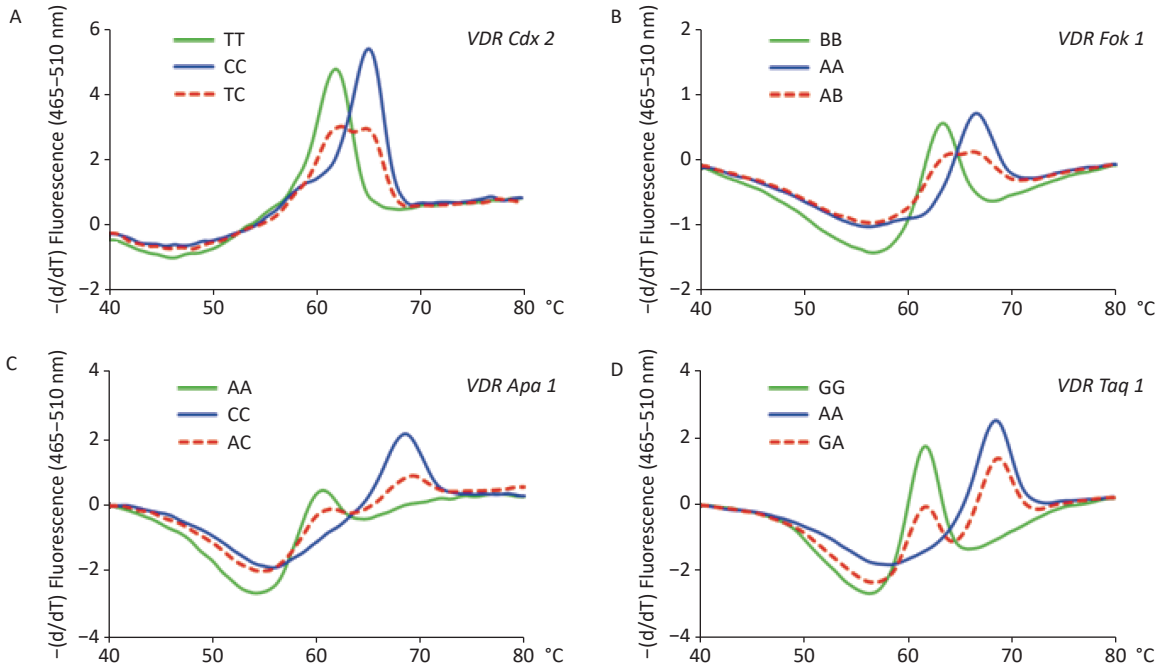

Supplementary Figure S1. Melting curve analyses on the polymorphisms of vitamin D receptor gene (*VDR*). Panel A: Melting curve of *VDR Cdx2* (rs11568820, A). Panel B: Melting curve of *Fok1* (rs2228570, B). Panel C: Melting curve of *VDR Apa1* (rs7975232, C). Panel D: Melting curve of *VDR Taq1* (rs731236, D).

Supplementary Table S1. The information of molecular beacon probes and primers for genotyping the four single nucleotide polymorphisms (SNPs) of vitamin D receptor gene (*VDR*)

NCBI rs ID	SNP name	Alleles[a]	Position[b]	Oligo name	Oligo sequence, 5'–3' direction[c]	Length of amplicon, bp
rs11568820	*Cdx2*	C > T	promoter region, chr12:47908762	Probe	cctgaTTACTGTGACCTAGTTTACTCAGG	179
				Forward primer	CAATGAAAGCAAACCAAGGGGTCTTC	
				Backward primer	AGGAAGGAAAAGAGGATAGAGAAAAT	
rs2228570	*Fok1*	A > B[d]	exon 2, chr12:47879112	Probe	ccgcGGGATGGAGGCAATGGCGG	178
				Forward primer	CACTGACTCTGGCTCTGACCGT	
				Backward primer	GCAGCCTTCACAGGTCATA	
rs7975232	*Apa1*	C > A	intron 8, chr12:47845054	Probe[e]	ctTGGGCCCCTCACTGCTCAAg	185
rs731236	*Taq1*	A > G	exon 9, chr12:47844974	Probe[e]	cgcGGATGGCCTCAATCAGCGCG	
				Forward primer	GGCGGCAGCGGATGTACG	
				Backward primer	GCCGTTGAGTGTCTGTGT	

