Supplemental Data

# Gene-centric Association Signals for Lipids

and Apolipoproteins Identified

via the HumanCVD BeadChip

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Figure S1. Population Structure

ANALYSIS 1: A multidimensional scaling plot based on the pairwise Identity-By-State distances of all QC-passed samples (5441) and SNPs (48032)
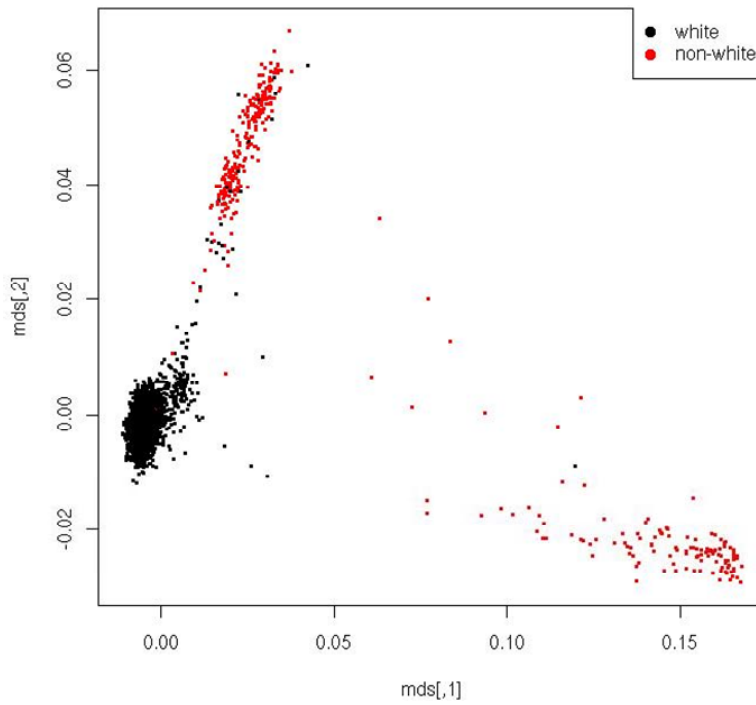
ANALYSIS 2: A multidimensional scaling plot based on the pairwise Identity-By-State distances of Caucasian samples (5067), showing 8 outliers circled in red.
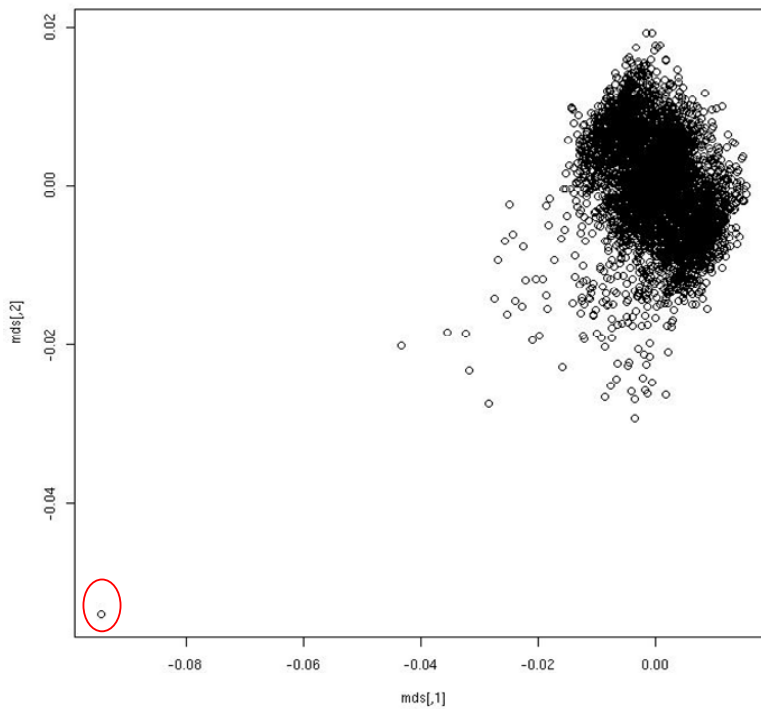
Figure S2 . Heat plot reflecting the relationship between the five traits with SNPs that that were significant at the cut-off of 10^{-5} for at least one of the traits. White shows the strongest association m, red the weakest.
