

SUPPLEMENTARY INFORMATION

Interaction Effects of Lipoprotein Lipase Polymorphisms with Lifestyle on Lipid Levels in a Korean Population: A Cross-sectional Study

Jung-A Pyun¹, Sunshin Kim¹, KyungChae Park², Inkyung Baik³, Nam H Cho⁴, InSong Koh⁵, Jong-Young Lee⁶, Yoon Shin Cho⁶, Young Jin Kim⁶, Min Jin Go⁶, Eugene Shim⁷, KyuBum Kwack^{1*}, Chol Shin⁸

¹Department of Biomedical Science, College of Life Science, CHA University, Seongnam 463-836, Korea, ²Department of Family Medicine, CHA Bundang Medical Center, CHA University School of Medicine, Seongnam 463-712, Korea, ³Department of Foods and Nutrition, College of Natural Sciences, Kookmin University, Seoul 136-702, Korea, ⁴Department of Preventive Medicine, Ajou University School of Medicine, Suwon 443-749, Korea, ⁵Department of Physiology, Hanyang University College of Medicine, Seoul 133-791, Korea, ⁶Center for Genome Science, National Institute of Health, Osong 363-951, Korea, ⁷National Hypertension Center, Yonsei University Health System, Seoul 120-752, Korea, ⁸Division of Pulmonary and Critical Care Medicine, Department of Internal Medicine, Korea University Ansan Hospital, Korea University College of Medicine, Ansan 425-707, Korea

Supplementary Table 1. SNPs associated with lipid concentrations by using stage 1 and imputed data

Study	SNP	Position	Gene	Function	Alleles	HDLc		TG		LDLc		TCHL	
						Effect ^a	p-value ^b	Effect ^a	p-value ^b	Effect ^a	p-value ^b	Effect ^a	p-value ^b
Imputed	rs255	19811901	<i>LPL</i>	Intron	T>C	1.25	6.80×10^{-11}	-8.7	1.90×10^{-6}	0.72	0.24	0.74	0.35
Imputed	rs256	19811967	<i>LPL</i>	Intron	C>T	1.26	3.90×10^{-11}	-8.9	1.20×10^{-6}	0.7	0.26	0.69	0.39
Stage 1	rs263	19812812	<i>LPL</i>	Intron	G>A	1.23	1.20×10^{-10}	-8.8	1.70×10^{-6}	0.7	0.26	0.69	0.39
Imputed	rs264	19813180	<i>LPL</i>	Intron	G>A	1.26	3.30×10^{-11}	-9.0	8.90×10^{-7}	0.71	0.25	0.7	0.38
Stage 1	rs271	19813702	<i>LPL</i>	Intron	C>T	1.27	2.50×10^{-11}	-9.0	7.20×10^{-7}	0.7	0.25	0.69	0.39
Imputed	rs301	19816934	<i>LPL</i>	Intron	T>C	1.38	5.20×10^{-12}	-9.3	7.40×10^{-8}	1.06	0.1	0.8	0.28
Imputed	rs312	19817997	<i>LPL</i>	Intron	G>C	0.37	0.25	1.1	0.69	-1.45	0.13	-0.76	0.36
Imputed	rs316	19818436	<i>LPL</i>	Synonymous	C>A	0.43	0.18	0.8	0.76	-1.22	0.2	-0.5	0.5
Imputed	rs319	19818976	<i>LPL</i>	Intron	A>C	0.58	0.01	-1.7	0.4	0.51	0.53	0.61	0.33
Imputed	rs325	19819328	<i>LPL</i>	Intron	T>C	1.74	5.40×10^{-13}	-14.8	3.20×10^{-12}	2.3	3.70×10^{-3}	1.34	0.1
Imputed	rs327	19819536	<i>LPL</i>	Intron	A>C	1.34	1.30×10^{-11}	-9.1	7.60×10^{-8}	1.11	0.08	0.82	0.26
Imputed	rs328	19819724	<i>LPL</i>	Nonsense	C>G	1.75	4.60×10^{-13}	-14.8	3.60×10^{-12}	2.34	3.20×10^{-3}	1.39	0.09
Imputed	rs330	19820396	<i>LPL</i>	Intron	G>A	0.43	0.18	0.6	0.88	-1.14	0.22	-0.48	0.49
Imputed	rs331	19820405	<i>LPL</i>	Intron	G>A	1.33	1.10×10^{-11}	-8.9	1.30×10^{-7}	1.1	0.08	0.83	0.25
Imputed	rs12679834	19820433	<i>LPL</i>	Intron	T>C	1.73	6.10×10^{-13}	-14.5	9.90×10^{-12}	2.33	3.20×10^{-3}	1.39	0.09
Imputed	rs10099160	19821815	<i>LPL</i>	Intron	T>G	0.59	9.60×10^{-3}	-1.8	0.37	0.6	0.45	0.71	0.28
Imputed	rs11570891	19822810	<i>LPL</i>	Intron	C>T	1.84	3.20×10^{-14}	-14.9	1.20×10^{-12}	2.33	2.90×10^{-3}	1.43	0.08
Imputed	rs4922115	19822830	<i>LPL</i>	3' UTR	G>A	0.42	0.19	0.9	0.81	-1.22	0.18	-0.55	0.45
Stage 1	rs11570892	19823617	<i>LPL</i>	3' UTR	T>C	0.45	0.17	1.3	0.63	-1.59	0.09	-0.78	0.37
Imputed	rs3735964	19824045	<i>LPL</i>	3' UTR	C>A	1.84	1.70×10^{-14}	-14.6	3.70×10^{-12}	2.34	2.50×10^{-3}	1.52	0.06
Stage 1	rs3200218	19824071	<i>LPL</i>	3' UTR	T>C	0.45	0.03	-2.0	0.44	0.8	0.31	0.76	0.26
Imputed	rs13702	19824492	<i>LPL</i>	3' UTR	T>C	1.42	3.60×10^{-13}	-9.2	3.60×10^{-8}	1.01	0.11	0.8	0.27
Imputed	rs1059611	19824563	<i>LPL</i>	3' UTR	T>C	1.84	1.20×10^{-14}	-14.7	2.90×10^{-12}	2.35	2.40×10^{-3}	1.53	0.06
Imputed	rs3916027	19824868	-	Near gene 3'	G>A	1.42	3.50×10^{-13}	-9.3	3.20×10^{-8}	1.04	0.1	0.81	0.26

