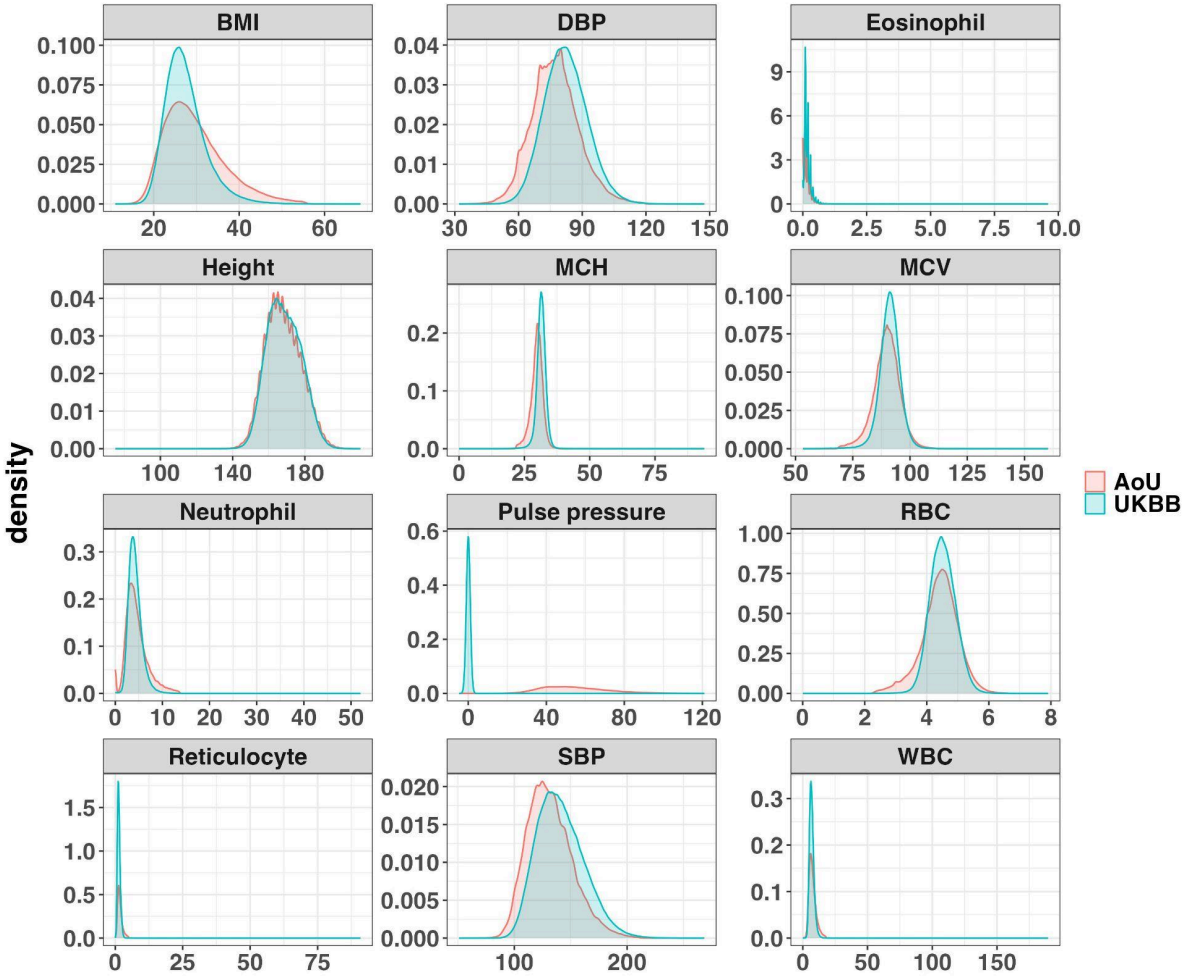
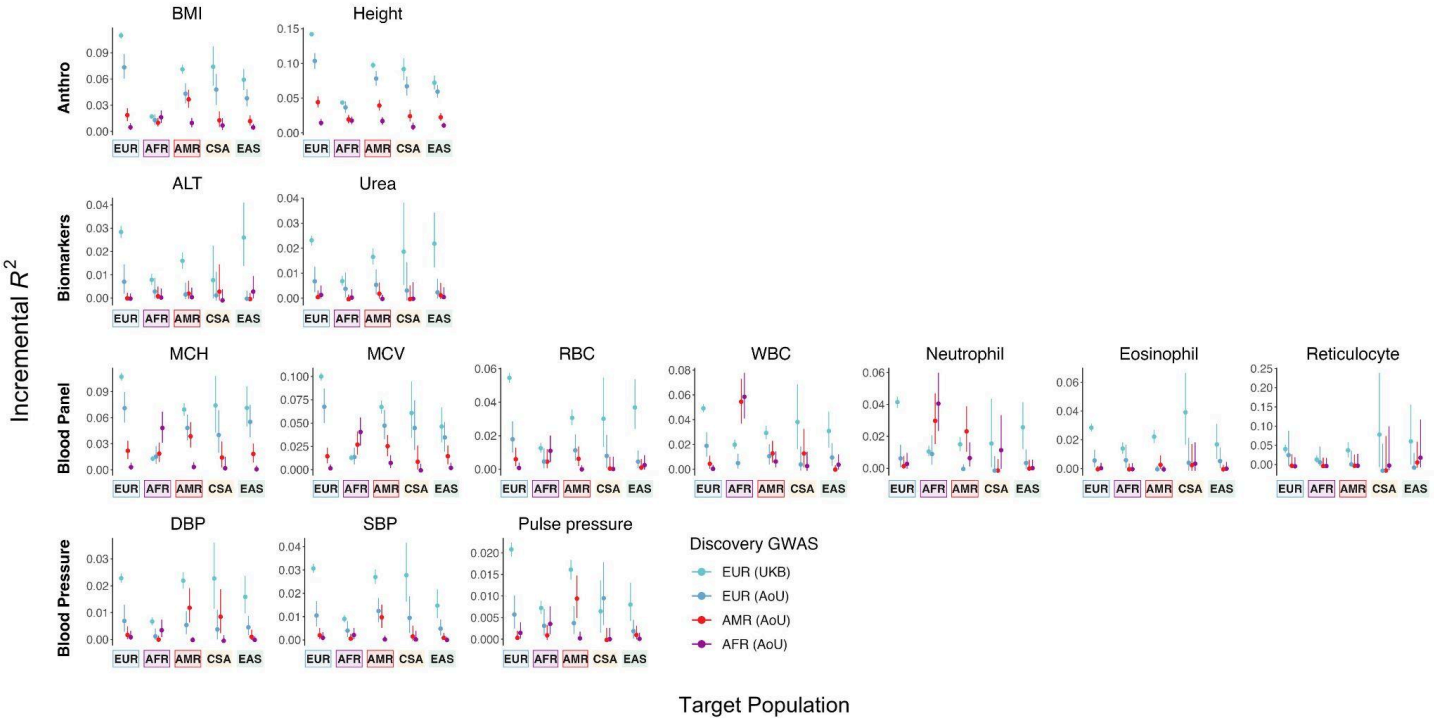
Supplementary Figures

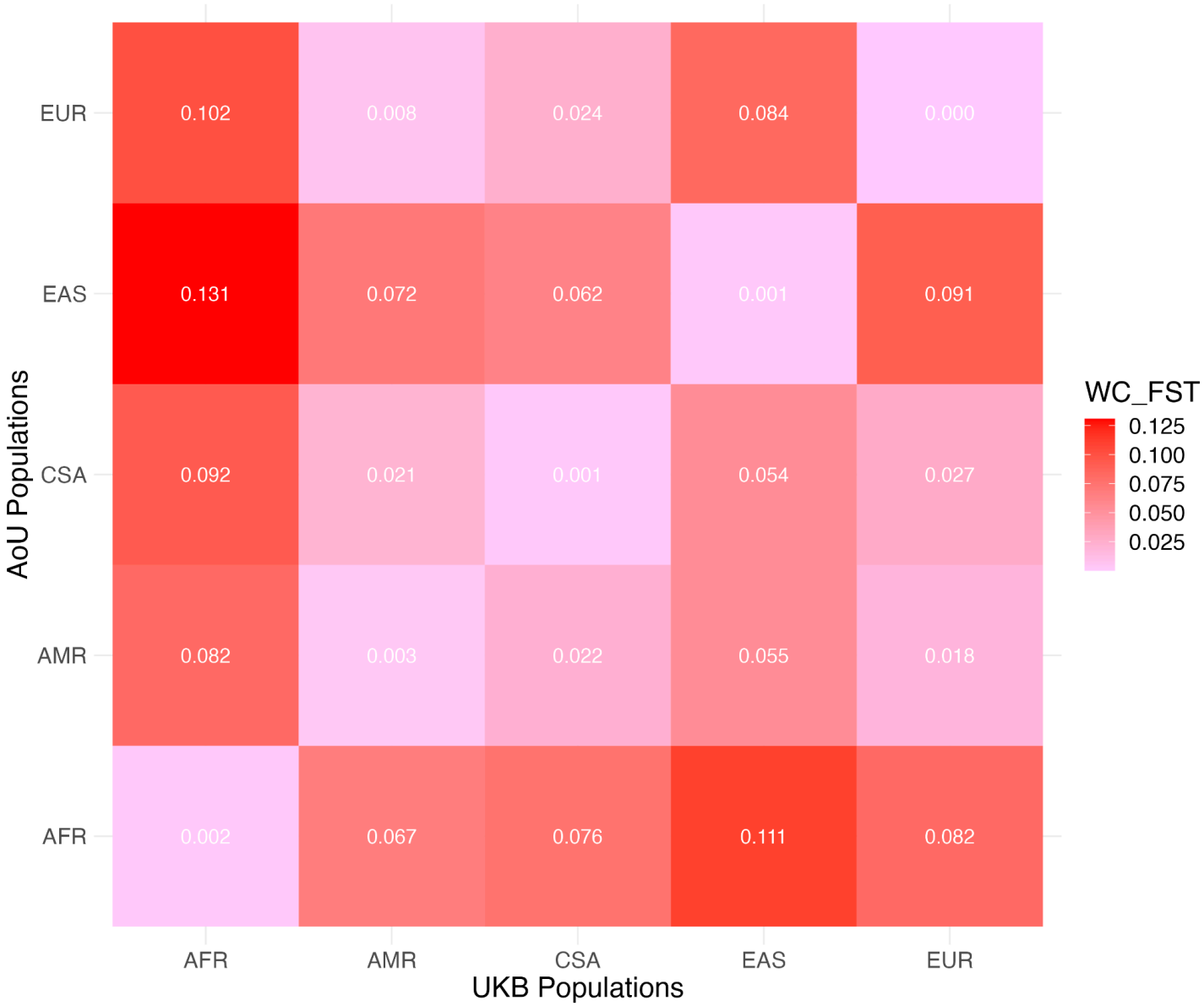
Supplementary Figure 1. Effect size comparisons. Effect sizes of genome-wide significant (GWS), clumped variants ascertained in AoU and UKB GWAS. Effect sizes from UKB GWAS are represented on x-axes; effect sizes from AoU GWAS are represented on y-axes. A) Quantitative phenotypes. B) Binary phenotypes.



