Supplemental Methods

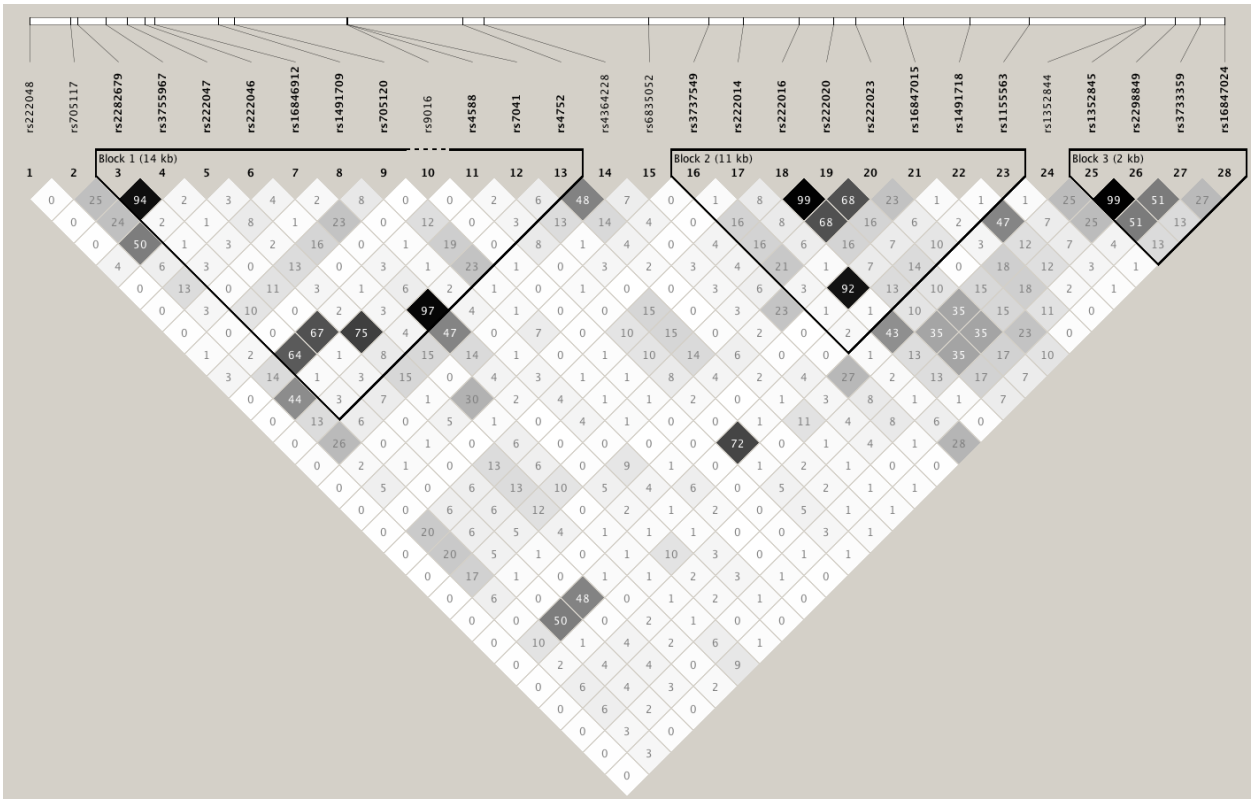
Candidate GWAS-associated SNP selection

Two genome-wide associations studies in Caucasians were reviewed to develop a list of candidate 25(OH)D-associated SNPs [7, 8]. From the study by Ahn *et al* [8], we included the following SNPs associated with 25(OH)D at a GWAS significance level: rs2282679 in *GC*, rs3829251 in *DHCR7/NADSYN1*, and rs2060793 in *CYP2R1*. The association of rs6599638 in c10orf88 with 25(OH)D was not confirmed in a replication sample, and consequently not included in the current study. In the second GWAS study by Wang *et al* [7], the SNPs most strongly associated with serum 25(OH)D from each associated gene were included in our preliminary list: rs2282679 in *GC*, rs12785878 in *DHCR7/NADSYN1*, rs10741657 in *CYP2R1*, and rs6013897 in *CYP24A1*. Finally, SNPs strongly associated with 25(OH)D at GWAS or near-GWAS level significance and in strong LD with the most significant SNPs identified in GWAS [7, 8] were included: rs7041 and rs1155563 in *GC,* rs1993116 in *CYP2R1*, and rs11234027 in *NADSYN1.*