Note. [a]The usages of these alleles are consistent to those used in the NCBI dbSNP database. [b]Location of the allelic bases on the *VDR* and chromosome 12. [c]In the probe sequence, the lowercase letters at the 5' or 3' end are adaptor bases, and the highlighted letters are one of the alleles in the SNP locus. [d]B, degenerate base standing for C, G, and T, i.e. not A. [e]*Apa1* and *Taq1* were detected with their respective probe on the same qPCR amplicon.

Supplementary Table S2. Hardy-Weinberg equilibrium tests on the vitamin D receptor gene polymorphisms, *Cdx2* (rs11568820), *Fok1* (rs2228570), *Apa1* (rs7975232), and *Taq1* (rs731236)

Genotype	*n*	Genotype frequency, %			χ^2	*P* value[*]
Cdx2		**TT**	**CT**	**CC**		
DL	1,142	20.0	47.0	34.0	2.06	0.15
ND	845	19.0	51.0	30.0	0.80	0.37
total	1,987	19.0	49.0	32.0	0.26	0.61
Fok1		**BB**	**AB**	**AA**		
DL	1,142	28.0	52.0	20.0	2.38	0.12
ND	845	28.0	50.0	22.0	0.06	0.81
total	1,987	28.0	51.0	21.0	1.75	0.19
Apa1		**AA**	**AC**	**CC**		
DL	1,142	10.0	39.0	51.0	4.85	**0.03**
ND	845	9.0	42.0	49.0	0.09	0.76
total	1,987	9.0	40.0	50.0	2.14	0.14
Taq1		**GG**	**AG**	**AA**		
DL	1,142	0.5	8.0	90.0	2.73	0.10
ND	845	0.5	11.0	91.0	0.60	0.44
total	1,987	1.0	9.0	90.0	3.01	0.08

Note. Abbreviations: B, degenerate base standing for C, G, and T; DL, dyslipidemia; ND, non-dyslipidemia. [*]Hardy-Weinberg equilibrium analyses test for the genotypes of the four SNPs.

Supplementary Table S3. Comparisons of the genotypic and allelic frequencies of vitamin D receptor gene polymorphisms, *Cdx2* (rs11568820), *Fok1* (rs2228570), *Apa1* (rs7975232), and *Taq1* (rs731236) between dyslipidemia (DL) and non-dyslipidemia (ND) adults

Genotype	Female				Male			
	DL, % *n* = 236	ND, % *n* = 888	χ^2	*P* value	DL, % *n* = 299	ND, % *n* = 564	χ^2	*P* value
Cdx2								
TT	17.8	19.4	0.955	0.620	20.4	19.1	0.390	0.823
CT	50.0	51.6			43.8	45.9		
CC	32.2	29.1			35.8	34.9		
T	42.8	45.2	0.841	0.359	42.3	42.1	0.006	0.937
C	57.2	54.8			57.7	57.9		
Fok1								
AA	15.3	23.3	11.658	**0.003**	16.7	21.6	3.871	0.144
AB	48.7	50.2			53.2	52.8		
BB	36.0	26.5			30.1	25.5		
A	39.6	48.4	11.618	**0.001**	43.3	48.0	3.528	0.060
B	60.4	51.6			56.7	52.0		
Apa1								
AA	9.3	9.9	0.120	0.942	8.7	9.0	0.304	0.859
AC	41.1	40.1			41.5	39.5		
CC	49.6	50.0			49.8	51.4		
A	29.9	30.0	0.001	0.972	29.4	28.8	0.073	0.787
C	70.1	70.0			70.6	71.2		
Taq1								
AA	91.5	88.9	1.496	0.476	91.0	91.3	0.256	0.921
AG	8.1	10.7			8.7	8.2		
GG	0.4	0.5			0.3	0.5		
A	95.6	94.2	1.305	0.253	95.3	95.4	0.005	0.946
G	4.4	5.8			4.7	4.6		

Note. Abbreviations: B, degenerate base standing for C, G, and T.

