Supplementary Material

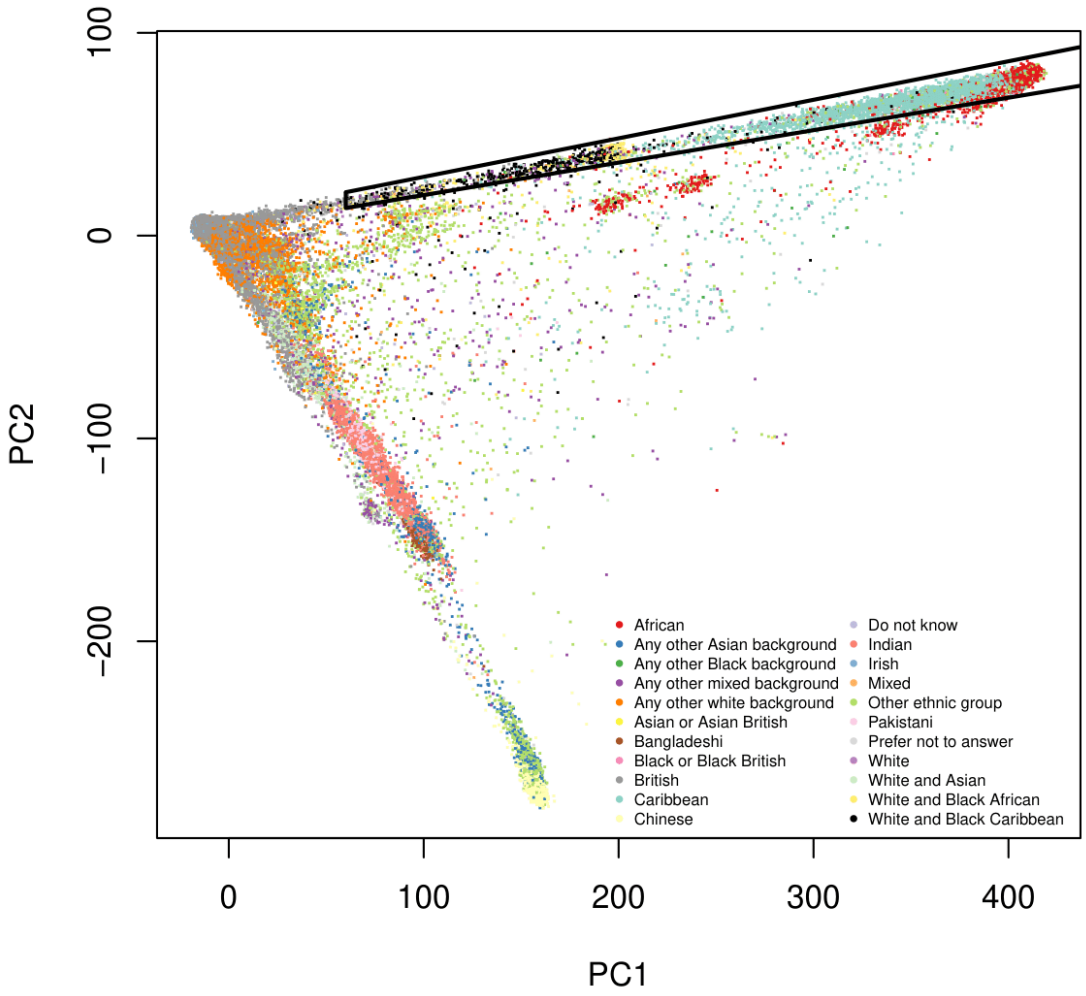


Figure S1. Principal component analysis (PCA) of UK Biobank individuals. PC1 separates Africans and Europeans. We selected 8,813 individuals with African or admixed African and European ancestry based on PCA, shown in the boxed area.

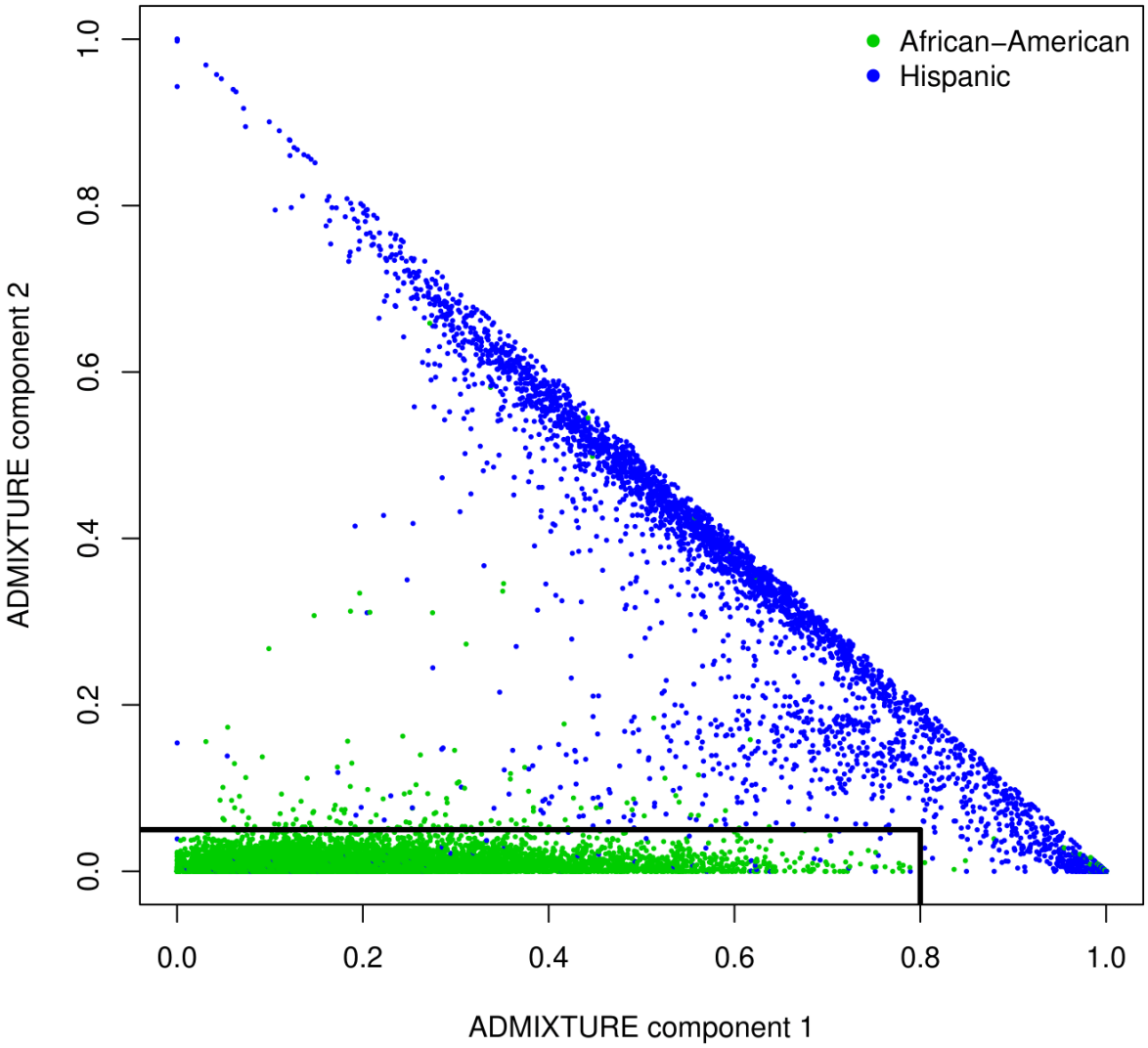


Figure S2. ADMIXTURE analysis of Women's Health Initiative (WHI) individuals. We ran unsupervised ADMIXTURE (k=3) and identified 7,285 individuals with self-reported "African American" ancestry with at most 0.8 of the first ADMIXTURE component (interpreted as the European component) and at most 0.05 of the second ADMIXTURE component (interpreted as the Native American component).

