

Supplementary Tables

Table S1: Genotyping and quality control methods in the participating studies.

Study	Array	Calling algorithm	Pre-imputation variant exclusion criteria			No of SNPs used for imputation	Genomic control parameter
			Per SNP callrate	HWE p	MAF		
ARIC	Affymetrix 6.0	Birdseed	<95%	<10 ⁻⁵	<1%	669,450	1.036
CHS	Illumina 370 CNV BeadChip	BeadStudio	<96%	<10 ⁻⁶	<5%	306,655	1.009
DCCT/EDIC	Illumina 1 M BeadChip	Genome Studio	-	<10 ⁻⁶	<1%	947,519	-
GOOD	Illumina 610	BeadStudio	<98%	<10 ⁻⁶	<1%	553,191	-
Indiana	Illumina Quad 660 Beadchip	Birdseed2	<95%	<10 ⁻⁴	<3%	539,566	1.175
LURIC	Affymetrix 6.0	Birdseed2	<98%	<10 ⁻⁴	<1%	686,195	-
MrOS	Illumina Human Omni1_Quad_v1-0 B	BeadStudio	<97%	<10 ⁻⁴	<1%	740,713	1.023
MESA	Affymetrix 6.0	Birdseed	<96%	<10 ⁻⁶	<5%	934,940	1.020
NESDA	Perlegen + Affymetrix 6.0	Genotyper, BeadStudio, Birdseed	<95%	<10 ⁻⁵	<1%	1,110,706	1.015
OGP-Talana	Affymetrix 500K	BRLMM	<95%	<10 ⁻⁶	<5%	362,151	1.007
SHIP-1	Affymetrix SNP 6.0	Birdseed2	≤90%	<10 ⁻⁴	none	869,224	1.019
SHIP-Trend	Illumina Omni 2.5	GenCall	≤90%	<10 ⁻⁴	none	1,782,967	1.005
TwinsUK	Illumina 317, Illumina 610	Illuminous	<96%	<10 ⁻⁶	< 5%	918,282	1.002
Amish	Affymetrix 500K, Affymetrix 6.0	Birdseed	<95%	<10 ⁻⁷	< 1%	366,169	-

Table S2: Imputation and analysis methods in the participating studies.

Study	Imputation software	Imputation Backbone / NCBI build	Filtering of imputed genotypes	Statistical analysis software	PCA Software used	No of SNPs used for analysis	Trait transformation of PTH	Analysis method	Adjustments
ARIC	IMPUTE2	1000G (March 2012 release) / Build 37	none	R, SAS, SNPTEST	EIGENSTRAT	Whites 23M Blacks 27M	natural logarithm	linear regression	age, sex, field centers, seasons, eGFR, eGFR ² , BMI, and PCs 1-10
CHS	BIMBAM	1000G / Build 37	none	R, STATA, ProABEL, METAL, MANTRA	EIGENSTRAT		natural logarithm	linear regression	age, sex, study site, PCs 1-10
DCCT/EDIC	IMPUTE2	1000G / Build 37	none	R, SNPTEST, SAS	EIGENSTRAT	30M	natural logarithm	linear regression	age, sex, season, eGFR, eGFR ² , BMI, PCs 1-3
GOOD	MACH1.0	HapMap CEU, release 22, build 36	none	R, PLINK	N/A		natural logarithm	linear regression	Age, season, eGFR, BMI
Indiana	IMPUTE2	1000G (March 2012 release) / Build 37	none	GWAF	N/A	30M	natural logarithm	linear mixed effects model	age, season
LURIC	IMPUTE2	1000G / Build 37	none	R, SPSS, SNPTEST	GCTA		natural logarithm	linear regression	age, sex, seasons, PCs 1-3
MrOS	MINIMAC	HapMap2	R ² <0.3	R	R	2.4M	natural logarithm	linear regression	age, study site, PCs 1-10
MESA	IMPUTE 2	1000G / Build 37	none	R, STATA, ProbABEL, METAL, MANTRA	EIGENSTRAT	6.3M	natural logarithm	linear regression	age, sex, study site, PCs 1-10
NESDA	MINIMAC	1000G (March 2012 release) / Build 37	none	SAS, SPSS, PLINK	EIGENSTRAT	30M	natural logarithm	linear regression	age, sex, seasons, waves & chips of genotyping, BMI, eGFR and eGFR ² , PCs 1-3,
OGP-Talana	IMPUTE2	1000G / Build 37	none	R, ProbABEL	EIGENSTRAT	4.1M	natural logarithm	linear regression	age, sex, PCs 1-10

