms: phenotypic assortment based on mate choice[15,16], partner interaction and convergence in phenotype over time[14,17], or social homogamy where individuals pair according to social or environmental background. Here, we present theory and an analytical approach to test for genetic evidence of assortative mating and find a correlation in genetic value among partners for a range of phenotypes. Across three independent samples of 24,662 spousal pairs in total, we infer a correlation at trait-associated loci between partners for height (0.200, 0.004 standard error, SE) that matched the phenotypic correlation (0.201, 0.004 SE), and a correlation at trait-associated loci for BMI (0.143, 0.007 SE) that was significantly lower than the phenotypic value (0.228, 0.004 SE). We extend our analysis to the UK Biobank study (7,780 pairs), finding evidence of a correlation at trait-associated loci for waist-to-hip ratio (0.101, 0.041 SE), systolic blood pressure (0.138, 0.064 SE) and educational attainment (0.654, 0.014 SE). Our results imply that mate choice, combined with widespread pleiotropy among traits, affects the genomic architecture of traits in humans.

Under direct phenotypic assortment for a heritable trait, pairing of phenotypically similar individuals will increase the proportion of homozygous progeny, create a directional build-up of gametic phase disequilibria after many generations[16,18–20], affect trait correlations between relatives[16,21,22] and influence traits that are genetically correlated. In contrast, there are no genetic consequences in the population if partner similarity arises by an environmental correlation from either social homogamy or an interaction between couples after pairing. Despite the fact that phenotypic similarity between partners for traits such as height and intelligence was first quantified over a century ago[16,20,22,23], the genetic consequences of assortative mating remain unresolved, because many confounding factors affect partner similarity, making it difficult to distinguish among the different mechanisms. As elegantly summarized in the first ever textbook on quantitative genetics: "Assortative mating in man, however, probably seldom arises purely in this way [phenotypic resemblance as a cause of assortative mating] and caution is needed in applying the results to human data"[24].

Studies have attempted to address this question empirically using classical twin designs[13], finding mixed evidence for partner similarity due to initial choice for many phenotypes[1]. A number of recent studies have used genomic data to examine the genetic similarity between couples, by estimating the genome-wide sharing of single-nucleotide polymorphisms (SNPs) and testing whether the observed correlation is greater than expected in the population[25–27]. We show here that an extremely large sample size would be required in order to detect a deviation from expectation in genome-wide sharing (Supplementary Note, Supplementary Figure 1), which implies that results based on SNP sharing are most likely to be explained by other factors[28]. For example, if a phenotype is correlated with social, cultural or ethnic status, and there is social homogamy, then partners will generally be genetically similar[29–31], but this will not affect the genetic architecture of traits in the population. A recent study of 13,068 pairs of adult male–female partners living in the same household found that the genotype of a person is correlated with the height of their partner[32], with both genetic and environmental effects contributing to the observed phenotypic correlation of height between partners[32]. However, examining mate choice in a variance component framework when the data contains close relatives[32] is unlikely to separate confounded environmental

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Table 1 | Phenotypic and genetic correlations among partners for height.

Cohort	Spousal pairs	Number of SNP markers	Phenotypic correlation among pairs (95% CI)	BLUP predictor regression coefficient (SE)	Estimated genetic association among pairs (SE)		Heritability of mate choice (SE)		MLMA predictor regression variance explained (R^2)	
					Male partner	Female partner	Male partner	Female partner	Male partner	Female partner
Composite Sample of ARIC, HRS, LL and MCTFR cohorts	5,044	1,135,785	0.200 (0.186, 0.221)	1.082 (0.040)	0.175 (0.035)	0.185 (0.034)	0.027 (0.065)	0.044 (0.066)	0.005	0.011
23andMe research participant cohort	11,908	1,134,501	0.210 (0.193, 0.227)	1.112 (0.022)	0.213 (0.023)	0.220 (0.023)	0.086 (0.029)	0.005 (0.029)	0.008	0.010
UK Biobank	7,780	1,162,900	0.190 (0.180, 0.210)	1.090 (0.020)	0.191 (0.033)	0.192 (0.030)	0.046 (0.045)	0.005 (0.044)	0.008	0.012

The initial analysis was conducted in a dataset that was a composite of the Atherosclerosis in Communities (ARIC), Health and Retirement (HRS), LifeLines (LL), and Minnesota Center for Twin and Family Research (MCTFR) cohort studies, and the analysis was repeated in the UK Biobank and the 23andMe research participant cohort. Imputed HapMap3 single nucleotide polymorphisms (SNPs) were used and the number of SNPs passing QC in each analysis is shown. Male partner and female partner refer to the focal individual used in the analysis. MLMA refers to mixed linear model association analysis of mate choice, and the SNP estimates gained were then used to predict height in an independent sample. BLUP, best linear unbiased predictor.

Table 2 | Phenotypic and genetic correlations among partners for BMI.

Cohort	Spousal pairs	Number of SNP markers	Phenotypic correlation among pairs (95% CI)	BLUP predictor regression coefficient (SE)	Estimated genetic association among pairs (SE)		Heritability of mate choice (SE)	
					Male partner	Female partner	Male partner	Female partner
Composite Sample of ARIC, HRS, LL and MCTFR cohorts	5,044	1,135,785	0.193 (0.168, 0.229)	0.997 (0.058)	0.099 (0.047)	0.080 (0.048)	0.025 (0.066)	0.001 (0.066)
23andMe research participant cohort	11,908	1,134,501	0.271 (0.255, 0.288)	0.880 (0.033)	0.159 (0.034)	0.215 (0.033)	0.015 (0.029)	0.063 (0.030)
UK Biobank	7,780	1,162,900	0.205 (0.170, 0.235)	0.987 (0.029)	0.117 (0.038)	0.158 (0.047)	0.030 (0.045)	0.014 (0.043)

The initial analysis was conducted in a dataset that was a composite of the Atherosclerosis in Communities (ARIC), Health and Retirement (HRS), LifeLines (LL), and Minnesota Center for Twin and Family Research (MCTFR) cohort studies, and the analysis was repeated in the UK Biobank and the 23andMe research participant cohort. Imputed HapMap3 SNPs were used and the number of SNPs passing QC in each analysis is shown. Male partner and female partner refer to the focal individual used in the analysis. BLUP, best linear unbiased predictor.

and genetic factors that affect partner similarity, meaning that the causes and genetic consequences of assortative mating remain obscured (Supplementary Note). In this study, we devise an analytical framework that is unbiased by environmental confounding or population stratification, to estimate the genetic association between partners for a phenotype, allowing for a determination of the degree to which phenotypic similarity of mates reflects a correlation among partners at trait-associated loci.