Imputed	rs4921684	19825128	-	Near gene 3'	C>T	0.43	0.18	1.0	0.79	-1.18	0.2	-0.5	0.49
Imputed	rs2197089	19826373	-	Near gene 3'	G>A	1.31	3.90×10^{-15}	-8.3	5.60×10^{-8}	1.18	0.03	0.96	0.08
Imputed	rs10105606	19827848	-	Near gene 3'	C>A	1.45	8.10×10^{-14}	-9.5	1.30×10^{-8}	1.07	0.09	0.84	0.23
Stage 1	rs2410616	19828679	-	Near gene 3'	G>A	0.4	0.19	1.1	0.72	-0.99	0.27	-0.34	0.6
Imputed	rs2410617	19828893	-	Near gene 3'	T>A	0.46	0.14	0.2	0.98	-0.92	0.32	-0.29	0.64
Imputed	rs1561750	19830766	-	Intergenic	T>C	0.39	0.21	-0.5	0.87	-1.05	0.26	-0.5	0.57
Imputed	rs1011685	19830769	-	Intergenic	C>T	1.95	2.20×10^{-16}	-14.9	4.60×10^{-13}	2.41	1.70×10^{-3}	1.69	0.04
Imputed	rs10096633	19830921	-	Intergenic	C>T	1.9	6.40×10^{-16}	-15.0	3.80×10^{-13}	2.28	2.70×10^{-3}	1.5	0.06
Imputed	rs1372339	19831798	-	Intergenic	A>G	0.37	0.23	-0.5	0.89	-0.93	0.31	-0.42	0.62
Imputed	rs17091872	19831977	-	Intergenic	G>A	0.37	0.23	-0.5	0.89	-0.93	0.31	-0.42	0.62
Stage 1	rs17482753	19832646	-	Intergenic	G>T	1.88	1.10×10^{-15}	-14.8	6.00×10^{-13}	2.26	2.90×10^{-3}	1.49	0.06
Imputed	rs4922116	19832778	-	Intergenic	G>A	0.37	0.23	-0.5	0.89	-0.93	0.31	-0.42	0.62
Imputed	rs1441777	19833571	-	Intergenic	T>C	0.37	0.23	-0.5	0.89	-0.94	0.31	-0.42	0.61
Imputed	rs10097668	19833729	-	Intergenic	T>C	0.64	5.70×10^{-3}	-2.2	0.31	0.41	0.61	0.53	0.39
Imputed	rs17091891	19843171	-	Intergenic	T>C	1.89	7.40×10^{-16}	-14.9	4.10×10^{-13}	2.22	3.40×10^{-3}	1.45	0.07
Imputed	rs12678919	19844222	-	Intergenic	A>G	1.94	4.20×10^{-16}	-14.8	6.20×10^{-13}	2.33	2.40×10^{-3}	1.61	0.05
Imputed	rs7819706	19844415	-	Intergenic	A>G	1.89	7.30×10^{-16}	-15.0	2.50×10^{-13}	2.26	2.90×10^{-3}	1.46	0.06
Imputed	rs7841189	19845376	-	Intergenic	C>T	1.89	6.90×10^{-16}	-15.1	2.30×10^{-13}	2.26	2.90×10^{-3}	1.46	0.06
Stage 1	rs12545984	19847259	-	Intergenic	G>A	0.33	0.28	-0.7	0.91	-0.97	0.29	-0.5	0.58
Stage 1	rs10503669	19847690	-	Intergenic	G>T	1.89	2.00×10^{-15}	-14.9	4.60×10^{-13}	2.07	7.00×10^{-3}	1.26	0.11
Stage 1	rs17410962	19848080	-	Intergenic	G>A	1.88	1.00×10^{-15}	-15.0	2.80×10^{-13}	2.25	3.00×10^{-3}	1.45	0.07
Imputed	rs17091905	19849757	-	Intergenic	G>A	1.89	7.90×10^{-16}	-15.1	2.10×10^{-13}	2.24	3.20×10^{-3}	1.43	0.07
Stage 1	rs17411031	19852310	-	Intergenic	C>G	1.42	2.10×10^{-13}	-10.3	4.50×10^{-9}	0.96	0.12	0.67	0.31
Stage 1	rs17489282	19852518	-	Intergenic	G>A	1.38	8.80×10^{-13}	-10.1	9.60×10^{-9}	0.94	0.13	0.61	0.35
Stage 1	rs4922117	19852586	-	Intergenic	A>G	1.42	2.50×10^{-13}	-10.1	6.80×10^{-9}	0.88	0.16	0.62	0.36
Imputed	rs1372345	19852948	-	Intergenic	C>A	0.26	0.42	-0.2	0.79	-1	0.28	-0.5	0.56
Imputed	rs2410618	19853500	-	Intergenic	G>A	1.4	4.10×10^{-13}	-10.2	5.30×10^{-9}	0.98	0.11	0.68	0.31

Imputed	rs2410620	19854660	-	Intergenic	C>T	1.4	4.10×10^{-13}	-10.2	5.30×10^{-9}	0.98	0.11	0.68	0.31
Imputed	rs2410621	19854682	-	Intergenic	T>C	1.4	4.10×10^{-13}	-10.2	5.30×10^{-9}	0.98	0.11	0.68	0.31
Imputed	rs2410623	19854889	-	Intergenic	A>G	1.4	4.70×10^{-13}	-10.2	7.30×10^{-9}	1.04	0.09	0.74	0.26
Stage 1	rs17411126	19855272	-	Intergenic	T>C	1.41	2.90×10^{-13}	-10.3	5.10×10^{-9}	1.01	0.1	0.71	0.29
Imputed	rs2165558	19856260	-	Intergenic	T>G	1.39	1.80×10^{-12}	-10.6	4.70×10^{-9}	1.07	0.09	0.72	0.28
Imputed	rs4523270	19856539	-	Intergenic	T>C	1.41	3.50×10^{-13}	-10.2	6.00×10^{-9}	1.05	0.09	0.74	0.26
Imputed	rs2103325	19858343	-	Intergenic	C>T	1.41	3.20×10^{-13}	-10.2	6.00×10^{-9}	1.05	0.09	0.74	0.26
Imputed	rs1581675	19858499	-	Intergenic	T>A	1.34	2.40×10^{-11}	-9.9	7.00×10^{-8}	0.72	0.26	0.39	0.56
Imputed	rs2119690	19859539	-	Intergenic	G>A	1.41	3.40×10^{-13}	-10.0	8.00×10^{-9}	1.06	0.09	0.77	0.25
Imputed	rs2165556	19859627	-	Intergenic	C>T	1.41	3.40×10^{-13}	-10.0	8.00×10^{-9}	1.06	0.09	0.76	0.25
Imputed	rs12541912	19859791	-	Intergenic	G>C	1.41	3.40×10^{-13}	-10.0	8.00×10^{-9}	1.06	0.09	0.76	0.25
Imputed	rs4083261	19861226	-	Intergenic	T>C	1.4	4.90×10^{-13}	-10.0	8.80×10^{-9}	1.08	0.08	0.78	0.24
Imputed	rs1441766	19862788	-	Intergenic	A>T	1.4	4.10×10^{-13}	-10.0	7.50×10^{-9}	1.08	0.08	0.77	0.24
Imputed	rs6999813	19863471	-	Intergenic	T>A	1.91	1.90×10^{-15}	-14.7	1.70×10^{-12}	2.54	1.10×10^{-3}	1.75	0.03
Imputed	rs2119689	19863507	-	Intergenic	C>T	1.4	4.20×10^{-13}	-10.1	6.60×10^{-9}	1.11	0.07	0.79	0.23
Imputed	rs1441762	19864687	-	Intergenic	G>A	1.4	4.60×10^{-13}	-10.1	6.40×10^{-9}	1.12	0.07	0.8	0.23
Imputed	rs2083637	19865175	-	Intergenic	A>G	1.41	3.40×10^{-13}	-10.1	5.50×10^{-9}	1.11	0.07	0.79	0.23
Imputed	rs2083636	19865263	-	Intergenic	T>G	1.4	3.40×10^{-13}	-10.1	5.40×10^{-9}	1.11	0.07	0.79	0.23
Imputed	rs894211	19865747	-	Intergenic	C>T	1.39	5.70×10^{-13}	-9.9	6.20×10^{-9}	1.08	0.08	0.73	0.27
Stage 1	rs765547	19866274	-	Intergenic	C>T	1.41	3.20×10^{-13}	-10.0	4.10×10^{-9}	1.15	0.06	0.8	0.23
Imputed	rs765548	19866594	-	Intergenic	C>T	1.39	5.60×10^{-13}	-9.9	5.90×10^{-9}	1.07	0.08	0.73	0.27
Imputed	rs9644637	19867220	-	Intergenic	T>C	1.39	5.60×10^{-13}	-9.9	5.90×10^{-9}	1.07	0.08	0.73	0.27
Stage 1	rs11986942	19867445	-	Intergenic	G>C	1.39	6.20×10^{-13}	-9.9	6.80×10^{-9}	1.04	0.09	0.7	0.29
Stage 1	rs1837842	19868290	-	Intergenic	T>C	1.39	5.40×10^{-13}	-9.7	8.10×10^{-9}	1.03	0.1	0.7	0.29
Imputed	rs1441756	19868386	-	Intergenic	A>C	1.39	5.50×10^{-13}	-9.9	5.80×10^{-9}	1.08	0.08	0.74	0.27
Imputed	rs4406409	19868971	-	Intergenic	T>C	1.39	6.20×10^{-13}	-9.9	6.30×10^{-9}	1.07	0.08	0.73	0.28
Stage 1	rs1919484	19869676	-	Intergenic	C>T	1.39	6.90×10^{-13}	-9.9	6.30×10^{-9}	1.07	0.08	0.73	0.27