Supplementary Table S4. Genetic model comparison of *Cdx2* (rs11568820) in vitamin D receptor gene between dyslipidemia (DL) and non-dyslipidemia (ND) adults

Gene	Additive model			Dominant model		Recessive model		Homozygous model		Allelic model	
models	TT	CT	CC	TT + CT	CC	TT	CT + CC	TT	CC	T	C
DL											
n	103	249	183	352	183	103	432	103	183	455	615
%	19.3	46.5	34.2	65.8	34.2	19.3	80.7	36.0	64.0	42.5	57.5
ND											
n	280	717	455	997	455	280	1,172	280	455	1,277	1,627
%	19.3	49.4	31.3	68.7	31.3	19.3	80.7	38.1	61.9	44.0	56.0
Total											
n	383	966	638	1,349	638	383	1,604	383	638	1,732	2,242
%	19.3	48.6	32.1	67.9	32.1	19.3	80.7	37.5	62.5	43.6	56.4
χ^2	1.54			1.48		0.00		0.38		0.67	
P value	0.46			0.22		0.99		0.54		0.41	

Supplementary Table S5. Genetic model comparison of *Apa1* (rs7975232) in vitamin D receptor gene between dyslipidemia (DL) and non-dyslipidemia (ND) adults

Gene models	Additive model			Dominant model		Recessive model		Homozygous model		Allelic model	
	AA	AC	CC	AA + AC	CC	AA	AC + CC	AA	CC	A	C
DL											
n	48	221	266	269	266	48	487	48	266	317	753
%	9.0	41.3	49.7	50.3	49.7	9.0	91.0	15.3	84.7	29.6	70.4
ND											
n	139	579	734	718	734	139	1,313	139	734	857	2,047
%	9.5	39.9	50.6	49.4	50.6	9.6	90.4	15.9	84.1	29.5	70.5
Total											
n	187	800	1,000	987	1,000	187	1,800	187	1,000	1,174	2,800
%	9.4	40.3	50.3	49.7	50.3	9.4	90.6	15.8	84.2	29.5	70.5
χ^2	0.40			0.11		0.17		0.10		0.01	
P value	0.82			0.74		0.68		0.79		0.94	

Supplementary Table S6. Genetic model comparison of *Taq1* (rs731236) in vitamin D receptor gene between dyslipidemia (DL) and non-dyslipidemia (ND) adults

Gene models	Additive model			Dominant model		Recessive model		Homozygous model		Allelic model	
	GG	AG	AA	GG + AG	AA	GG	AG + AA	GG	AA	G	A
DL											
n	2	45	488	47	488	2	533	2	488	49	1,021
%	0.4	8.4	91.2	8.8	91.2	0.4	99.6	0.4	99.6	4.6	95.4
ND											
n	7	141	1,304	148	1,304	7	1,445	7	1,304	155	2,749
%	0.5	9.6	89.9	10.2	89.8	0.5	99.5	0.5	99.5	5.3	94.7
Total											
n	9	186	1,792	195	1,792	9	1,978	9	1,792	204	3,770
%	0.5	9.4	90.2	9.8	90.2	0.5	99.5	0.5	99.5	5.1	94.9
χ^2	0.89			0.88		0.00		0.11		0.92	
P value	0.64			0.35		1.00		0.74		0.34	

Supplementary Table S7. Logistic regression analyses of lipids with SNPs of *VDR* in adult females with adjustment for age, body mass index, dietary 25-hydroxyvitamin D, and the sunshine time per week