We first analysed height and body mass index (BMI) in three independent samples: a composite sample of 5,044 couples taken from a range of publicly available cohort studies; a sample of 7,780 couples from the UK Biobank study; and a sample of 11,908 couples from the 23andMe research participant cohort (Supplementary Table 1). In all samples, we selected heterosexual couples of European ethnicity, and we ensured that there were no close relatives within the data. We began by estimating the phenotypic correlation among couples for height and BMI after accounting for age and sex differences in both traits. We then predicted an individual's phenotype from a genome-wide genetic predictor created from their partner's genotype. To create the genetic predictor, we devised a random-effects approach. We first re-analysed results from recent genetic studies of height[33] and BMI[34] to ensure that the samples used in our study were independent of the discovery samples. We then re-estimated the SNP effects (SNPs on HapMap3) in a random-effect model that converts the least-squares SNP estimates into approximate best linear unbiased predictors (summary statistic BLUP, or SBLUP; see Methods). The SBLUP approach maximizes prediction power as it creates a genetic predictor with BLUP properties[35,36] (Supplementary Figure 2). From summary statistics of the meta-analysed genome-wide association study (GWAS), our SBLUP predictors for height and BMI had BLUP properties (slope of the regression of phenotype on genetic predictor of ~1, Tables 1,2), and explained 18% of the phenotypic variation of height and 8% of the phenotypic variation of BMI, as compared with estimates of 17% and 7%, respectively, obtained by using genetic predictors made directly from GWAS summary statistics[33,34].

We subsequently estimated the regression coefficient from a linear regression of the phenotype of a female on the SBLUP genetic predictor of their male partner, and vice versa, within a mixed-effects model. To further account for population stratification, we adjusted the genetic predictor by the first 20 principal components generated from genotype data prior to the analysis[33,34,37]. We demonstrate by theory (Supplementary Methods) and through simulation (Supplementary Figures 2, 3 and 4) that if there is direct assortative mating for a phenotype, and the predictor has BLUP properties, then the regression coefficient from a linear regression of the phenotype of one partner on the genetic predictor of the other is expected to equal the phenotypic correlation among couples. Furthermore, we show by theory (Supplementary Methods) and simulation (Supplementary Figure 5) that indirect assortment for an unmeasured genetically correlated trait would also create a correlation among couples at trait-associated loci for the recorded phenotype, with the value dependent on the phenotypic and genetic correlations of the different phenotypes, the ratio of their heritability, and the