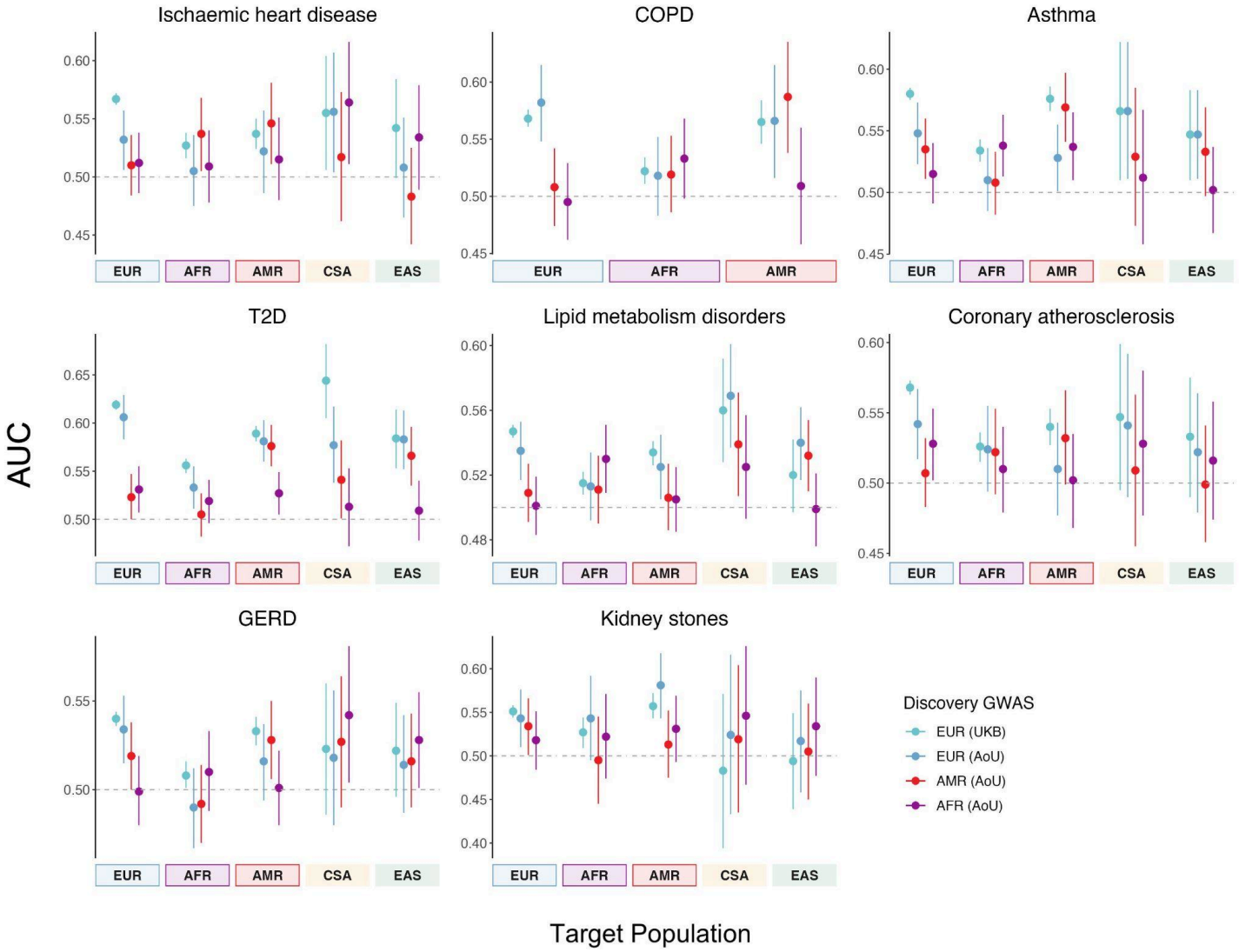
Supplementary Figure 2. Phenotype distributions of quantitative traits in AoU vs. UKB. Phenotype values are represented on x-axes. Blue curves represent distribution in UKB and red curves represent distribution in AoU. (BMI = body mass index; DBP = diastolic blood pressure; Eosinophil = eosinophil count; MCH = mean corpuscular hemoglobin; MCV = mean corpuscular volume; Neutrophil = neutrophil count; RBC = red blood cell count; Reticulocyte = reticulocyte percentage; SBP = systolic blood pressure; WBC = white blood cell count)



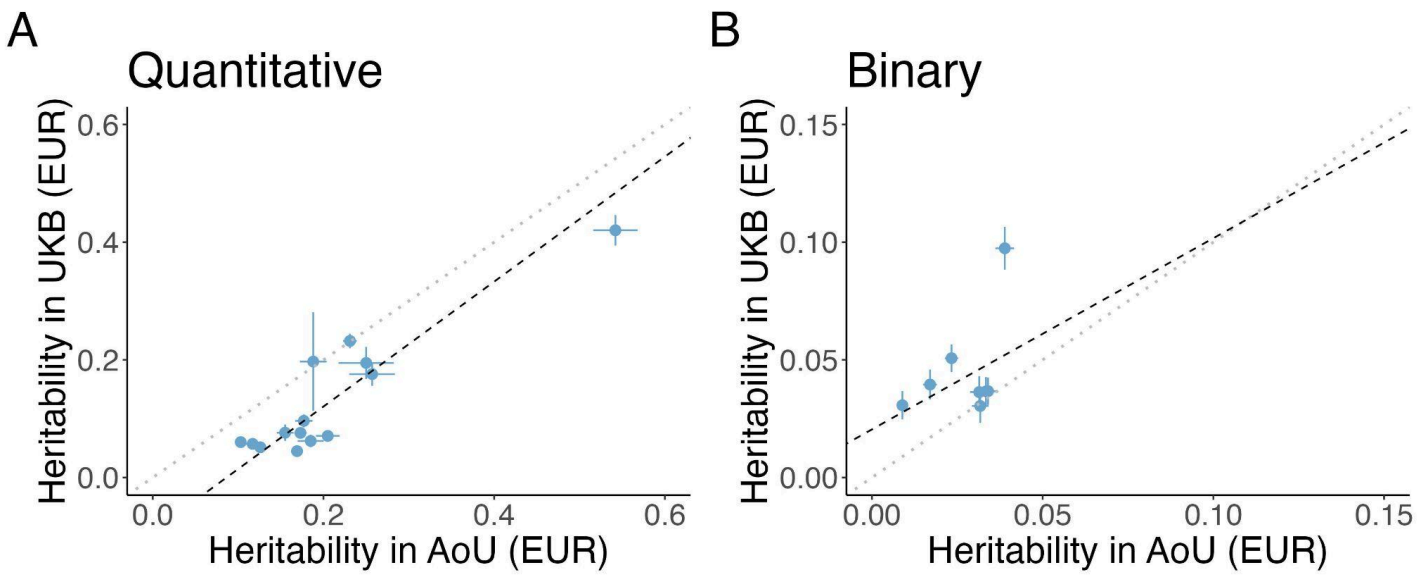
Supplementary Figure 3. Performance of PRS derived from single-ancestry discovery GWAS from AoU and UKB for quantitative traits. Quantitative traits are divided into categories: anthropometric traits, biomarkers, blood panel traits, and blood pressure traits. PRS were constructed from PRS-CS applied to