Gene models	TG ≥ 1.7 *vs*. < 1.7 mmol/L		TC ≥ 5.2 *vs*. < 5.2 mmol/L		LDLC ≥ 3.4 *vs*. < 3.4 mmol/L		HDLC < 1.0 *vs*. ≥ 1.0 mmol/L	
	P	*OR* (95% *CI*)	*P*	*OR* (95% *CI*)	*P*	*OR* (95% *CI*)	*P*	*OR* (95% *CI*)
Apa1 (rs7975232)								
Add.: AA *vs*. AC *vs*. CC	0.47	1.11 (0.84–1.47)	0.48	0.93 (0.76–1.14)	0.38	1.12 (0.87–1.43)	0.93	1.03 (0.52–2.04)
Dom.: AA + AC *vs*. CC	0.59	1.10 (0.77–1.59)	0.35	0.88 (0.67–1.15)	0.59	1.09 (0.79–1.50)	0.87	1.08 (0.44–2.64)
Rec.: AA *vs*. AC + CC	0.84	1.06 (0.59–1.92)	0.88	0.97 (0.63–1.49)	0.33	1.29 (0.78–2.12)	0.99	1.01 (0.23–4.45)
Hom.: AA *vs*. CC	0.16	0.21 (0.03–1.86)	0.52	1.35 (0.54–3.34)	0.16	2.09 (0.75–5.81)	0.71	1.63 (0.13–20.27)
Alle.: A *vs*. C	0.45	1.12 (0.83–1.51)	0.38	0.91 (0.73–1.13)	0.54	1.08 (0.84–1.40)	0.79	1.11 (0.53–2.33)
Cdx2 (rs11568820)								
Add.: TT *vs*. CT *vs*. CC	0.15	0.83 (0.64–1.07)	0.77	0.97 (0.81–1.17)	0.79	1.03 (0.83–1.29)	0.38	0.76 (0.40–1.42)
Dom.: TT + CT *vs*. CC	0.10	0.73 (0.50–1.06)	0.30	0.86 (0.65–1.14)	0.70	1.07 (0.76–1.49)	0.79	0.88 (0.35–2.23)
Rec.: TT *vs*. CT + CC	0.65	0.90 (0.57–1.41)	0.49	1.12 (0.81–1.55)	0.97	0.99 (0.67–1.46)	0.20	0.38 (0.09–1.68)
Hom.: TT *vs*. CC	0.42	0.66 (0.23–1.85)	0.27	1.45 (0.75–2.82)	0.51	1.32 (0.58–3.02)	0.27	0.28 (0.03–2.71)
Alle.: T *vs*. C	0.11	0.81 (0.62–1.05)	0.98	1.00 (0.83–1.21)	0.79	0.97 (0.77–1.22)	0.45	0.77 (0.40–1.50)
Fok1 (rs2228570)								
Add.: BB *vs*. AB *vs*. AA	0.57	1.08 (0.84–1.39)	0.35	1.09 (0.91–1.31)	**0.03**	1.28 (1.03–1.59)	0.68	1.13 (0.62–2.07)
Dom.: BB + AB *vs*. AA	0.51	1.16 (0.75–1.80)	0.64	1.08 (0.79–1.47)	0.18	1.31 (0.89–1.92)	0.57	0.76 (0.29–1.99)
Rec.: BB *vs*. AB + AA	0.70	1.08 (0.73–1.59)	0.29	1.16 (0.88–1.54)	**0.03**	1.45 (1.04–2.00)	0.22	1.72 (0.72–4.14)
Hom.: BB *vs*. AA	0.22	0.55 (0.21–1.44)	0.68	1.15 (0.60–2.20)	**0.02**	2.86 (1.16–7.08)	0.98	1.03 (0.14–7.63)
Alle.: B *vs*. A	0.30	1.15 (0.88–1.49)	0.27	1.11 (0.92–1.34)	0.05	1.26 (1.00–1.58)	0.37	1.36 (0.70–2.65)
Taq1 (rs731236)								
Add.: GG *vs*. AG *vs*. AA	0.08	0.55 (0.28–1.08)	0.35	0.82 (0.54–1.25)	0.85	0.95 (0.58–1.58)	0.87	0.89 (0.20–3.87)
Dom.: GG + AG *vs*. AA	0.11	0.57 (0.28–1.13)	0.41	0.83 (0.53–1.29)	0.94	0.98 (0.58–1.66)	0.98	0.98 (0.21–4.64)
Rec.: GG *vs*. AG + AA	1.00	0.00 (0.00–NA)	0.45	0.42 (0.04–3.99)	0.96	1.06 (0.11–10.06)	1.00	0.00 (0.00–NA)
Hom.: GG *vs*. AA	NA	NA (NA–NA)	NA	NA (NA–NA)	NA	NA (NA–NA)	NA	NA (NA–NA)
Alle.: G *vs*. A	0.12	0.59 (0.30–1.15)	0.27	0.79 (0.51–1.21)	0.75	0.92 (0.56–1.53)	0.86	0.87 (0.19–4.09)

