

SUPPLEMENTARY MATERIAL

Table S1. Features of classical hyperlipoproteinemia (HLP) phenotypes

WHO ICD number	Frederickson HLP phenotype	MIM number	Lipids	Lipoproteins	Genetics
E78.3	HLP type 1 Familial chylomicronemia (LPL deficiency)	238600	↑TG	↑CM	Primarily pediatric and young adults; Monogenic; AR due to mutant <i>LPL</i> or <i>APOC2</i>
E78.0	HLP type 2A Familial hypercholesterolemia (FH)	143890	↑TC	↑LDL	Monogenic; Heterozygous form due to mutant <i>LDLR</i> , <i>APOB</i> or <i>PCSK9</i> ; Homozygous form due to mutant <i>LDLR</i> or <i>ARH</i>
E78.4	HLP type 2B (HLP2B) Combined hyperlipoproteinemia (CHL)	144250	↑TC, ↑TG	↑VLDL, ↑LDL	Polygenic, multiple etiologies, some cases due to <i>USF1</i> , <i>APOB</i> or <i>LPL</i> ; Common <i>APOA5</i> SNPs associated (ref. 22)
E78.2	HLP type 3 Dysbetalipoproteinemia (DBL)	107741	↑TC, ↑TG	↑IDL	Polygenic; <i>APOE</i> E2/E2 homozygosity or mutant <i>APOE</i> necessary but not sufficient; Common <i>APOA5</i> SNPs associated (ref. 22)
E78.1	HLP type 4 Primary hypertriglyceridemia (HTG)	144600 and 145750	↑TG	↑VLDL	Polygenic; Common <i>APOA5</i> SNPs associated (ref. 22)
E78.3	HLP type 5 Mixed hyperlipidemia (MHL)	144650	↑TC, ↑TG	↑VLDL, ↑CM	Polygenic; rare mutations in <i>LPL</i> , <i>APOC2</i> and <i>APOA5</i> in ~10% of cases (ref. 20); Common <i>APOA5</i> , <i>TRIB1</i> , <i>TBL2</i> , <i>GCKR</i> and <i>GALNT2</i> SNPs associated (ref. 21)

abbreviations: WHO, World Health Organization; ICD, International Classification of Diseases; HLP, hyperlipoproteinemia; MIM, Mendelian Inheritance in Man; LPL, lipoprotein lipase; TG, triglyceride; TC, total cholesterol; CM, chylomicrons; VLDL, very-low density lipoprotein; LDL, low-density lipoprotein; IDL, intermediate-density lipoprotein; AR, autosomal recessive; *LPL*, gene encoding LPL; *APOC2*, gene encoding apolipoprotein (apo) C-II; *APOB*, gene encoding apo B; *PCSK9*, gene encoding proprotein convertase subtilisin/kexin type 9; *ARH*, gene encoding autosomal recessive hypercholesterolemia protein; *USF1*, gene encoding upstream stimulatory factor 1; *APOE*, gene encoding apo E; *APOA5*, gene encoding apo A-V; *TRIB1*, gene encoding homologue of *Drosophila Tribbles 1*; *TBL2* locus containing genes encoding transducin-beta-like-2 and MLX interacting protein-like (also called carbohydrate response element binding protein [ChREBP]); *GCKR*, gene encoding glucokinase receptor; *ANGPTL3*, gene encoding angiopoietin-like 3; *GALNT2*, gene encoding UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase

