SUPPLEMENTAL MATERIAL

Supplementary Figures:

Table S1. Genome wide significant SNPs from Genome-wide association results for Glucose change among PEAR-2 Blacks.

SNP	CHR	BP	Nearest Gene	Minor Allele	MAF	PEAR-2 Chlorthalidone Response	
						β	P-value
rs201505549	9	19,743,120	SLC24A2	D	0.0556	15.41	$2.11x10^{-09}$
rs61824877	1	200,242,632	69kb 3’ of C1orf98	A	0.0606	12.74	$4.82x10^{-09}$
rs10919872	1	200,239,052	73kb 3’ of C1orf98	A	0.06002	12.50	$1.13Ex10^{-08}$
rs2241868	1	120,293,169	HMGCS2	C	0.06579	12.87	$1.37x10^{-08}$
rs10923897	1	120,297,295	HMGCS2	G	0.06579	12.87	$1.37x10^{-08}$
rs12406668	1	120,303,055	HMGCS2	T	0.06579	12.87	$1.37x10^{-08}$
rs61824876	1	200,238,124	74kb 3’ of C1orf98	T	0.05978	12.39	$1.63x10^{-08}$
rs10919866	1	200,230,636	81kb 3’ of C1orf98	A	0.05922	12.12	$3.84x10^{-08}$
rs9927344	16	12,388,109	SNX29	T	0.11819	9.61	$3.86x10^{-08}$
rs9943291	1	120,292,290	HMGCS2	G	0.0637	12.51	$4.17x10^{-08}$

CHR: chromosome; BP: Base-Pair Position: hg19 position. MAF: Minor Allele Frequency; **β**: regression coefficient for allele Minor Allele; D: deletion

Table S2. SNPs which met suggestive significance level 1X10^{-6} in the genome wide association with respect to chlorthalidone induced glucose change in PEAR-2 Whites

SNP	**CHR**	**BP**	**Nearest Gene**	**A1**	**MAF**	**Imputation Quality (Rsq)**	**Pear-2 Chlorthalidone**	
							β	**P**
rs79405723	7	131336198	PODXL	C	0.16	0.60	5.80	2.72x10^{-07}
rs112255998	16	88263085	BANP	G	0.06	0.72	8.28	4.17 x10^{-07}
rs72891473	6	66586528	MCART3P	T	0.05	0.89	9.80	7.67 x10^{-07}
rs79557329	2	167709963	XIRP2	A	0.13	0.97	5.90	8.99 x10^{-07}

CHR: chromosome; BP: Base-Pair Position: hg19 position. MAF: Minor Allele Frequency; β: regression coefficient for allele Minor Allele; SE: standard error of the beta coefficient.

Table S3. Details of the top associations for Blacks in Whites

Top Associations for Blacks										
SNP	CHR	BP	Nearest Gene	Minor Allele	PEAR-2 Chlorthalidone Response (Blacks)			PEAR-2 Chlorthalidone Response (Whites)		
					MAF	**β**	**P-value**	MAF	**β**	**P-value**
rs201505549	9	19,743,120	SLC24A2	D	0.0556	15.41	$2.11x10^{-09}$	SNP removed due to QC (very low MAF)		
rs61824877	1	200,242,632	69kb 3’ of C1orf98	A	0.0606	12.74	$4.82x10^{-09}$	0.1298	-3.60	0.006
rs9927344	16	12,388,109	SNX29	T	0.11819	9.61	$3.86x10^{-08}$	SNP removed due to QC (very low MAF)		
rs9943291	1	120,292,290	HMGCS2	G	0.0637	12.51	$4.17x10^{-08}$	0.0853	1.39	0.34

CHR: chromosome; Position: hg19 position. A1: allele 1; A2: allele 2; BP: Base Pair position

Table S4. Details of the top associations for Whites in Blacks

Top Associations for Whites										
SNP	**CHR**	**BP**	**Nearest Gene**	**Minor Allele**	**PEAR-2 Chlorthalidone Response (Whites)**			**PEAR-2 Chlorthalidone Response (Blacks)**		
					MAF	**β**	**P-value**	**MAF**	**β**	**P-value**
rs79405723	7	131336198	PODXL	C	0.1675	5.80	2.72x10^{-07}	0.1645	0.811	0.63
rs112255998	16	88263085	BANP	G	0.0614	8.28	4.17 x10^{-07}	SNP removed due to QC (very low MAF)		
rs72891473	6	66586528	MCART3P	T	0.0519	9.80	7.67 x10^{-07}	SNP removed due to QC (very low MAF)		
rs79557329	2	167709963	XIRP2	A	0.1308	5.90	8.99 x10^{-07}	SNP removed due to QC (very low MAF)		