SHIP-1	IMPUTE	Build 36	duplicate RSID	QUICKTEST, R, InforSense, InterSystems Caché	EIGENSTRAT	2.7M	natural logarithm	linear regression	age, sex, PCs 1-10
SHIP-Trend	IMPUTE	Build 36	duplicate RSID	QUICKTEST, R, InforSense, InterSystems Caché	EIGENSTRAT	3.4M	natural logarithm	linear regression	age, sex, PCs 1-10
TwinsUK	IMPUTE2	HapMap	none	GenABEL, STATA13	NA	2.5M	natural logarithm	linear regression	age, sex, seasons, eGFR, eGFR ² , BMI
Amish	IMPUTE2	1000G / Build 37	MAF 0.001 and info < 0.02	MMAF	NA		natural logarithm	linear regression	age, sex, season

PCs indicates principal components

Table S3: Details of PTH and covariate measurement of participating studies

[illegible]

Table S4: Additional Mineral Metabolite Laboratory Methods

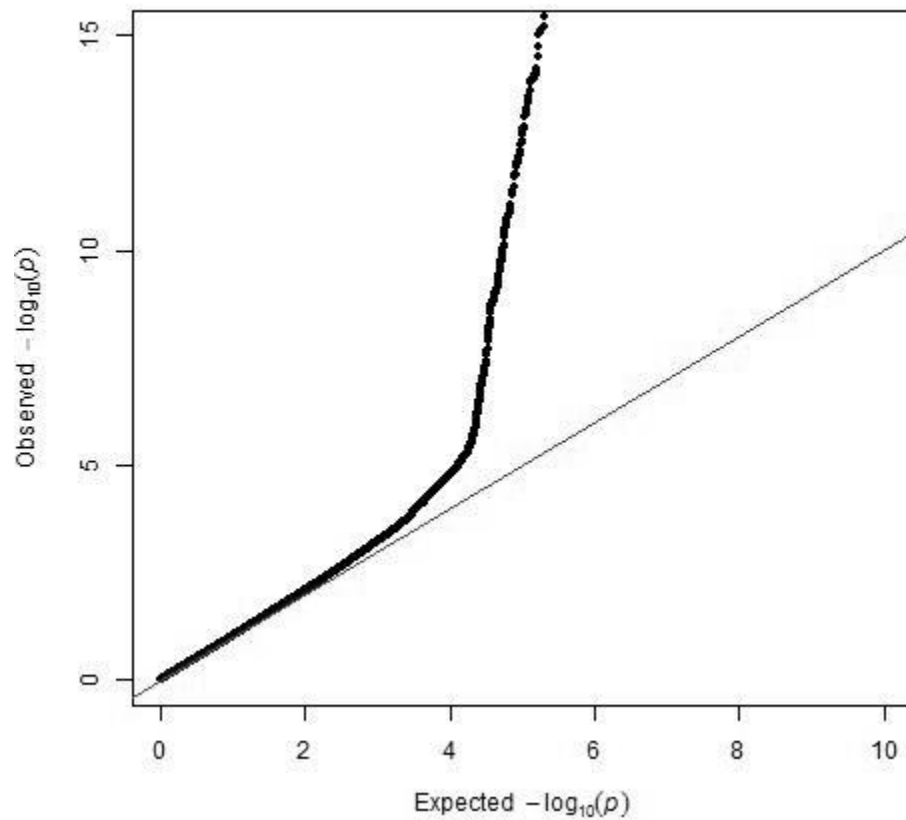
Study	MESA	LURIC	ARIC
<i>Serum Calcium</i>	Indirect potentiometry, DxC Synchron analyzer (Beckman-Coulter Inc, Brea, CA.) ⁶⁷	o-cresolphthalein-complex assay, CA/Hitachi 717 Roche, Mannheim, Germany	o-cresolphthalein-complex assay, CA/Hitachi 717 Roche, Mannheim, Germany
<i>Serum Phosphate</i>	Timed-rate colorimetric reaction method. ⁶⁷	-	Ammonium molybdate
<i>25(OH)D</i>	Mass spectrometry ⁶⁸	-	Mass spectrometry (AB Sciex 5500, Framingham, Massachussets)
<i>24,25(OH)₂D</i>	Mass spectrometry ⁶⁸	-	-
<i>Urine phosphorus</i>	Cobas 6000 analyzer (Roche Diagnostics) in 24-hour urine specimens. Lower limit of detection: 3.4mg/dl CV: 1.4% - 1.7%	-	-
<i>Fractional excretion of phosphorus</i>	[urine phosphorus (mg/dl)/serum phosphorus (mg/dl)]×[serum creatinine (mg/dl)/urine creatinine (mg/dl)]×100	-	-
<i>Urine calcium</i>	Indirect potentiometry with calcium ion-selective electrode		
<i>Serum Fibroblast growth factor-23</i>	Kainos immunoassay (FGF-23 ELISA Kit; Kainos Laboratories Inc. Tokyo, Japan). Interassay CV for singlicate high and low control samples:6.7% and 12.4%, respectively. ⁶⁹	-	Kainos immunoassay (FGF-23 ELISA Kit; Kainos Laboratories Inc. Tokyo, Japan). Interassay CV for singlicate high and low control samples:8.8% and 16.6%, respectively.