Note. Abbreviations: Add., additive model; Alle., allelic model; B, degenerate base standing for C, G, and T; *CI*, confidential interval; Dom., dominant model; HDLC, high-density lipoprotein cholesterol; Hom., homozygous model; LDLC, low-density lipoprotein cholesterol; NA, not available; *OR*, odds ratio; Rec., recessive model; SNPs, single nucleotide polymorphisms; TC, total cholesterol; TG, triglyceride; *VDR*, vitamin D receptor gene.

Supplementary Table S8. Logistic regression analyses of lipids with SNPs of *VDR* in adult males with adjustment for age, body mass index, dietary 25-hydroxyvitamin D, and the sunshine time per week

Gene models	TG ≥ 1.7 *vs*. < 1.7 mmol/L		TC ≥ 5.2 *vs*. < 5.2 mmol/L		LDLC ≥ 3.4 *vs*. < 3.4 mmol/L		HDLC < 1.0 *vs*. ≥ 1.0 mmol/L	
	P	*OR* (95% *CI*)	*P*	*OR* (95% *CI*)	*P*	*OR* (95% *CI*)	*P*	*OR* (95% *CI*)
Apa1 (rs7975232)								
Add.: AA *vs*. AC *vs*. CC	0.55	1.08 (0.85–1.37)	0.95	0.99 (0.79–1.24)	0.92	0.99 (0.75–1.30)	0.11	1.72 (0.88–3.35)
Dom.: AA + AC *vs*. CC	0.49	1.12 (0.82–1.51)	0.46	0.90 (0.68–1.19)	0.74	0.94 (0.67–1.34)	0.13	2.11 (0.81–5.51)
Rec.: AA *vs*. AC + CC	0.77	1.08 (0.64–1.83)	0.23	1.35 (0.83–2.20)	0.82	1.07 (0.58–1.97)	0.51	1.54 (0.43–5.53)
Hom.: AA *vs*. CC	0.74	1.18 (0.45–3.11)	0.25	1.72 (0.69–4.29)	0.56	1.36 (0.49–3.82)	0.31	3.00 (0.37–24.68)
Alle.: A *vs*. C	0.47	1.10 (0.86–1.41)	0.66	1.05 (0.84–1.33)	0.83	0.97 (0.73–1.29)	0.35	1.39 (0.70–2.77)
Cdx2 (rs11568820)								
Add.: TT *vs*. CT *vs*. CC	0.65	0.96 (0.78–1.17)	0.09	0.85 (0.71–1.03)	0.46	0.92 (0.73–1.16)	0.12	1.62 (0.89–2.95)
Dom.: TT + CT *vs*. CC	0.88	0.98 (0.72–1.33)	0.14	0.81 (0.61–1.07)	0.64	0.92 (0.65–1.30)	0.57	1.32 (0.50–3.50)
Rec.: TT *vs*. CT + CC	0.57	0.90 (0.62–1.30)	0.20	0.80 (0.57–1.13)	0.40	0.83 (0.54–1.28)	**0.04**	2.68 (1.06–6.75)