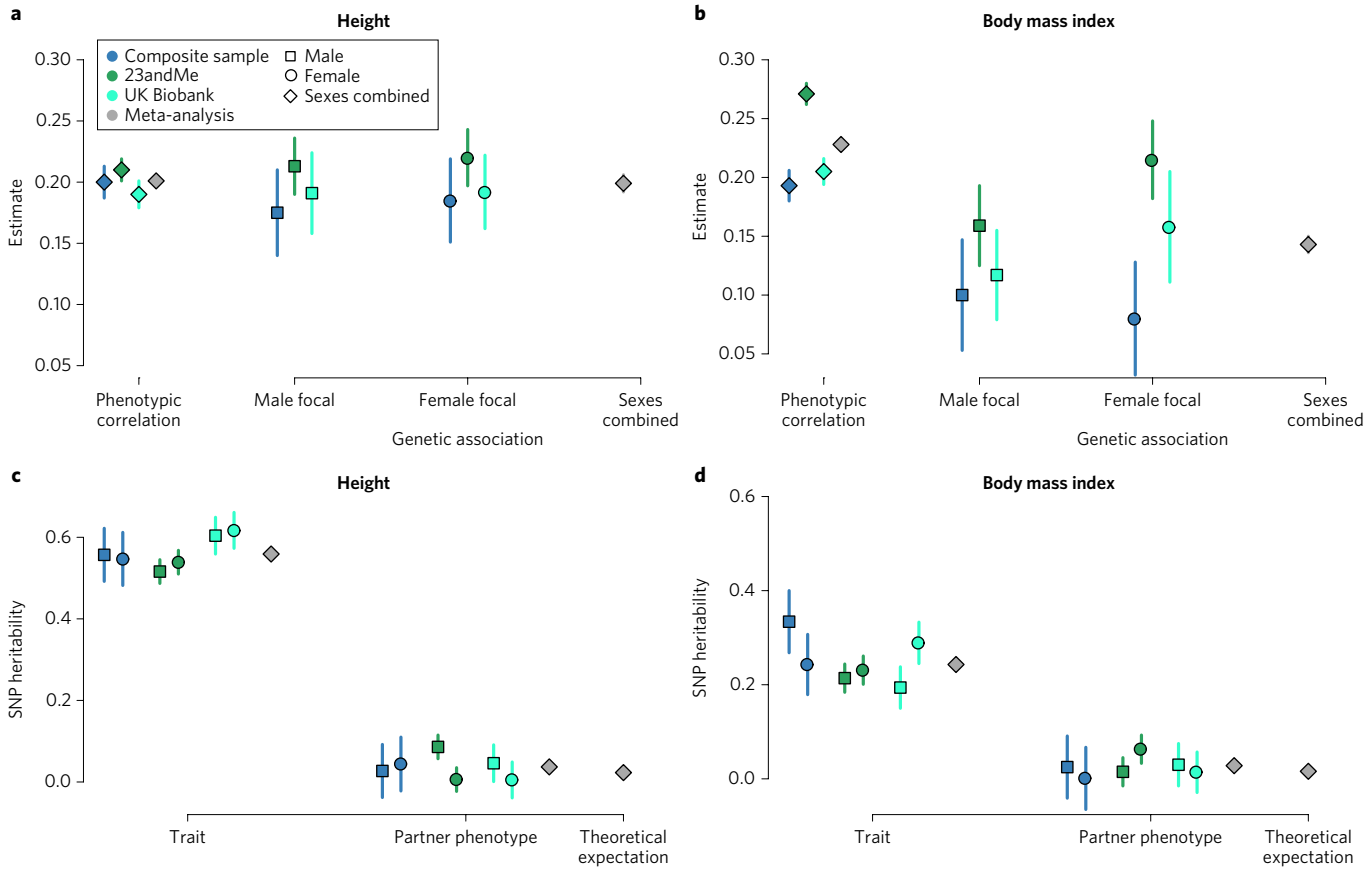

Figure 1 | Assortative mating for height and BMI creates a correlation at trait-associated loci among partners. In blue ($N = 5{,}044$ couples) are the results of analysis conducted in a dataset that was a composite of the Atherosclerosis in Communities, Health and Retirement, LifeLines, and Minnesota Center for Twin and Family Research cohort studies. The analysis was repeated in the UK Biobank (cyan, $N = 7{,}710$) and 23andMe research participant cohort (green, $N = 11{,}908$), and then the results were meta-analysed (grey). **a**,**b**, The phenotypic correlation among spousal pairs is shown, after correcting for age and sex differences. 'Male focal' and 'female focal' refer to the focal individual used in the analysis to estimate the genetic association among partners for height (**a**) and BMI (**b**), with the combined meta-analysis value across studies in grey. **c**,**d**, Trait refers to the SNP heritability for height (**c**) and BMI (**d**), in males, females, and meta-analysed across sexes and studies. From the meta-analysis value, a theoretical expectation was derived for the heritability estimate gained when treating the phenotype of an individual's partner as the phenotype of that individual, and then partner phenotype refers to those estimates gained from the data. Error bars give the SE of the estimates.

degree of partner assortment (Supplementary Methods). Therefore, our approach provides a direct estimate of the correlation among couples at trait-associated loci but cannot differentiate between direct assortment on a phenotype and assortment on a genetically correlated trait. However, our approach does differentiate between assortative mating based on selection of phenotypic characteristics and assortative mating based on shared social or environmental factors, because under only social/environmental homogamy we would not expect an association between genetic predictors of phenotype within the mixed-effect model of equation (1). This is because the equation accounts for population stratification, both by regressing principal components from the genetic predictor, and by fitting a relationship matrix estimated from the SNP markers.

We find evidence for a genetic basis of assortative mating for both height and BMI in all samples (Tables 1,2, Fig. 1). Across all samples, the meta-analysed phenotypic correlation among partners was 0.201 for height (0.004 SE) and 0.228 for BMI (0.004 SE; Tables 1,2, Fig. 1). For height, the meta-analysed value of the regression coefficient from a linear regression of the SBLUP genetic predictor of males and the phenotype of their female partner, and vice versa (meta-analysed value 0.200 with SE of 0.007, Table 2, Fig. 1a), did not significantly differ from the phenotypic correlation. For BMI, the meta-analysed estimate of the regression coefficient was 0.143 (0.007 SE), which was lower than the phenotypic correlation (Table 2, Fig. 1b). The regression coefficients did not differ when using either the male or female partner as the focal individual (Tables 1 and 2; Fig. 1a and b). For both phenotypes, the regression coefficient was significantly different from the expectation of zero under only social homogamy or partner interaction (Supplementary Figure 3), and we demonstrate that correlation in ancestry among partners in our data would not drive the results we present (Supplementary Figure 6). For height, obtaining a genetic estimate equal to the phenotypic estimate under indirect assortment would require a combination of a partner correlation that is greater than 0.2, for a trait that has a genetic correlation of >0.5 with height, and a heritability of >0.8, which is unlikely given that there is no evidence for a trait fitting these criteria. Therefore, our results suggest that there is direct assortative mating on height across all studies. For BMI, there may be indirect assortment on a genetically correlated trait, or there may be a combination of direct assortment and environmental factors that lead to phenotypic similarity among partners. For example, couples may additionally converge in phenotype over time, creating a mismatch in phenotypic and genetic estimates. Regardless of the mechanism, we find evidence of assortment at height- and BMI-associated loci implying gametic phase disequilibrium at those loci in the human population.

We estimated the heritability (h^2_{SNP}) associated with common SNPs for realized phenotypic mate choice in unrelated individuals,

by treating an individual's partner's phenotype as their own, and we tested this estimate against a derived theoretical expectation (Supplementary Methods, Supplementary Figure 7). The meta-analysed estimate of h^2_{SNP} for height was 0.559 (0.012) and that for BMI was 0.243 (0.012) across samples, with no evidence for significant differences among samples or sexes (Fig. 1d). Using these meta-analysis estimates and the phenotypic partner correlations, we calculated expectations of the h^2_{SNP} for realized phenotypic mate choice of 0.023 for height and 0.016 for BMI (Supplementary Methods and Supplementary Figure 7). The estimates of h^2_{SNP} for partner phenotype were not significantly different from their expectation, giving meta-analysis values of 0.030 (0.012) for height and 0.026 (0.012) for BMI (Tables 1,2, Fig. 1c and d). Finally, we conducted a mixed linear model association analysis of assortative mating for height, in which we tested for associations between the phenotype of an individual and the genotype of their partner. We created a genetic predictor from the SNP estimates gained from this analysis and used this to predict height in an independent sample of individuals from the combined cohorts that were not part of, or related to, the couples used in the analysis (Supplementary Table 1). The genetic predictor generated from the SNP results of the composite sample was significantly associated with height in the independent prediction sample (Table 1, prediction $R^2=0.011$, $p<2\times10^{-16}$ for the female focal analysis; prediction $R^2=0.005$, $p<4\times10^{-6}$ for the male focal analysis), and this result was replicated in both the UK Biobank and 23andMe samples (Table 1). These results also conformed to our expectation from theory and simulation (Supplementary Methods and Supplementary Figure 8). Taken together, these analyses suggest that the same loci underlie the trait and assortment on the trait, and provide further support for a correlation among partners at height- and BMI-associated loci.

We then extended our analysis to a range of phenotypes in the UK Biobank study. Of the 7,780 couples identified using household information (see Methods) with both phenotypic and genotypic data, all had measures of educational attainment (years), 4,323 had measures of bone mineral density, 7,773 had measures of waist-to-height ration (WHR) and 7,173 had measures of blood pressure. We corrected the phenotypes for age and sex differences and standardized to a *z*-score before estimating the phenotypic correlation. To estimate the genetic association, we reanalysed summary statistics from recent genetic studies[38–41] to create SBLUP statistics, and we then predicted an individual's phenotype from a genome-wide SBLUP genetic predictor created from their partner's genotype.