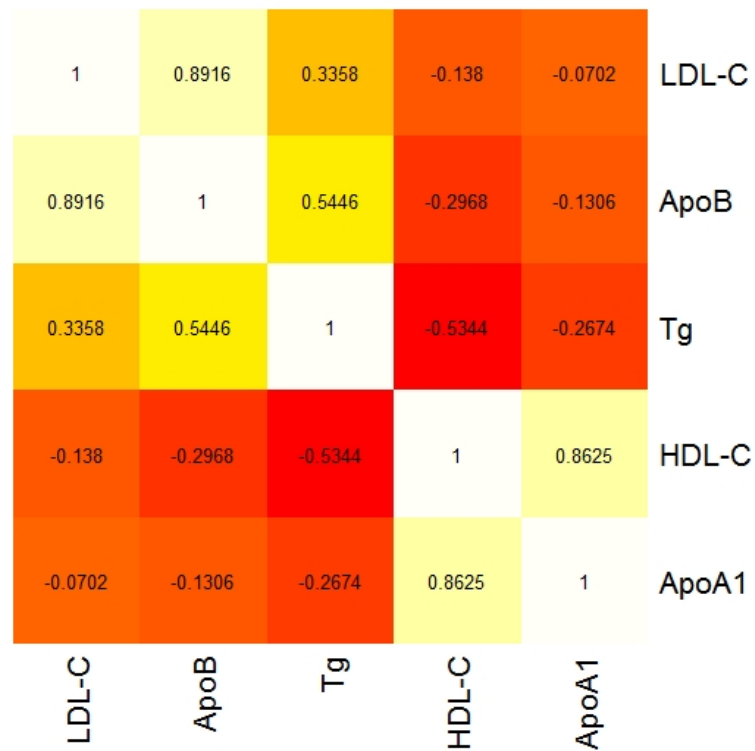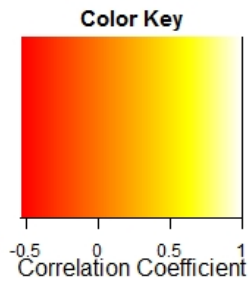
Figure S3a Haploview plots for ApoB showing the SNPs significant by univariate analysis (at $p<10^{-5}$) and those retained after variable selection (red boxes). For the Chromosome 19 *APOE* locus those SNPs in orange are no longer retained when the *APOE* rs rs429358 and rs7412defining the common alleles were included into the analysis
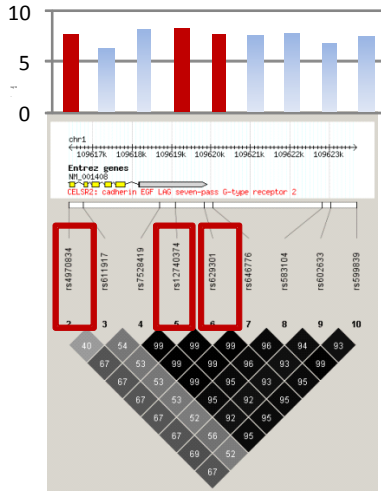
Chr1 *CELSR2*
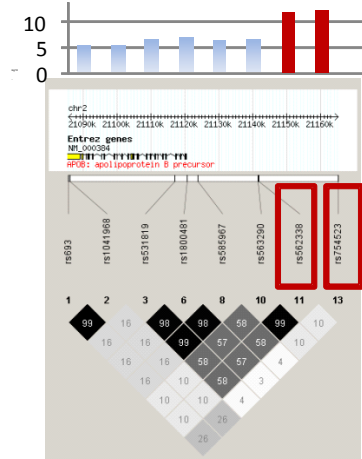
Chr2 *APOB*
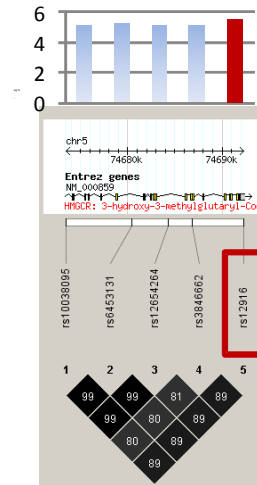
Chr5 *HMGCR*
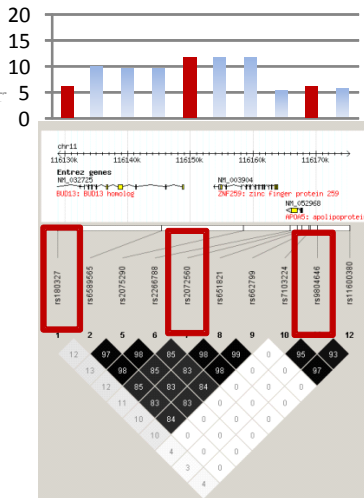
Chr11 *BUD13/ZNF259/APOA5*
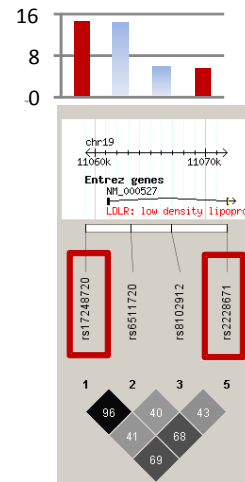
Chr19 *LDLR*
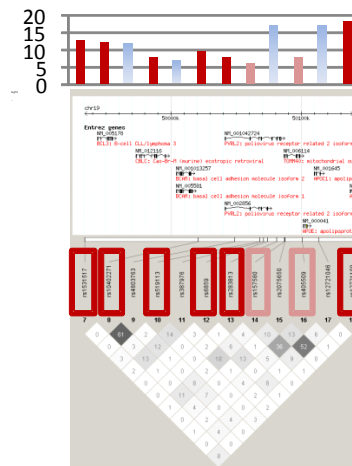
Chr19 *APOE* cluster