EUR GWAS from UKB and AoU, as well as AMR and AFR GWAS from AoU. Target populations from AoU are shown on x-axes and target populations with ancestry-matched PRS are outlined; PRS performance as measured by incremental R^2 is shown on y-axes.



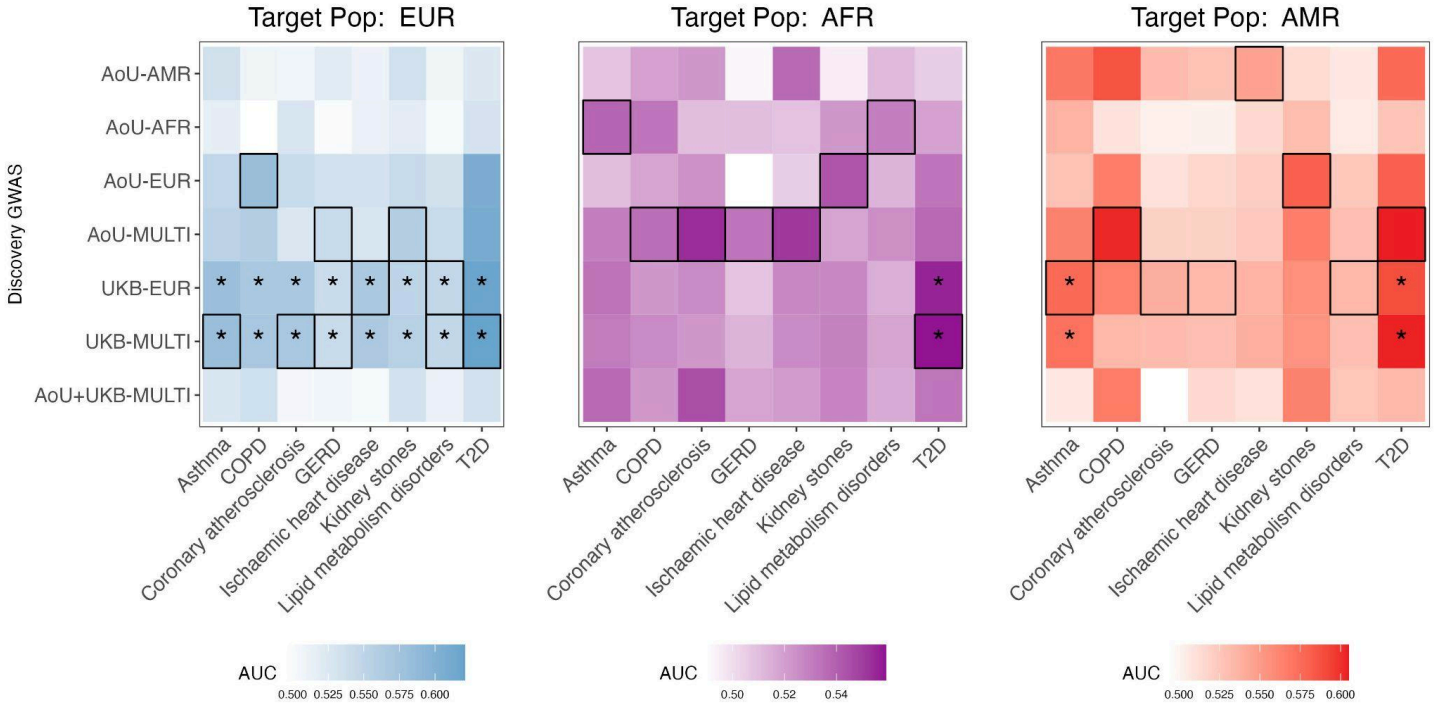
Supplementary Figure 4. Genetic distance between populations in AoU and UKB. Population genetic differentiation, as measured by Wright's fixation index, F_{st}, between genetic ancestry groups in UKB vs. AoU.



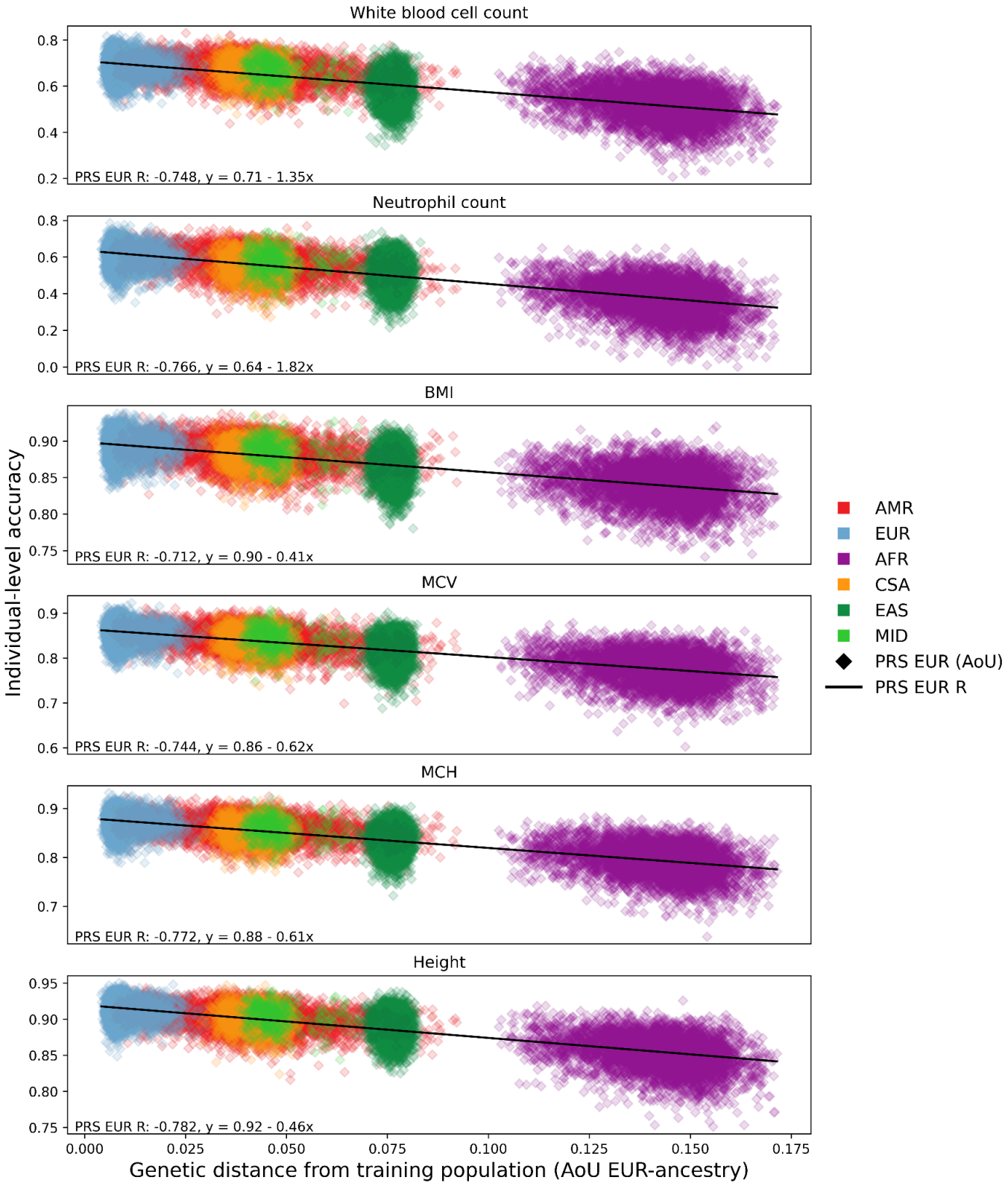
Supplementary Figure 5. Performance of PRS derived from single-ancestry discovery GWAS from AoU and UKB for binary phenotypes. PRS were constructed from PRS-CS applied to EUR GWAS from UKB and AoU, as well as AMR and AFR GWAS from AoU. Target populations from AoU are shown on x-axes and target populations with ancestry-matched PRS are outlined; PRS performance as measured by AUC is shown on y-axes.