Table S5: PTH-increasing allele frequency across 1000 Genomes Super Populations

SNP	Nearest gene	Chr	Position	PTH-increasing allele ^a	PTH-increasing allele frequency				
					1000 Genomes Super Population				
					EAS	EUR	AFR	AMR	SAS
rs6127099	<i>CYP24A1</i>	20	52731402	T	0.34	0.34	0.21	0.50	0.36
rs4074995	<i>RGS14</i>	5	176797343	G	0.86	0.71	0.92	0.77	0.76
rs219779	<i>CLDN14</i>	21	37833751	G	0.99	0.75	0.69	0.78	0.86
rs4443100	<i>RTDRI</i>	22	23372864	G	0.01	0.32	0.20	0.18	0.21
rs73186030	<i>CASR</i>	3	122013465	T	0.04	0.14	0.01	0.11	0.19

^a From analyses in European Americans.

Supplementary Figure S1. QQ Plot for Serum Parathyroid Hormone GWAS



Quantile-quantile plot showing observed p-values of the parathyroid hormone meta-analysis versus expected p-values by chance.

Supplementary Figure S2. Regional Association Plots

Regional association plot showing $-\log_{10}$ (p-values) for all SNPs ordered by their chromosomal position within all regions reaching p-values $< 5 \times 10^{-8}$ in the discovery screen, as well as the parathyroid hormone gene region. Each SNP is colored according to its correlation with the SNP showing the lowest p-value (index SNP) within the region as specified in the color scheme.