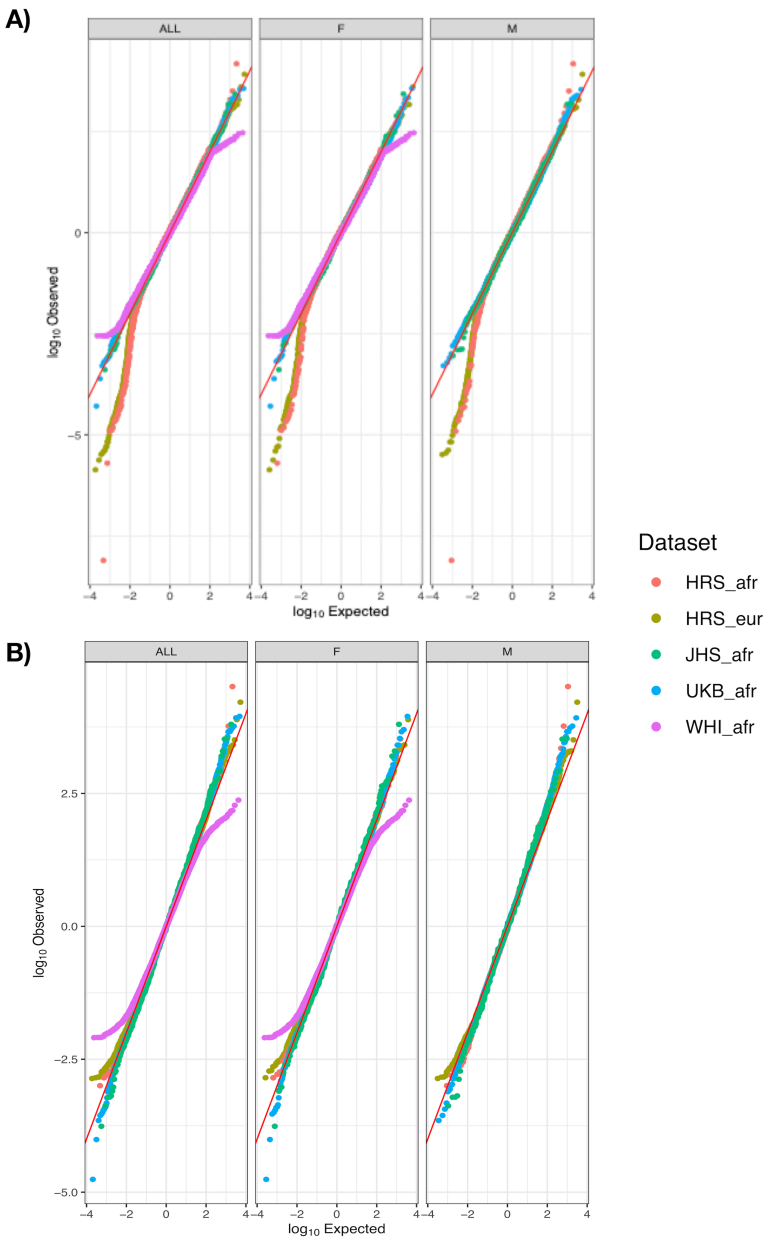


Figure S3. Q-Q plot of residual height in each dataset. **A:** before filtering; **B:** after filtering out individuals from WHI and HRS datasets according to the following criteria. WHI: individuals with a height more than 2 standard deviations away from the mean; HRS_afr and HRS_eur: individuals with height lower than the mean minus 2 standard deviations (mean and sd calculated sex-specific). X-axis, expected values under a normal distribution. F, females; M, males; ALL, males and females. Residuals obtained after regressing out confounding factors as follows: height~sex+Dataset+sex*Dataset+age+age*Dataset+age*sex+age^2+age^2*Dataset+age^2*sex.