We find evidence for a correlation among partners at trait-associated loci for WHR, blood pressure and educational attainment (Fig. 2). In contrast, there was no evidence for either a phenotypic correlation for bone mineral density, or a correlation at bone mineral density associated loci, among partners (Fig. 2). Our findings for blood pressure, WHR and BMI probably reflect assortment on some combination of these phenotypes, or an alternative component of metabolism, given previous evidence for a genetic correlation between metabolic syndrome traits such as BMI, WHR and blood pressure[42]. For educational attainment, the correlation at trait-associated loci (0.654, 0.014 SE) was significantly higher than the phenotypic correlation (0.412, 0.011 SE). Previous studies indicate that a genetic predictor for educational attainment explains more variation in cognitive performance than educational attainment[43], and provide evidence[41,43] for a genetic correlation between educational attainment and cognitive performance that is higher than the phenotypic correlation of ~0.5. A partner correlation of ~0.65 for an unmeasured trait of cognitive performance with heritability ~0.7 that has phenotypic correlation ~0.6 and genetic correlation ~0.8 with educational attainment, and a heritability for educational attainment of ~0.35, would result in the estimates that we obtain here (Supplementary Methods). We support these results by directly estimating the correlation among partners for genetic predictors of both height and

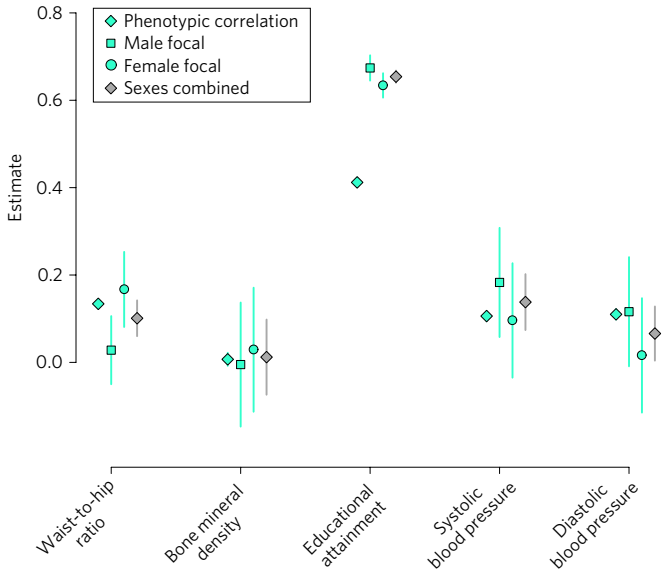

Figure 2 | Genetic evidence for assortative mating across a range of phenotypes in the UK Biobank study. Of the 7,780 couples identified in the UK Biobank with both phenotypic and genotypic data, all had measures of educational attainment (years), 4,323 had measures of bone mineral density, 7,773 had measures of waist-to-hip ratio and 7,173 had measures of blood pressure. We corrected the phenotypes for age and sex differences and standardized to a *z*-score before estimating the phenotypic correlation. To estimate the genetic association, we reanalysed summary statistics from recent genetic studies to create SBLUP statistics (see Methods). 'Male focal' (square) and 'female focal' (circle) refer to the focal individual used in the analysis to estimate the genetic association among partners, and 'sexes combined' refers to the meta-analysed value.

educational attainment, calculated from the ordinary least-squares association study estimates (Supplementary Figure S9). For educational attainment, we find that this direct estimate of the correlation at genetic value among partners is higher than the expected value given a phenotypic correlation of 0.4. In contrast, for height, the correlation at genetic value among partners conforms to the expectation given a phenotypic correlation of 0.2. While these findings on phenotypes other than height and BMI require replication that was not feasible in this study, they suggest that in addition to height there is phenotypic assortment in the UK population on traits that are associated with educational attainment and metabolism that creates a correlation among partners at trait-associated loci.

In summary, we show that the observed similarity in height, metabolic traits and educational attainment between partners reflects a correlation at trait-associated loci to differing degrees across traits. For height, there is likely to be direct phenotypic assortment, which is why our findings support a recent study[32], despite the potential for bias by environmental confounding in that study. Secondary assortment on a genetically correlated trait probably leads to a correlation at trait-associated loci for educational attainment. Finally, for BMI, WHR and blood pressure there may be indirect assortment on a genetically correlated metabolic trait, or there may be a combination of direct assortment and environmental sharing that leads to phenotypic similarity among partners. For many phenotypes, shared environment probably plays a role in both phenotypic variation and mate choice. Our approach, which is free of environmental confounding, enables a direct estimation of the degree to which assortative mating creates a genetic correlation among partners at trait-associated loci for any phenotype in populations of any species.

Our results represent a snapshot of contemporary assortative mating in the human population, and we do not know whether mate

choice was historically consistent, or whether equilibrium has been reached. If we assume equilibrium and an equilibrium heritability of 0.7 for height and 0.4 for BMI[44], then our estimates of the degree to which the phenotypic correlation reflects a correlation at genetic values predict that the additive genetic variance and heritability are inflated by 17% and 5% for height, and 7% and 4% for BMI, respectively, relative to a population with random mating (see eq. 7.19 of previous work[45]). For educational attainment, assuming an equilibrium heritability of 0.4 implies an inflation of 27% and 24% for the additive genetic variance and heritability, respectively. These results have implications for the interpretation of resemblance between relatives and for estimates of genetic parameters in populations.

Methods

We define assortative mating to be a phenotypic assortment that creates a directional build-up of gametic phase disequilibria at the underlying trait loci[15,16,18,19,45]. Phenotypic assortment can be based either directly on a phenotype, or indirectly on the phenotype of a genetically correlated trait. We distinguish this from assortative mating under heterogamy/homogamy where assortment occurs based on the environment (culture, social status, ethnicity), which can create a correlation in trait value if the phenotype is correlated with these environmental factors. Cultural homogamy can also create a correlation in genetic similarity among individuals if there is correlated population stratification among couples[46]. Our aim is to control for population stratification in order to quantify assortative mating genome-wide for height and BMI within populations.