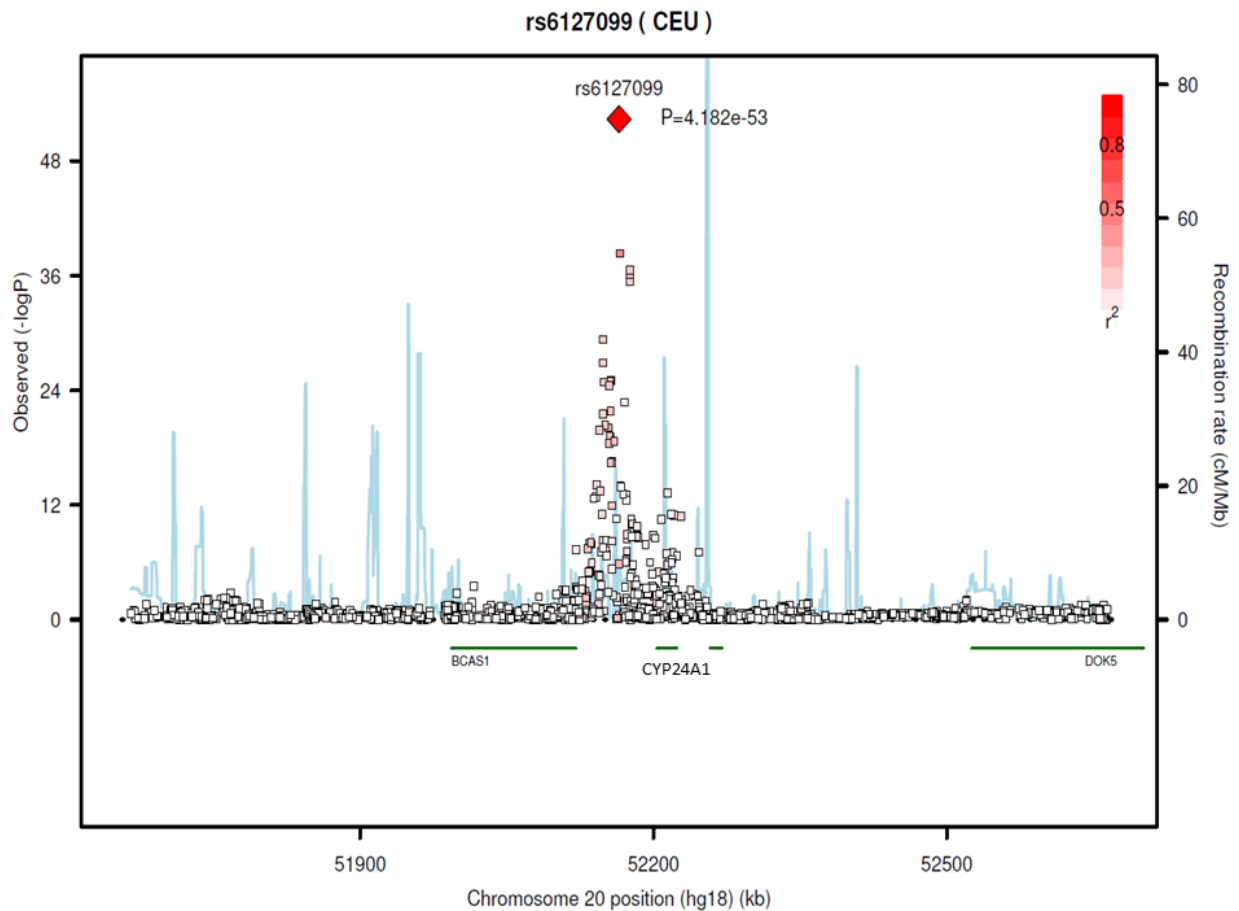


Figure S2a. Regional Association Plot for rs6127099

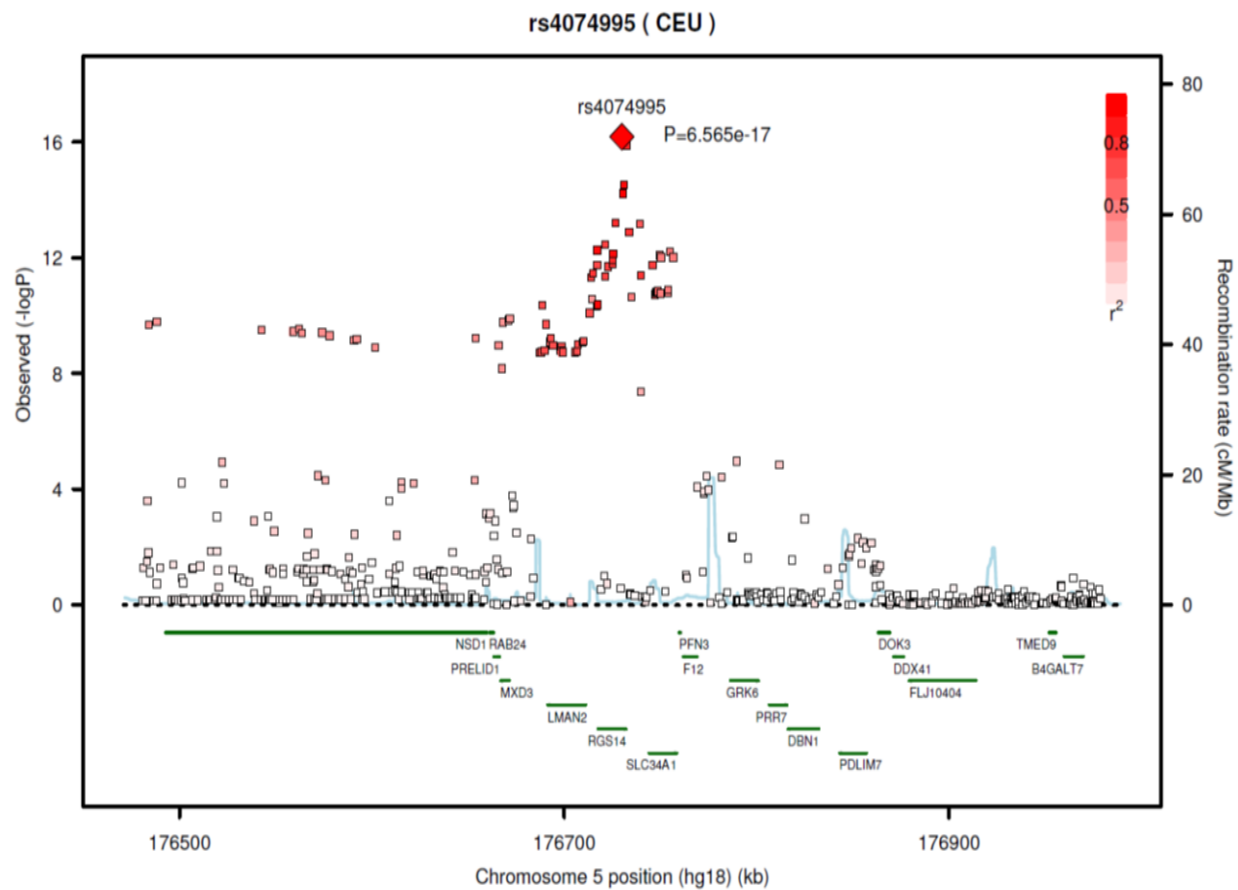