Figure S3b. Haploview plots for ApoAI showing the SNPs significant by univariate analysis (at $p<10^{-5}$) and those retained after variable selection (red boxes)

Chr15 *LIPC*

Chr16 *CETP*
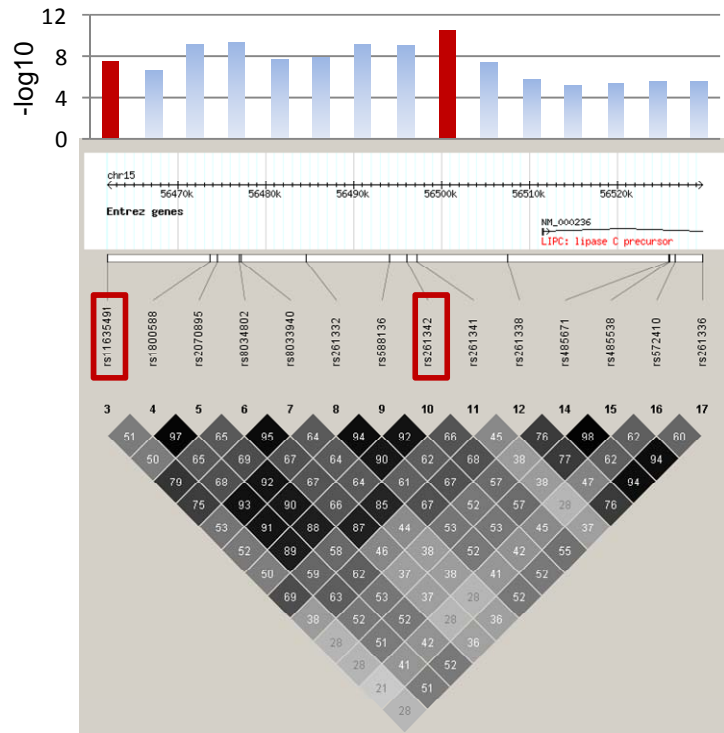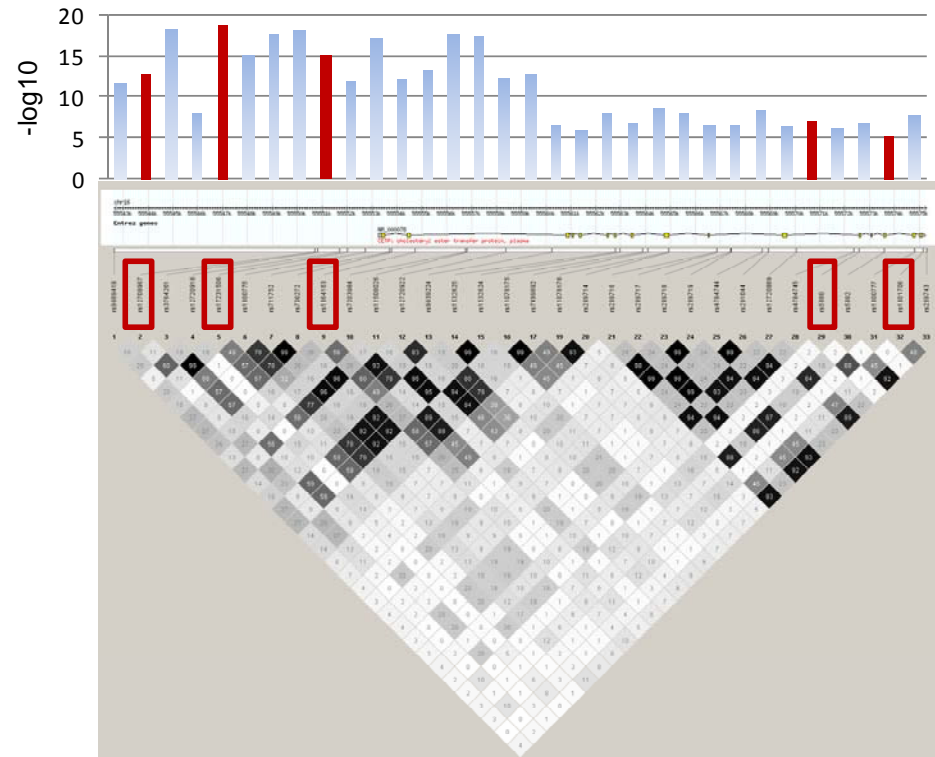
Figure S4. Frequency distribution of the gene count score and the effect of gene score on a) HDL-C, b) ApoAI, c) apoB, d) apoB/apoAI. The odds ratio for occupancy of the extreme 10% of the trait distribution at different cut points of the respective gene score distributions are presented below each histogram. The medians (interquartile ranges) of the gene counts were 28 (26-30) for apoB, 12 (10-14) for HDL-C, 10 (8-11) for apoAI, and 25 (24-26) for apoB/apoAI.
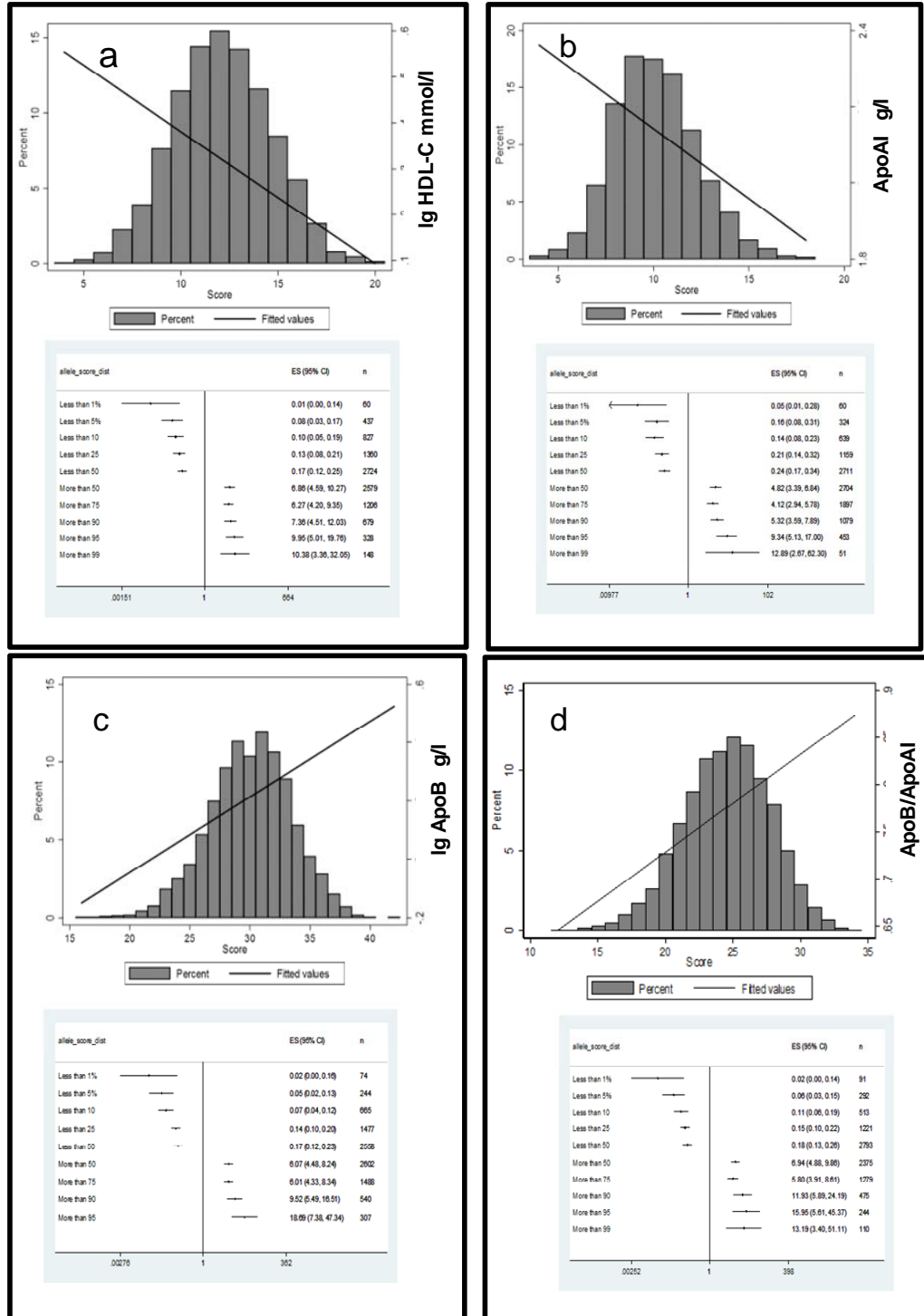
Figure S5a-d The figures shows the SNP coverage of the IBC CVD chip compared to the Illumina 550K, Illumina 300K and Affy5.0 GWAS chips using the UCSC Genome Browser (http://genome.ucsc.edu/). The IBC CVD chip has much denser coverage for loci with a high likelihood of functional significance and candidate loci that are potentially involved in phenotypes of interest