Data. *Composite cohort sample.* We used a composite sample of data across a number of cohort studies (Supplementary Table 1). We selected heterosexual couples by identifying individuals of European ethnicity who had (i) a child together (inferred from genotype data and/or known pedigree structure), (ii) SNP genotype data, and (iii) phenotype data for height and BMI. Within each cohort, we adjusted the phenotype for age and standardized to *z*-scores in males and females separately, which removed differences in both mean and variance between males and females, and across cohorts. We then removed any couples that contained an outlying individual with a phenotypic value >7 SD from the mean.

All of the composite sample cohorts were independently imputed to a 1000 Genomes reference panel, using identical quality control (QC) procedures on the initial datasets of per-SNP missing data rate of <0.01, minor allele frequency >0.01, per-person missing data rate <0.01, and Hardy–Weinberg disequilibrium p-value $<1\times10^{-6}$. Imputation was performed in two stages. First, the target data were haplotyped using HAPI-UR. Second, Impute2 was used to impute the haplotypes to the 1,000-genome reference panel (release 1, version 3). We then extracted best-guess genotypes at common SNPs typed in the HapMap 3 European sample with imputation info score >0.5. We conducted principal component analysis within each cohort and removed individuals with principal eigenvector values that were >7 SD from the mean. We calculated allele frequencies within each of the cohorts and removed any SNPs with allele frequency differences across cohorts larger than 0.2. We then combined the cohorts together and conducted an additional round of QC of per-SNP missing data rate of <0.01, minor allele frequency >0.01, per-person missing data rate <0.01 and Hardy–Weinberg disequilibrium p-value $<1\times10^{-6}$. Finally, we removed one of any pair of individuals with estimated relatedness in a genetic relatedness matrix (see below) greater than a threshold of 0.05. All QC was conducted using PLINK v1.9.

23andMe research participant cohort. We repeated our analysis using data from the 23andMe research participant cohort, which is drawn from the customer base of 23andMe, a consumer genetics company. This cohort has been described in detail previously[47,48]. Participants provided informed consent and answered survey questions online, under a protocol approved by the external institutional review board Ethical & Independent Review Services (E&I Review), which is accredited by the Association for the Accreditation of Human Research Protection Programs. Couples were selected who had at least one child in the database, and for whom self-reported height and weight were available. Relatives were then excluded, by removing one from any pair of individuals that shared more than 700 cM of total identity by descent. Participant genotype data were phased out of sample using a modified version of BEAGLE, and were then imputed in batches of 8,000 to 9,000 individuals against the September 2013 release of the 1000 Genotypes Project haplotypes using Minimac2, with five rounds and 200 states for parameter estimation. Analyses were limited to 15.5 million SNPs with imputed $R^2>0.5$ averaged across all batches and $R^2>0.3$ in every batch.

UK Biobank Sample. We repeated our analyses using data from the UK Biobank following a recent study[32]. The UK Biobank Axiom (UKBA) array from Affymetrix was custom-designed for the purpose of genotyping the UK Biobank participants. The UKBA array is being used to genotype ~450,000 of the ~500,000 UK Biobank participants. The other ~50,000 samples were genotyped on the closely related UK BiLEVE (UKBL) array. The UKBA array is an updated version of the UKBL array that includes additional markers, which replaced a small fraction of the markers used for genome-wide coverage. The UKBL cohort and the rest of UK Biobank differ only in small details of the DNA processing stage and the two SNP arrays are very similar with over 95% common marker content. The ~50,000 samples genotyped on the UKBL array are included in the interim release. After QC procedures have been applied (see Supplementary Methods), the interim UK Biobank data release contains genotypes for 152,736 samples that passed sample QC (~99.9% of total samples), and 806,466 SNPs that passed SNP QC in at least one batch (>99% of the array content).

Imputed genotype data are provided as part of the data release. Prior to imputation, genotypes SNPs on the UKBA chip and UKBL chip were removed if (i) they were missing across multiple batches, (ii) they were multiallelic or (iii) they were of minor allele frequency, <1%. 1,037 sample outliers were also removed. These filters resulted in a dataset with 641,018 autosomal SNPs in 152,256 samples. The result of the imputation process using a merged reference panel from the UK10K and 1000 Genomes data (Supplementary Methods) is a dataset with 73,355,667 SNPs, short indels and large structural variants in 152,249 individuals. Selecting out only SNPs with imputation 'info score' >0.3 and minor allele count >=5 gives ~40M SNPs in 152,249 individuals. Principal component analysis and the self-declared ethnicity were used to derive a 'White British' subset of samples. In addition, samples were excluded if they had (i) at least one identified closely related sample ($r>0.1$); (ii) a genetically inferred sex that did not match the self-reported gender; (iii) ~500 extreme heterozygosity or missing genotype outliers. These filters resulted in a dataset with 112,338 samples, and further exclusion of one individual from a pair with an estimate SNP marker relatedness greater than 0.05 using GCTA (Supplementary Methods) resulted in a final sample of 108,042 samples. We then selected out 1,162,900 HapMap3 SNPs. BMI and height were recorded for every individual, and we selected only the first recorded measures. We then adjusted both phenotypes for age (factor with levels for each age between 40 and 73) and sex differences. BMI and height phenotypes 5 SD away from the mean were not included in the analyses. Both phenotypes were then converted to *z*-scores with zero mean and variance of 1.

From this set of 108,042 individuals, we used household sharing information to identify pairs of individuals who were less than 10 years apart in age, who both reported living with their spouse, in the same location, for the same length of time, with the same number of people in their household, and who had parents of different ages. This provided a set of 7,780 couples with complete height, BMI and genotype data. From these couples, 4,323 couples had complete bone mineral density data (UK Biobank unique data identifier 3148.0.0), 7,773 had measures of WHR (UK Biobank unique data identifier 48-0.0 and 49-0.0), 7,173 had measures of blood pressure (UK Biobank unique data identifiers 4079-0.0 and 4080-0.0) and all 7,780 had reported their educational attainment (UK Biobank unique data identifier 6138-0.0). We converted educational attainment to a continuous yearly measure as in a previous study[41]. We then adjusted the phenotypes for age (factor with levels for each age between 40 and 73) and sex differences, removed individuals 5 SD away from the mean, and standardized the phenotype to a *z*-score with zero mean and variance of 1.

Statistical analysis. *Phenotypic correlation.* We began by estimating the phenotypic correlation among couples for all phenotypes after accounting for age and sex differences in both traits.