Table S2. Genotype counts and frequencies of candidate genes in HLP types

		Type 2A	Type 2B	Type 3	Type 4	Type 5	Controls
<i>APOA5</i> p.S19W	SS	72 (87.8%)	53 (77.9%)	29 (69.1%)	41 (85.4%)	98 (67.1%)	221 (91.3%)
	SW	9 (11.0%)	14 (20.6%)	12 (28.6%)	6 (12.5%)	41 (28.1%)	17 (7.0%)
	WW	1 (1.2%)	1 (1.5%)	1 (2.4%)	1 (2.1%)	7 (4.79%)	4 (1.7%)
<i>APOA5</i> -1131T>C	TT	70 (85.4%)	57 (83.8%)	30 (71.4%)	31 (64.6%)	99 (67.8%)	219 (90.5%)
	TC	11 (13.4%)	11 (16.2%)	11 (26.2%)	17 (35.4%)	38 (26.0%)	23 (9.5%)
	CC	1 (1.2%)	0	1 (2.4%)	0	9 (6.2%)	0
<i>APOA5</i> rs6589566	AA	70 (85.4%)	55 (80.9%)	30 (71.4%)	32 (66.7%)	96 (65.8%)	212 (88.0%)
	AG	11 (13.4%)	13 (19.1%)	11 (26.2%)	16 (33.3%)	41 (28.1%)	29 (12.0%)
	GG	1 (1.2%)	0	1 (2.4%)	0	9 (6.2%)	0
<i>APOA5</i> rs12286037	CC	72 (87.8%)	52 (76.5%)	29 (69.05%)	41 (85.4%)	97 (66.4%)	221 (91.7%)
	CT	9 (11.0%)	15 (22.1%)	12 (28.6%)	6 (12.5%)	43 (29.5%)	16 (6.7%)
	TT	1 (1.22%)	1 (1.5%)	1 (2.4%)	1 (2.1%)	6 (4.1%)	4 (1.7%)
<i>BUD13</i> rs964184	CC	61 (74.4%)	41 (60.3%)	22 (53.7%)	28 (58.3%)	58 (40.0%)	193 (79.8%)
	CG	18 (22.0%)	24 (35.3%)	12 (29.3%)	16 (33.3%)	62 (42.8%)	45 (18.6%)
	GG	3 (3.7%)	3 (4.4%)	7 (17.1%)	4 (8.3%)	25 (17.2%)	4 (1.7%)
<i>BUD13</i> rs28927680	CC	70 (87.5%)	52 (76.5%)	31 (73.8%)	38 (82.6%)	95 (65.5%)	218 (90.1%)
	CG	9 (11.3%)	15 (22.1%)	9 (21.4%)	7 (15.2%)	43 (30.0%)	20 (8.3%)
	GG	1 (1.3%)	1 (1.5%)	2 (4.8%)	1 (2.17%)	7 (4.8%)	4 (1.7%)
<i>APOC3M</i> -482C>T	CC	47 (57.3%)	33 (48.5%)	21 (50%)	20 (41.7%)	68 (46.6%)	115 (47.5%)
	CT	32 (39.0%)	31 (45.6%)	13 (31.0%)	21 (43.8%)	64 (43.8%)	115 (47.5%)
	TT	3 (3.7%)	4 (5.9%)	8 (19.1%)	7 (14.6%)	14 (9.6%)	12 (5.0%)
<i>TRIB1</i> rs17321515	AA	30 (36.6%)	28 (41.2%)	15 (35.7%)	15 (31.3%)	61 (41.8%)	66 (27.3%)
	AG	39 (47.6%)	36 (52.9%)	25 (59.5%)	29 (60.4%)	69 (47.3%)	114 (47.1%)
	GG	13 (15.9%)	4 (5.9%)	2 (4.8%)	4 (8.3%)	16 (11.0%)	62 (25.6%)
<i>TRIB1</i> rs2954029	AA	30 (39.5%)	28 (41.2%)	16 (40.0%)	15 (32.6%)	64 (44.8%)	68 (28.3%)
	AT	34 (44.7%)	36 (52.9%)	22 (55.0%)	28 (60.9%)	66 (46.2%)	114 (47.5%)
	TT	12 (15.8%)	4 (5.9%)	2 (5.0%)	3 (6.5%)	13 (9.1%)	58 (24.2%)
<i>TBL2</i> rs17145738	CC	65 (79.3%)	61 (89.7%)	36 (85.7%)	43 (89.6%)	126 (86.3%)	175 (72.3%)
	CT	16 (19.5%)	7 (10.3%)	5 (11.9%)	5 (10.4%)	18 (12.3%)	62 (25.6%)
	TT	1 (1.2%)	0	1 (2.4%)	0	2 (1.4%)	5 (2.1%)
<i>BAZ1B</i> rs2074755	CC	0	0	0	0	2 (1.4%)	5 (2.1%)
	CT	17 (20.7%)	10 (14.7%)	6 (14.3%)	5 (10.4%)	17 (11.7%)	63 (26.3%)