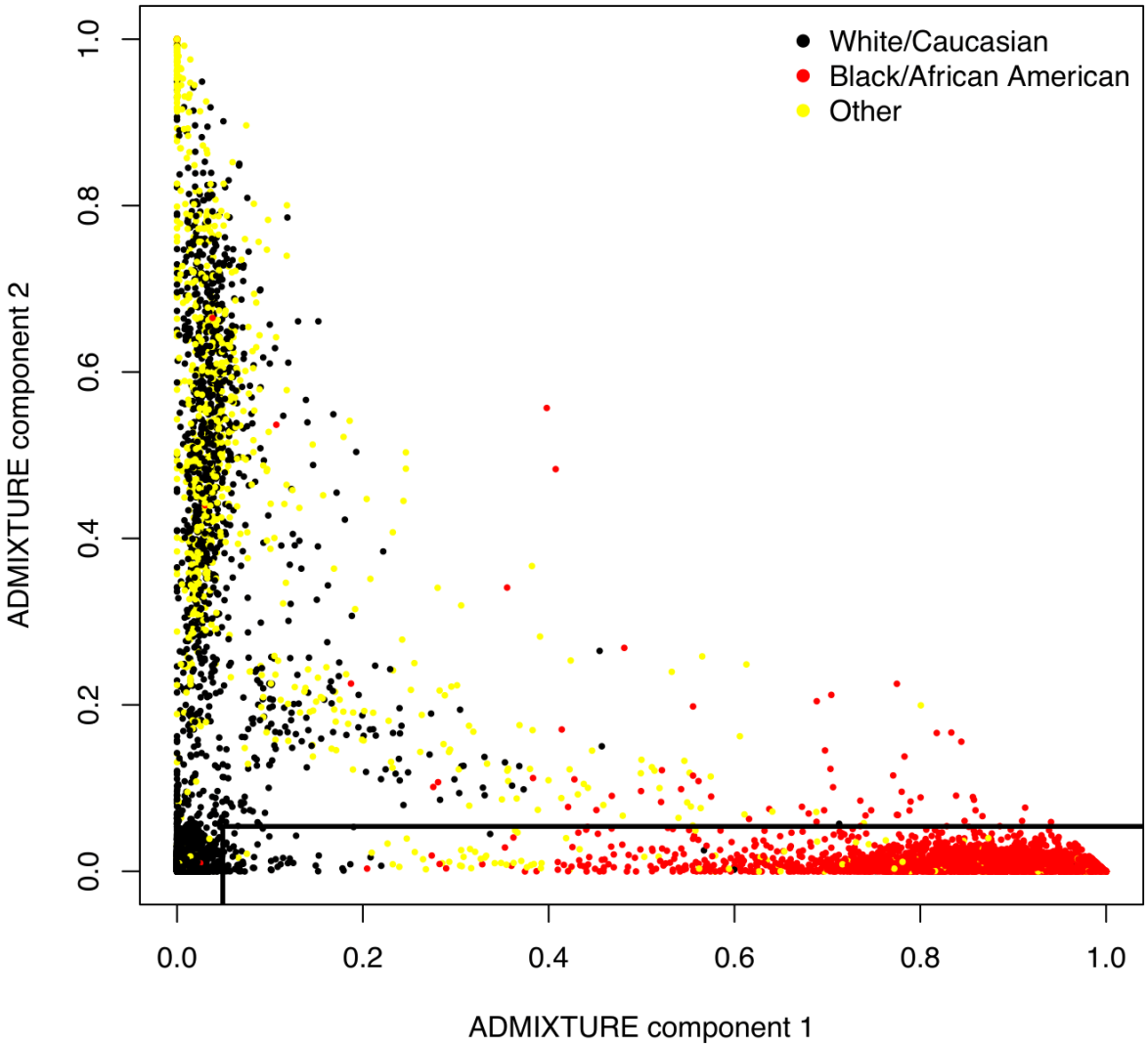


Figure S4. ADMIXTURE analysis of Health and Retirement Study (HRS) individuals. We ran unsupervised ADMIXTURE (k=3) and identified 2,322 individuals with self-reported "Black/African American" ancestry with at least 0.05 of the first ADMIXTURE component (assumed to be African) and at most 0.05 of the second ADMIXTURE component (assumed to be Native American).

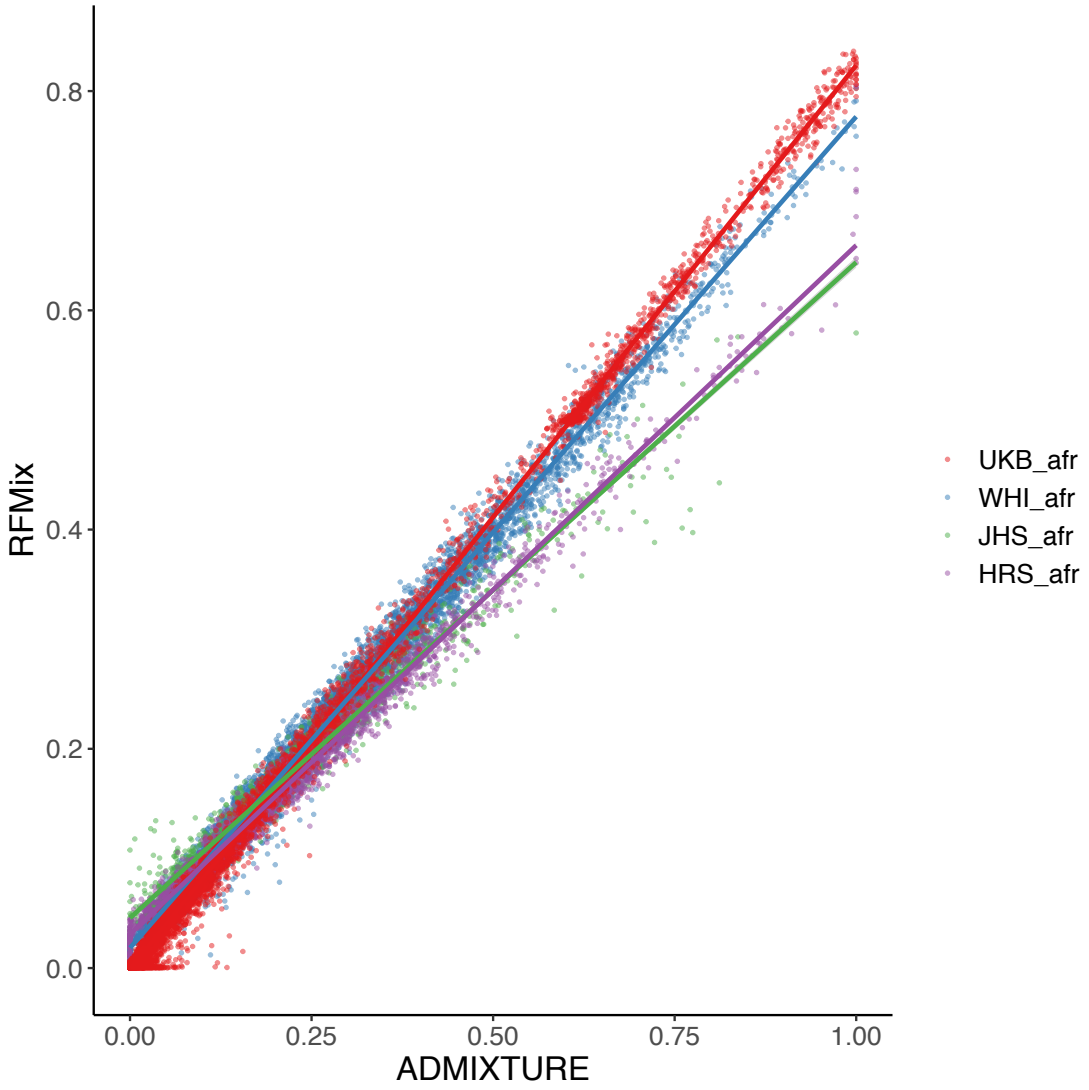


Figure S5. Comparison between ADMIXTURE and RFMix estimates for genome-wide ancestry. For RFMix, the average across all sites was used. Colored lines display linear regressions for each dataset. HRS_afr, Health and Retirement Study African Americans (*N*=2,322); WHI_afr, Women's Health Initiative African Americans (*N*=7,285); JHS_afr, Jackson Heart Study African Americans (*N*=1,774); UKB_afr, individuals with European and African admixture in the UK Biobank (*N*=8,813). Correlations are: 0.994 (WHI_afr), 0.982 (JHS_afr), 0.999 (UKB_afr), 0.993 (HRS_afr), 0.993 (ALL). The RFMix proportions are more likely to be correct because of the fact that we selected individuals with at least some African Ancestry, which will bias the ADMIXTURE results. Empirically, the RFMix proportions show a spike at 50% ancestry – likely to be from individuals with one parent of African ancestry and one of European ancestry. This spike is at ~60% European ancestry in the ADMIXTURE proportions suggesting that the ADMIXTURE European ancestry proportions are overestimated by a factor of around 1.2.