a) *SH2B3* locus
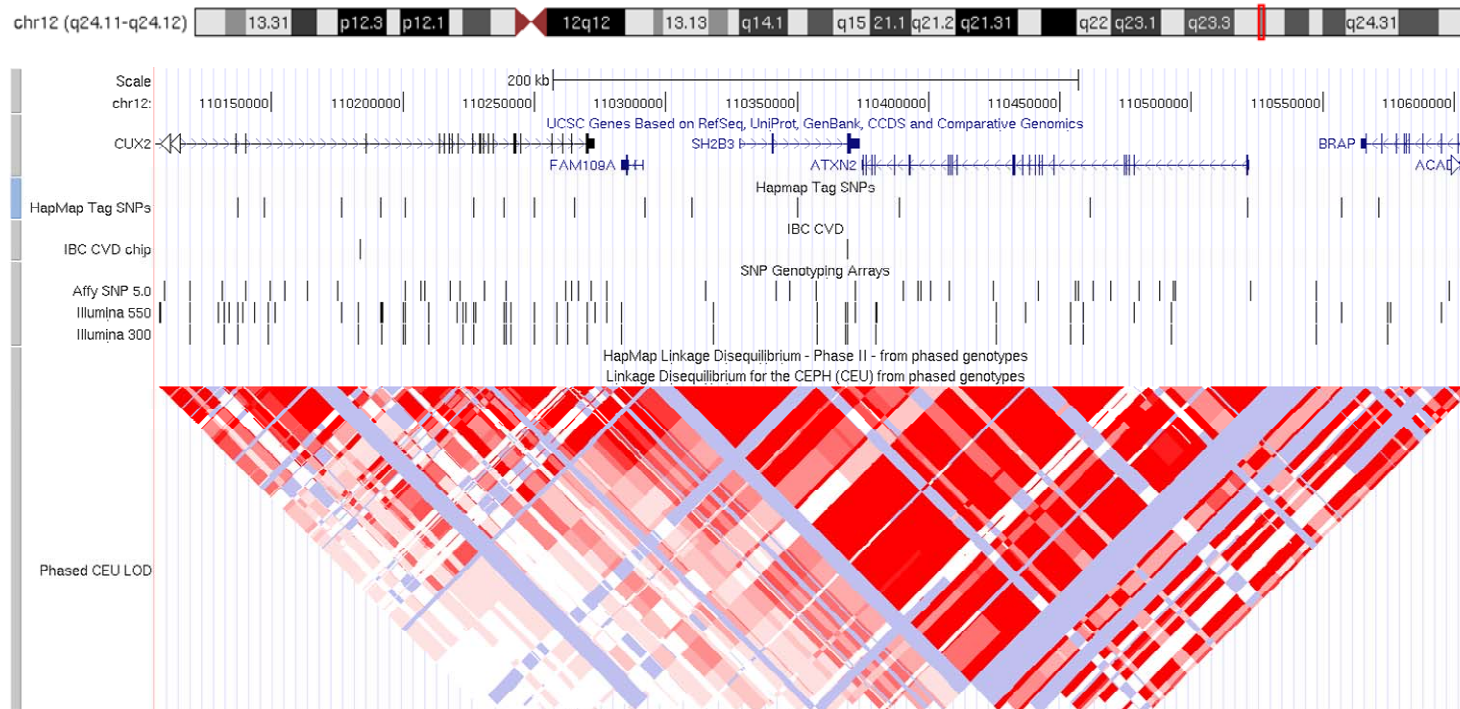
chr12:110,105,771-110,608,345

b) *APOE* locus

Chr19:49,921,182-50,164,991

c) *LDLR* locus
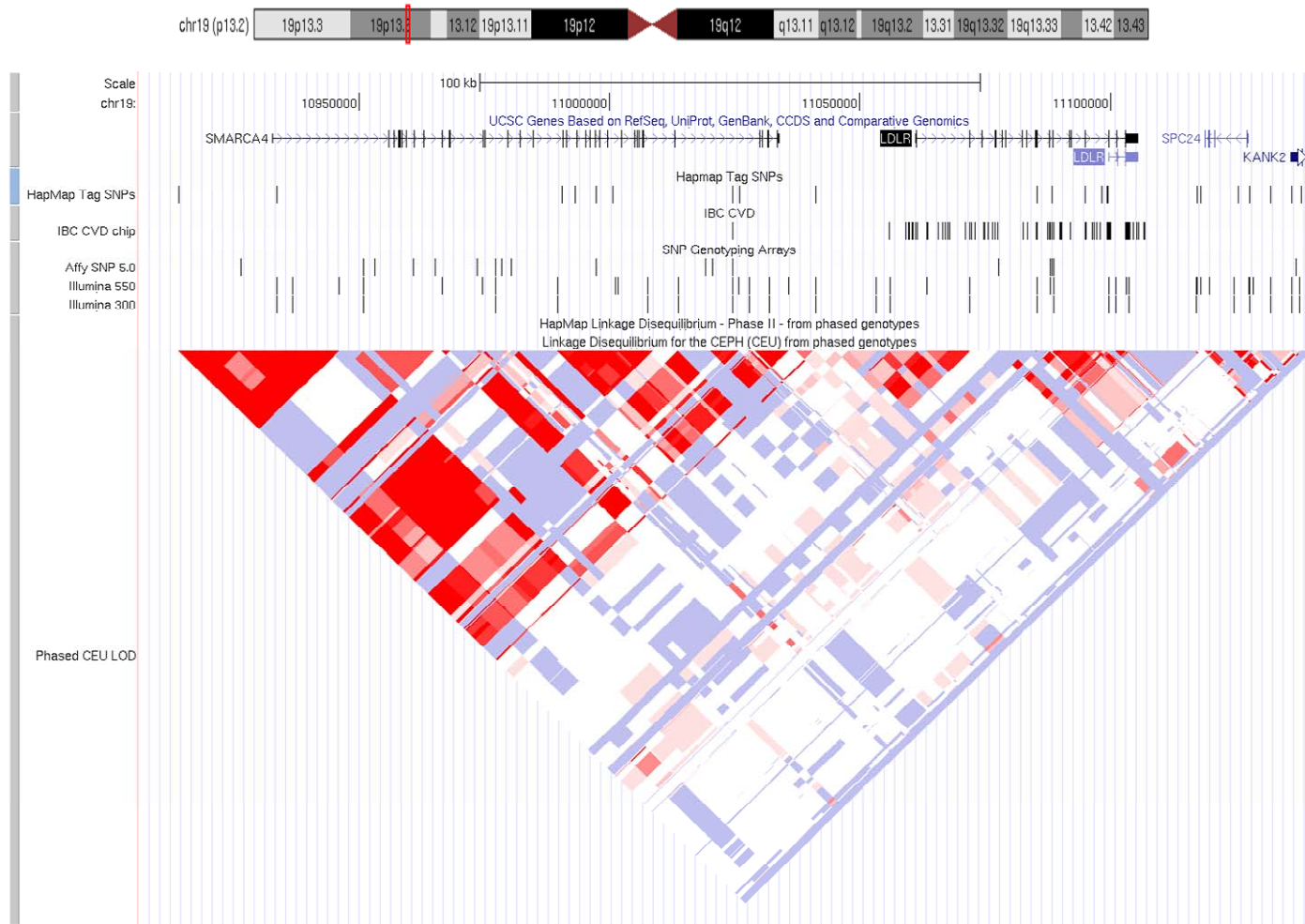
chr19:10,906,104-11,141,894