	TT	65 (79.3%)	58 (85.3%)	36 (85.7%)	43 (89.6%)	126 (86.9%)	172 (71.7%)
<i>GCKR</i> rs780094	AA	12 (14.8%)	21 (30.9%)	6 (14.3%)	8 (16.7%)	43 (29.5%)	35 (14.5%)
	GA	39 (48.2%)	30 (44.1%)	23 (54.8%)	21 (43.8%)	69 (47.3%)	120 (49.6%)
	GG	30 (37.0%)	17 (25.0%)	13 (31.0%)	19 (39.6%)	34 (23.3%)	87 (36.0%)
<i>GCKR</i> rs1260326	CC	29 (35.4%)	15 (22.1%)	11 (26.2%)	19 (39.6%)	32 (21.9%)	84 (34.7%)
	CT	39 (47.6%)	31 (45.6%)	24 (57.1%)	20 (41.7%)	67 (45.9%)	123 (50.8%)
	TT	14 (17.1%)	22 (32.4%)	7 (16.6%)	9 (18.8%)	47 (32.2%)	35 (14.5%)
<i>CILP2</i> rs16996148	GG	71 (86.59%)	59 (86.8%)	38 (90.5%)	40 (83.3%)	130 (89.0%)	196 (81.0%)
	GT	11 (13.4%)	9 (13.2%)	4 (9.5%)	8 (16.7%)	16 (11.0%)	46 (19.0%)
<i>SF4</i> rs10401969	CC	1 (1.2%)	0	0	0	0	2 (0.8%)
	CT	11 (13.4%)	9 (13.2%)	2 (4.8%)	7 (14.6%)	13 (8.9%)	38 (15.8%)
	TT	70 (85.4%)	59 (86.8%)	40 (95.2%)	41 (85.4%)	133 (91.1%)	200 (83.3%)
<i>APOE</i> isotype	2/2	0	3 (4.4%)	42 (100%)	0	1 (0.68%)	0
	3/2	6 (7.3%)	6 (8.8%)	0	6 (12.5%)	28 (19.2%)	31 (12.8%)
	3/3	59 (72.0%)	37 (54.4%)	0	24 (50%)	76 (52.1%)	151 (62.4%)
	4/2	0	1 (1.5%)	0	2 (4.2%)	6 (4.1%)	3 (1.2%)
	4/3	14 (17.1%)	19 (27.9%)	0	15 (31.3%)	30 (20.6%)	51 (21.1%)
	4/4	3 (3.7%)	2 (2.9%)	0	1 (2.1%)	5 (3.4%)	6 (2.5%)
<i>LPL</i> S447X	SS	67 (81.7%)	55 (80.9%)	36 (85.7%)	46 (95.8%)	134 (91.8%)	203 (83.9%)
	SX	15 (18.3%)	13 (19.1%)	6 (14.3%)	1 (2.1%)	12 (8.2%)	39 (16.1%)
	XX	0	0	0	1 (2.1%)	0	0
<i>LPL</i> rs10503669	AC	13 (15.9%)	12 (17.7%)	5 (11.9%)	2 (4.2%)	11 (7.6%)	39 (16.2%)
	CC	69 (84.2%)	56 (82.4%)	37 (88.1%)	46 (95.8%)	134 (92.4%)	202 (83.8%)
		0	0	0	0	0	0
<i>LPL</i> rs17482753	GG	66 (81.5%)	56 (82.4%)	36 (85.7%)	45 (95.7%)	135 (92.5%)	198 (82.5%)
	GT	15 (18.5%)	12 (17.7%)	6 (14.3%)	1 (2.1%)	11 (7.5%)	42 (17.5%)
	TT	0	0	0	1 (2.1%)	0	0
<i>LPL</i> rs6993414	AA	67 (81.7%)	56 (82.4%)	37 (88.1%)	45 (93.8%)	132 (91.0%)	199 (82.9%)
	AG	14 (17.1%)	12 (17.7%)	4 (9.5%)	3 (6.3%)	13 (9.0%)	40 (16.7%)
	GG	1 (1.2%)	0	1 (2.4%)	0	0	1 (0.42%)
<i>ANGPTL3</i> rs12130333	CC	54 (65.9%)	49 (72.1%)	31 (75.6%)	32 (66.67%)	103 (70.6%)	140 (57.9%)
	CT	25 (30.5%)	18 (26.5%)	10 (24.4%)	12 (25.0%)	41 (28.1%)	90 (37.2%)
	TT	3 (3.7%)	1 (1.5%)	0	4 (8.3%)	2 (1.4%)	12 (5.0%)
<i>ANGPTL3</i> rs1748195	CC	36 (43.9%)	38 (55.9%)	24 (57.1%)	20 (41.7%)	89 (61.0%)	106 (43.8%)