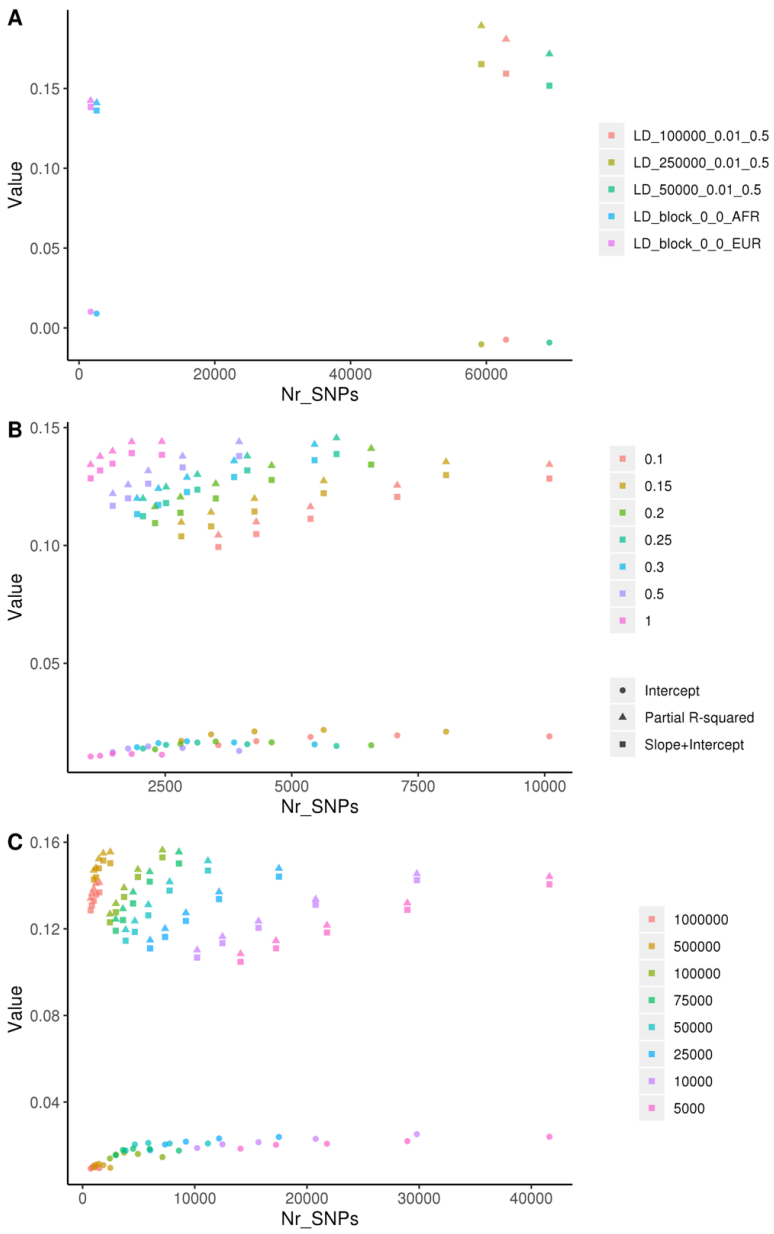


Figure S6. The predictive power of height PRS as a function of the number of SNPs included in the PRS. **A**: LD clumping methods (r^2>0.5, p<0.01, window sizes 50-250 Kb) and LD blocks pruning strategy[3]. **B**: Genetic and **C**: physical clumping. Values are for the HRS_eur dataset. Broadly, including more SNPs in the PRS increases partial-R^2 (ρ=0.36 for UKB_eur, p=0.0011), although this masks subtler patterns. For example, when using a clumping strategy with a fixed window size, increasing the p-value threshold (more SNPs) leads to higher predictive power. On the other hand, when using a fixed p-value, increasing window sizes (fewer SNPs) also improves prediction**.**

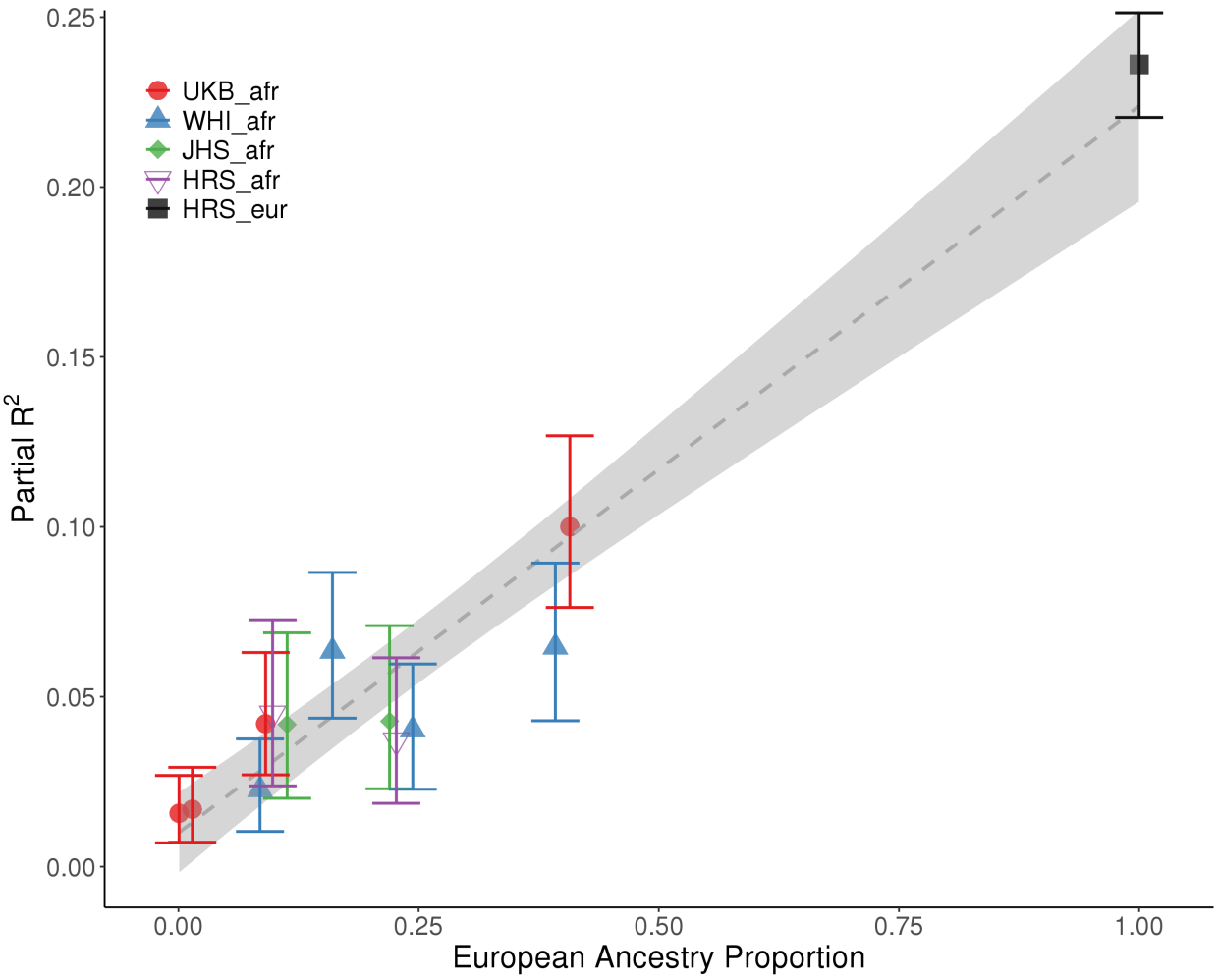


Figure S7. As Figure 1, but using effect sizes estimated assuming an infinitesimal model (LDpred). Each quantile has between 816 and 2,175 individuals, and plotted values represents the median of each bin. Vertical bars represent 95% confidence intervals estimated from case resampling bootstrap (1,000 replicates). The dashed line shows the regression with standard errors shaded in light gray.The dashed line is the weighted linear regression, and gray shadowing represents the 95 confidence interval.