Hom.: TT *vs*. CC	0.06	2.25 (0.97–5.23)	0.82	0.92 (0.42–1.99)	0.74	1.17 (0.47–2.95)	0.19	4.84 (0.46–51.14)
Alle.: T vs C	0.62	0.95 (0.76–1.18)	0.14	0.86 (0.70–1.05)	0.45	0.91 (0.71–1.17)	0.30	1.42 (0.73–2.73)
Fok1 (rs2228570)								
Add.: BB *vs*. AB *vs*. AA	0.50	0.93 (0.75–1.15)	0.08	0.84 (0.69–1.02)	0.77	1.04 (0.81–1.33)	**0.02**	2.26 (1.12–4.56)
Dom.: BB + AB *vs*. AA	0.75	0.94 (0.65–1.36)	0.30	0.84 (0.59–1.17)	0.63	1.11 (0.72–1.72)	0.23	2.48 (0.57–10.90)
Rec.: BB *vs*. AB + AA	0.47	0.89 (0.64–1.23)	0.08	0.76 (0.56–1.03)	0.97	0.99 (0.68–1.45)	**0.03**	2.75 (1.12–6.74)
Hom.: BB *vs*. AA	0.89	1.06 (0.48–2.35)	0.80	1.11 (0.52–2.35)	0.82	1.11 (0.45–2.73)	0.82	0.79 (0.10–6.34)
Alle.: B *vs*. A	0.50	0.93 (0.75–1.15)	0.19	0.87 (0.71–1.07)	0.53	1.08 (0.84–1.39)	0.09	1.85 (0.91–3.76)
Taq1 (rs731236)								
Add.: GG vs AG *vs*. AA	0.67	1.12 (0.67–1.86)	0.70	1.10 (0.68–1.76)	0.30	0.72 (0.38–1.35)	0.64	0.69 (0.15–3.19)
Dom.: GG + AG *vs*. AA	0.69	1.12 (0.65–1.91)	0.75	1.09 (0.66–1.79)	0.42	0.76 (0.40–1.47)	0.85	0.86 (0.19–3.97)
Rec.: GG *vs*. AG + AA	0.83	1.27 (0.15–11.06)	0.47	2.36 (0.23–24.37)	1.00	0.00 (0.00–NA)	1.00	0.00 (0.00–NA)
Hom.: GG *vs*. AA	NA	NA (NA–NA)	NA	NA (NA–NA)	NA	NA (NA–NA)	NA	NA (NA–NA)
Alle.: G *vs*. A	0.65	1.13 (0.67–1.89)	0.68	1.11 (0.68–1.79)	0.31	0.72 (0.38–1.37)	0.71	0.75 (0.17–3.37)

***Note*.** Abbreviations: Add., additive model; Alle., allelic model; B, degenerate base standing for C, G, and T; *CI*, confidential interval; Dom., dominant model; HDLC, high-density lipoprotein cholesterol; Hom., homozygous model; LDLC, low-density lipoprotein cholesterol; NA, not available; *OR*, odds ratio; Rec., recessive model; SNPs, single nucleotide polymorphisms; TC, total cholesterol; TG, triglyceride; *VDR*, vitamin D receptor gene.