Imputed	rs1569213	19870735	-	Intergenic	G>A	1.42	3.40×10^{-13}	-10.7	2.10×10^{-9}	1.11	0.08	0.73	0.28
Imputed	rs1372343	19871320	-	Intergenic	C>T	1.38	7.10×10^{-13}	-9.7	1.30×10^{-8}	0.94	0.13	0.64	0.32
Imputed	rs1372340	19871372	-	Intergenic	G>A	1.38	7.10×10^{-13}	-9.7	1.30×10^{-8}	0.94	0.13	0.64	0.32
Imputed	rs2410626	19871487	-	Intergenic	C>G	0.36	0.25	0.2	0.89	-1.47	0.13	-0.92	0.34
Imputed	rs2410627	19871513	-	Intergenic	T>C	1.38	7.10×10^{-13}	-9.7	1.30×10^{-8}	0.94	0.13	0.64	0.32
Stage 1	rs7461115	19871540	-	Intergenic	G>C	1.39	7.20×10^{-13}	-9.7	1.40×10^{-8}	0.96	0.12	0.66	0.3
Imputed	rs2898494	19871580	-	Intergenic	C>G	0.36	0.25	0.2	0.89	-1.47	0.13	-0.92	0.34
Imputed	rs2410629	19871637	-	Intergenic	T>C	1.39	6.70×10^{-13}	-9.7	1.30×10^{-8}	0.95	0.13	0.64	0.32
Imputed	rs2898495	19871892	-	Intergenic	A>G	1.42	2.30×10^{-13}	-10.0	5.30×10^{-9}	0.99	0.11	0.68	0.28
Imputed	rs4593558	19872008	-	Intergenic	A>G	1.42	2.30×10^{-13}	-10.0	5.30×10^{-9}	0.99	0.11	0.68	0.28
Imputed	rs6986010	19872780	-	Intergenic	T>C	1.42	2.30×10^{-13}	-10.0	5.30×10^{-9}	0.99	0.11	0.68	0.28
Imputed	rs17489539	19873582	-	Intergenic	T>A	1.42	2.30×10^{-13}	-10.0	5.30×10^{-9}	0.99	0.11	0.68	0.28
Imputed	rs4922119	19874153	-	Intergenic	C>T	1.42	2.30×10^{-13}	-10.0	5.30×10^{-9}	0.99	0.11	0.68	0.28
Imputed	rs4375019	19874498	-	Intergenic	T>A	1.42	2.30×10^{-13}	-10.0	5.30×10^{-9}	0.99	0.11	0.68	0.28
Imputed	rs4333617	19875004	-	Intergenic	A>G	1.41	2.90×10^{-13}	-10.0	5.40×10^{-9}	0.98	0.12	0.67	0.29
Imputed	rs2410630	19875100	-	Intergenic	C>T	1.41	2.90×10^{-13}	-10.0	5.40×10^{-9}	0.98	0.12	0.67	0.29
Imputed	rs6586886	19875408	-	Intergenic	G>A	1.42	2.50×10^{-13}	-10.0	5.30×10^{-9}	0.99	0.11	0.68	0.28
Imputed	rs4403423	19875554	-	Intergenic	A>G	0.4	0.2	0.1	0.87	-1.27	0.19	-0.69	0.48
Imputed	rs7016880	19876746	-	Intergenic	G>C	1.86	7.50×10^{-15}	-15.1	5.20×10^{-13}	2.38	2.10×10^{-3}	1.55	0.06
Imputed	rs7007609	19876797	-	Intergenic	T>C	1.86	7.50×10^{-15}	-15.1	5.20×10^{-13}	2.38	2.10×10^{-3}	1.55	0.06
Imputed	rs7007797	19876970	-	Intergenic	T>G	1.86	7.50×10^{-15}	-15.1	5.20×10^{-13}	2.38	2.10×10^{-3}	1.55	0.06
Imputed	rs7004149	19877208	-	Intergenic	A>G	1.86	5.70×10^{-15}	-15.1	4.30×10^{-13}	2.37	2.30×10^{-3}	1.54	0.06
Imputed	rs7004158	19877233	-	Intergenic	A>G	1.86	5.70×10^{-15}	-15.1	4.30×10^{-13}	2.37	2.30×10^{-3}	1.54	0.06
Imputed	rs6983430	19877253	-	Intergenic	G>C	1.86	5.70×10^{-15}	-15.1	4.30×10^{-13}	2.37	2.30×10^{-3}	1.54	0.06
Imputed	rs12678603	19877732	-	Intergenic	C>T	1.85	7.30×10^{-15}	-15.0	7.50×10^{-13}	2.39	2.00×10^{-3}	1.58	0.05
Imputed	rs12678604	19877773	-	Intergenic	C>G	1.85	7.30×10^{-15}	-15.0	7.50×10^{-13}	2.39	2.00×10^{-3}	1.58	0.05
Stage 1	rs7013777	19878356	-	Intergenic	A>G	1.39	4.80×10^{-13}	-10.0	7.50×10^{-9}	0.93	0.13	0.63	0.31