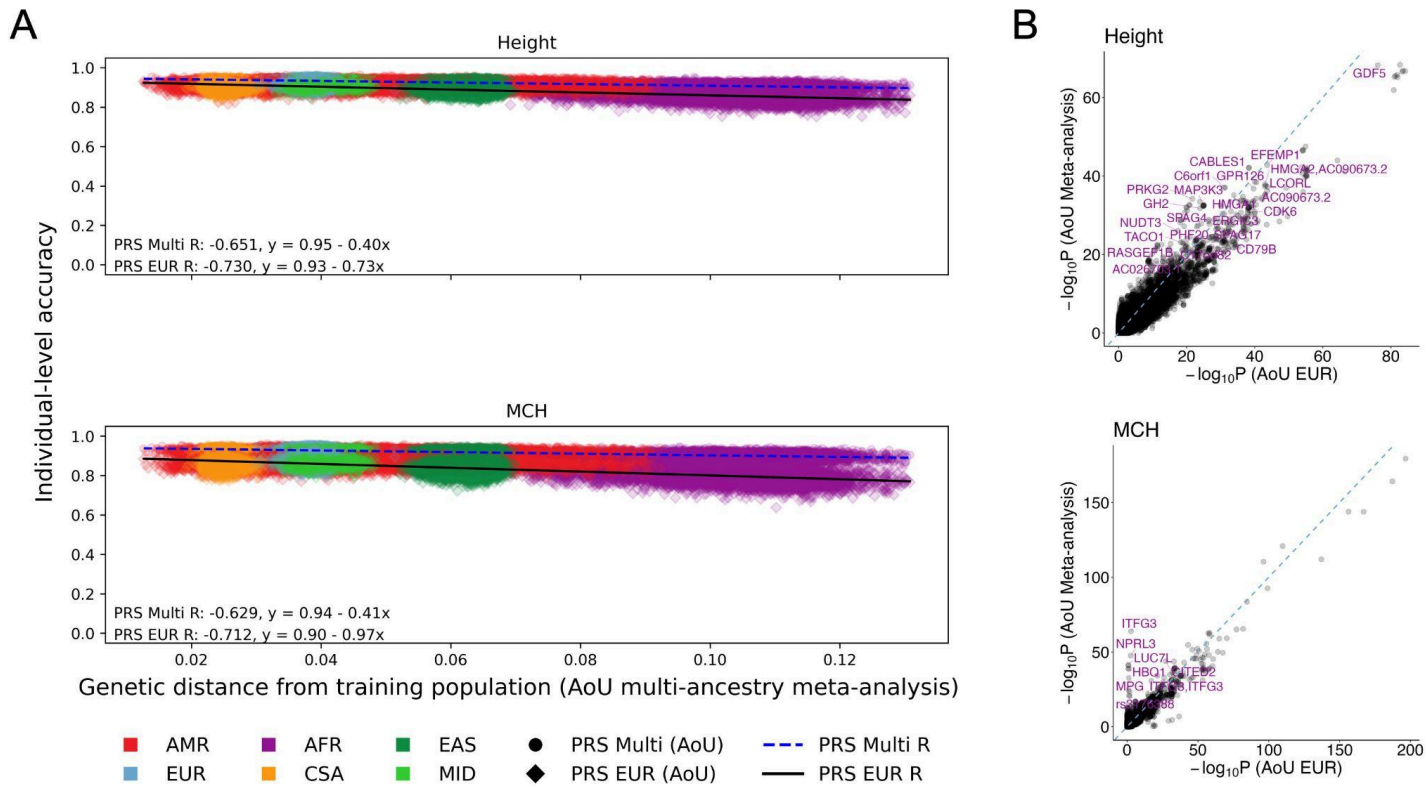
Supplementary Figure 6. Comparison of SNP-based heritability estimates derived from AoU and UKB. Each point represents a phenotype. SNP-based heritability was estimated from EUR GWAS using LDSC. Dotted line is x=y line; dashed line is slope estimated from York regression analysis. A) 14 quantitative phenotypes. B) 8 binary phenotypes with at least 10,000 cases and >0.03 heritability estimates from AoU EUR GWAS.



Supplementary Figure 7. Performance of all PRS models for binary phenotypes. PRS derived from discovery GWAS, denoted on y-axis, for binary phenotypes denoted on x-axis. PRS model with highest AUC per trait is outlined. Asterisk indicates AUC significantly greater than 0.5 (t-test, $p < 0.05$).



Supplementary Figure 8. Individual-level accuracy for PRS derived from AoU EUR GWAS. Each point represents a target individual in AoU. The x-axis