	CG	39 (47.6%)	26 (38.2%)	18 (42.9%)	21 (43.8%)	52 (35.6%)	110 (45.5%)
	GG	7 (8.5%)	4 (5.9%)	0	7 (14.6%)	5 (3.4%)	26 (10.7%)
<i>GALNT2</i> rs4846914	AA	30 (36.6%)	21 (30.9%)	16 (38.1%)	11 (22.9%)	40 (27.4%)	84 (34.7%)
	AG	41 (50.0%)	38 (55.9%)	18 (42.9%)	25 (52.1%)	67 (45.9%)	135 (55.8%)
	GG	11 (13.4%)	9 (13.2%)	8 (19.1%)	12 (25.0%)	39 (26.7%)	23 (9.5%)
<i>PSRC1</i> rs599839	AA	59 (72.0%)	49 (72.1%)	26 (61.9%)	30 (62.5%)	84 (57.5%)	152 (62.8%)
	AG	18 (22.0%)	17 (25%)	14 (33.3%)	16 (33.3%)	56 (38.4%)	78 (32.2%)
	GG	5 (6.1%)	2 (2.9%)	2 (4.8%)	2 (4.2%)	6 (4.1%)	12 (5.0%)
<i>LDLR</i> rs6511720	GG	63 (76.8%)	55 (80.9%)	33 (78.6%)	39 (81.3%)	117 (80.1%)	185 (76.5%)
	GT	19 (23.2%)	13 (19.1%)	8 (19.1%)	9 (18.8%)	25 (17.1%)	55 (22.7%)
	TT	0	0	1 (2.4%)	0	4 (2.7%)	2 (0.8%)
<i>APOB</i> rs693	CC	22 (26.8%)	16 (23.5%)	11 (26.8%)	16 (34.0%)	39 (26.7%)	64 (26.5%)
	CT	38 (46.3%)	30 (44.1%)	20 (48.8%)	25 (53.2%)	68 (46.6%)	119 (49.2%)
	TT	22 (26.8%)	22 (32.4%)	10 (24.4%)	6 (12.8%)	39 (26.7%)	59 (24.4%)
<i>SELP</i> rs3917820	AG	18 (22.2%)	12 (17.7%)	7 (17.5%)	11 (23.4%)	40 (27.6%)	62 (25.8%)
	GG	63 (77.8%)	56 (82.4%)	33 (82.5%)	36 (76.6%)	105 (72.4%)	178 (74.2%)
<i>LIPC</i> rs4775041	CC	9 (11.0%)	7 (10.3%)	5 (11.9%)	2 (4.2%)	20 (13.7%)	23 (9.5%)
	CG	35 (42.7%)	32 (47.1%)	16 (38.1%)	12 (25.0%)	57 (39.0%)	86 (35.5%)
	GG	38 (46.3%)	29 (42.7%)	21 (50%)	34 (70.8%)	69 (47.3%)	133 (55.0%)

Abbreviations: as in Table 2.