d) *BMPR2* locus

chr2:202,949,295 -203,140,719
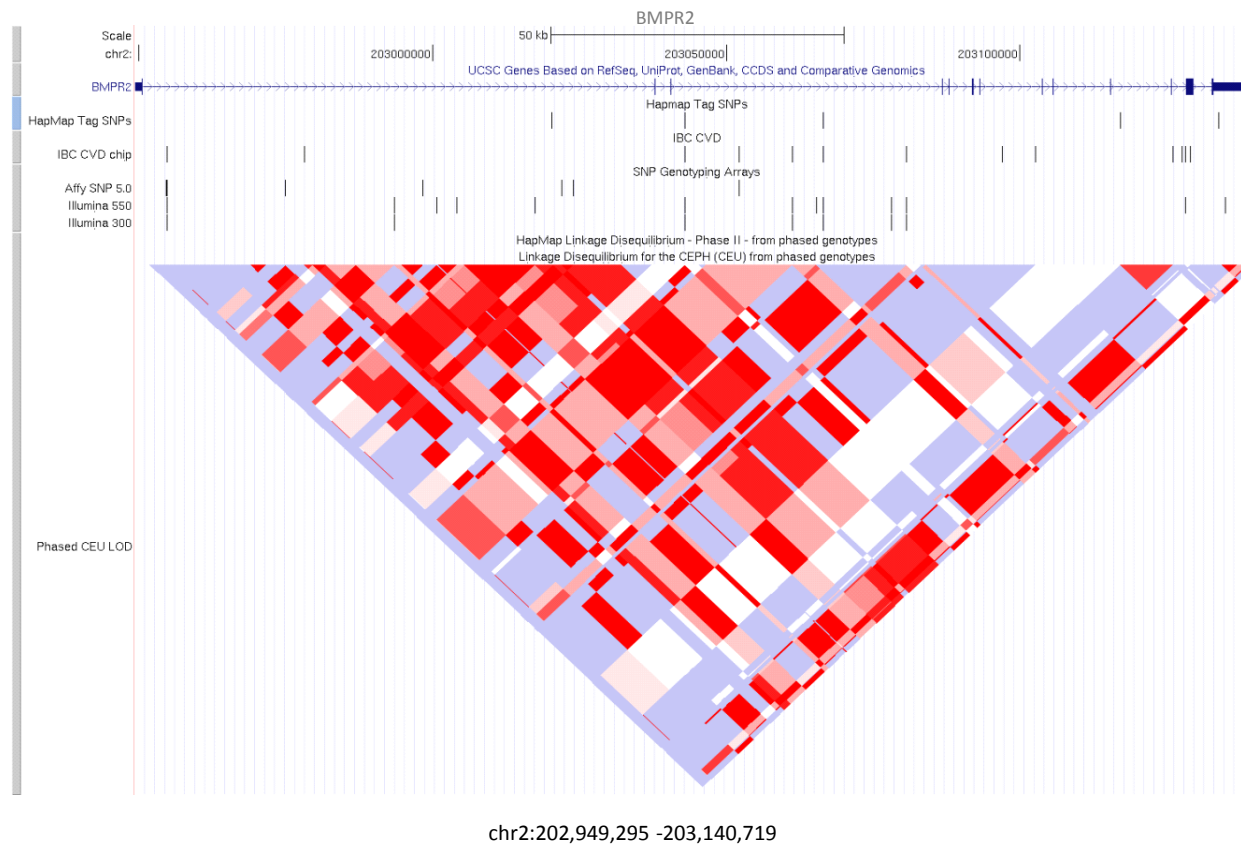
Table S1. Details of the five studies used in the meta-analyses and genotyping methodology

	Whitehall II [1]	BWHHS [2]	BRIGHT[3]	ASCOT[4]	NORDIL [5]
Design	Prospective observational	Prospective observational	Cases (from case-control)	DNA repository from randomized trial	DNA repository from randomized trial
n	5058	3313	1751, but see below	1262, but see below	1935
Males (%)	73.5	0	40	82	50.5
Mean age (yrs)	49	69	58	63	56
Proportion receiving lipid lowering medication (%)	0.8	7	11.3	12.6	not analysed
Genotyping platform	IBC chip	IBC chip	IBC chip	IBC chip	IBC chip
Calling algorithm	Gencall	Gencall	Illuminus	Illuminus	Illuminus
Contribution to current analysis	Index study	Meta-analysis	Meta-analysis	Meta-analysis	Meta-analysis

BRIGHT and ASCOT

Sample sizes for BRIGHT are as follows:

without age/sex covariates: 1646 for LDL-C, and 1751 for other lipid phenotypes

with age/sex covariates: 1599 for LDL-C, and 1700 for other lipid phenotypes

Sample sizes for ASCOT are as follows:

1169 for LDL-C, 1192 for TG, and 1262 for HDLC

For both BRIGHT and ASCOT, % males, mean age and % on LLA were calculated using largest

sample size (resp. 1751 and 1262)

References

1. Marmot,M.G., Smith,G.D., Stansfeld,S., Patel,C., North,F., Head,J., White,I., Brunner,E., and Feeney,A. (1991). Health inequalities among British civil servants: the Whitehall II study. Lancet *337*, 1387-1393

2. Lawlor,D.A., Bedford,C., Taylor,M., and Ebrahim,S. (2003). Geographical variation in cardiovascular disease, risk factors, and their control in older women: British Women's Heart and Health Study. J. Epidemiol. Community Health *57*, 134-140

3. Caulfield,M., Munroe,P., Pembroke,J., Samani,N., Dominiczak,A., Brown,M., Benjamin,N., Webster,J., Ratcliffe,P., O'Shea,S. et al. (2003). Genome-wide mapping of human loci for essential hypertension. Lancet *361*, 2118-2123

4. Sever,P.S., Dahlof,B., Poulter,N.R., Wedel,H., Beevers,G., Caulfield,M., Collins,R., Kjeldsen,S.E., McInnes,G.T., Mehlsen,J. et al. (2001). Rationale, design, methods and baseline demography of participants of the Anglo-Scandinavian Cardiac Outcomes Trial. ASCOT investigators. J. Hypertens. *19*, 1139-1147

5. Hansson,L., Hedner,T., Lund-Johansen,P., Kjeldsen,S.E., Lindholm,L.H., Syvertsen,J.O., Lanke,J., de,F.U., Dahlof,B., and Karlberg,B.E. (2000). Randomised trial of effects of calcium antagonists compared with diuretics and beta-blockers on cardiovascular morbidity and mortality in hypertension: the Nordic Diltiazem (NORDIL) study. Lancet *356*, 359-365

Table S2. SNP p Values Adjusted for Age and Gender for the 195 SNPs Associated with Lipid Traits

Excel file available online at http://www.cell.com/AJHG.