Imputed	rs11989309	19880330	-	Intergenic	C>T	1.88	7.80×10^{-15}	-15.0	1.00×10^{-12}	2.47	1.60×10^{-3}	1.67	0.04
Imputed	rs1919485	19882721	-	Intergenic	T>G	0.33	0.29	0.6	0.66	-1.32	0.17	-0.67	0.49
Imputed	rs7816447	19882950	-	Intergenic	T>C	1.88	8.10×10^{-15}	-14.9	1.40×10^{-12}	2.44	1.80×10^{-3}	1.65	0.04
Imputed	rs1919486	19883287	-	Intergenic	A>T	0.33	0.29	0.6	0.65	-1.32	0.17	-0.67	0.49
Imputed	rs1919487	19883530	-	Intergenic	T>A	1.38	2.80×10^{-12}	-9.9	1.40×10^{-8}	0.83	0.2	0.53	0.42
Imputed	rs4543558	19888329	-	Intergenic	C>G	1.39	2.80×10^{-12}	-9.9	1.50×10^{-8}	0.88	0.17	0.6	0.37
Imputed	rs2178296	19889125	-	Intergenic	G>T	1.42	8.40×10^{-13}	-10.0	9.80×10^{-9}	0.86	0.18	0.58	0.39
Imputed	rs7837677	19889872	-	Intergenic	C>T	0.39	0.2	0.5	0.73	-1.42	0.14	-0.75	0.44
Imputed	rs4574859	19890322	-	Intergenic	G>A	0.35	0.26	1.2	0.63	-1.41	0.14	-0.65	0.48
Imputed	rs10103634	19890612	-	Intergenic	G>A	1.5	2.10×10^{-16}	-11.7	9.00×10^{-13}	1.66	5.40×10^{-3}	1	0.1
Stage 1	rs4442164	19892181	-	Intergenic	A>G	0.23	0.52	3.6	0.27	-1.76	0.07	-0.87	0.35
Stage 1	rs4244457	19899046	-	Intergenic	C>T	1.39	8.40×10^{-17}	-9.6	5.70×10^{-10}	0.96	0.08	0.75	0.2
Imputed	rs2178298	19899697	-	Intergenic	G>T	0.36	0.25	0.3	0.67	-1.51	0.12	-0.7	0.45
Imputed	rs1406502	19902067	-	Intergenic	C>T	0.36	0.24	0.3	0.67	-1.51	0.12	-0.7	0.45
Imputed	rs1406501	19902177	-	Intergenic	T>C	0.32	0.31	0.4	0.6	-1.51	0.11	-0.69	0.45
Imputed	rs2049749	19902769	-	Intergenic	C>A	0.36	0.24	0.3	0.67	-1.5	0.12	-0.69	0.45
Imputed	rs2178297	19902830	-	Intergenic	G>A	0.36	0.24	0.3	0.67	-1.5	0.12	-0.69	0.45
Stage 1	rs4449813	19903320	-	Intergenic	G>A	0.35	0.32	1.3	0.62	-1.77	0.08	-0.96	0.41
Stage 1	rs1590120	19903355	-	Intergenic	T>C	0.34	0.26	0.7	0.64	-1.46	0.13	-0.67	0.46
Imputed	rs1581674	19903423	-	Intergenic	G>T	0.36	0.24	0.3	0.67	-1.5	0.12	-0.69	0.45
Stage 1	rs12544475	19906693	-	Intergenic	T>C	0.35	0.27	0.6	0.59	-1.39	0.14	-0.59	0.49
Imputed	rs7015401	19909426	-	Intergenic	G>T	0.31	0.33	1.0	0.5	-1.47	0.13	-0.65	0.46
Imputed	rs1569211	19914106	-	Intergenic	C>G	0.29	0.37	1.0	0.49	-1.5	0.12	-0.71	0.43

SNP, single nucleotide polymorphism; HDLC, high density lipoprotein cholesterol; TG, triglyceride; LDLC, low density lipoprotein cholesterol; TCHL, total cholesterol; *LPL*, lipoprotein lipase; UTR, untranslated region.

^aUnstandardized coefficients of untransformed values (effect). Effect sizes (mg/dL) of minor alleles assessed in an additive manner; ^bp-values of the minor allele (assessed in an additive manner) adjusted for residence area, age, gender and body mass index.

Supplementary Table 2. Association of *LPL* SNPs with lipid concentrations at stage 2

SNP	Position	Function	Alleles	HDLc		TG		LDLc		TCHL	
				Effect ^a	p-value ^b	Effect ^a	p-value ^b	Effect ^a	p-value ^b	Effect ^a	p-value ^b
rs343	19810787	Intron	C>A	0.68	0.08	-7.52	0.12	2.16	0.05	1.82	0.11
rs253	19811417	Intron	C>T	0.85	4.2×10^{-3}	-7.42	3.6×10^{-3}	0.87	0.27	0.59	0.56
rs263	19812812	Intron	G>A	1.53	5.5×10^{-6}	-8.58	3.3×10^{-3}	1.57	0.09	1.82	0.07
rs271	19813702	Intron	C>T	1.53	5.1×10^{-6}	-8.71	2.2×10^{-3}	1.51	0.10	1.74	0.08
rs326	19819439	Intron	T>C	2.05	1.5×10^{-9}	-12.17	9.1×10^{-7}	-0.20	0.83	-3.7×10^{-3}	0.80
rs327	19819536	Intron	A>C	2.05	1.6×10^{-9}	-12.27	5.9×10^{-7}	-0.30	0.74	-0.11	0.90
rs12679834	19820433	Intron	T>C	3.26	3.1×10^{-14}	-13.70	1.3×10^{-6}	-0.45	0.69	0.72	0.40
rs11570892	19823617	3' UTR	T>C	-0.03	0.92	-7.60	0.11	9.0×10^{-3}	0.99	-1.15	0.48
rs3200218	19824071	3' UTR	T>C	-0.67	0.09	-3.81	0.25	-0.36	0.74	-1.65	0.13

LPL, lipoprotein lipase; SNP, single nucleotide polymorphism; HDLc, high density lipoprotein cholesterol; TG, triglyceride; LDLc, low density lipoprotein cholesterol; TCHL, total cholesterol; UTR, untranslated region.

^aUnstandardized coefficients of untransformed values (effect). Effect sizes (mg/dL) of minor alleles assessed in an additive manner; ^bp-values of the minor allele (assessed in an additive manner) adjusted for age, gender and body mass index.