Table S3. Univariate odds ratios (with 95% confidence intervals) for association of candidate genotypes with HLP types

		Type 2A	Type 2B	Type 3	Type 4	Type 5
<i>APOA5</i> p.S19W	W_DOM	1.95 (0.99, 3.83) 0.0486	2.78 (1.50, 5.17) 0.0008	4.57 (2.31, 9.06) <0.0001	3.37 (1.83, 6.19) <0.0001	5.65 (3.47, 9.20) <0.0001
	W_REC	1.04 (0.12, 9.43) 0.9707	1.01 (0.11, 9.14) 0.9928	1.77 (0.19, 16.10) 0.6085	2.15 (0.39, 11.93) 0.3691	4.28 (1.24, 14.81) 0.0129
<i>APOA5</i> -1131T>C	C_DOM	1.85 (0.97, 3.53) 0.0593	2.31 (1.26, 4.22) 0.0054	3.16 (1.55, 6.45) 0.001	4.22 (2.34, 7.66) <0.0001	4.59 (2.87, 7.34) <0.0001
	C_REC	4.47 (0.28, 72.18) 0.248	4.23 (0.26, 68.23) 0.2692	7.94 (0.49, 129.0) 0.0844	5.48 (0.34, 86.61) 0.1787	24.1 (3.03, 192) <0.0001
<i>APOA5</i> rs6589566	G_DOM	1.29 (0.66, 2.56) 0.4566	2.18 (1.20, 3.94) 0.0091	2.94 (1.45, 5.96) 0.0019	3.71 (2.04, 6.73) <.0001	3.97 (2.46, 6.40) <.0001
	G_REC	3.53 (0.22, 57.99) 0.3359	3.40 (0.21, 54.85) 0.3598	6.45 (0.40, 104.8) 0.1327	4.39 (0.27, 71.00) 0.2555	21.94 (2.78, 173.05) <.0001
<i>APOA5</i> rs12286037	T_DOM	1.59 (0.75, 3.36) 0.2226	2.82 (1.48, 5.36) 0.0011	4.76 (2.31, 9.84) <.0001	3.23 (1.63, 6.42) 0.0005	5.67 (3.36, 9.58) <.0001
	T_REC	0.89 (0.10, 8.10) 0.9203	0.84 (0.09, 7.57) 0.8733	1.59 (0.17, 14.49) 0.6799	2.25 (0.40, 12.55) 0.3411	3.22 (0.89, 11.58) 0.0594
<i>BUD13</i> rs964184	G_DOM	1.56 (0.91, 2.08) 0.1011	2.73 (1.66, 4.50) <.0001	3.61 (1.89, 6.91) <.0001	4.02 (2.35, 6.87) <.0001	6.02 (3.93, 9.24) <.0001
	G_REC	2.39 (0.66, 8.66) 0.1718	2.95 (0.88, 9.91) 0.0666	9.58 (3.06, 29.99) <.0001	5.51 (1.80, 16.94) 0.0009	10.90 (4.38, 27.13) <.0001
<i>BUD13</i> rs28927680	G_DOM	1.52 (0.74, 3.12) 0.2483	2.67 (1.43, 4.99) 0.0015	3.21 (1.51, 6.83) 0.0016	2.80 (1.41, 5.58) 0.0025	5.31 (3.19, 8.83) <.0001
	G_REC	0.88 (0.10, 7.94) 0.9065	1.70 (0.31, 9.41) 0.5413	3.32 (0.59, 18.63) 0.1492	2.36 (0.42, 13.17) 0.3122	3.85 (1.11, 13.35) 0.0231
<i>APOC3M</i> -482C>T	T_DOM	0.68 (0.43, 1.00) 0.1165	0.88 (0.56, 1.38) 0.5831	0.79 (0.43, 1.46) 0.4486	1.23 (0.74, 2.05) 0.4246	1.00 (0.69, 1.45) 0.9978
	T_REC	0.52 (0.15, 1.80) 0.2951	1.42 (0.62, 3.25) 0.4100	3.25 (1.37, 7.72) 0.0050	1.91 (0.82, 4.42) 0.1253	1.53 (0.77, 3.02) 0.2223
<i>TRIB1</i> rs17321515	G_DOM	0.66 (0.41, 1.07) 0.0895	0.56 (0.35, 0.90) 0.015	0.76 (0.41, 1.41) 0.377	0.90 (0.52, 1.55) 0.7112	0.53 (0.36, 0.78) 0.0012
	G_REC	0.59 (0.32, 1.08) 0.0851	0.19 (0.07, 0.47) <0.0001	0.28 (0.10, 0.81) 0.0125	0.35 (0.15, 0.78) 0.0078	0.39 (0.22, 0.68) 0.0007
<i>TRIB1</i> rs2954029	T_DOM	0.61 (0.37, 0.99) 0.0469	0.57 (0.35, 0.93) 0.0229	0.69 (0.38, 1.35) 0.2797	0.79 (0.45, 1.38) 0.401	0.50 (0.33, 0.75) 0.0006
	T_REC	0.64 (0.33, 1.22) 0.1734	0.25 (0.10, 0.59) 0.0007	0.36 (0.12, 1.04) 0.0491	0.34 (0.14, 0.83) 0.0133	0.34 (0.18, 0.63) 0.0004
<i>TBL2</i> rs17145738	T_DOM	0.91 (0.53, 1.57) 0.7304	0.38 (0.20, 0.78) 0.0061	0.53 (0.23, 1.22) 0.1316	0.29 (0.12, 0.69) 0.2929	0.52 (0.31, 0.87) 0.0128
	T_REC	1.12 (0.23, 5.35) 0.8901	0.54 (0.07, 4.37) 0.5579	1.03 (0.13, 8.37) 0.9812	0.32 (0.02, 5.57) 0.7512	0.67 (0.14, 3.19) 0.6128
<i>BAZ1B</i> rs2074755	C_DOM	0.70 (0.40, 1.23) 0.2171	0.43 (0.23, 0.81) 0.0073	0.46 (0.20, 1.06) 0.0739	0.25 (0.10, 0.59) 0.0007	0.41 (0.24, 0.69) 0.0006
	C_REC	0.23 (0.01, 4.07)* 0.1563	0.22 (0.01, 3.94)* 0.1496	0.44 (0.02, 7.81)* 0.3052	0.29 (0.02, 5.22)* 0.2421	0.90 (0.23, 3.57) 0.8919