Approximate best linear unbiased genetic predictor. We predicted an individual's phenotype from a genome-wide genetic predictor created from their partner's genotype. To create the genetic predictor, we devised a random-effect approach (Supplementary Methods). We first re-analysed results from recent genetic studies of height[33] and BMI[34] to ensure that the samples used in our study were independent of the discovery samples. For the extended UK Biobank analysis, we used results from genetic studies of bone mineral density[38], systolic and diastolic blood pressure[39], WHR[40] and educational attainment[41], ensuring that the UK Biobank sample was not included within the discovery meta-analysis. We then re-estimated the SNP effects (SNPs on HapMap3) in a random-effect model that converts the least-squares SNP estimates into approximate best linear unbiased predictors (summary statistic BLUP: SBLUP; Supplementary Methods). The SBLUP approach maximizes prediction power, as it creates a genetic predictor with BLUP properties[35,36] (Supplementary Figure 2).

Prediction accuracy of a predictor with BLUP properties. We then estimated the amount of variation in height and BMI that can be explained by a predictor with BLUP properties. To do this, we estimated principal components of the HapMap 3 best-guess imputed SNPs for the combined cohort and we selected the top 20 principal components to create a $N\times P$ matrix $\mathbf{Z}$ of eigenvectors across the P selected principal components. We then regressed the estimated genetic predictor onto the eigenvectors as $\hat{\mathbf{g}}_m=\mu+\mathbf{Z}\boldsymbol{\beta}_m+\mathbf{e}_m$ and $\hat{\mathbf{g}}_f=\mu+\mathbf{Z}\boldsymbol{\beta}_f+\mathbf{e}_f$ for males (m)

and females (f), respectively, where μ is the mean and $\boldsymbol{\beta}$ is a $P \times 1$ vector of the regression coefficients, and e is the residual error. We adjusted the predictors as $\hat{\mathbf{g}}_{\mathrm{P_m}} = \hat{\mathbf{g}}_{\mathrm{m}} - \mathbf{Z}\hat{\boldsymbol{\beta}}_{\mathrm{m}}$ and $\hat{\mathbf{g}}_{\mathrm{P_f}} = \hat{\mathbf{g}}_{\mathrm{f}} - \mathbf{Z}\hat{\boldsymbol{\beta}}_{\mathrm{f}}$. We then regressed the phenotypic values onto the adjusted genetic predictors as $\mathbf{y}_{\mathrm{m}} = \mu + \hat{\mathbf{g}}_{\mathrm{P_m}} + \mathbf{e}$ and $\mathbf{y}_{\mathrm{f}} = \mu + \hat{\mathbf{g}}_{\mathrm{P_f}} + \mathbf{e}$, where $\mathbf{y}_{\mathrm{m}}$ and $\mathbf{y}_{\mathrm{f}}$ are $N \times 1$ vectors and represent the phenotype for males and females, respectively. In the UK Biobank sample and the 23andMe cohort, the same approach was followed, with the top 20 principal components computed from a subset of genotyped SNPs[47,48]. This approach removes population stratification (associated with the leading axes of genetic variation) in the predictor, before estimating the amount of variation in height and BMI explained by the genetic predictor, and the slope of the relationship between phenotype and genetic predictor[49–52]. These two parameters are key to the later analysis.

Predicting an individual's phenotype from the genotype of their partner. To estimate the degree to which assortative mating creates a genetic correlation at trait-associated loci, we first determined the relationship between the genetic predictor of males and the phenotype of their female partner, and vice versa, as:

$$\mathbf{y}_{\mathrm{m}} = \mu_{\mathrm{m}} + \hat{\mathbf{g}}_{\mathrm{P_f}} + \mathbf{u}_{\mathrm{m}} + \mathbf{e}_{\mathrm{m}};\ \mathbf{y}_{\mathrm{f}} = \mu_{\mathrm{f}} + \hat{\mathbf{g}}_{\mathrm{P_m}} + \mathbf{u}_{\mathrm{f}} + \mathbf{e}_{\mathrm{f}} \quad (1)$$

where $\mathbf{u}$ is an $N \times 1$ vector of the total genetic effects of the individuals, with $\mathbf{u} = N(0, \mathbf{A}\sigma^2_{\mathrm{G}})$. Here, $\mathbf{A}$ is the genetic relationship matrix between either males (when estimating $\mathbf{u}_{\mathrm{m}}$) or females (when estimating $\mathbf{u}_{\mathrm{f}}$), with its jlth element being $A_{jl} = \frac{1}{N}\sum_{i=1}^{N} \frac{(x_{ij} - 2p_i)(x_{il} - 2p_i)}{2p_i(1-p_i)}$ where p_i is the frequency of the minor allele of the imputed HapMap3 common SNP i, and x is the SNP genotype (best guess for the combined cohort and rounded imputed diploid dosage for the 23andMe cohort). The genetic relationship matrix accounts for population stratification in the phenotype, as it is equivalent to fitting all the principal components within the model. Equation (1) was estimated using the GREML function in GCTA v1.25. Under different types of assortative mating, we derive the expectation of the regression coefficient from a linear regression of the phenotype of males on the genetic predictor of their female partners, and vice versa, in the Supplementary Methods.

Common SNP heritability of realized mate choice. We then estimated the heritability associated with common SNPs (h^2_{SNP}) for realized mate choice of height and BMI as:

$$\mathbf{y}_{\mathrm{m}} = \mu_{\mathrm{m}} + \mathbf{Z}\boldsymbol{\beta}_{\mathrm{m}} + \mathbf{u}_{\mathrm{f}} + \mathbf{e}_{\mathrm{m}},\ \mathbf{y}_{\mathrm{f}} = \mu_{\mathrm{f}} + \mathbf{Z}\boldsymbol{\beta}_{\mathrm{f}} + \mathbf{u}_{\mathrm{m}} + \mathbf{e}_{\mathrm{f}} \quad (2)$$

with notation the same as above. Equation (2) controls for population stratification by fitting the effects of the first 20 principal components estimated within the 23andMe data before then estimating the effects $\mathbf{u} = N(0, \mathbf{A}\sigma^2_{\mathrm{G}})$. We selected Hapmap3 common SNPs from the best-guess imputed SNP data to estimate $\mathbf{A}$, and thus σ^2_{G} is the variance explained by those SNPs. Equation (2) was estimated using the GREML function in GCTA v 1.25. Again, we derive the expectation of the regression coefficient from a linear regression of the phenotype of males on the genetic predictor of their female partners, and vice versa, in the Supplementary Methods.

