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Online Resource 4 Association between individual risk SNPs and change in TC, LDL-C, HDL-C and TG after treatment[a]

Association of TC SNPs with change in TC after treatment

SNP	Gene	Effect	SE	*P**	*n*	r^2	*P* treatment x gene**	Risk allele	Risk allele freq.	Original SNP (LD r^2)[b]
rs3764261	*CETP*	0.008	0.118	0.894	269	0.071	0.82	T	0.36	
rs1532085	*LIPC*	-0.096	0.121	0.110	275	0.078	0.92	A	0.43	
rs1367117	*APOB*	-0.020	0.116	0.737	271	0.070	0.23	A	0.30	
rs4299376	*ABCG5,ABCG8*	0.018	0.112	0.763	286	0.071	0.02	G	0.32	
rs6882076	*TIMD4,HAVCR1*	-0.039	0.112	0.504	287	0.073	0.75	C	0.64	
rs1260326	*GCKR*	-0.135	0.118	0.021	281	0.089	0.81	T	0.39	
rs2954029	*TRIB1*	-0.039	0.128	0.509	272	0.092	0.85	A	0.53	
rs2131925	*ANGPTL3,DOCK7*	-0.085	0.113	0.143	283	0.079	0.20	T	0.63	rs3850634 (1.0), rs1167998 (1.0)
rs174546	*FADS1,FADS2,FADS3*	-0.002	0.117	0.973	267	0.083	0.41	T	0.71	rs174550 (1.0)

Association of LDL-C SNPs with change in LDL-C after treatment

SNP	Gene	Effect	SE	*P**	*n*	r^2	*P* treatment x gene**	Risk allele	Risk allele freq.	Original SNP (LD r^2)[b]
rs3764261	*CETP*	-0.092	0.070	0.138	269	0.020	0.64	G	0.63	rs247616 (1.0)
rs1367117	*APOB*	-0.003	0.069	0.969	271	0.013	0.57	A	0.30	
rs4299376	*ABCG5,ABCG8*	0.038	0.066	0.525	286	0.010	0.91	G	0.32	
rs6882076	*TIMD4,HAVCR1*	0.039	0.067	0.557	287	0.014	0.97	C	0.64	
rs2954029	*TRIB1*	0.057	0.076	0.350	272	0.019	0.75	A	0.53	rs2954022 (0.94)
rs2131925	*ANGPTL3,DOCK7*	-0.027	0.067	0.651	283	0.014	0.49	T	0.63	rs3850634 (1.0)
rs174546	*FADS1,FADS2,FADS3*	-0.039	0.076	0.535	267	0.014	0.22	T	0.71	

Association of HDL-C SNPs with change in HDL-C after treatment

SNP	Gene	Effect	SE	*P**	*n*	r^2	*P* treatment x gene**	Risk allele	Risk allele freq.	Original SNP (LD r^2)[b]
rs3764261	*CETP*	-0.037	0.036	0.304	269	0.015	0.26	G	0.63	
rs1532085	*LIPC*	0.056	0.037	0.362	275	0.018	0.57	G	0.57	
rs4846914	*GALNT2*	-0.082	0.037	0.184	269	0.028	0.16	G	0.47	
rs4149268	*ABCA1*	0.015	0.036	0.681	280	0.014	0.84	C	0.58	
rs2954029	*TRIB1*	0.009	0.039	0.879	272	0.016	0.78	A	0.53	rs10808546 (1.0)
rs174546	*FADS1,FADS2,FADS3*	-0.064	0.036	0.312	267	0.021	0.92	T	0.29	rs174547 (1.0)

Association of TG SNPs with change in TG after treatment[c]

SNP	Gene	Effect	SE	*P**	*n*	r^2	*P* treatment x gene**	Risk allele	Risk allele freq.	Original SNP (LD r^2)[b]
rs3764261	*CETP*	0.053	0.043	0.389	269	0.047	0.84	G	0.63	rs7205804 (1.0)
rs4846914	*GALNT2*	-0.183	0.019	0.916	269	0.042	0.97	G	0.47	
rs6882076	*TIMD4,HAVCR1*	0.089	0.040	0.133	287	0.046	0.11	C	0.64	rs1553318 (1.0)
rs1260326	*GCKR*	0.026	0.043	0.539	281	0.042	0.38	T	0.39	
rs2954029	*TRIB1*	0.075	0.047	0.116	272	0.049	0.94	A	0.53	
rs2131925	*ANGPTL3,DOCK7*	-0.001	0.041	0.852	283	0.039	0.35	T	0.63	
rs439401	*APOE,APOC1,APOC2*	0.030	0.041	0.470	286	0.043	0.21	C	0.63	
rs174546	*FADS1,FADS2,FADS3*	-0.510	0.043	0.321	267	0.039	0.05	T	0.29	

[a] Data are the coefficients of associations of SNP with the change in trait (final value - baseline value) presented as effect size and standard error derived from linear regression models of SNP against change in trait after 12 months. The proportion of explained variance is indicated by r^2 and *n* is the number of participants in each subgroup.

[b] The original SNP identified in GWAS and the LD r^2 value to the proxy SNP used in this analysis.

[c] TG data was logged for analysis and is presented in that form.

BMI Body mass index; *GWAS* genome-wide association study; *HDL-C* high density lipoprotein cholesterol; *LD* linkage disequilibrium; *LDL-C* low density lipoprotein-cholesterol; *SE* standard error; *SNP* single nucleotide polymorphism; *TC* total cholesterol; *TG* triglyceride.

*Significance of association of SNP with the change in trait derived from linear regression models. *P*-values for adjusted for BMI, age, gender, ethnicity and treatment.

**Significance of interaction between genotypes and treatment assessed by univariate ANOVA. *P*-values for adjusted for BMI, age, gender and ethnicity.