

Supplementary Figures

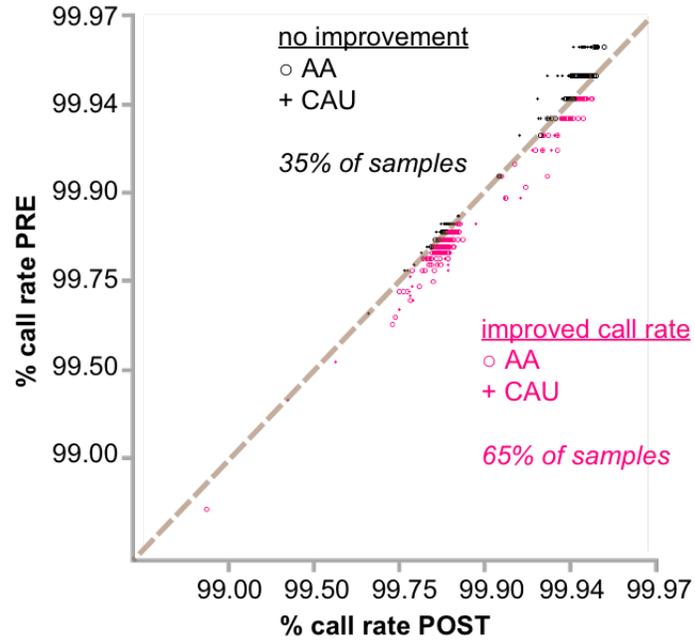


Figure S1: Summary of sample call rates prior to and post data-driven and custom analysis of SNPs. Samples in magenta (65%) experienced an increase in Call Rate due to the data-driven custom analysis. Circle (o) or plus (+) symbols indicate Americans of either African (AA) or European (CAU) descent. The AA subjects benefited more from customer clustering than persons of European descent.

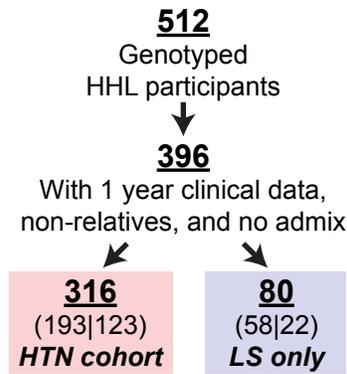


Figure S2: HHL stratification of intervention participation. A total of 512 HHL participants were genotyped. After one year, 396 subjects remained to be used for SNP association analyses. 316 subjects received the HTN intervention, making up the *HTN cohort* described in this report. 80 subjects did not receive the HTN intervention and only participated in the lifestyle (LS) intervention, referred to as the *LS only* cohort. The number of AA vs CAU subjects in each cohort is indicated (AA|CAU).