Mixed linear model association analysis of realized mate choice. To identify the genomic regions associated with realized mate choice and test for a single genetic basis of the trait and mate choice, which implies direct assortment on phenotype, we conducted a mixed linear model association analysis[53] as:

$$\mathbf{y}_{\mathrm{m}} = \mu_{\mathrm{m}} + \mathbf{X}_{\mathrm{f}i}\beta_i + \mathbf{u}_{\mathrm{m}} + \mathbf{e}_{\mathrm{m}};\ \mathbf{y}_{\mathrm{f}} = \mu_{\mathrm{f}} + \mathbf{X}_{\mathrm{m}i}\beta_i + \mathbf{u}_{\mathrm{f}} + \mathbf{e}_{\mathrm{f}} \quad (3)$$

with notation the same as above, where β_i is the regression coefficient, $\mathbf{X}_{\mathrm{m}i}$ and $\mathbf{X}_{\mathrm{f}i}$ are $N \times 1$ vectors of genotypes for each SNP $i = 1, \ldots, k$ (coded as 0, 1 or 2 defining the number of reference alleles), for males and females respectively, $\boldsymbol{u}_{\mathrm{m}}$ and $\boldsymbol{u}_{\mathrm{f}}$ are the polygenic effects (random effect) for males and females respectively, and $\mathbf{e}$ is the residual. We selected HapMap3 common SNPs (MAF ≥ 0.01) from the best-guess imputed SNP data in equation (3) as we did for equations (1) and (2). Equation (3) was estimated using the MLMA function in GCTA v1.25. Again, we derive the expectation of the regression coefficient from a linear regression of the phenotype of males on the genetic predictor of their female partners and vice versa in the Supplementary Methods[54,55].

Simulation study. To support our results we conducted a simulation study using real genotype data that is described in full in the Supplementary Methods.

Data availability. We utilize publicly available dbGaP data from the Atherosclerosis Risk in Communities (ARIC) Study (dbGaP phs000090.v1.p1), Health and Retirement Study (HRS: dbGaP phs000428.v1.p1), and Resource for Genetic Epidemiology Research on Adult Health and Aging (GERA: dbGaP phs000674.v1.p1). We also use data from the UK Biobank which is a publicly available resource on request. Access to individual-level phenotypic, genetic and partner identity data from the 23andMe cohort, ARIC, TWINGENE, Minnesota Center for Twin and Family Research (MCTFR) and the LifeLines Study is available with the obtainment of a research agreement. The summary data that support the findings of the study are available from M.R.R. upon request.

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References

1. Zietsch, B. P., Verweij, K. J. H., Heath, A. C. & Martin, N. G. Variation in human mate choice: simultaneously investigating heritability, parental influence, sexual imprinting, and assortative mating. *Am. Nat.* **177,** 605–616 (2011).
2. Silventoinen, K., Kaprio, J., Lahelma, E., Viken, R. J. & Rose, R. J. Assortative mating by body height and BMI: Finnish twins and their spouses. *Am. J. Hum. Biol.* **15,** 620–627 (2003).
3. Maes, H., Neale, M. & Eaves, L. Genetic and environmental factors in relative body weight and human adiposity. *Behav. Genet.* **27,** 325–351 (1997).
4. Keller, M. C. *et al.* The genetic correlation between height and IQ: Shared genes or assortative mating? *PLoS Genet.* **9,** e1003451 (2013).
5. Eaves, L. J. Assortative mating and intelligence: An analysis of pedigree data. *Heredity (Edinb.)* **30,** 199–210 (1973).
6. Eaves, L. J. & Heath, A. C. Detection of the effects of asymmetric assortative mating. *Nature* **289,** 205–206 (1981).
7. Vandenberg, S. G. Assortative mating, or who marries whom? *Behav. Genet.* **2,** 127–157 (1972).
8. Hippisley-Cox, J. Married couples' risk of same disease: Cross sectional study. *Br. Med. J.* **325,** 636 (2002).
9. Willemsen, G. Assortative mating may explain spouses' risk of same disease. *Br. Med. J.* **326,** 396a–396 (2003).
10. Ajslev, T. A. *et al.* Assortative marriages by body mass index have increased simultaneously with the obesity epidemic. *Front. Genet.* **3,** 125 (2012).
11. Eaves, L. *et al.* Comparing the biological and cultural inheritance of personality and social attitudes in the Virginia 30,000 study of twins and their relatives. *Twin Res.* **2,** 62–80 (1999).
12. Heath, A. C. *et al.* No decline in assortative mating for educational level. *Behav. Genet.* **15,** 349–369 (1985).
13. Heath, A. C. & Eaves, L. J. Resolving the effects of phenotype and social background on mate selection. *Behav. Genet.* **15,** 15–30 (1985).
14. Heath, A. C., Eaves, L. J., Nance, W. E. & Corey, L. A. Social inequality and assortative mating: Cause or consequence? *Behav. Genet.* **17,** 9–17 (1987).
15. Falconer, D. & Mackay, T. F. C. *Introduction to Quantitative Genetics* (Pearson Prentice Hall, 1996).
16. Fisher, R. A. The correlation between relatives on the supposition of Mendelian inheritance. *Trans. R. Soc. Edinb.* **52,** 399–433 (1918).
17. Nance, W. E., Corey, L. A., Rose, R. J. & Eaves, L. J. Relevance of the marriages of twins to the causal analysis of nonrandom mating. *Prog. Clin. Biol. Res.* **69** (Pt B), 61–71 (1981).
18. Crow, J. F. & Kimura, M. *An Introduction to Population Genetics Theory* (Harper and Row, 1970).
19. Wilson, S. R. The correlation between relatives under the multifactorial model with assortative mating. *Ann. Hum. Genet.* **37,** 189–204 (1973).
20. Wright, S. Systems of mating. III. Assortative mating based on somatic resemblance. *Genetics* **6,** 144–161 (1921).
21. Eaves, L. J., Last, K., Martin, N. G. & Jinks, J. L. A progressive approach to non-additivity and genotype-environmental covariance in the analysis of human differences. *Br. J. Math. Stat. Psychol.* **30,** 1–42 (1977).
22. Pearson, K. & Lee, A. On the laws of inheritance in man I. Inheritance of physical characters. *Biometrika* **2,** 357–462 (1903).
23. Galton, F. Measurement of character. *Fortn. Rev.* **36,** 179–185 (1884).
24. Falconer, D. S. *Introduction to Quantitative Genetics* (Ronald, 1960).
25. Zou, J. Y. *et al.* Genetic and socioeconomic study of mate choice in Latinos reveals novel assortment patterns. *Proc. Natl Acad. Sci. USA* **112,** 13621–13626 (2015).
26. Guo, G., Wang, L., Liu, H. & Randall, T. Genomic assortative mating in marriages in the United States. *PLoS ONE* **9,** e112322 (2014).
27. Domingue, B. W., Fletcher, J., Conley, D. & Boardman, J. D. Genetic and educational assortative mating among US adults. *Proc. Natl Acad. Sci. USA* **111,** 7996–8000 (2014).
28. Abdellaoui, A., Verweij, K. J. H. & Zietsch, B. P. No evidence for genetic assortative mating beyond that due to population stratification. *Proc. Natl Acad. Sci. USA* **111,** E4137 (2014).
29. Abdellaoui, A. *et al.* Association between autozygosity and major depression: stratification due to religious assortment. *Behav. Genet.* **43,** 455–467 (2013).
30. Abdellaoui, A. *et al.* Educational attainment influences levels of homozygosity through migration and assortative mating. *PLoS ONE* **10,** e0118935 (2015).