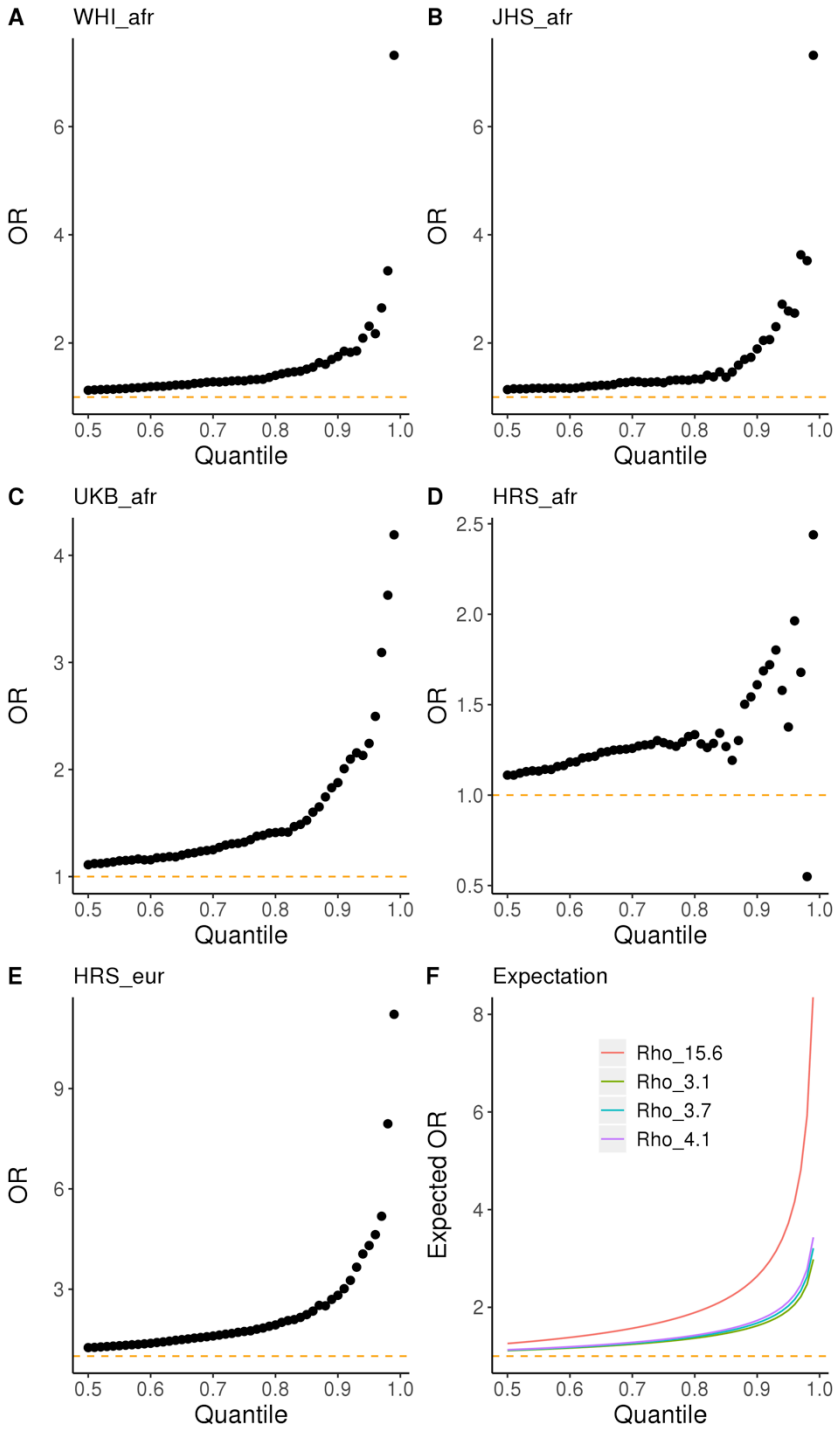


Figure S8. The ability of PRS to predict tallness. **A-E**: Odds-ratio (OR) for being above the *q*-th quantile of height, conditional on being above the *q*-th quantile of PRS, for different datasets. **F**: expected OR assuming a bivariate normal distribution for PRS and disease risk on the liability scale. Different *rho* values reflect partial-R^2 detected empirically for each dataset (0.156 for HRS_eur, 0.041 for UKB_afr, 0.36 for WHI_afr, 0.38 for JHS_afr and 0.31 for HRS_afr).