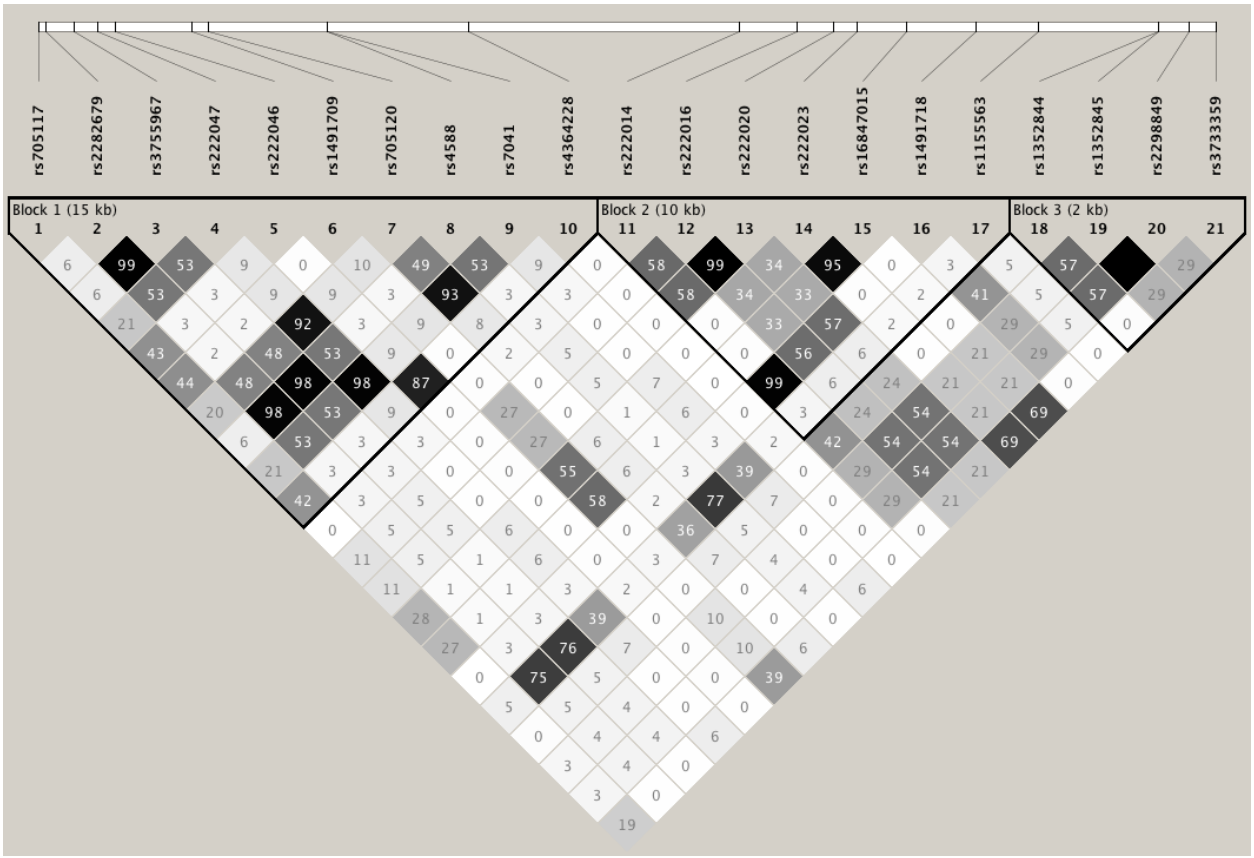
Two SNPs (rs6013897 and rs11234027) were not in the Health ABC African-American database, leaving a final set of 8 candidate SNPs in three genomic loci, which are considered in Table 2 of the manuscript: rs7041, rs2282679, and rs1155563 in *GC*; rs2060793, rs10741657, rs1993116 in *CYP2R1*; and rs12785878 and rs3829251 in *DHCR7/NADSYN1*.