Supplementary Table 3. Association between haplotypes including *LPL* SNPs and lipid concentrations by using stage 1 and imputed data

Block	HT	Haplotype frequency			HDLC		TG		LDLC		TCHL	
		++	+-	--	Effect ^a	p-value ^b	Effect ^a	p-value ^b	Effect ^a	p-value ^b	Effect ^a	p-value ^b
B1	HT1: CTAAT	356	2,425	4,751	1.26	4.4×10^{-11}	-8.99	9.2×10^{-7}	0.70	0.26	0.67	0.40
	HT2: TCGGC	4,725	2,448	359	-1.24	8.1×10^{-11}	8.77	1.5×10^{-6}	-0.72	0.24	-0.72	0.37
B2	HT1 ^c	3,014	3,327	921	-1.30	4.2×10^{-15}	8.00	1.9×10^{-8}	-1.22	0.02	-1.05	0.06
	HT2 ^d	68	1,421	5,773	0.58	0.01	-3.85	0.17	0.95	0.26	0.86	0.29
	HT3 ^e	104	1,480	5,678	1.99	7.8×10^{-16}	-15.07	5.6×10^{-13}	2.25	5.1×10^{-3}	1.42	0.09
	HT4 ^f	2	288	6,972	0.34	0.68	-9.42	0.15	-1.03	0.58	-1.56	0.44
	HT5 ^g	21	836	6,405	0.19	0.62	2.08	0.42	-0.90	0.41	-0.31	0.92
	HT6 ^h	0	225	7,037	-0.45	0.52	11.55	0.19	0.70	0.74	1.37	0.36

LPL, lipoprotein lipase; SNP, single nucleotide polymorphism; HT, haplotype; HDLC, high density lipoprotein cholesterol; TG, triglyceride; LDLC, low density lipoprotein cholesterol; TCHL, total cholesterol; B, block.

^aUnstandardised coefficients of untransformed values (effect). Effect sizes (mg/dL) of haplotypes assessed in an additive manner; ^bp-values of the haplotype (assessed in an additive manner) adjusted for residence area, age, gender and body mass index; ^cHaplotype 1 in block 2:

TGCATACGGTTCGTCTTTGCGCGTTCAGGGTTAACGGGGCGACGCTATTTCTGCGTATCGATCCCTGTATCGCGCTGCTAATTCTACGAGTTAA
GCCACTTATTCGCGGACGCTCGGTGTGC; ^dHaplotype 2 in block 2:

TGCCTACGGTGCCTTGCACGTTCCAGGGTCTAACGGGGCGACGCTATTTCTGCGTATCGATCCCTGTATCGCGCTGCTAATTCTACGAGTTA
AGCCACTTATTCGCGAATGCTCGGTGTGC; ^eHaplotype 3 in block 2:

CGCACC GGACTTGTATCCACAAGTTTTAGTGTTTCGGTGTAAAGAGCATCGCGCTAATCCTATAGGTTTCCCCCTATAACCCCGGCATAGTAACCGG
GCTGGTTCAACGTCGAATGCTCGGTGTGC; ^fHaplotype 4 in block 2:

TGCATACGGTTCGTCTTTGCGCGTTCAGGGTTAACGGGGCGACGCTATTTCTGCGTATCGATCCCTGTATCGCGCTGCTAATTCTACGAGTTAA
GCCACTTATTCGCGAATGCTCGGTGTGC; ^gHaplotype 5 in block 2:

CCAATCCAATTCACCTCTATAAAACCCGAGACTTAACAGGGGAGAATCGCGCTAATCCTTTAGGTTTCCCCCTATAGCCGCGGCATAGTAGGTTA
AGCCGCGTTATGTTAGGTTTCAAACCTCTG; ^hHaplotype 6 in block 2:

TGCCTACGGTGCCTTGCACGTTCCAGGGTCTAACGGGGCGACGCTATTTCTGCGTATCGATCCCTGTATCGCGCTGCTAATTCTACGAGTTA
AGCCACTTATTCGCGGACGCTCGGTGTGC.

Supplementary Table 4. Association between haplotypes including *LPL* SNPs and lipid concentrations at stage 1

Block	HT	Haplotype frequency			HDLC		TG		LDLC		TCHL	
		++	+-	--	Effect ^a	p-value ^b	Effect ^a	p-value ^b	Effect ^a	p-value ^b	Effect ^a	p-value ^b
B1	HT1: AT	356	2,426	4,754	1.25	5.2×10^{-11}	-8.98	9.3×10^{-7}	0.70	0.26	0.66	0.41
	HT2: GC	4,725	2,451	360	-1.25	5.7×10^{-11}	8.81	1.3×10^{-6}	-0.70	0.25	-0.72	0.37
B2	HT1: TGGGGGCGATCGTCGA	3,258	3,408	870	-1.27	5.0×10^{-15}	7.88	3.4×10^{-8}	-1.15	0.03	-0.94	0.08
	HT2: CGGGGGCGATCGTCGA	97	1,623	5,816	0.42	0.04	-1.92	0.43	0.88	0.26	0.81	0.24
	HT3: TGTGTAGAGCTCCTCG	119	1,550	5,867	1.92	5.4×10^{-16}	-15.02	7.3×10^{-13}	2.20	4.4×10^{-3}	1.42	0.08
	HT4: TAGAGGGAGCTCCTCG	43	1,144	6,349	0.35	0.22	-1.00	0.95	-0.91	0.33	-0.44	0.63

LPL, lipoprotein lipase; SNP, single nucleotide polymorphism; HT, haplotype; HDLC, high density lipoprotein cholesterol; TG, triglyceride; LDLC, low density lipoprotein cholesterol; TCHL, total cholesterol; B, block.

^aUnstandardised coefficients of untransformed values (effect). Effect sizes (mg/dL) of haplotypes assessed in an additive manner; ^bp-values of the haplotype (assessed in an additive manner) adjusted for residence area, age, gender and body mass index.