Figure S2b. Regional Association Plot for rs4074995

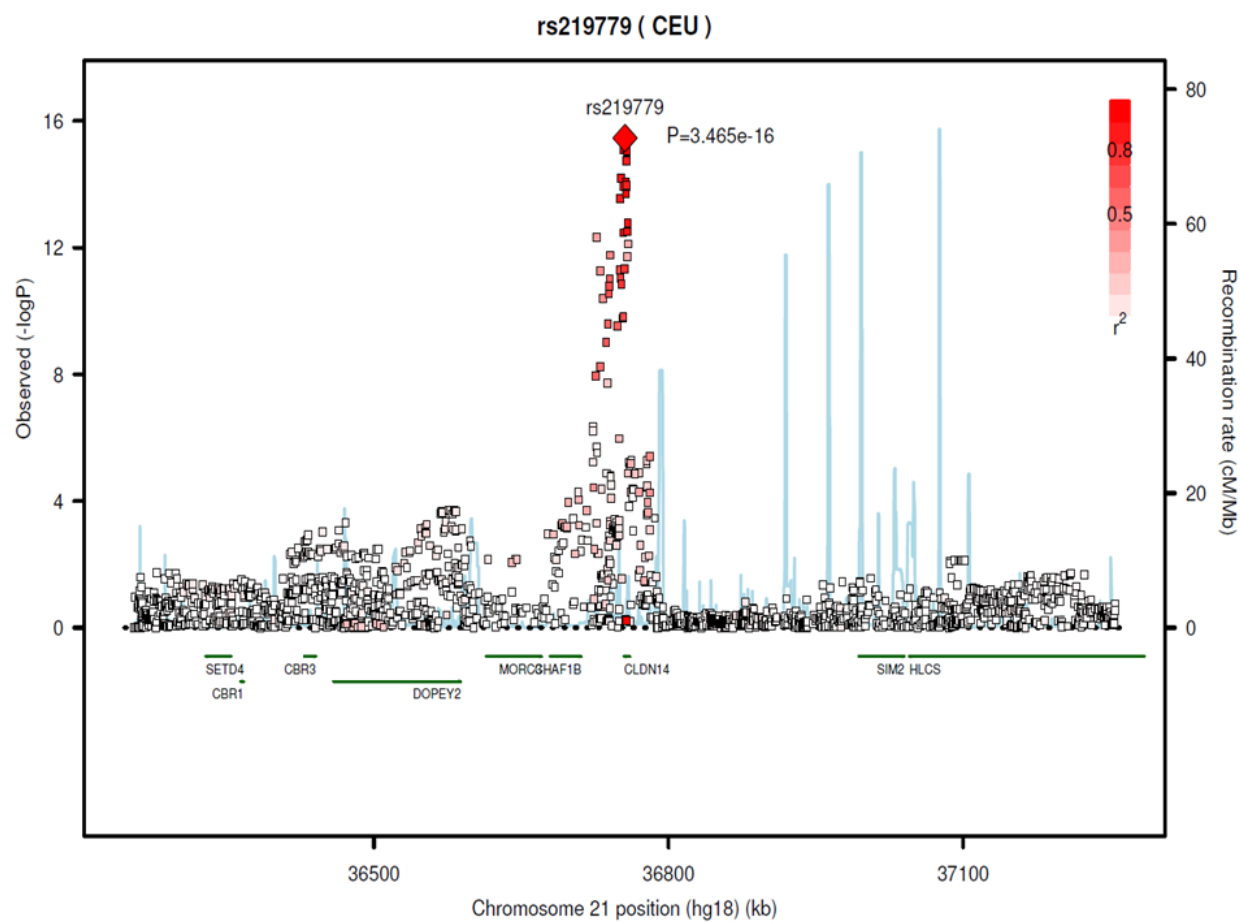