Supplemental Figure 1. Linkage disequilibrium (LD) plots of *GC* in Health ABC African Americans (A) and Health ABC European Americans (B), based on directly genotyped SNPs only. Shading represents linkage (R^2), where black shading represents complete linkage between SNPs and white shading represents no linkage. Inset triangles represent LD blocks.

A



B


rs705117
rs2282679
rs3755967
rs222047
rs222046
rs1491709
rs705120
rs4588
rs7041
rs4364228
rs222014
rs222016
rs222020
rs222023
rs16847015
rs1491718
rs1155563
rs1352844
rs1352845
rs2298849
rs3733359
Block 1 (15 kb)
Block 2 (10 kb)
Block 3 (2 kb)

Supplemental Table 1 Imputed SNPs in genes[1] identified in published GWAS of serum 25-hydroxyvitamin D [25(OH)D] phenotype in Caucasians, associated with serum 25(OH)D at *P*<0.10 in African American participants of the Health, Aging and Body Composition cohort

SNP	Gene[1]	Chr	Position	Coded allele	Freq.	β[2] ± SE	*P*[3]
rs222040	*GC*	4	72835796	A	0.43	0.86 ± 0.41	0.04
rs842999	*GC*	4	72830554	C	0.17	1.15 ± 0.58	0.05
rs10500804	*CYP2R1*	11	14866849	G	0.16	1.31 ± 0.56	0.02
rs11819875	*CYP2R1*	11	14873873	G	0.48	0.95 ± 0.41	0.02
rs12794714	*CYP2R1*	11	14870151	A	0.16	1.30 ± 0.56	0.02
rs7928249	*DHCR7/NADSYN1*	11	70838711	A	0.55	0.82 ± 0.42	0.05
rs12800438	*DHCR7/NADSYN1*	11	70848651	A	0.41	0.78 ± 0.43	0.07
rs7131218	*DHCR7/NADSYN1*	11	70859450	C	0.84	0.98 ± 0.54	0.07
rs7938885	*DHCR7/NADSYN1*	11	70847691	C	0.41	0.77 ± 0.43	0.07
rs4944062	*DHCR7/NADSYN1*	11	70864942	G	0.59	0.76 ± 0.42	0.07
rs2276362	*DHCR7/NADSYN1*	11	70852100	A	0.60	0.76 ± 0.43	0.08
rs4423214	*DHCR7/NADSYN1*	11	70850902	C	0.59	0.75 ± 0.43	0.08
rs7129788	*DHCR7/NADSYN1*	11	70849373	A	0.14	0.98 ± 0.58	0.09
rs2276360	*DHCR7/NADSYN1*	11	70847195	C	0.44	0.72 ± 0.43	0.09

[1] In total, 69, 14 and 122 SNPs were imputed in *GC*, *CYP2R1*, and *DHCR7/NADSYN1*, respectively; only those with P<0.10 are shown in table

[2] Estimated change in serum 25(OH)D per copy of **coded** allele, calculated in a multivariate regression model adjusted for age, gender, study site, season of blood draw, and principal components

[3] Nominal *P*-value.

Supplemental Table 2 Comparison of frequencies for GWAS-associated SNPs between Caucasians and Africans (gene frequencies from HapMap populations, CEU[1] and YRI[2], as reported in dbSNP)

SNP	Allele[3]	Gene	CEU[1] Frequency	YRI[2] Frequency	Health ABC African American Frequency
rs7041	A/T	*GC*	0.43	0.90	0.82
rs2282679	G/C	*GC*	0.26	0.04	0.10
rs1155563	C	*GC*	0.29	0.05	0.11
rs2060693	A	*CYP2R1*	0.39	0.35	0.37
rs10741657	A	*CYP2R1*	0.37	0.22	0.28
rs1993116	A/T	*CYP2R1*	0.40	0.26	0.28
rs12785878	G	*DHCR7/NADSYN1*	0.27	0.84	0.73
rs3829251	A	*DHCR7/NADSYN1*	0.17	0.27	0.23

[1] CEU: Utah residents with Northern and Western European ancestry from the CEPH collection

[2] YRI: Yoruba population in Ibadan, Nigeria

[3] For three SNPs, the coded allele in Health ABC differed from the allele reported in dbSNP; in these instances, allele frequencies for the complementary allele are reported.