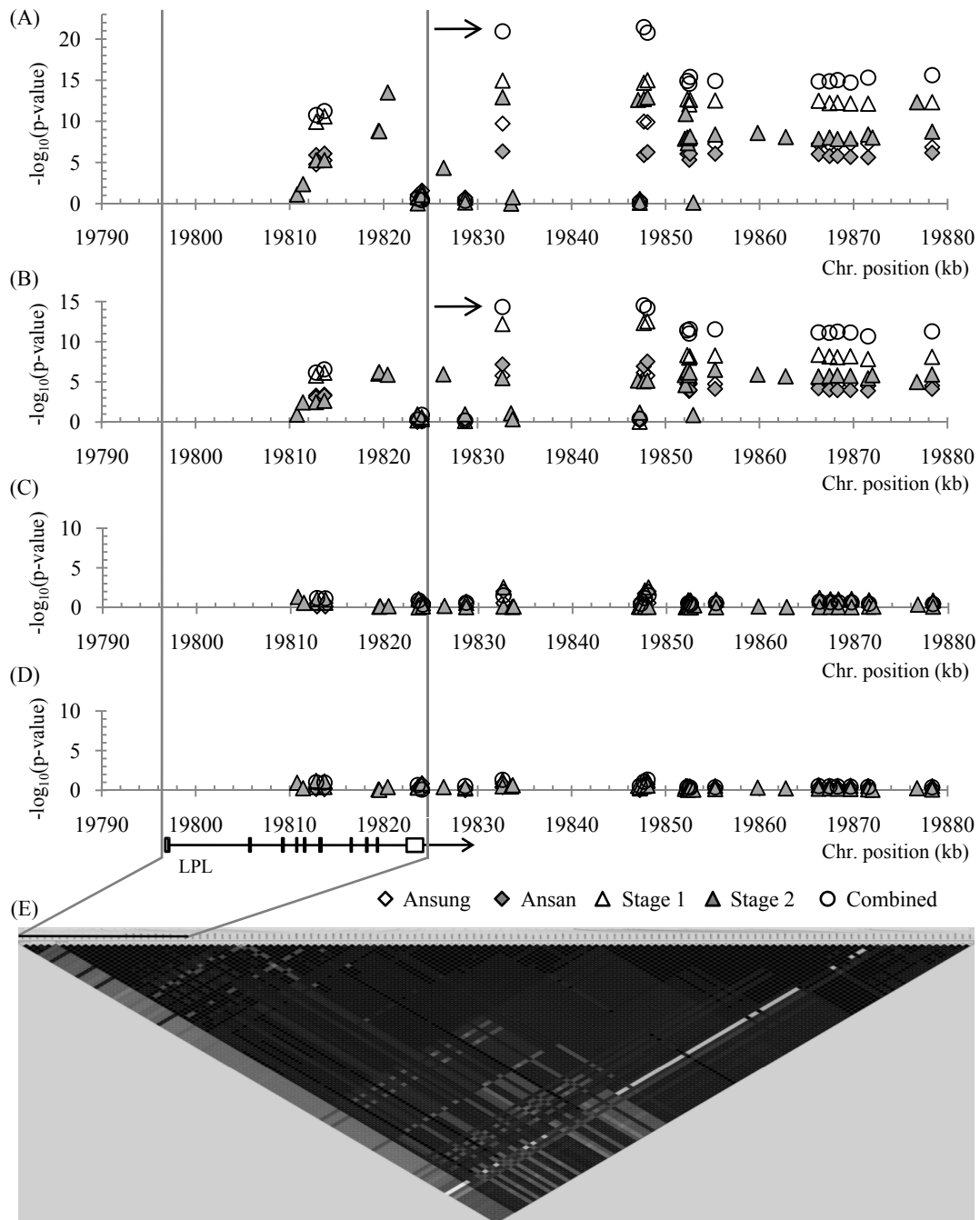
Supplemental Table 5. Association between haplotypes including *LPL* SNPs and lipid concentrations at stage 2

Block	HT	Haplotype frequency			HDLC		TG		LDLC		TCHL	
		++	+-	--	Effect ^a	p-value ^b	Effect ^a	p-value ^b	Effect ^a	p-value ^b	Effect ^a	p-value ^b
B1	HT1: ATAT	53	851	2,799	0.77	0.05	-7.27	0.14	2.28	0.04	2.08	0.08
	HT2: CTAT	13	504	3,186	2.37	7.1×10^{-6}	-8.28	7.5×10^{-3}	-0.37	0.80	0.57	0.70
	HT3: CTGC	50	727	2,926	-0.60	0.13	-1.92	0.66	-0.51	0.65	-1.43	0.17
	HT4: CCGC	1,712	1,644	347	-0.85	4.1×10^{-3}	7.58	2.8×10^{-3}	-0.92	0.25	-0.61	0.55
B2	HT1 ^c	36	690	2,902	3.27	1.1×10^{-12}	-12.84	1.5×10^{-5}	-0.55	0.65	0.74	0.42
	HT2 ^d	1,452	1,695	481	-1.39	1.9×10^{-6}	10.71	1.3×10^{-6}	0.07	0.93	0.32	0.89
	HT3 ^e	0	87	3,541	-2.77	0.05	11.21	0.14	2.92	0.39	1.86	0.62
	HT4 ^f	12	362	3,254	0.20	0.70	-9.46	0.12	0.76	0.64	-0.40	0.78
	HT5 ^g	2	136	3,490	1.32	0.22	-8.71	0.40	-0.08	0.98	-0.11	0.86
	HT6 ^h	40	680	2,908	-0.33	0.37	-4.65	0.22	-0.76	0.53	-1.95	0.10

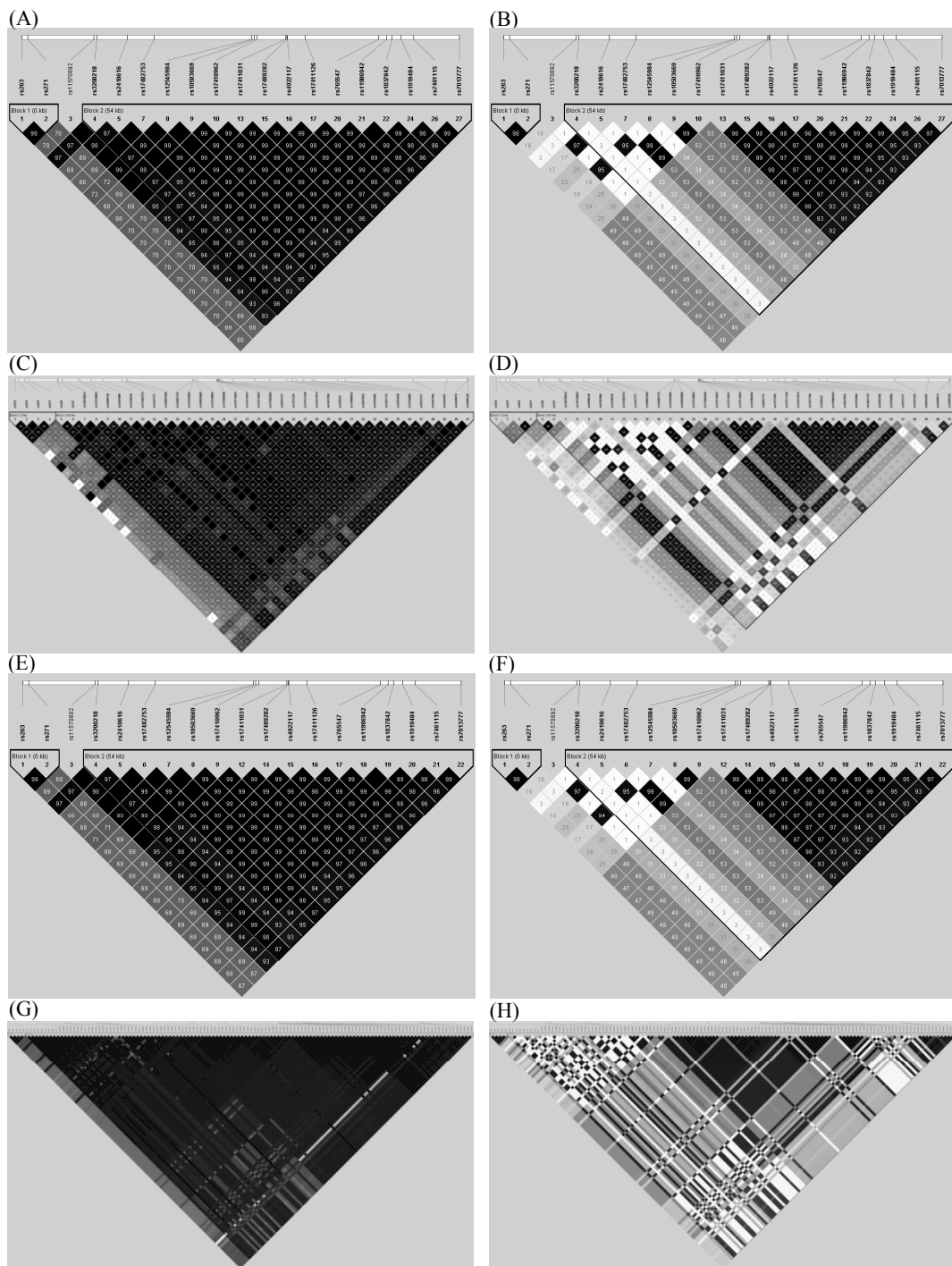
LPL, lipoprotein lipase; SNP, single nucleotide polymorphism; HT, haplotype; HDLC, high density lipoprotein cholesterol; TG, triglyceride; LDLC, low density lipoprotein cholesterol; TCHL, total cholesterol; B, block.