<i>GCKR</i> rs780094	A_DOM	0.90 (0.56, 1.45) 0.6747	1.32 (0.81, 2.16) 0.2694	1.26 (0.67, 2.38) 0.4793	0.97 (0.58, 1.64) 0.9238	1.82 (1.18, 2.79) 0.0058
	A_REC	0.82 (0.42, 1.60) 0.5657	2.46 (1.47, 4.11) 0.0005	0.88 (0.38, 2.05) 0.7713	1.40 (0.75, 2.62) 0.2891	2.26 (1.46, 3.50) 0.0002
<i>GCKR</i> rs1260326	T_DOM	0.96 (0.58, 1.56) 0.8588	1.31 (0.79, 2.19) 0.2924	1.74 (0.85, 3.53) 0.1249	1.03 (0.60, 1.76) 0.9268	1.68 (1.08, 2.61) 0.0215
	T_REC	1.02 (0.53, 1.95) 0.9502	2.60 (1.52, 4.42) 0.0003	1.25 (0.57, 2.73) 0.5814	1.43 (0.75, 2.73) 0.2727	2.64 (1.67, 4.17) <0.0001
<i>CILP2</i> rs16996148	T_DOM	0.61 (0.31, 1.18) 0.1385	0.64 (0.33, 1.22) 0.1754	0.34 (0.12, 1.00) 0.0406	0.83 (0.43, 1.60) 0.5772	0.48 (0.27, 0.86) 0.0115
		no homozygous T	no homozygous T	no homozygous T	no homozygous T	no homozygous T
<i>SF4</i> rs10401969	C_DOM	0.83 (0.44, 1.57) 0.5682	0.73 (0.38, 1.41) 0.3488	0.19 (0.05, 0.81) 0.013	0.74 (0.36, 1.53) 0.4142	0.42 (0.22, 0.80) 0.007
	C_REC	1.75 (0.16, 19.55) 0.6441	0.67 (0.03, 14.05)* 0.4404	1.26 (0.06, 26.69)* 0.5753	0.87 (0.04, 18.41)* 0.5002	0.41 (0.02, 8.65)* 0.3257
<i>APOE</i> isotype	NON-E3	0.85 (0.53, 1.36) 0.4916	1.52 (0.98, 2.33) 0.0586	180.4 (11.1, 2942)* <0.0001	1.14 (0.71, 1.81) 0.5919	2.04 (1.43, 2.89) <0.0001
<i>LPL</i> p.S447X	X447DOM	1.39 (0.76, 2.56) 0.287	0.90 (0.48, 1.68) 0.7342	1.07 (0.46, 2.51) 0.8712	0.48 (0.20, 1.16) 0.097	0.49 (0.26, 0.94) 0.0302
		no homozygous X	no homozygous X	no homozygous X	no homozygous X	no homozygous X
<i>LPL</i> rs10503669	A_DOM	0.84 (0.44, 1.60) 0.5979	0.83 (0.44, 1.57) 0.57	0.67 (0.27, 1.65) 0.3809	0.34 (0.13, 0.89)* 0.0213	0.36 (0.18, 0.71) 0.0024
	A_REC	no homozygous A	no homozygous A	no homozygous A	13.11 (0.53, 325.19)* 0.0371	no homozygous A
<i>LPL</i> rs17482753	T_DOM	0.97 (0.53, 1.79) 0.9253	0.91 (0.49, 1.67) 0.7584	0.82 (0.37, 1.85) 0.6385	0.26 (0.09, 0.73) 0.0066	0.34 (0.17, 0.68) 0.0013
	T_REC	1.17 (0.05, 29.00)* 0.5946	1.11 (0.04, 27.45)* 0.5844	2.03 (0.08, 50.65)* 0.687	4.36 (0.27, 70.55) 0.2579	0.68 (0.03, 16.86)* 0.4854
<i>LPL</i> rs6993414	G_DOM	0.95 (0.52, 1.75) 0.8765	0.80 (0.42, 1.51) 0.4938	0.77 (0.33, 1.81) 0.5488	0.38 (0.15, 0.99) 0.0408	0.47 (0.22, 0.78) 0.0055
	G_REC	3.60 (0.50, 25.94) 0.1744	0.69 (0.03, 14.58)* 0.4489	3.45 (0.31, 38.76) 0.2867	0.86 (0.04, 18.01)* 0.4955	0.42 (0.02, 8.78)* 0.3295
<i>ANGPTL3</i> rs12130333	T_DOM	0.75 (0.46, 1.22) 0.2473	0.73 (0.45, 1.18) 0.1971	0.87 (0.47, 1.62) 0.6559	0.75 (0.44, 1.28) 0.2929	0.69 (0.46, 1.04) 0.0738
	T_REC	0.70 (0.20, 2.40) 0.5637	0.92 (0.30, 2.76) 0.8775	0.88 (0.20, 3.89) 0.8638	1.20 (0.39, 3.62) 0.7512	0.28 (0.06, 1.20) 0.0676
<i>ANGPTL3</i> rs1748195	G_DOM	0.93 (0.58, 1.49) 0.7651	0.70 (0.44, 1.11) 0.1278	0.60 (0.32, 1.11) 0.1037	1.02 (0.60, 1.71) 0.9483	0.47 (0.32, 0.70) 0.0002
	G_REC	0.63 (0.27, 1.47) 0.2822	1.00 (0.49, 2.06) 0.9907	0.33 (0.08, 1.43) 0.121	1.09, (0.50, 2.37) 0.8341	0.26 (0.10, 0.67) 0.003