Table S3a. All SNPs significantly associated with LDL-C

SNP	CHR	BP	GENE	Alleles		MAF	Common HMZ mean mmol/l	HTZ mean mmol/l	Rare HMZ mean mmol/l	Beta	P-value	R2 (univariate)	Chr R2
				1	2								
rs11591147	1	55278235	PCSK9	C	A	0.02	4.38	3.84	2.98	-0.55	9.28E-12	6.98E-02	0.07
rs4970834	1	109616403	CELSR2	G	A	0.18	4.42	4.27	4.08	-0.16	5.18E-09		
rs611917	1	109616775	CELSR2	A	G	0.31	4.44	4.31	4.26	-0.11	1.97E-06		
rs7528419	1	109618715	CELSR2	A	G	0.21	4.43	4.27	4.14	-0.15	2.41E-09		
rs12740374	1	109619113	CELSR2	C	A	0.21	4.43	4.28	4.12	-0.15	1.82E-09		
rs629301	1	109619829	CELSR2	A	C	0.21	4.43	4.28	4.14	-0.15	6.50E-09		
rs646776	1	109620053	PSRC1	A	G	0.21	4.43	4.28	4.14	-0.14	1.03E-08		
rs583104	1	109622830	PSRC1	A	C	0.22	4.43	4.28	4.15	-0.14	1.15E-08		
rs602633	1	109623034	PSRC1	C	A	0.20	4.43	4.27	4.17	-0.14	3.15E-08		
rs599839	1	109623689	PSRC1	A	G	0.22	4.42	4.29	4.16	-0.14	4.31E-08		
rs693	2	21085700	APOB	A	G	0.48	4.48	4.34	4.27	-0.11	3.86E-08	7.05E-02	0.07
rs1041968	2	21086309	APOB	A	G	0.48	4.48	4.34	4.27	-0.11	5.32E-08		
rs10199768	2	21097505	APOB	C	A	0.44	4.29	4.36	4.49	0.10	6.58E-07		
rs531819	2	21117144	APOB	C	A	0.15	4.41	4.26	4.11	-0.16	4.91E-08		
rs1367117	2	21117405	APOB	G	A	0.33	4.30	4.39	4.53	0.12	2.63E-08		
rs12714264	2	21119023	APOB	T	A	0.13	4.41	4.26	4.09	-0.16	1.23E-07		
rs1800481	2	21120715	APOB	G	A	0.15	4.41	4.26	4.10	-0.16	4.95E-08		
rs934197	2	21120966	APOB	G	A	0.33	4.30	4.40	4.53	0.12	3.43E-08		
rs585967	2	21124059	APOB	C	A	0.15	4.41	4.26	4.10	-0.16	3.28E-08		
rs7575840	2	21126995	APOB	C	A	0.35	4.30	4.38	4.56	0.12	7.84E-08		
rs563290	2	21141731	APOB	A	G	0.18	4.43	4.23	4.20	-0.18	1.33E-11		
rs562338	2	21141826	APOB	G	A	0.18	4.43	4.24	4.16	-0.18	1.21E-11		
rs754524	2	21165046	APOB	A	C	0.28	4.31	4.40	4.57	0.12	1.69E-07		
rs754523	2	21165196	APOB	A	G	0.33	4.30	4.37	4.60	0.13	2.86E-09		
rs4299376	2	43926080	ABCG8	A	C	0.32	4.28	4.42	4.53	0.13	8.70E-10		
rs10038095	5	74673467	HMGCR	A	T	0.38	4.28	4.40	4.51	0.12	4.29E-08	5.87E-02	0.06
rs10474434	5	74680437	HMGCR	C	A	0.23	4.31	4.42	4.57	0.12	2.05E-06		
rs6453131	5	74680462	HMGCR	A	C	0.38	4.27	4.40	4.50	0.11	4.59E-08		
rs17238484	5	74684252	HMGCR	C	A	0.23	4.31	4.43	4.57	0.12	1.79E-06		
rs12654264	5	74684359	HMGCR	T	A	0.38	4.27	4.40	4.50	0.11	5.76E-08		
rs3846662	5	74686840	HMGCR	A	G	0.43	4.27	4.38	4.49	0.11	5.17E-08		

rs12916	5	74692295	*HMGCR*	A	G	0.41	4.26	4.39	4.51	0.12	6.66E-09		
rs3804231	5	74732535	*COL4A3BP*	G	A	0.13	4.33	4.46	4.62	0.14	5.15E-06		
rs4704220	5	74793312	*COL4A3BP*	G	A	0.39	4.30	4.38	4.49	0.09	8.05E-06		
rs6589565	11	116145447	*BUD13*	G	A	0.07	4.34	4.50	4.94	0.19	3.33E-06	5.63E-02	0.06
rs2075290	11	116158506	*ZNF259*	A	G	0.07	4.34	4.49	4.94	0.18	6.05E-06		
rs2266788	11	116165896	*APOA5*	A	G	0.07	4.34	4.49	4.94	0.18	5.43E-06		
rs2072560	11	116167036	*APOA5*	G	A	0.06	4.34	4.51	5.33	0.22	2.36E-07		
rs651821	11	116167789	*APOA5*	A	G	0.06	4.34	4.50	5.33	0.21	6.90E-07		
rs662799	11	116168917	*APOA4*	A	G	0.06	4.34	4.50	5.33	0.21	7.19E-07		
rs3764261	16	55550825	*CETP*	C	A	0.33	4.43	4.33	4.23	-0.11	1.06E-06	5.61E-02	0.06
rs17231506	16	55552029	*CETP*	G	A	0.32	4.44	4.33	4.22	-0.11	5.02E-07		
rs1529729	19	11024562	*SMARCA4*	A	G	0.45	4.28	4.39	4.44	0.09	6.71E-06	1.11E-01	0.11
rs17248720	19	11059187	*LDLR*	G	A	0.13	4.45	4.14	3.81	-0.31	7.86E-25		
rs6511720	19	11063306	*LDLR*	C	A	0.13	4.45	4.14	3.85	-0.30	7.30E-24		
rs8102912	19	11066975	*LDLR*	G	A	0.23	4.44	4.26	4.19	-0.16	2.24E-11		
rs8110695	19	11067530	*LDLR*	T	A	0.22	4.43	4.27	4.21	-0.14	1.12E-08		
rs2228671	19	11071912	*LDLR*	G	A	0.13	4.42	4.21	4.18	-0.18	6.52E-10		
rs2569559	19	11075533	*LDLR*	A	C	0.23	4.43	4.27	4.22	-0.14	1.74E-08		
rs1531517	19	49934013	*BCL3*	G	A	0.07	4.40	4.17	4.08	-0.22	6.26E-08		
rs10402271	19	50021054	*PVRL2*	A	C	0.33	4.26	4.44	4.53	0.15	2.06E-12		
rs4803763	19	50049131	*PVRL2*	G	C	0.26	4.29	4.43	4.58	0.15	2.20E-10		
rs519113	19	50068124	*PVRL2*	C	G	0.24	4.42	4.31	4.18	-0.12	9.37E-07		
rs387976	19	50070900	*PVRL2*	A	C	0.35	4.43	4.34	4.22	-0.10	5.98E-06		
rs6859	19	50073874	*PVRL2*	G	A	0.41	4.27	4.38	4.52	0.12	3.53E-08		
rs283813	19	50081014	*PVRL2*	T	A	0.07	4.39	4.23	3.70	-0.19	2.51E-06		
rs157580	19	50087106	*TOMM40*	A	G	0.40	4.47	4.34	4.21	-0.11	1.03E-07		
rs2075650	19	50087459	*TOMM40*	A	G	0.14	4.31	4.51	4.87	0.23	1.14E-14		
rs12721046	19	50113094	*APOC1*	G	A	0.15	4.30	4.51	4.74	0.21	7.58E-14		
rs12721109	19	50139061	*APOC2*	G	A	0.02	4.39	3.82	4.32	-0.54	5.06E-14		