^aUnstandardised coefficients of untransformed values (effect). Effect sizes (mg/dL) of haplotypes assessed in an additive manner; ^bp-values of the haplotype (assessed in an additive manner) adjusted for age, gender and body mass index; ^cHaplotype 1 in block 2: CCCTTTGTAATGTAAGCAGGCGATCCTCGCGATGT; ^dHaplotype 2 in block 2: TATTCGGAACGGGTGCTGAGTCTCGTCGAGAACGT;

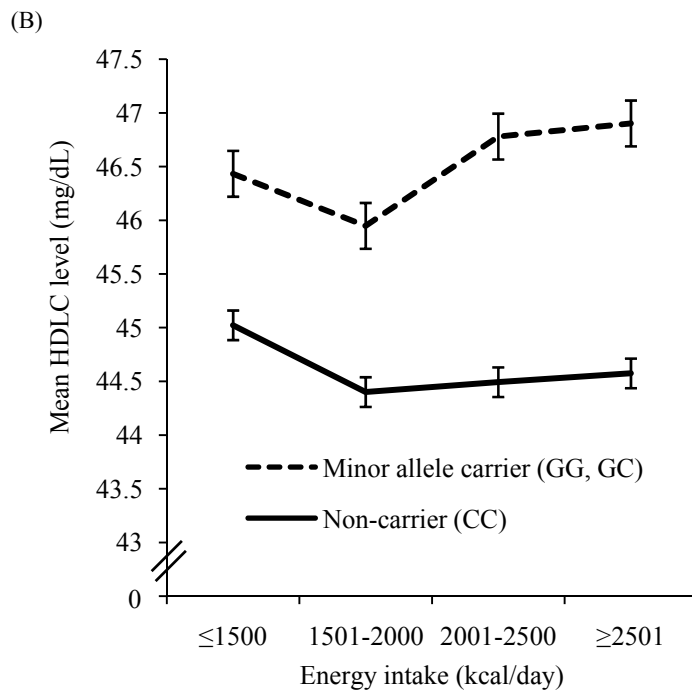
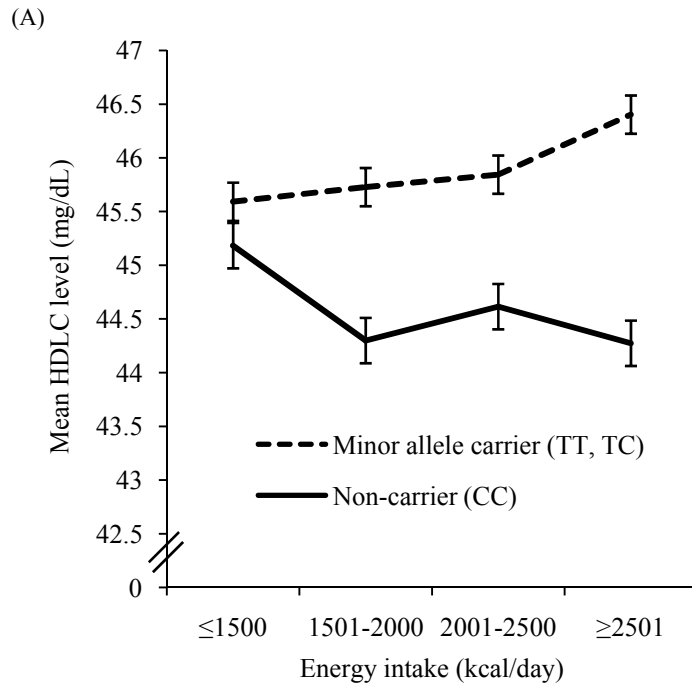
^eHaplotype 3 in block 2: TATTCTGGAGCGGGTCTGAGTCTCGTCGAGAACGT; ^fHaplotype 4 in block 2: CCTCTTAGGACAGGAGG-CAGTCGATCCTCGGGGTAC; ^gHaplotype 5 in block 2: TATTCGGAACGGGTGCTGAGTCTCGTCGAGAATGT; ^hHaplotype 6 in block 2: TATTCTGGAGCGGGTCTGAGTCTCGTCGAGAATGT.

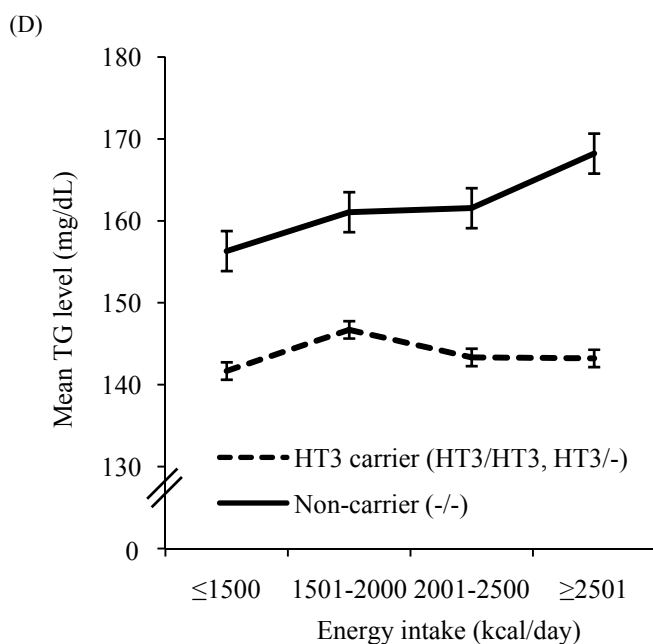
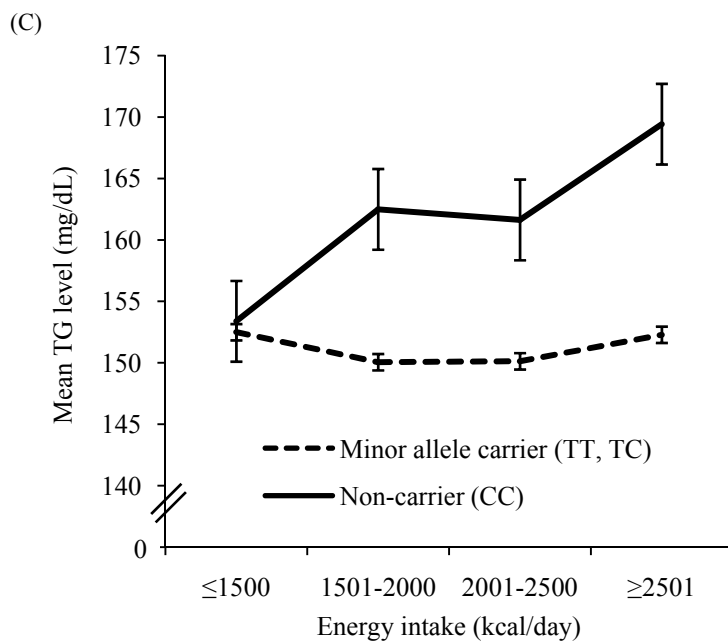