Figure S2c. Regional Association Plot for rs219779

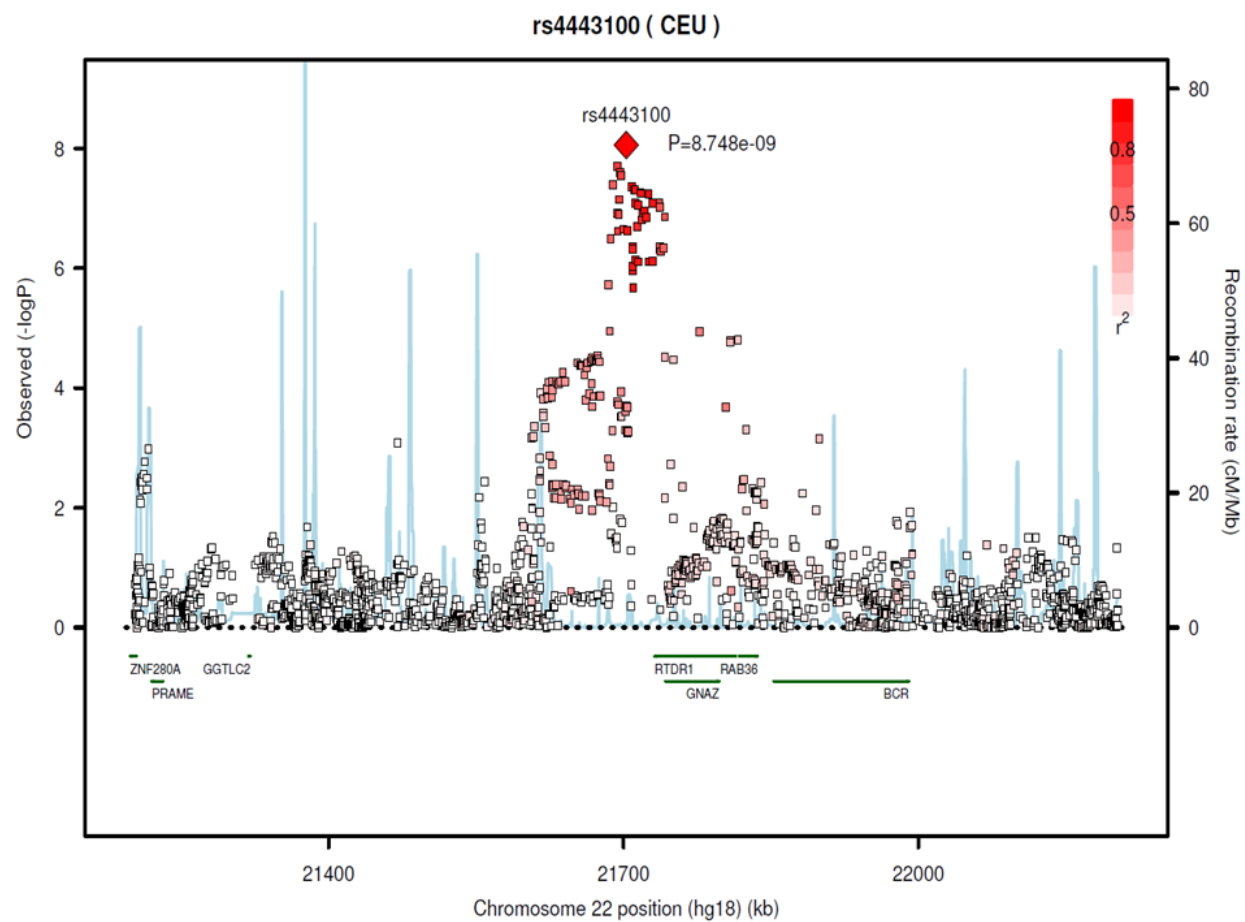


Figure S2d. Regional Association