HMZ, homozygote ; HTZ, heterozygote

Table S3b. All SNPs significantly associated with ApoB

SNP	CHR	BP	GENE	Alleles		MAF	Common HMZ mean g/l	HTZ mean g/l	Rare HMZ mean g/l	Beta	P-value	R2 (univariate)	Chr R2
				1	2								
rs11591147	1	55278235	PCSK9	C	A	0.02	1.28	1.14	0.94	-0.12	1.89E-10	7.91E-03	0.08
rs4970834	1	109616403	CELSR2	G	A	0.18	1.29	1.25	1.18	-0.03	2.00E-08	6.00E-03	
rs611917	1	109616775	CELSR2	A	G	0.31	1.29	1.25	1.23	-0.03	6.69E-07	4.86E-03	
rs7528419	1	109618715	CELSR2	A	G	0.21	1.29	1.25	1.19	-0.03	8.09E-09	6.92E-03	
rs12740374	1	109619113	CELSR2	C	A	0.21	1.29	1.25	1.19	-0.03	4.70E-09	7.18E-03	
rs629301	1	109619829	CELSR2	A	C	0.21	1.29	1.25	1.19	-0.03	1.76E-08	6.67E-03	
rs646776	1	109620053	PSRC1	A	G	0.21	1.29	1.25	1.19	-0.03	2.40E-08	6.55E-03	
rs583104	1	109622830	PSRC1	A	C	0.22	1.29	1.25	1.19	-0.03	2.18E-08	6.37E-03	
rs602633	1	109623034	PSRC1	C	A	0.20	1.29	1.25	1.20	-0.03	2.21E-07	5.64E-03	
rs599839	1	109623689	PSRC1	A	G	0.22	1.29	1.25	1.20	-0.03	4.79E-08	5.96E-03	
rs693	2	21085700	APOB	A	G	0.48	1.29	1.27	1.25	-0.02	5.69E-06	3.06E-03	0.08
rs1041968	2	21086309	APOB	A	G	0.48	1.29	1.27	1.25	-0.02	7.80E-06	2.95E-03	
rs531819	2	21117144	APOB	C	A	0.15	1.28	1.25	1.20	-0.03	3.21E-07	4.55E-03	
rs12714264	2	21119023	APOB	T	A	0.13	1.28	1.24	1.21	-0.04	1.60E-07	4.64E-03	
rs1800481	2	21120715	APOB	G	A	0.15	1.28	1.25	1.19	-0.03	7.41E-07	4.36E-03	
rs585967	2	21124059	APOB	C	A	0.15	1.28	1.24	1.20	-0.03	2.48E-07	4.63E-03	
rs563290	2	21141731	APOB	A	G	0.18	1.29	1.23	1.20	-0.04	7.38E-13	9.29E-03	
rs562338	2	21141826	APOB	G	A	0.18	1.29	1.24	1.19	-0.04	6.00E-13	9.24E-03	
rs754523	2	21165196	APOB	A	G	0.33	1.25	1.27	1.32	0.02	1.11E-06	4.15E-03	
rs4299376	2	43926080	ABCG8	A	C	0.32	1.25	1.28	1.32	0.03	7.60E-08	5.74E-03	
rs10038095	5	74673467	HMGCR	A	T	0.38	1.25	1.28	1.31	0.02	8.05E-06	3.98E-03	0.07
rs6453131	5	74680462	HMGCR	A	C	0.38	1.25	1.28	1.31	0.02	6.34E-06	4.07E-03	
rs12654264	5	74684359	HMGCR	T	A	0.38	1.25	1.28	1.30	0.02	9.25E-06	3.90E-03	
rs3846662	5	74686840	HMGCR	A	G	0.43	1.25	1.27	1.30	0.02	8.57E-06	3.86E-03	
rs12916	5	74692295	HMGCR	A	G	0.41	1.25	1.27	1.31	0.02	3.34E-06	4.56E-03	
rs180327	11	116128869	BUD13	A	G	0.36	1.24	1.29	1.29	0.02	7.70E-07	5.02E-03	0.08
rs6589565	11	116145447	BUD13	G	A	0.07	1.26	1.33	1.46	0.06	2.01E-10	7.59E-03	
rs2075290	11	116158506	ZNF259	A	G	0.07	1.26	1.33	1.46	0.06	4.73E-10	7.23E-03	
rs2266788	11	116165896	APOA5	A	G	0.07	1.26	1.33	1.45	0.06	3.42E-10	7.34E-03	