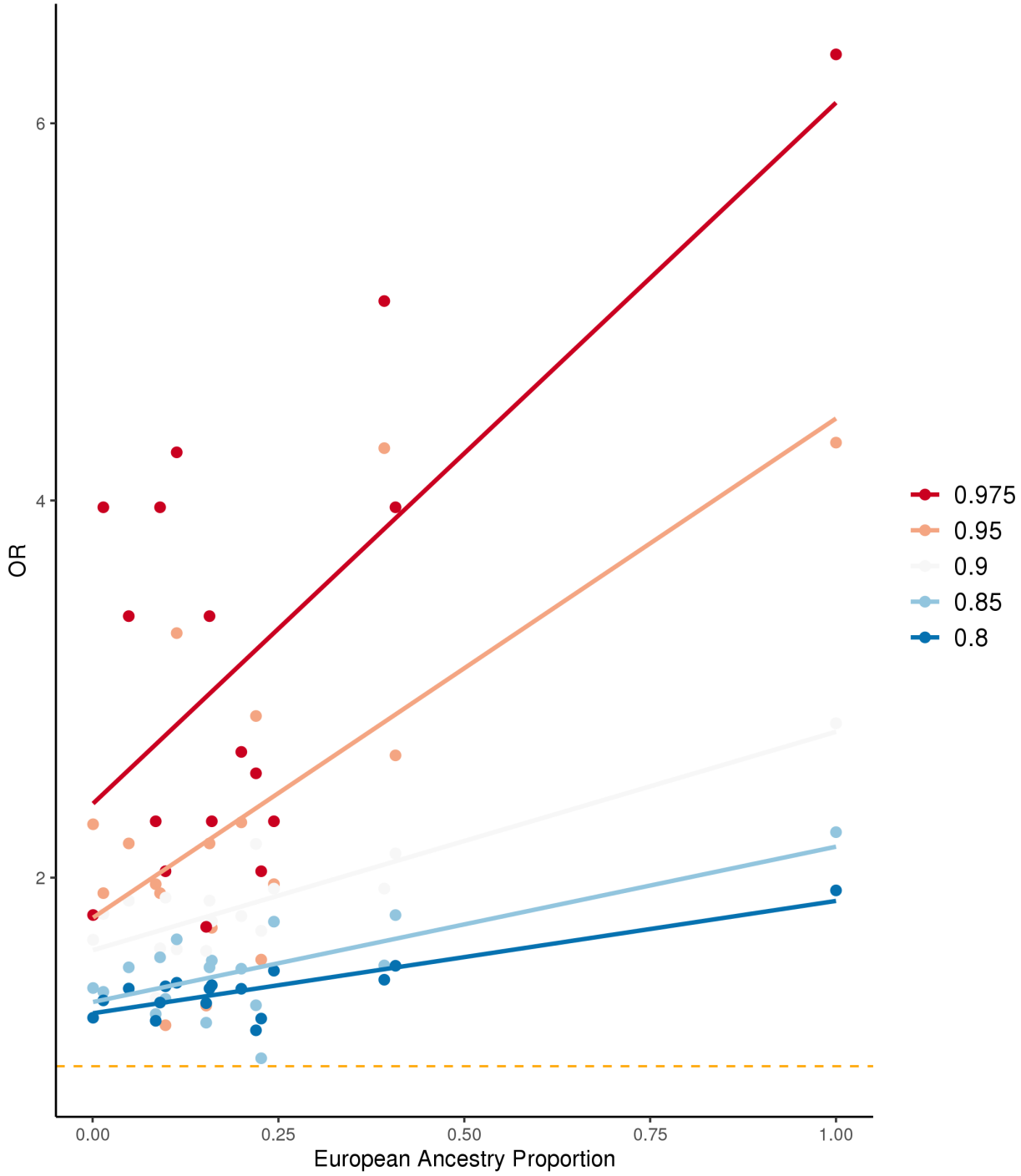
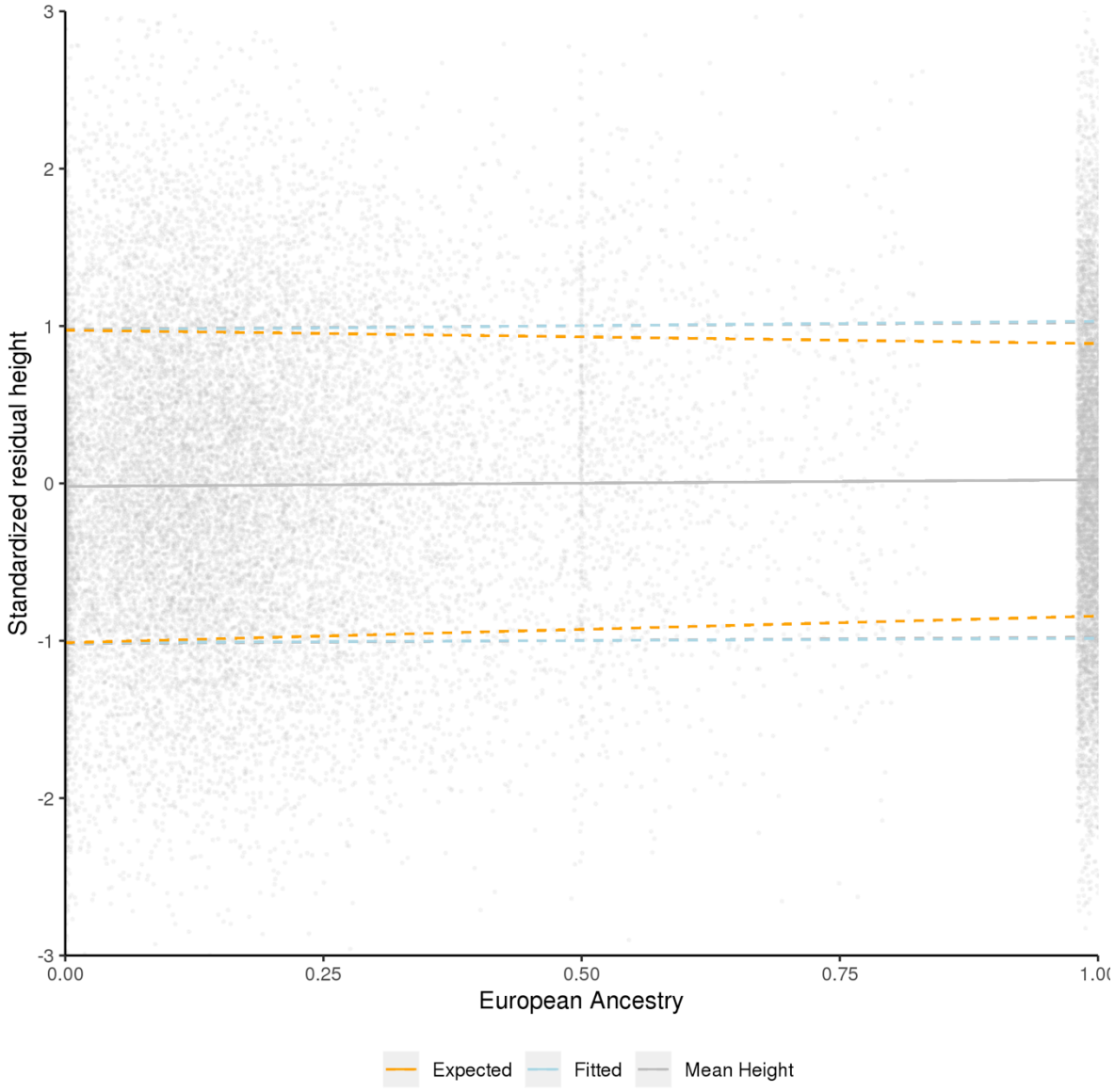


Figure S9. Odds-ratio for 'tallness' as a function of European ancestry proportion. All datasets are pooled together. OR is the probability of being in above the n^{th} quantile of residual height (after regressing out sex, age, age^2, study) given that an individual is above the n^{th} quantile of PRS, divided by 1-). Dashed line is OR=1.



S10. Phenotypic variance. Gray lines show mean height, and dashed lines show ∓ 1 sd. In orange, we show the expected sd if it were negatively dependent on European ancestry. In blue, we show the fitted model with variable variance, which is not significantly different from the constant variance model (green). We reject the model (orange line) whereby the phenotypic variance in people with 100% European ancestry is 76% that of people with 0% European ancestry.

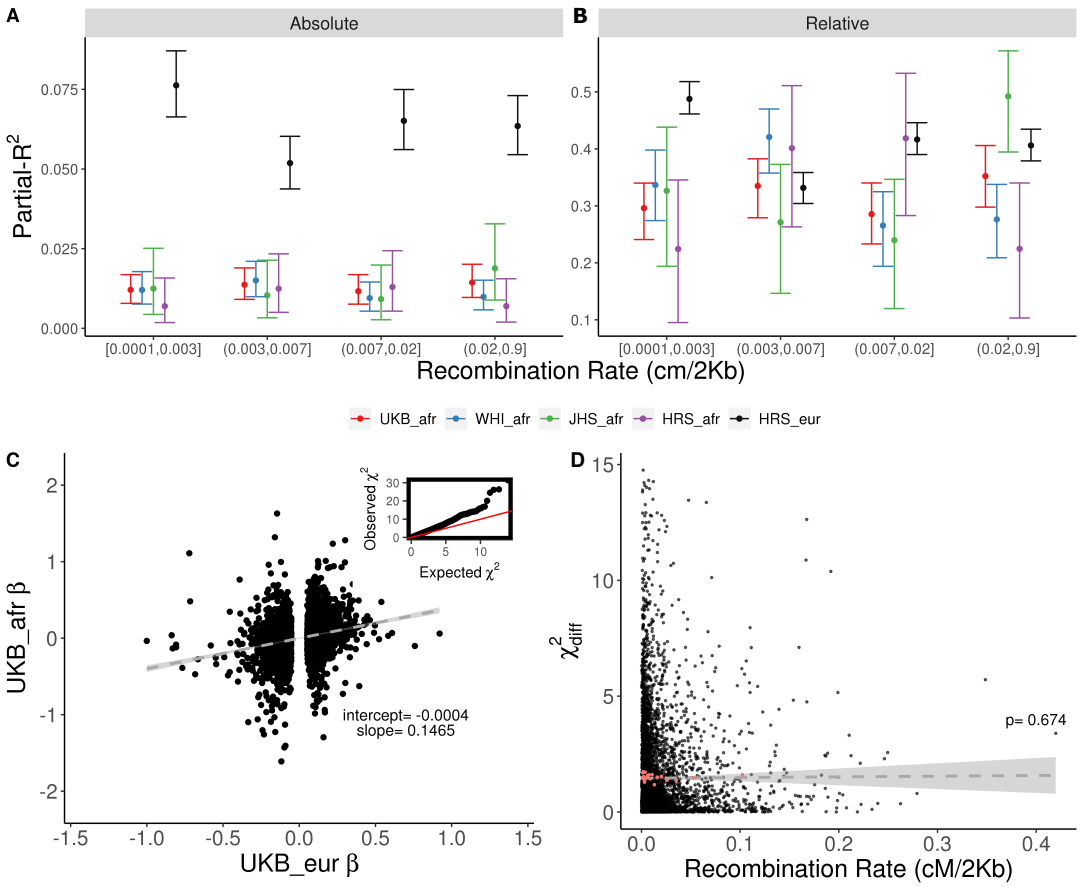


Figure S11. Effect of recombination rates on predictive power with a European recombination map