<i>GALNT2</i> rs4846914	G_DOM	0.85 (0.53, 1.37) 0.5079	0.97 (0.60, 1.56) 0.8963	0.80 (0.44, 1.47) 0.4756	1.06 (0.62, 1.83) 0.829	1.24 (0.82, 1.88) 0.3019
	G_REC	0.80 (0.40, 1.58) 0.5158	1.03 (0.55, 1.93) 0.9348	1.81 (0.89, 3.64) 0.0956	1.57 (0.84, 2.96) 0.1584	2.17 (1.38, 3.42) 0.0007
<i>PSRC1</i> rs599839	G_DOM	0.60 (0.36, 1.01) 0.0539	0.57 (0.34, 0.96) 0.0348	1.07 (0.57, 1.99) 0.8403	1.02 (0.60, 1.74) 0.9371	1.23 (0.83, 1.83) 0.2941
	G_REC	1.33 (0.47, 3.92) 0.5682	0.77 (0.21, 2.76) 0.6878	1.52 (0.42, 5.55) 0.5211	0.67 (0.15, 3.05) 0.604	1.10 (0.43, 2.80) 0.8493
<i>LDLR</i> rs6511720	T_DOM	0.77 (0.44, 1.33) 0.3467	0.50 (0.27, 0.92) 0.0235	0.71 (0.34, 1.50) 0.3721	0.71 (0.38, 1.32) 0.2743	0.64 (0.40, 1.03) 0.0656
	T_REC	0.50 (0.03, 9.81)* 0.357	0.48 (0.02, 9.29)* 0.3438	2.28 (0.23, 22.34) 0.4685	1.50 (0.15, 14.59) 0.7275	2.81 (0.62, 12.71) 0.1618
<i>APOB</i> rs693	T_DOM	0.87 (0.51, 1.46) 0.5888	1.49 (0.84, 2.63) 0.173	0.95 (0.48, 1.88) 0.8773	0.90 (0.50, 1.60) 0.7122	0.94 (0.61, 1.45) 0.7747
	T_REC	1.04 (0.61, 1.79) 0.878	1.22 (0.73, 2.05) 0.4403	1.01 (0.50, 2.04) 0.9716	0.75 (0.39, 1.41) 0.3676	1.10 (0.71, 1.71) 0.6635
<i>SELP</i> rs3917820	A_DOM	0.91 (0.53, 1.58) 0.7405	0.68 (0.38, 1.21) 0.1902	0.56 (0.24, 1.30) 0.1719	0.91 (0.49, 1.68) 0.7578	1.08 (0.70, 1.68) 0.7239
	A_REC	no homozygous A	no homozygous A	no homozygous A	14.2 (0.57, 354.0)* 0.0298	no homozygous A
<i>LIPC</i> rs4775041	C_DOM	1.15 (0.72, 1.85) 0.5413	1.42 (0.90, 2.28) 0.1331	0.90 (0.49, 1.64) 0.7213	0.50 (0.29, 0.86) 0.0108	1.14 (0.77, 1.68) 0.5054
	C_REC	1.05 (0.50, 2.24) 0.8851	0.79 (0.35, 1.77) 0.56	0.96 (0.36, 2.59) 0.937	0.79 (0.32, 1.97) 0.6165	1.29 (0.71, 2.33) 0.3979