Plot for rs4443100

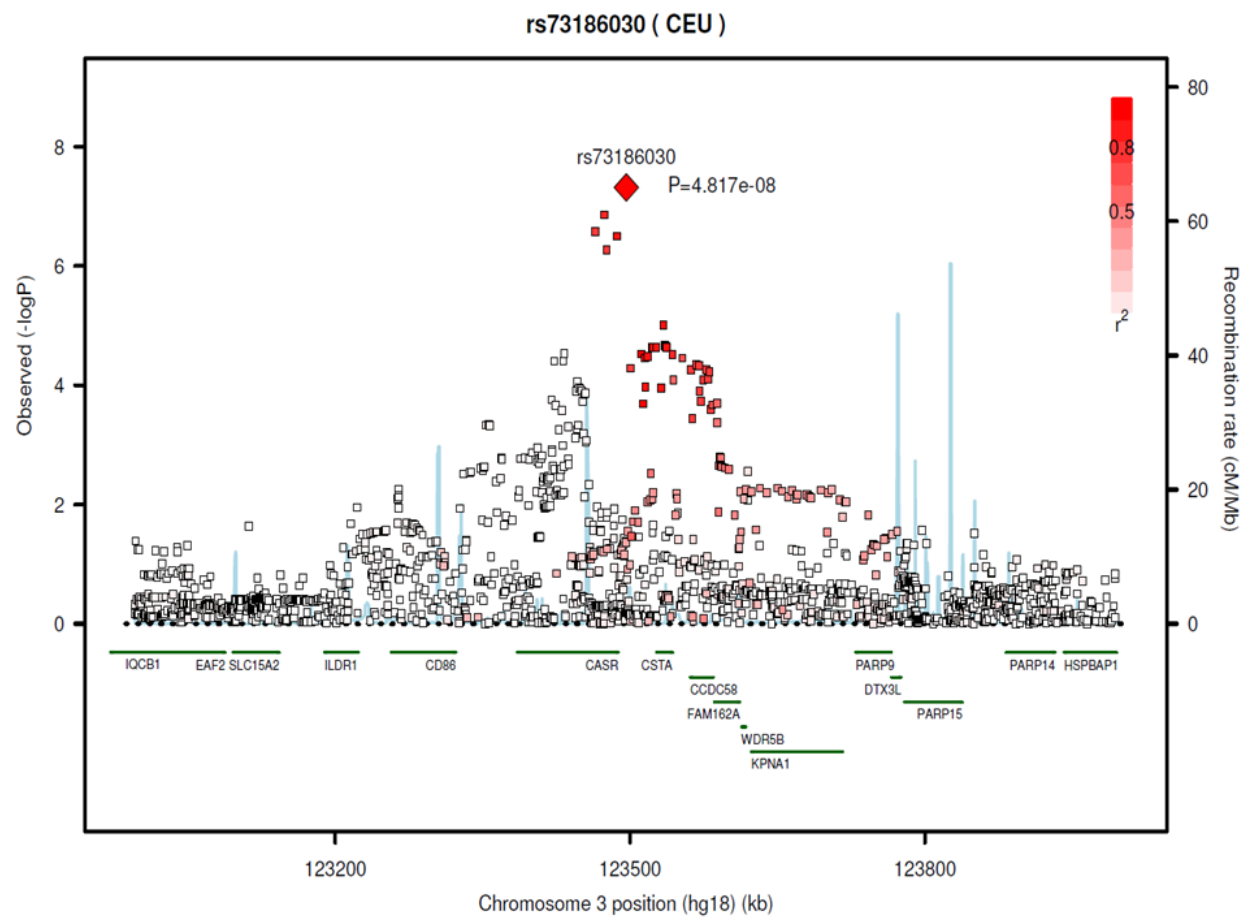


Figure S2e. Regional Association Plot for rs73186030