CHR: chromosome; Position: hg19 position. A1: allele 1; A2: allele 2; BP: Base Pair position

Table S5. Genome Wide Significant signals from the meta-analysis of Chlorthalidone induced glucose change in PEAR-2 and Hydrochlorothiazide induced glucose change in PEAR Blacks

SNP	CHR	BP	A1	A2	PEAR-2 P-value	PEAR P-Value	Meta-analysis P-value	Nearest Gene
11:92331394:A_AT	11	92331394	I	R	$2.22x10^{-4}$	$1.72x10^{-5}$	$1.72x10^{-08}$	FAT3
1:120292290	1	120292290	G	T	$4.17x10^{-08}$	0.046194	$3.71x10^{-08}$	HMGCS2

CHR: chromosome; Position: hg19 position. A1: allele 1; A2: allele 2; BP: Base Pair position

Table S6. SNPs which met suggestive significance level $1X10^{-6}$ in the meta-analysis of Chlorthalidone induced glucose change in PEAR-2 and Hydrochlorothiazide induced glucose change in PEAR Whites

SNP	CHR	BP	A1	A2	PEAR-2	PEAR	Meta-analysis	Nearest Gene
					P-value	P-Value	P-value	
12:52807944	12	52807944	C	T	6.76E-05	0.0004	1.39E-07	7.8kb 5' of KRT82
12:52803608	12	52803608	A	G	7.27E-05	0.0004	1.48E-07	3.4kb 5' of KRT82
6:5337596	6	5337596	C	T	1.45E-06	0.0388	2.11E-07	FARS2
6:131801262	6	131801262	A	G	0.0002	0.0007	5.81E-07	93kb 5' of ARG1

CHR: chromosome; Position: hg19 position. A1: allele 1; A2: allele 2; BP: Base Pair position

Figure S1. The overall analyses flowchart of the study depicting the total number of participants that were excluded from the analysis, the final number of participants included in the analysis and the various steps of the analysis framework.