A and **B**: PRS SNPs from each dataset were separately binned into quartiles of European recombination rate. Y-axis, partial-R^2, absolute (**A**) and relative (**B**), obtained for subsets of SNPs divided by the total partial-R^2 for each dataset (**Table 1**). Confidence intervals were obtained by nonparametric bootstrap 95% confidence intervals obtained by the percentile method on 1,000 bootstrap replicates by case resampling and dividing by total confidence intervals. **C**: correlation between PRS SNPs effect sizes from Europeans and Admixed Africans in the WHI_afr dataset. The inset shows a qq-plot of χ^2_{diff} for PRS SNPs. The dashed line shows the regression with standard errors shaded in light gray. **D**: y-axis, χ^2_{diff} statistic for the difference in β between European and Admixed African populations (**Equation 1**) in the WHI_afr dataset; x-axis, recombination rate in cM/20Kb. Cut-off at 15 for display purposes excludes 10 data points. Dashed line shows the regression with standard errors shaded in light gray. Red points represent the median recombination rate for each of 20 bins (quantiles) of recombination rate.

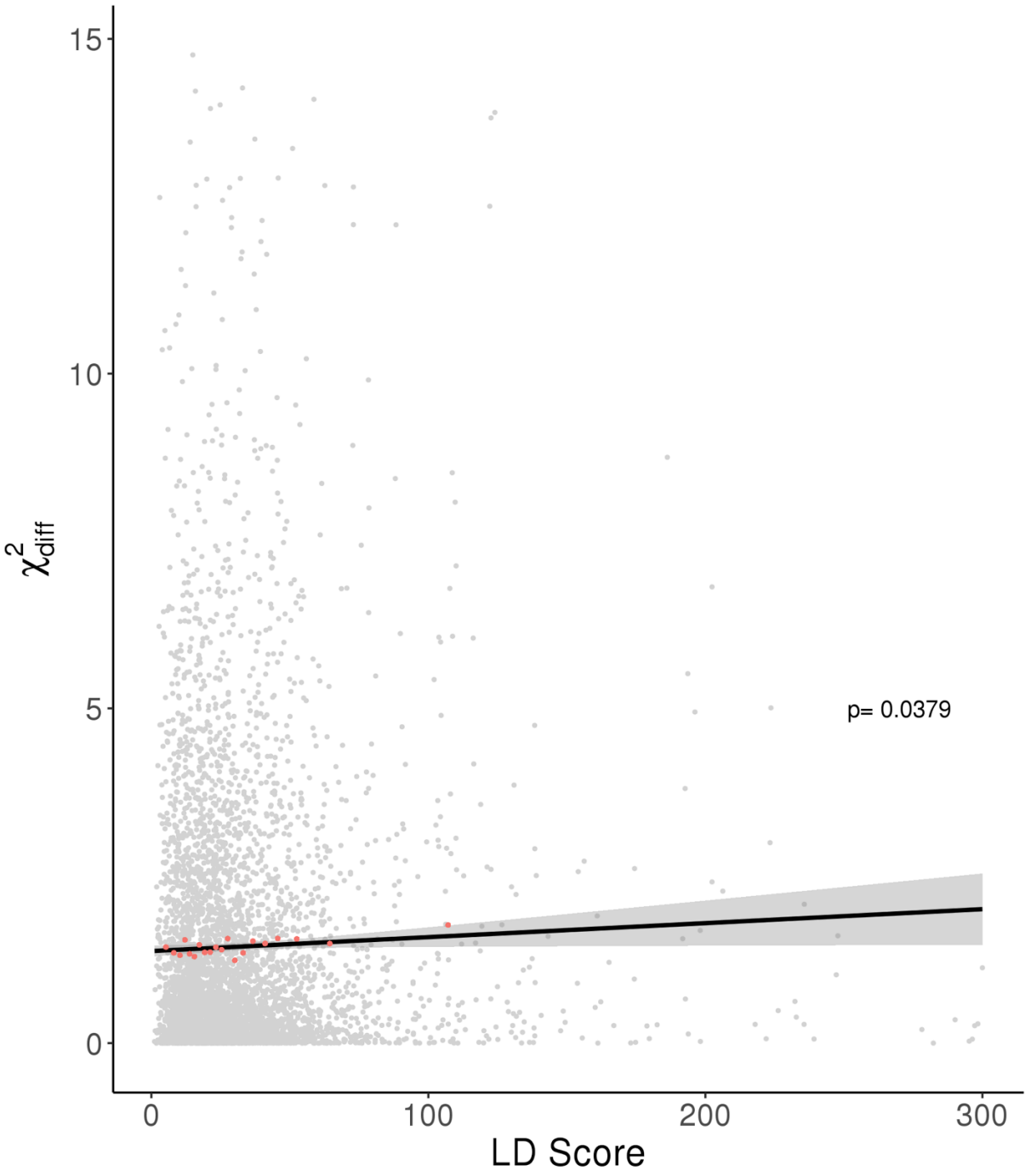


Figure S12. χ^2_{diff} against European LD score. The black line is the linear regression with confidence intervals in gray. Red points represent the median recombination distance and LD score values for 20 bins and mean χ^2_{diff} values.

