Web table D Association of genotypes with total cholesterol (mmol/l) (phase 3 and phase 7)

Gene	Genotype	Number	Phase 3	Phase 7	Beta-value (standard error) all years combined
ADAMTS9	GG	2878	6.46 (1.13)	5.77 (1.03)	0
	GA	1857	6.43 (1.12)	5.71 (1.00)	-0.045 (0.026)
	AA	297	6.40 (1.14)	5.61 (1.09)	-0.118 (0.054)
	P value^1		0.51	0.009	
	P value^2		0.37	0.007	0.01
BCL11A	AA	2728	6.45 (1.12)	5.74 (1.02)	0
	AG	1909	6.45 (1.14)	5.73 (1.02)	-0.020 (0.026)
	GG	380	6.39 (1.10)	5.78 (1.04)	-0.003 (0.048)
	P value^1		0.70	0.66	
	P value^2		0.63	0.60	0.63
CALPN10	GG	2945	6.47 (1.13)	5.76 (1.03)	0
	GA	2150	6.46 (1.15)	5.75 (1.01)	-0.003 (0.025)
	AA	378	6.33 (1.10)	5.61 (0.98)	-0.118 (0.048)
	P value^1		0.11	0.03	
	P value^2		0.11	0.12	0.01*
CDC123, CAMK1D	AA	3464	6.44 (1.11)	5.74 (1.00)	0
	AG	1448	6.46 (1.18)	5.75 (1.07)	0.009 (0.027)
	GG	124	6.35 (1.14)	5.69 (1.11)	-0.112 (0.080)
	P value^1		0.61	0.73	
	P value^2		0.71	0.68	0.65
CDKALI	GG	4463	6.43 (1.12)	5.73 (1.02)	0
	GA	543	6.58 (1.14)	5.83 (1.03)	0.095 (0.040)
	AA	24	6.52 (1.38)	5.42 (1.02)	-0.117 (0.180)
	P value^1		0.02	0.03	
	P value^2		0.01	0.03	0.05
CDKN	AA	3257	6.42 (1.12)	5.73 (1.02)	0

	AG	1543	6.49 (1.12)	5.77 (1.02)	0.067 (0.027)
	GG	149	6.55 (1.19)	5.65 (1.14)	0.016 (0.074)
	P value^1		0.06	0.20	
	P value^2		0.10	0.17	0.04
FTO	TT	1953	6.47 (1.17)	5.74 (1.03)	0
	TC	2716	6.43 (1.11)	5.76 (1.01)	-0.000 (0.026)
	CC	938	6.48 (1.12)	5.73 (1.05)	0.019 (0.035)
	P value^1		0.35	0.71	
	P value^2		0.38	0.63	0.65
HHEX	GG	2635	6.44 (1.15)	5.76 (1.04)	0
	GA	1968	6.45 (1.11)	5.71 (1.02)	-0.027 (0.026)
	AA	405	6.45 (1.10)	5.71 (0.93)	-0.039 (0.047)
	P value^1		0.93	0.22	
	P value^2		0.91	0.30	0.24
HNF1A	CC	5106	6.45 (1.13)	5.75 (1.02)	0
	CT	301	6.42 (1.14)	5.65 (1.05)	-0.064 (0.052)
	TT	5	6.95 (0.76)	6.54 (0.95)	0.758 (0.399)
	P value^1		0.60	0.05	
	P value^2		0.52	0.06	0.06*
IGF2BP2	CC	2362	6.46 (1.15)	5.76 (1.04)	0
	AC	2182	6.43 (1.11)	5.72 (1.01)	-0.037 (0.026)
	AA	485	6.43 (1.09)	5.70 (0.98)	-0.023 (0.044)
	P value^1		0.67	0.26	
	P value^2		0.63	0.21	0.26
JAZF1	AA	1269	6.51 (1.16)	5.79 (1.06)	0
	AG	2453	6.42 (1.10)	5.75 (1.00)	-0.047 (0.030)
	GG	1304	6.42 (1.13)	5.68 (1.03)	-0.098 (0.035)
	P value^1		0.09	0.02	
	P value^2		0.05	0.04	0.005

KCNJ11	CC	2313	6.45 (1.13)	5.72 (1.02)	0
	CT	2478	6.46 (1.13)	5.77 (1.04)	0.036 (0.025)
	TT	720	6.44 (1.18)	5.72 (0.95)	0.004 (0.038)
	P value[1]		0.93	0.12	
	P value[2]		P=0.88	P=0.17	P=0.51
NOTCH2	CC	4024	6.43 (1.12)	5.74 (1.02)	0
	AC	949	6.52 (1.13)	5.76 (1.02)	0.059 (0.032)
	AA	62	6.23 (1.20)	5.58 (1.01)	-0.190 (0.113)
	P value[1]		0.04	0.37	
	P value[2]		0.03	0.30	0.39
PPARG	CC	4290	6.44 (1.15)	5.74 (1.03)	0
	CG	1138	6.50 (1.07)	5.78 (1.00)	0.039 (0.029)
	GG	86	6.59 (1.31)	5.70 (1.06)	0.010 (0.096)
	P value[1]		P=0.17	0.47	
	P value[2]		P=0.17	0.55	0.24
SLC30A8	GG	2416	6.43 (1.11)	5.77 (1.02)	0
	GA	2177	6.46 (1.15)	5.71 (1.01)	-0.016 (0.026)
	AA	428	6.42 (1.10)	5.71 (1.09)	-0.022 (0.046)
	P value[1]		0.55	0.18	
	P value[2]		0.58	0.23	0.49
TCF2 (HNF1B)	AA	1395	6.35 (1.06)	5.72 (1.00)	0
	AG	2446	6.48 (1.15)	5.74 (1.03)	0.067 (0.030)
	GG	1154	6.47 (1.15)	5.75 (1.03)	0.058 (0.035)
	P value[1]		0.002	0.63	
	P value[2]		0.003	0.60	0.08
TCF7L2	AA	2365	6.42 (1.14)	5.75 (1.02)	0
	AG	2173	6.45 (1.13)	5.72 (1.04)	-0.000 (0.026)
	GG	467	6.47 (1.06)	5.74 (0.97)	0.011 (0.045)
	P value[1]		0.60	0.66	

	P value[2]		0.62	0.68	0.87
THADA	AA	3953	6.44 (1.14)	5.73 (1.03)	0
	AG	1003	6.46 (1.09)	5.79 (0.99)	0.054 (0.031)
	GG	75	6.38 (1.16)	5.64 (0.97)	-0.144 (0.103)
	P value[1]		0.81	0.19	
	P value[2]		0.63	0.16	0.42
TSPAN8, LGR5	AA	1762	6.42 (1.12)	5.70 (1.04)	0
	AG	2424	6.47 (1.14)	5.77 (1.02)	0.053 (0.028)
	GG	838	6.43 (1.12)	5.74 (1.01)	0.024 (0.037)
	P value[1]		0.41	0.12	
	P value[2]		0.30	0.08	0.28
VEGFA	GG	2611	6.45 (1.12)	5.74 (1.02)	0
	GA	2008	6.43 (1.12)	5.73 (1.01)	-0.018 (0.026)
	AA	400	6.53 (1.23)	5.83 (1.10)	0.106 (0.047)
	P value[1]		0.28	0.17	
	P value[2]		0.19	0.15	0.26

Results are mean (standard deviation)

[1] ANOVA, unadjusted

[2] ANOVA, adjusted for age and gender.

*recessive model

B(se) is the coefficient for overall genotype effect estimated from a mixed model with age at phase1 and gender included as fixed covariates.

The change in cholesterol over time is allowed to vary between subjects.