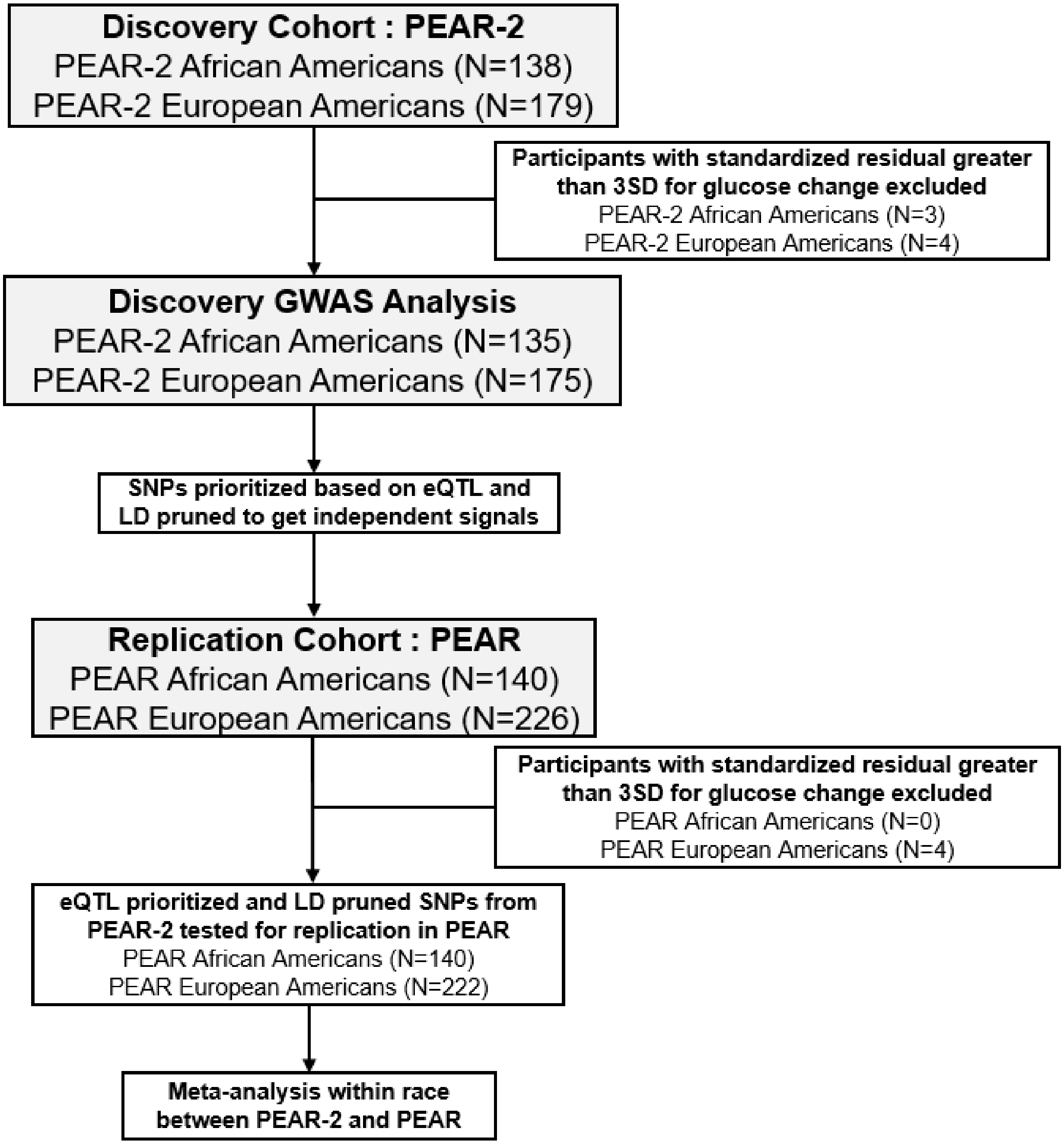


Figure S2. Regional plot for rs9943291 (HMGCS2 gene) the GWAS of glucose change post chlorthalidone treatment.