represents the genetic distance (GD) of each target individual from the EUR discovery group in AoU. The y-axis shows the PRS accuracy, which was scaled to enable cross-trait comparisons of decay in accuracy as a function of GD; as a result, proportions of genetic liability explained by PRS for each individual are not represented here. R was calculated as the correlation between GD and PRS accuracy from a two-sided Pearson correlation test. The colors represent genetic ancestry groups as inferred by PCA.



Supplementary Figure 9. **Individual-level accuracy for height and MCH PRS derived from AoU multi-ancestry meta-analyses.** A) Individual-level accuracy derived from AoU multi-ancestry meta-analyses and EUR GWAS across target individuals in AoU, represented by each point. The x-axis represents the genetic distance (GD) of each target individual from the combined discovery populations included in the AoU multi-ancestry meta-analyses. The y-axis shows the PRS accuracy, which was scaled to enable cross-trait comparisons of decay in accuracy as a function of GD; as a result, proportions of genetic liability explained by PRS for each individual are not represented here. R was calculated as the correlation between GD and PRS accuracy from a two-sided Pearson correlation test. The colors represent genetic ancestry groups as inferred by PCA. B) Comparison of GWAS significance in AoU multi-ancestry meta-analyses and AoU EUR GWAS for height and MCH. SNPs tested in both the AoU multi-ancestry meta-analyses and EUR GWAS are represented by each point. SNPs reaching genome-wide significance ($p < 5e-8$) in the AoU meta-analysis and AoU AFR GWAS for each phenotype are annotated. Dashed lines indicate y=x; x- and y-axis scales are specific to each phenotype and differ according to scale of significance in meta-analyses vs. EUR GWAS.