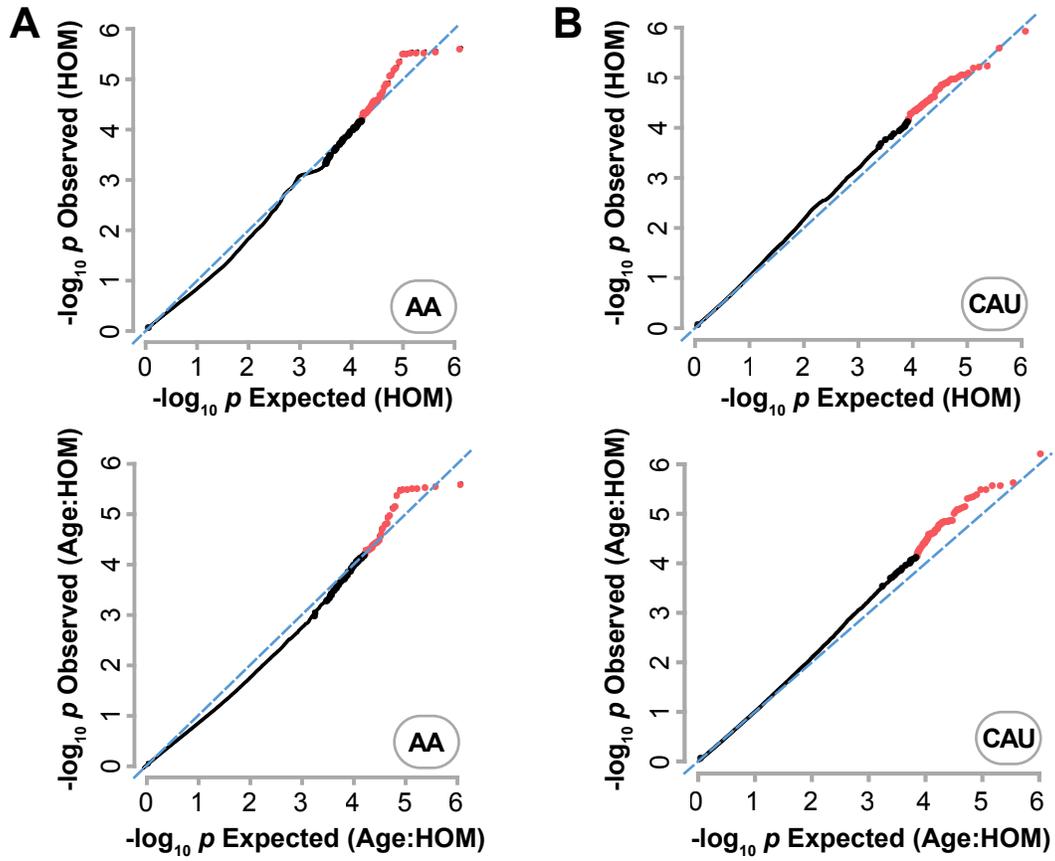


Figure S3: Q-Q plots of the SNP main effect and SNP-Age interaction effect. The observed versus expected values of the inverse log of the p values ($-\log_{10}$) for the homozygous main effect term (HOM, **top**) or the SNP-Age interaction term (Age:HOM, **bottom**) are plotted on the Y or X axis, respectively in the AA (**A**) or CAU (**B**) cohort. P values were calculated from equation (2). Red points represent SNPs that associated with Δ SBP at $p > 1E-4$ and the dashed line represents theoretical distribution of p values.