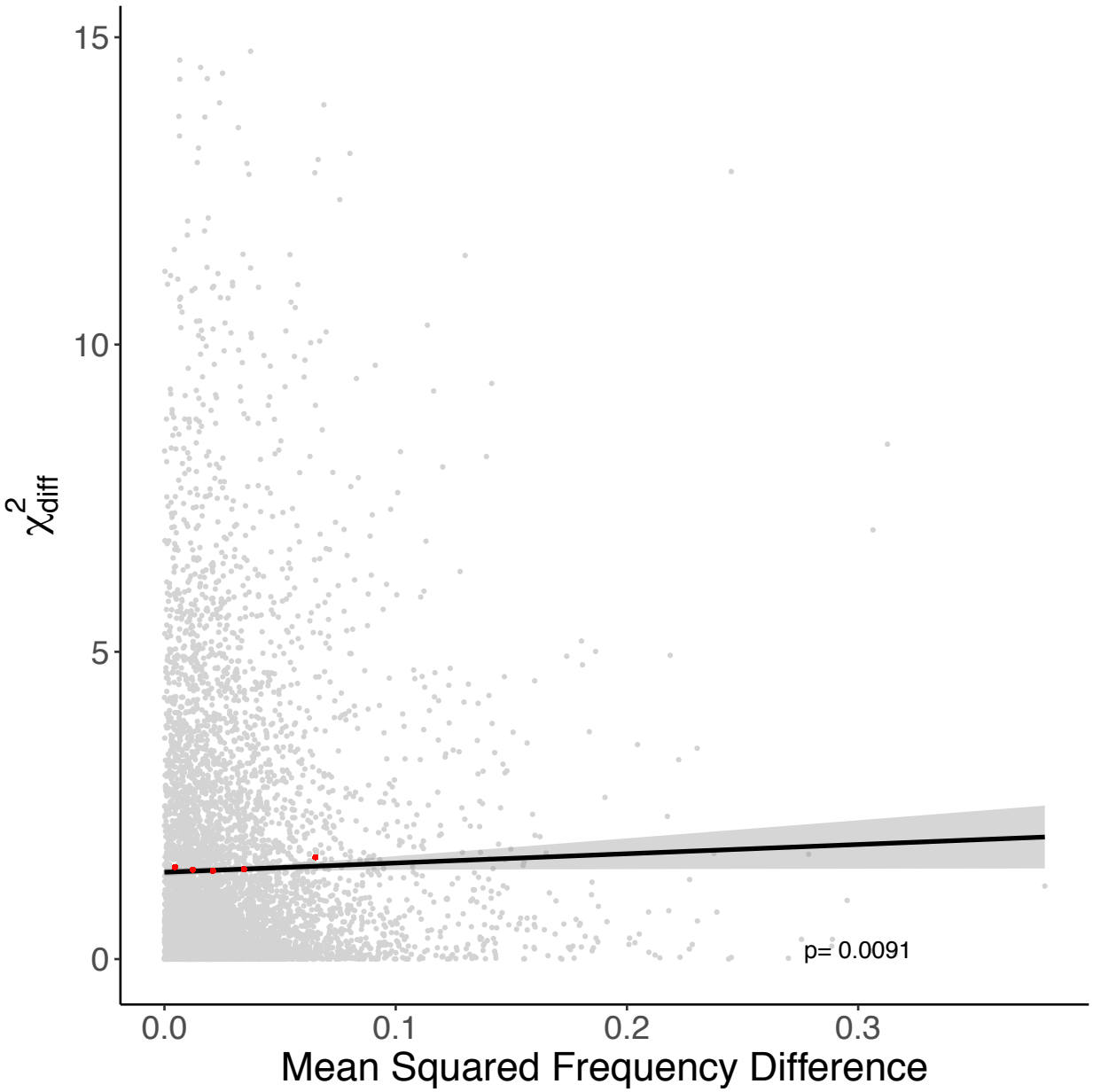


Figure S13. Differences in effect size as a function of allele frequency difference around PRS SNPs. X-axis, mean squared frequency difference for PRS SNPs for EUR and AFR in a 10 Kb window around each PRS SNP. Frequencies were calculated per dataset (HRS_eur, HRS_afr, UKB_eur, UKB_afr) for the causal allele. Y-axis, χ^2_{diff} of the difference in betas estimated for EUR and AFR. Cut-off at 15 for display purposes excludes 15 data points. In red, for visualization, are median squared frequency difference values for 5 bins of mean squared difference and the mean χ^2_{diff} for each bin.

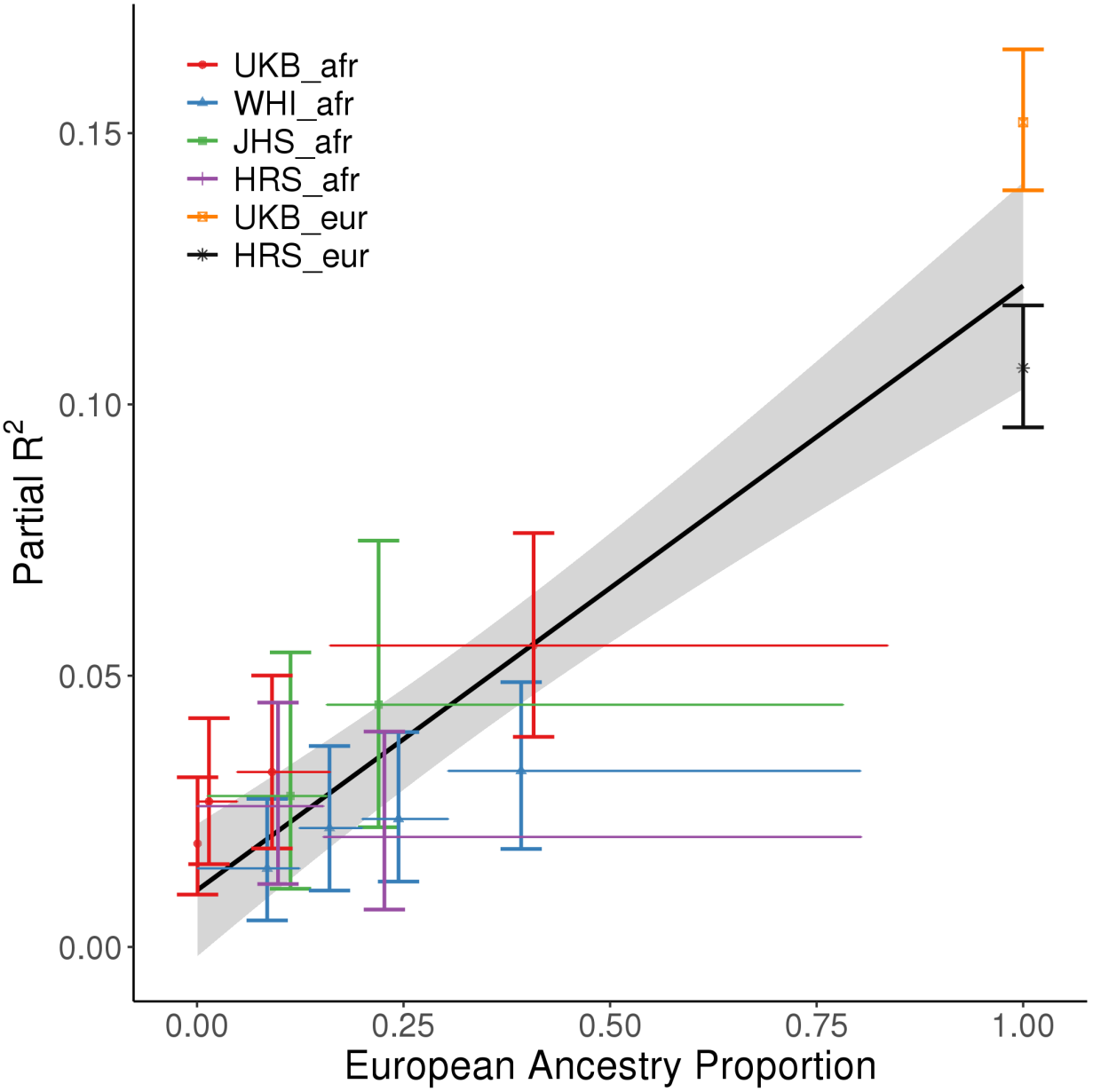


Figure S14. As Figure 1, but using effect sizes re-estimated within sibling pairs. Each admixed population is split up into quantiles of European ancestry proportion. Each quantile has between 816 and 2,175 individuals, and plotted values represents the median of each bin. Vertical bars represent 95% confidence intervals estimated from case resampling bootstrap (1,000 replicates). The black line shows the regression with standard errors shaded in light gray. Horizontal bars represent the range of European ancestry included in that bin. The black line is the weighted linear regression, and gray shadowing represents the 95% confidence interval.