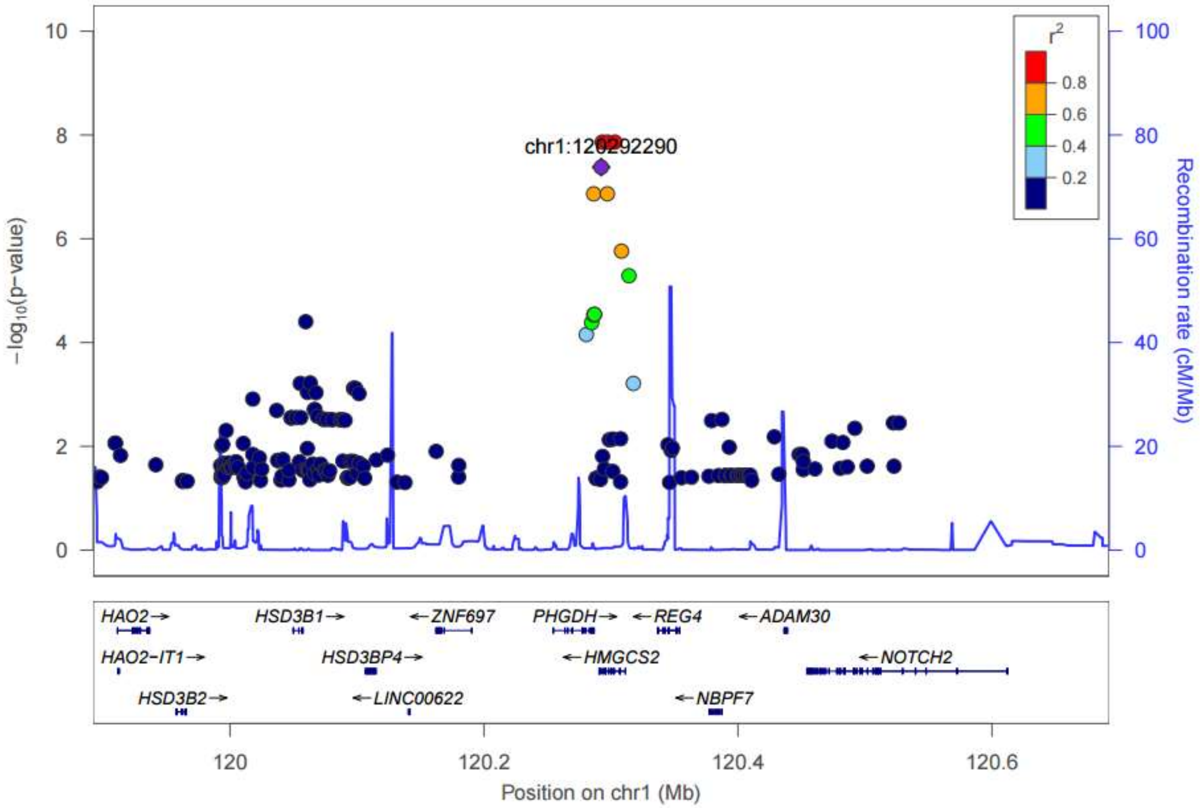
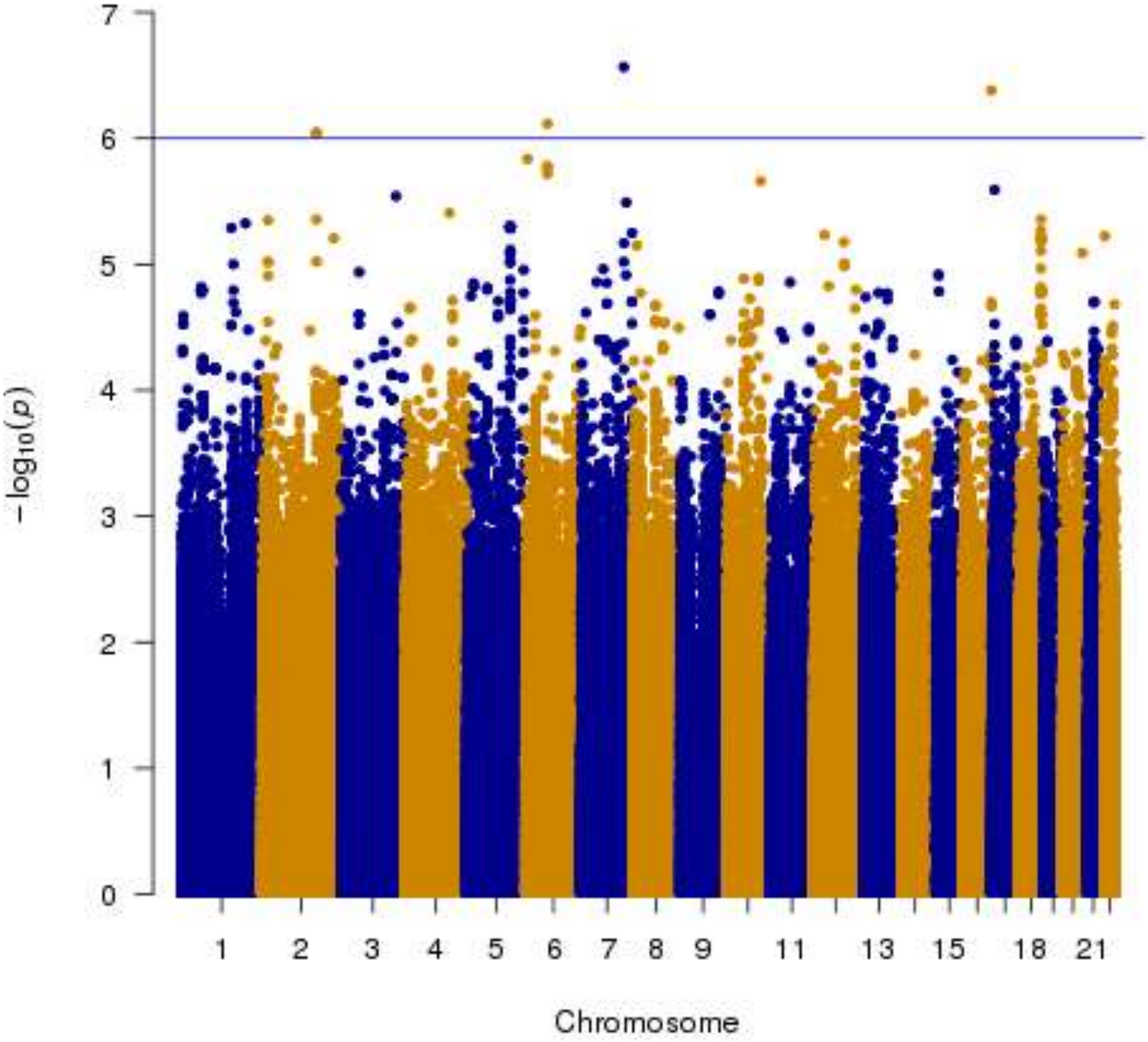


Figure S3. Manhattan plots of Glucose change post chlorthalidone treatment among PEAR-2 European American participants.



Suggestive significance threshold (Blue line): $p < 1 \times 10^{-6}$; PEAR-2: Pharmacogenomic Evaluation of Antihypertensive Response-2.