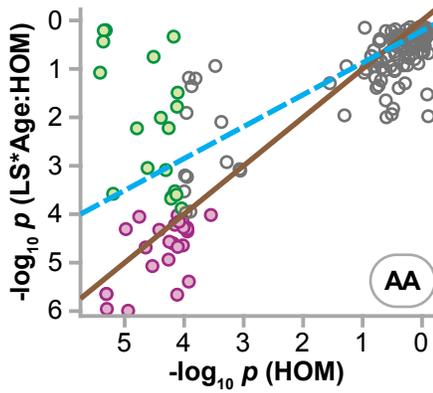
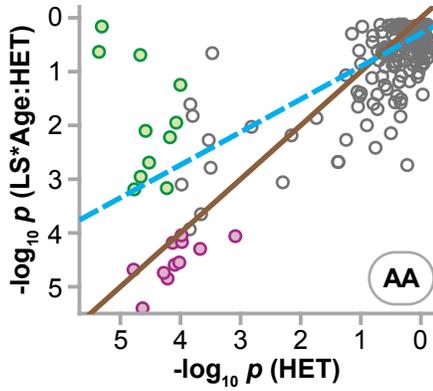
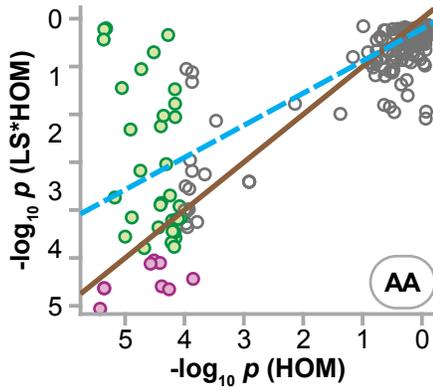
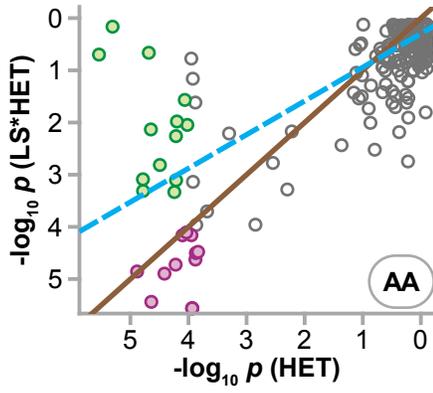
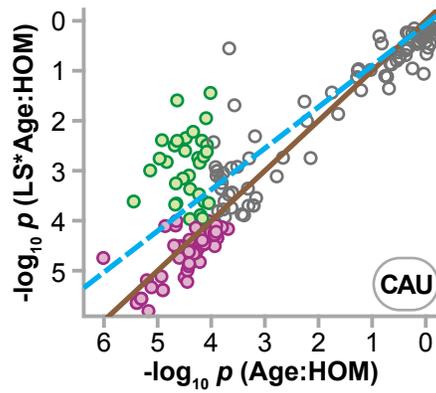
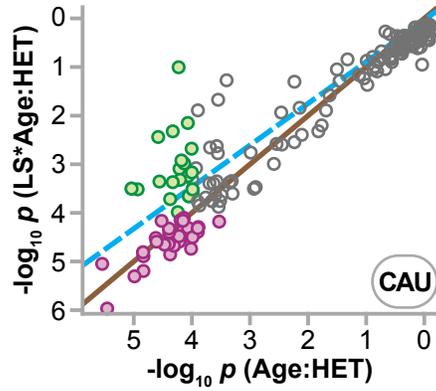
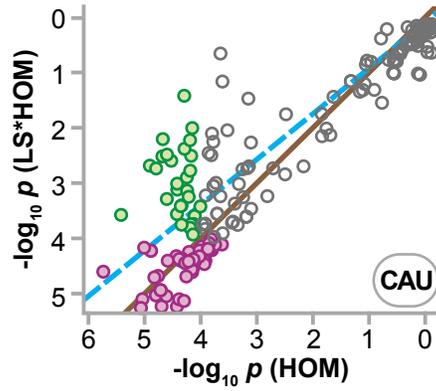
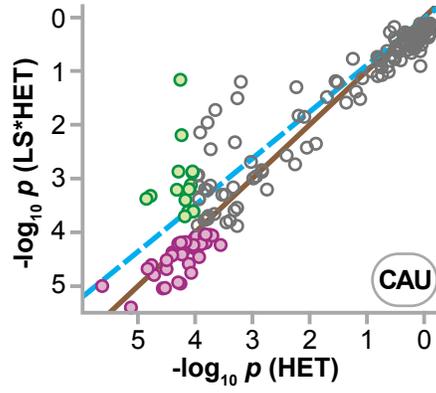
A**B**

Figure S4: Lifestyle co-participation correction on SNP discovery. The effect of including a lifestyle co-participation variable (LS) in the model for Δ SBP is represented by a scatter plot of the p values of the indicated main effect terms (HET, HOM) or interaction terms (Age:HET, Age:HOM) with or without the LS variable on either the Y or X axis, respectively in the AA (**A**) or CAU (**B**) cohort. Regression analysis (dashed line) indicates the overall effect of the correction by how far it deviates from no change (solid line). Individual SNPs that passed the discovery cutoff of $1E-4$ with the LS correction or SNPs that were confounded by LS participation and excluded from additional analyses are indicated by either magenta or green filled points, respectively. Open points represent additional SNPs with no association to Δ SBP ($p > 1E-4$).