31. Sebro, R., Hoffman, T. J., Lange, C., Rogus, J. J. & Risch, N. J. Testing for non-random mating: Evidence for ancestry-related assortative mating in the Framingham heart study. *Genet. Epidemiol.* **34,** 674–679 (2010).
32. Tenesa, A., Rawlik, K., Navarro, P. & Canela-Xandri, O. Genetic determination of height-mediated mate choice. *Genome Biol.* **16,** 269 (2016).
33. Wood, A. R. *et al.* Defining the role of common variation in the genomic and biological architecture of adult human height. *Nat. Genet.* **46,** 1173–1186 (2014).
34. Locke, A. E. *et al.* Genetic studies of body mass index yield new insights for obesity biology. *Nature* **518,** 197–206 (2015).
35. de Los Campos, G., Vazquez, A. I., Fernando, R., Klimentidis, Y. C. & Sorensen, D. Prediction of complex human traits using the genomic best linear unbiased predictor. *PLoS Genet.* **9,** e1003608 (2013).
36. Goddard, M. E., Wray, N. R., Verbyla, K. & Visscher, P. M. Estimating effects and making predictions from genome-wide marker data. *Stat. Sci.* **24,** 517–529 (2009).
37. Price, A. L. *et al.* Principal components analysis corrects for stratification in genome-wide association studies. *Nat. Genet.* **38,** 904–909 (2006).
38. Zheng, H.-F. *et al.* Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature* **526,** 112–117 (2015).
39. International Consortium for Blood Pressure Genome-Wide Association Studies *et al.* Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* **478,** 103–109 (2011).
40. Heid, I. M. *et al.* Meta-analysis identifies 13 new loci associated with waist–hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nat. Genet.* **42,** 949–960 (2010).
41. Okbay, A. *et al.* Genome-wide association study identifies 74 loci associated with educational attainment. *Nature* **533,** 539–542 (2016).
42. Vattikuti, S., Guo, J. & Chow, C. C. Heritability and genetic correlations explained by common SNPs for metabolic syndrome traits. *PLoS Genet.* **8,** e1002637 (2012).
43. Rietveld, C. A. *et al.* GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science* **340,** 1467–1471 (2013).
44. Yang, J. *et al.* Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. *Nat. Genet.* **47,** 1114–1120 (2015).
45. Lynch, M. & Walsh, B. *Genetics and Analysis of Quantitative Traits.* (Sinauer, 1998).
46. Yang, J. *et al.* Genomic inflation factors under polygenic inheritance. *Eur. J. Hum. Genet.* **19,** 807–812 (2011).
47. Eriksson, N. *et al.* Web-based, participant-driven studies yield novel genetic associations for common traits. *PLoS Genet.* **6,** e1000993 (2010).
48. Tung, J. Y. *et al.* Efficient replication of over 180 genetic associations with self-reported medical data. *PLoS ONE* **6,** e23473 (2011).
49. Yang, J. *et al.* Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. *Nat. Genet.* **44,** 369–375 (2012).
50. Yang, J., Lee, S. H., Goddard, M. E. & Visscher, P. M. GCTA: a tool for genome-wide complex trait analysis. *Am. J. Hum. Genet.* **88,** 76–82 (2011).
51. Haseman, J. K. & Elston, R. C. The investigation of linkage between a quantitative trait and a marker locus. *Behav. Genet.* **2,** 3–19 (1972).
52. Visscher, P. M. *et al.* Statistical power to detect genetic (co)variance of complex traits using SNP data in unrelated samples. *PLoS Genet.* **10,** e1004269 (2014).
53. Yang, J., Zaitlen, N. A., Goddard, M. E., Visscher, P. M. & Price, A. L. Advantages and pitfalls in the application of mixed-model association methods. *Nat. Genet.* **46,** 100–106 (2014).
54. Silventoinen, K., Kaprio, J. & Lahelma, E. Genetic and environmental contributions to the association between body height and educational attainment: A study of adult Finnish twins. *Behav. Genet.* **30,** 477–485 (2000).
55. Lin, D.-Y. & Sullivan, P. F. Meta-analysis of genome-wide association studies with overlapping subjects. *Am. J. Hum. Genet.* **85,** 862–872 (2009).

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M.R.R., J.Y. and P.M.V. conceived and designed the study. M.R.R., A.K. and M.G. analysed the data. M.R.R. devised and performed the simulations. A.A.E.V., W.J.P., A.A., B.Z., S.M. provided statistical support. 23andMe Inc., The LifeLines cohort, GIANT consortium, G.W.M., N.G.M., M.L., P.L., D.C., J.V.V.O., M.B.M., H.S., W.G.I., P.K.E.M, N.L.P, M.McG. and K.E.N. provided study oversight, sample collection and management. M.R.R. and P.M.V. derived the theory and wrote the manuscript. All collaborators reviewed and approved the final manuscript.

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Competing interests

The authors declare no competing interests.

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