Web table G Association of genotypes with high density lipoprotein-cholesterol (mmol/l) (phase 3 and phase 7). Results are geometric mean (approximate SD)

Gene	Genotype	Number	Phase 3	Phase 7	Beta-value (standard error) all years combined
ADAMTS9	GG	2878	1.38 (0.39)	1.52 (0.42)	0
	GA	1857	1.37 (0.37)	1.53 (0.41)	0.007 (0.007)
	AA	297	1.40 (0.39)	1.51 (0.40)	0.006 (0.014)
	P value[1]		0.63	0.60	
	P value[2]		0.79	0.32	0.70
BCL11A	AA	2728	1.37 (0.39)	1.51 (0.41)	0
	AG	1909	1.39 (0.39)	1.54 (0.43)	0.010 (0.007)
	GG	380	1.36 (0.38)	1.53 (0.42)	0.004 (0.013)
	P value[1]		0.11	0.21	
	P value[2]		0.23	0.41	0.31
CALPN10	GG	2945	1.37 (0.39)	1.52 (0.42)	0
	GA	2150	1.38 (0.39)	1.52 (0.42)	0.002 (0.0070
	AA	378	1.41 (0.39)	1.54 (0.42)	0.012 (0.013)
	P value[1]		0.19	0.57	
	P value[2]		0.40	0.79	0.39*
CDC123, CAMK1D	AA	3464	1.38 (0.39)	1.53 (0.41)	0
	AG	1448	1.36 (0.38)	1.51 (0.42)	-0.013 (0.007)
	GG	124	1.42 (0.43)	1.56 (0.52)	0.018 (0.022)
	P value[1]		0.12	0.21	
	P value[2]		0.10	0.18	0.60
CDKALI	GG	4463	1.38 (0.39)	1.52 (0.42)	0
	GA	543	1.39 (0.39)	1.53 (0.41)	0.003 (0.011)
	AA	24	1.50 (0.50)	1.49 (0.40)	0.035 (0.048)
	P value[1]		0.30	0.93	
	P value[2]		0.31	0.89	0.57
CDKN	AA	3257	1.38 (0.39)	1.52 (0.42)	0
	AG	1543	1.38 (0.39)	1.52 (0.42)	-0.001 (0.007)
	GG	149	1.37 (0.40)	1.54 (0.47)	-0.097 (0.020)
	P value[1]		0.94	0.89	
	P value[2]		0.83	0.99	0.62
FTO	TT	1953	1.39 (0.39)	1.53 (0.42)	0
	TC	2716	1.38 (0.39)	1.53 (0.42)	0.008 (0.007)
	CC	938	1.36 (0.38)	1.50 (0.41)	-0.013 (0.009)
	P value[1]		0.14	0.19	
	P value[2]		0.16	0.17	0.40
HHEX	GG	2635	1.38 (0.39)	1.52 (0.41)	0
	GA	1968	1.37 (0.38)	1.52 (0.43)	-0.002 (0.007)
	AA	405	1.38 (0.40)	1.52 (0.41)	0.002 (0.013)
	P value[1]		0.39	0.95	
	P value[2]		0.67	0.97	0.88

HNF1A	CC	5106	1.37 (0.39)	1.52 (0.42)	0
	CT	301	1.40 (0.39)	1.53 (0.42)	0.017 (0.014)
	TT	5	1.28 (0.22)	1.43 (0.22)	-0.066 (0.107)
	P value[1]		0.55	0.79	
	P value[2]		0.30	0.58	0.30
IGF2BP2	CC	2362	1.38 (0.38)	1.52 (0.41)	0
	AC	2182	1.38 (0.40)	1.52 (0.43)	-0.002 (0.007)
	AA	485	1.39 (0.38)	1.56 (0.41)	0.012 (0.012)
	P value[1]		0.72	0.17	
	P value[2]		0.91	0.25	0.30
JAZF1	AA	1269	1.39 (0.39)	1.54 (0.43)	0
	AG	2453	1.38 (0.39)	1.52 (0.42)	-0.005 (0.008)
	GG	1304	1.37 (0.38)	1.51 (0.41)	-0.005 (0.009)
	P value[1]		0.53	0.25	
	P value[2]		0.97	0.54	0.79
KCNJ11	CC	2313	1.38 (0.39)	1.52 (0.42)	0
	CT	2478	1.38 (0.39)	1.52 (0.42)	-0.008 (0.007)
	TT	720	1.37 (0.38)	1.52 (0.42)	-0.001 (0.010)
			P=0.89	P=0.91	
			P=0.91	P=0.72	P=0.60
NOTCH2	CC	4024	1.38 (0.39)	1.52 (0.42)	0
	AC	949	1.38 (0.38)	1.52 (0.42)	0.005 (0.008)
	AA	62	1.41 (0.46)	1.57 (0.40)	0.015 (0.030)
	P value[1]		0.67	0.69	
	P value[2]		0.77	0.93	0.53
PPARG	CC	4290	1.38 (0.39)	1.52 (0.42)	0
	CG	1138	1.39 (0.39)	1.53 (0.43)	0.006 (0.008)
	GG	86	1.43 (0.44)	1.56 (0.43)	0.029 (0.026)
	P value[1]		0.37	0.38	
	P value[2]		0.44	0.43	0.23
SLC30A8	GG	2416	1.38 (0.39)	1.53 (0.42)	0
	GA	2177	1.37 (0.39)	1.51 (0.41)	-0.009 (0.007)
	AA	428	1.37 (0.39)	1.52 (0.43)	-0.003 (0.012)
	P value[1]		0.61	0.27	
	P value[2]		0.61	0.25	0.95
TCF2 (HNF1B)	AA	1395	1.38 (0.39)	1.53 (0.42)	0
	AG	2446	1.37 (0.39)	1.52 (0.42)	-0.009 (0.008)
	GG	1154	1.38 (0.38)	1.53 (0.42)	0.002 (0.009)
	P value[1]		0.73	0.64	
	P value[2]		0.29	0.25	0.42
TCF7L2	AA	2365	1.38 (0.39)	1.52 (0.42)	0
	AG	2173	1.37 (0.38)	1.51 (0.41)	0.0 (0.007)
	GG	467	1.42 (0.41)	1.58 (0.43)	0.035 (0.012)
	P value[1]		0.03	0.02	
	P value[2]		0.05	0.04	0.04
THADA	AA	3953	1.38 (0.39)	1.52 (0.42)	0

	AG	1003	1.37 (0.38)	1.52 (0.41)	-0.003 (0.008)
	GG	75	1.36 (0.39)	1.49 (0.40)	-0.021 (0.028)
	P value[1]		0.87	0.66	
	P value[2]		0.89	0.46	0.41
TSPAN8, LGR5	AA	1762	1.37 (0.39)	1.51 (0.41)	0
	AG	2424	1.38 (0.39)	1.53 (0.42)	0.014 (0.007)
	GG	838	1.38 (0.39)	1.54 (0.42)	0.013 (0.010)
	P value[1]		0.34	0.25	
	P value[2]		0.11	0.07	0.40
VEGFA	GG	2611	1.38 (0.39)	1.53 (0.42)	0
	GA	2008	1.37 (0.39)	1.52 (0.42)	-0.004 (0.007)
	AA	400	1.40 (0.40)	1.51 (0.43)	0.006 (0.013)
	P value[1]		0.53	0.64	
	P value[2]		0.38	0.71	0.99

[1] ANOVA, unadjusted

[2] ANOVA, adjusted for age and gender.

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..