Abbreviations: as in Table 2; DOM, dominant model evaluated for minor allele as indicated; REC, recessive model evaluated for minor allele as indicated; shown are odds ratios with 95% confidence intervals in parentheses followed by P-values.

Table S4. Linkage disequilibrium correlation coefficients of SNP genotypes studied**Chromosome 11 apolipoprotein gene cluster**

	<i>BUD13</i> rs964184	<i>APOA5</i> rs12286037	<i>APOA5</i> rs6589566	<i>APOA5</i> -1131T>C	<i>APOA5</i> p.S19W	<i>APOC3</i> -482C>T
<i>BUD13</i> rs28927680	0.5319	0.9053*	0.0689	0.0320	0.9244*	0.0449
<i>BUD13</i> rs964184		0.6388*	0.6880*	0.6192*	0.6089	0.1263
<i>APOA5</i> rs12286037			0.0793	0.0503	0.9529*	0.1247
<i>APOA5</i> rs6589566				0.8865*	0.0471	0.2859
<i>APOA5</i> -1131T>C					0.0543	0.2514
<i>APOA5</i> p.S19W						0.0044

Lipoprotein lipase gene locus

	<i>LPL</i> rs17482753	<i>LPL</i> rs10503669	<i>LPL</i> rs6993414
<i>LPL</i> p.S447X	0.7026*	0.5485*	0.6036*
<i>LPL</i> rs17482753		0.9577*	0.9086*
<i>LPL</i> rs10503669			0.9449*

Tribbles 1 gene locus

	<i>TRIB1</i> rs2954029
<i>TRIB1</i> rs17321515	0.9452*

Glucokinase receptor gene locus

	<i>GCKR</i> rs1260326
<i>GCKR</i> rs780094	0.9456*

Angiotensin like 3 gene locus

	<i>ANGPTL3</i> rs1748195
<i>ANGPTL3</i> rs12130333	0.6858*

Chromosome 7 gene locus

	<i>BAZ1B</i> rs2074755
<i>TBL2</i> rs17145738	0.9653*

Abbreviations: as in Table 2; *P<0.0001