Supplementary Fig. 1. (A-E) Plots of association ($-\log_{10}$ p-value) between single-nucleotide polymorphisms (SNPs) located on lipoprotein lipase (*LPL*) gene including 3' flanking region and lipid traits: (A) high-density lipoprotein cholesterol, (B) triglyceride, (C) low-density lipoprotein cholesterol, (D) total cholesterol. The human *LPL* gene is located from base 19796582 to 19824770 on chromosome 8. The linkage disequilibrium (LD) block partition was performed by using stage 1 and imputed data. A significantly associated SNP marked by an arrow was rs17482753 which is in strong LD with a nonsense SNP, rs328.

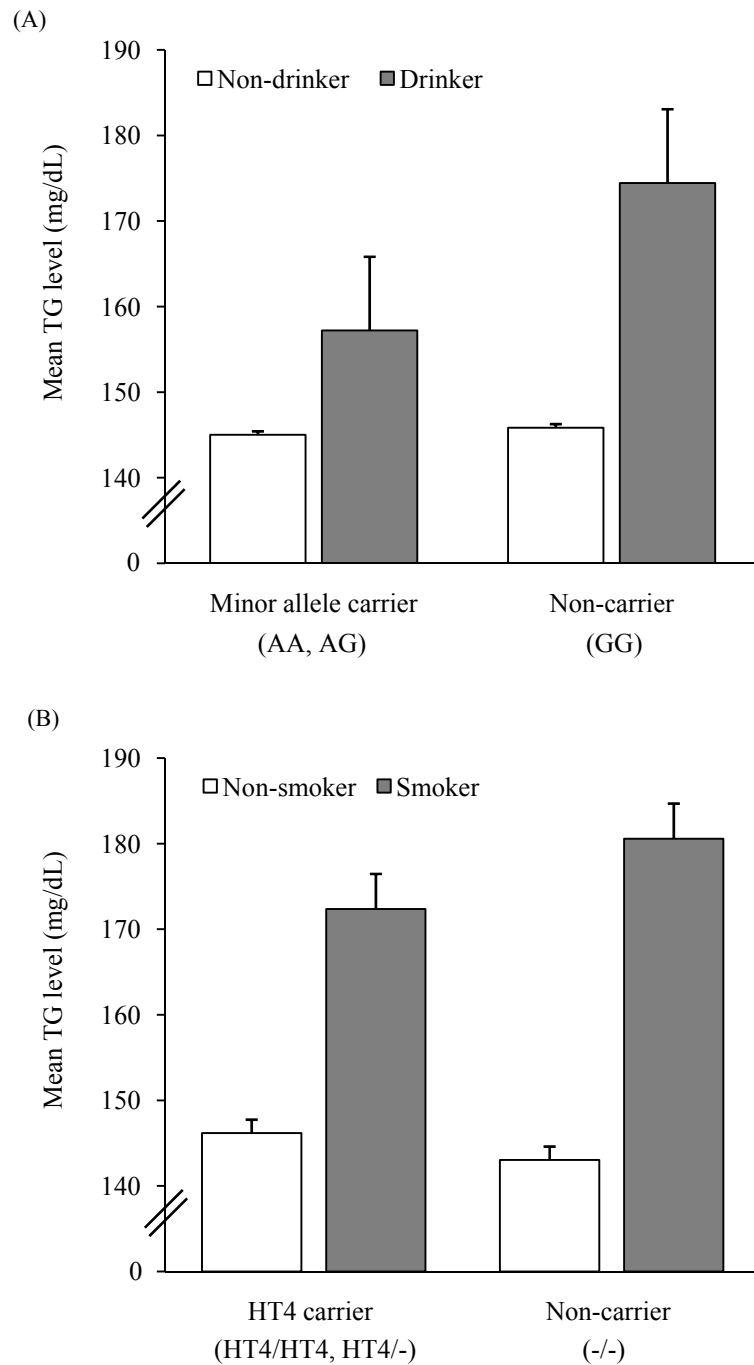


Supplementary Fig. 2. Linkage disequilibrium (LD) blocks for the region including lipoprotein lipase (*LPL*) single-nucleotide polymorphisms. (A, C, E, G) LD color by $|D'|$ values, (B, D, F, H) LD color by r^2 values. (A, B) stage 1, (C, D) stage 2, (E, F) combined data (stage 1 + 2), (G, H) imputed data.





Supplementary Fig. 3. Interaction effects of lipoprotein lipase (*LPL*) single-nucleotide polymorphisms (SNPs) and haplotype with daily energy intake on lipid levels. Interaction p-values were calculated by linear regression analyses, which includes main and interaction effects, adjusted for residence area, age, gender and body mass index. (A) Interaction effect of *LPL* SNP, rs271 ($r^2 = 0.99$ with rs263) with daily energy intake on high-density lipoprotein cholesterol (HDL) level ($p = 0.013$). (B) Interaction effect of *LPL* SNP, rs328 ($r^2 = 1$ with rs12679834) with daily energy intake on HDL level ($p = 0.033$). (C) Interaction effect of *LPL* SNP, rs271 ($r^2 = 0.99$ with rs263) with daily energy intake on triglyceride (TG) level ($p = 0.021$). (D). Interaction effect of haplotype 3 in block 2 (TGTGTAGAGCTCCTCG) with daily energy intake on TG level ($p = 0.027$). HT, haplotype.



Supplementary Fig. 4. Interaction effect of lipoprotein lipase (*LPL*) single-nucleotide polymorphisms (SNP) and haplotype with lifestyle factors on triglyceride (TG) level. Interaction p-value was calculated by linear regression analysis, which includes main and interaction effects, adjusted for residence area, age, gender and body mass index. (A). Interaction effect of *LPL* SNP, rs263 ($r^2 = 0.99$ with rs271) with alcohol consumption on TG level ($p = 0.017$). (B). Interaction effect of haplotype 4 in block 2 (TAGAGGGAGCTCCTCG) with cigarette smoking on TG level ($p = 0.022$). HT, haplotype.