Supplementary Table S9. Comparison of 25-hydroxyvitamin D concentration (nmol/L) across genotype models of *VDR* gene polymorphisms in adult males and females

Genotype	Female				Male			
comparison	*n*	Median	IQR	*P* value	*n*	Median	IQR	*P* value
Apa1 (rs7975232)								
Add: AA *vs*. AC *vs*. CC								
CC	561	58.97	[49.68–69.18]	0.35	439	63.18	[53.75–72.59]	0.83
AC	453	58.75	[49.16–68.63]		347	62.33	[52.65–73.59]	
AA	110	57.04	[48.40–65.71]		77	60.91	[52.44–73.32]	
Dom: AC + AA *vs*. CC								
AC + AA	563	58.53	[49.01–68.18]	0.47	424	62.12	[52.66–73.49]	0.54
CC	561	58.97	[49.68–69.18]		439	63.18	[53.75–72.59]	
Rec: AA *vs*. AC + CC								
AA	110	57.04	[48.40–65.71]	0.16	77	60.91	[52.44–73.32]	0.83
AC + CC	1,014	58.86	[49.50–68.82]		786	62.63	[53.24–72.72]	
Hom: AA *vs*. CC								
AA	110	57.04	[48.40–65.71]	0.15	77	60.91	[52.44–73.32]	0.74
CC	561	58.97	[49.68–69.18]		439	63.18	[53.75–72.59]	
Alle: A *vs*. C								
A	673	58.30	[48.86–67.20]	0.23	501	62.04	[52.66–73.38]	0.57
C	1,575	58.90	[49.54–68.88]		1,225	62.85	[53.38–72.66]	
Cdx2 (rs11568820)								
Add.: TT *vs*. CT *vs*. CC								
CC	334	59.17	[50.94–68.68]	0.20	304	61.79	[53.30–72.53]	0.69
CT	576	59.08	[48.96–69.29]		390	63.11	[53.50–72.93]	
TT	214	56.48	[48.30–67.03]		169	61.65	[51.85–72.31]	
Dom.: CT + TT *vs*. CC								
CT + TT	790	58.35	[48.80–68.56]	0.41	559	62.76	[53.14–72.88]	0.72
CC	334	59.17	[50.94–68.68]		304	61.79	[53.30–72.53]	
Rec.: TT *vs*. CT + CC								
TT	214	56.48	[48.30–67.03]	0.08	169	61.65	[51.85–72.31]	0.56
CT + CC	910	59.15	[49.50–69.12]		694	62.83	[53.46–72.73]	
Hom.: TT *vs*. CC								
TT	214	56.48	[48.30–67.03]	0.08	169	61.65	[51.85–72.31]	0.81
CC	334	59.17	[50.94–68.68]		304	61.79	[53.30–72.53]	
Alle: T *vs*. C								
T	1,004	58.00	[48.65–68.27]	0.13	728	62.59	[52.78–72.82]	0.93
C	1,244	59.15	[49.95–68.88]		998	62.61	[53.36–72.66]	
Fok1 (rs2228570)								
Add.: BB *vs*. AB *vs*. AA								
AA	243	57.56	[48.62–69.02]	0.83	172	63.52	[54.12–73.35]	0.47
AB	561	58.75	[49.14–69.11]		457	62.44	[53.50–72.16]	
BB	320	59.04	[49.98–67.16]		234	61.49	[51.87–72.67]	

