Supplementary Table 1. Analysis based on <u>controls only</u> (ATBC, CPS-II, CLUE II, and PLCO combined; n=1,312)

SNP[a]	Risk allele (freq)	Chr	Location[b]	Gene neighborhood	P-value[c,d]	Beta[e]	S.E.
rs2282679	C (0.26)	4	72827247	*GC*	1.4×10^{-11}	-0.39	0.06
rs3829251	A (0.19)	11	70872207	*NADSYN1/DHRC7*	0.11	-0.10	0.06
rs6599638	G (0.49)	10	124694139	*C10orf88*	4.0×10^{-3}	-0.15	0.05
rs2060793	A (0.41)	11	14866810	*CYP2R1*	0.25	0.06	0.05

FOOTNOTES TO SUPPLEMENTARY TABLES 1 AND 2

a. SNP identifier based on NCBI dbSNP

b. Chromosomal location based on NCBI Human Genome Build 35 coordinates

c. The result of 1 df test based on linear regression, using an additive model, after square root transformation of 25-hydroxy vitamin D levels – adjusted for age, vitamin D assay batch, study, case-control status, sex, body mass index, season of blood collection, vitamin D supplement intake, dietary vitamin D intake, region/latitude, and chosen eigenvectors to control population stratification.

d. The result of 1 df test based on logistic regression, using an additive model,– adjusted for age, vitamin D assay batch, study, case-control status, sex, body mass index, season of blood collection, vitamin D supplement intake, dietary vitamin D intake, region/latitude, and chosen eigenvectors to control population stratification.

e. The regression beta and standard error were based on the square root scale.

Supplementary Table 2. Binary outcome for vitamin D clinical deficiency (<25 nmol/L) (ATBC, CPS-II, CLUE II, PLCO combined; n=2,907)

SNP[a]	Risk allele (freq)	Chr	Location[b]	Gene Neighborhood	P-value[c]	OR
rs2282679	C (0.26)	4	72827247	*GC*	6.5×10^{-9}	1.83
rs3829251	A (0.19)	11	70872207	*NADSYN1/DHRC7*	0.11	1.18
rs6599638	G (0.49)	10	124694139	*C10orf88*	8.1×10^{-2}	1.17
rs2060793	A (0.41)	11	14866810	*CYP2R1*	0.21	0.89

Joint model: *GC* rs2282679 + *NADSYN1/DHCR7* rs3829251 + *C10orf88* rs6599638 + *CYPR1* rs2060793. Odds ratio of having one copy of high risk allele at each of the four loci is 2.97 (95% CI 2.00 - 4.39). The joint effect from the four SNPs is significant *(P* = 3.2×10^{-8}).