Continued

Genotype comparison	Female				Male			
	n	Median	IQR	*P* value	*n*	Median	IQR	*P* value
Dom.: BB + AB *vs*. AA								
BB + AB	881	58.87	[49.43–68.55]	0.54	691	62.30	[53.17–72.33]	0.40
AA	243	57.56	[48.62–69.02]		172	63.52	[54.12–73.35]	
Rec.: BB *vs*. AB + AA								
BB	320	59.04	[49.98–67.16]	0.87	234	61.49	[51.87–72.67]	0.27
AB + AA	804	58.37	[49.03–69.07]		629	62.80	[53.64–72.82]	
Hom.: BB *vs*. AA								
BB	320	59.04	[49.98–67.16]	0.62	234	61.49	[51.87–72.67]	0.24
AA	243	57.56	[48.62–69.02]		172	63.52	[54.12–73.35]	
Alle.: B *vs*. A								
B	1,201	58.92	[49.55–68.41]	0.65	925	62.16	[52.72–72.54]	0.24
A	1,047	58.32	[49.01–69.02]		801	62.99	[53.89–72.93]	
Taq1 (rs731236)								
Add.: GG vs AG *vs*. AA								
AA	1,005	58.53	[49.43–68.66]	0.92	787	62.37	[53.24–72.59]	0.50
AG	114	60.05	[48.85–67.77]		72	64.27	[52.80–75.16]	
GG	5	53.88	[37.14–74.36]		4	67.28	[66.31–71.96]	
Dom.: AG + GG *vs*. AA								
AG + GG	119	59.98	[48.95–67.63]	0.91	76	64.98	[53.28–74.37]	0.46
AA	1,005	58.53	[49.43–68.66]		787	62.37	[53.24–72.59]	
Rec.: GG vs AG + AA								
GG	5	53.88	[37.14–74.36]	0.68	4	67.28	[66.31–71.96]	0.30
AG + AA	1,119	58.73	[49.36–68.59]		859	62.56	[53.20–72.72]	
Hom.: GG *vs*. AA								
GG	5	53.88	[37.14–74.36]	0.68	4	67.28	[66.31–71.96]	0.29
AA	1,005	58.53	[49.43–68.66]		787	62.37	[53.24–72.59]	
Alle.: G *vs*. A								
G	124	59.97	[49.01–67.61]	0.84	80	65.45	[53.57–73.86]	0.34
A	2,124	58.64	[49.41–68.64]		1,646	62.49	[53.23–72.66]	

Note. Abbreviations: Add., additive model; Alle., allelic model; B, degenerate base standing for C, G, and T; Dom., dominant model; Hom., homozygous model; IQR, interquartile range; Rec., recessive model; *VDR*, vitamin D receptor gene.

Supplementary Table S10. Comparison of 25-hydroxyvitamin D concentration (nmol/L) in abnormal and normal lipid groups of adult males and females

Genotype comparison	Female				Male			
	n	Median	IQR	*P* value	*n*	Median	IQR	*P* value
TG								
≥ 2.3 mmol/L	92	57.79	[49.43–65.74]	0.40	213	59.58	[49.47–69.60]	**< 0.01**
< 2.3 mmol/L	1,032	58.80	[49.25–68.85]		650	63.43	[54.29–73.70]	
TC								
≥ 6.2 mmol/L	151	59.19	[47.87–72.64]	0.68	111	59.18	[49.73–71.13]	0.09
< 6.2 mmol/L	973	58.56	[49.55–68.31]		752	62.92	[53.42–72.93]	
LDLC								
≥ 4.1 mmol/L	29	56.70	[45.80–66.12]	0.52	17	55.45	[45.07–74.43]	0.20
< 4.1 mmol/L	1,095	58.78	[49.41–68.66]		846	62.65	[53.27–72.72]	
HDLC								
< 1.0 mmol/L	22	67.80	[59.52–78.05]	**< 0.01**	20	69.35	[57.83–83.61]	0.11
≥ 1.0 mmol/L	1,102	58.52	[49.13–68.44]		843	62.57	[53.19–72.59]	

***Note*.** Abbreviations: HDLC, high-density lipoprotein cholesterol; IQR, interquartile range; LDLC, low-density lipoprotein cholesterol; TC, total cholesterol; TG, triglyceride.

Supplementary Table S11. Simple linear regressions between serum 25-hydroxyvitamin D and lipid profiles

Lipid profiles	Female		Male	
	β	*P* value	*β*	*P* value
lg TG	< 0.001	0.902	−0.003	**< 0.001**
TC	0.001	0.647	−0.003	0.088
LDLC	−0.001	0.584	−0.003	**0.006**
HDLC	< 0.001	0.461	−0.001	**0.025**

***Note*.** Abbreviations: HDLC, high-density lipoprotein cholesterol; LDLC, low-density lipoprotein cholesterol; TC, total cholesterol; TG, triglyceride.