rs2072560	11	116167036	*APOA5*	G	A	0.06	1.26	1.34	1.58	0.07	1.40E-12	9.10E-03	
rs651821	11	116167789	*APOA5*	A	G	0.06	1.26	1.33	1.58	0.07	3.55E-12	8.69E-03	
rs662799	11	116168917	*APOA4*	A	G	0.06	1.26	1.33	1.58	0.07	5.18E-12	8.77E-03	
rs7103224	11	116169176	*APOA4*	G	A	0.08	1.28	1.22	1.28	-0.04	7.82E-06	3.98E-03	
rs9804646	11	116170289	*APOA4*	G	A	0.09	1.28	1.22	1.22	-0.04	1.25E-06	4.49E-03	
rs11600380	11	116175392	*APOA4*	A	G	0.08	1.28	1.22	1.26	-0.04	5.19E-06	4.02E-03	
rs3764261	16	55550825	*CETP*	C	A	0.33	1.29	1.26	1.23	-0.02	1.52E-06	4.32E-03	0.07
rs17231506	16	55552029	*CETP*	G	A	0.32	1.29	1.26	1.23	-0.02	1.36E-06	4.41E-03	
rs17248720	19	11059187	*LDLR*	G	A	0.13	1.29	1.22	1.14	-0.06	2.10E-15	1.22E-02	0.13
rs6511720	19	11063306	*LDLR*	C	A	0.13	1.29	1.22	1.15	-0.05	6.77E-15	1.18E-02	
rs8102912	19	11066975	*LDLR*	G	A	0.23	1.29	1.25	1.24	-0.03	1.26E-06	4.01E-03	
rs2228671	19	11071912	*LDLR*	G	A	0.13	1.28	1.24	1.23	-0.03	5.00E-06	4.22E-03	
rs1531517	19	49934013	*BCL3*	G	A	0.07	1.28	1.20	1.15	-0.07	1.96E-13	1.05E-02	
rs10402271	19	50021054	*PVRL2*	A	C	0.33	1.24	1.29	1.32	0.04	7.05E-13	9.93E-03	
rs4803763	19	50049131	*PVRL2*	G	C	0.26	1.25	1.29	1.34	0.04	2.75E-12	9.45E-03	
rs519113	19	50068124	*PVRL2*	C	G	0.24	1.29	1.25	1.22	-0.03	2.14E-08	6.27E-03	
rs387976	19	50070900	*PVRL2*	A	C	0.35	1.29	1.26	1.22	-0.03	1.54E-07	5.86E-03	
rs6859	19	50073874	*PVRL2*	G	A	0.41	1.24	1.28	1.32	0.03	1.49E-10	9.21E-03	
rs283813	19	50081014	*PVRL2*	T	A	0.07	1.28	1.23	1.09	-0.05	2.61E-08	5.41E-03	
rs157580	19	50087106	*TOMM40*	A	G	0.40	1.30	1.26	1.23	-0.02	6.55E-07	6.92E-03	
rs2075650	19	50087459	*TOMM40*	A	G	0.14	1.25	1.31	1.45	0.06	8.38E-18	1.50E-02	
rs405509	19	50100676	*APOE;PKP2*	C	A	0.48	1.25	1.27	1.30	0.03	1.89E-08	5.06E-03	
rs12721046	19	50113094	*APOC1*	G	A	0.15	1.25	1.32	1.41	0.06	1.01E-17	1.55E-02	
rs12721109	19	50139061	*APOC2*	G	A	0.02	1.28	1.10	1.05	-0.15	3.88E-19	1.67E-02	

HMZ, homozygote ; HTZ, heterozygote

Table S3c. All SNPs significantly associated with Triglycerides

SNP	CHR	BP	GENE	Alleles		MAF	Common HMZ mean mmol/l	HTZ mean mmol/l	Rare HMZ mean mmol/l	Beta	P-value	R2 (univariate)	Chr R2
				1	2								
rs1260326	2	27584444	*GCKR*	G	A	0.40	1.38	1.43	1.63	0.06	1.83E-07	5.67E-03	0.06
rs714052	7	72502805	*BAZ1B*	A	G	0.12	1.48	1.33	1.29	-0.09	4.38E-07	4.88E-03	0.07
rs2074755	7	72515102	*BAZ1B*	A	G	0.12	1.48	1.33	1.29	-0.09	2.94E-07	4.97E-03	
rs17145713	7	72542746	*BAZ1B*	G	A	0.20	1.50	1.36	1.25	-0.09	5.29E-10	7.11E-03	
rs12539316	7	72615834	*TBL2*	A	G	0.29	1.49	1.41	1.33	-0.05	9.39E-06	3.78E-03	
rs2286276	7	72625290	*TBL2*	G	A	0.29	1.49	1.41	1.33	-0.05	9.48E-06	3.73E-03	
rs11974409	7	72627326	*TBL2*	A	G	0.20	1.49	1.36	1.27	-0.08	5.66E-09	6.03E-03	
rs1051921	7	72645879	*MLXIPL*	G	A	0.20	1.49	1.36	1.28	-0.08	1.25E-08	5.60E-03	
rs17145750	7	72664314	*MLXIPL*	G	A	0.16	1.48	1.35	1.29	-0.07	1.48E-06	4.15E-03	
rs7800944	7	72673793	*MLXIPL*	A	G	0.29	1.49	1.41	1.33	-0.05	8.59E-06	3.79E-03	
rs253	8	19855697	*LPL*	G	A	0.45	1.53	1.44	1.34	-0.05	6.48E-06	4.68E-03	0.08
rs255	8	19856181	*LPL*	A	G	0.15	1.48	1.36	1.23	-0.07	2.46E-06	4.14E-03	
rs256	8	19856247	*LPL*	G	A	0.15	1.48	1.37	1.15	-0.07	2.07E-06	4.27E-03	
rs258	8	19856532	*LPL*	C	G	0.45	1.52	1.44	1.33	-0.05	8.69E-06	4.53E-03	
rs263	8	19857092	*LPL*	G	A	0.18	1.48	1.40	1.12	-0.07	3.09E-06	4.25E-03	
rs264	8	19857460	*LPL*	G	A	0.15	1.48	1.37	1.17	-0.07	2.51E-06	4.16E-03	
rs271	8	19857982	*LPL*	G	A	0.15	1.48	1.36	1.25	-0.08	6.59E-07	4.59E-03	
rs285	8	19859469	*LPL*	G	A	0.47	1.54	1.45	1.31	-0.07	2.65E-09	7.73E-03	
rs301	8	19861214	*LPL*	A	G	0.25	1.51	1.38	1.21	-0.08	2.17E-11	8.38E-03	
rs320	8	19863357	*LPL*	A	C	0.28	1.51	1.40	1.26	-0.08	1.79E-10	7.33E-03	
rs327	8	19863816	*LPL*	A	C	0.29	1.51	1.40	1.25	-0.08	2.40E-10	7.40E-03	
rs328	8	19864004	*LPL*	C	G	0.11	1.48	1.31	1.07	-0.11	8.42E-10	7.26E-03	
rs331	8	19864685	*LPL*	G	A	0.27	1.51	1.39	1.24	-0.08	1.73E-11	8.13E-03	
rs12679834	8	19864713	*LPL*	A	G	0.11	1.48	1.31	1.07	-0.11	1.06E-09	7.30E-03	
rs3289	8	19867472	*LPL*	A	G	0.03	1.43	1.70	1.04	0.16	3.16E-06	3.79E-03	
rs3208305	8	19867928	*LPL*	A	T	0.30	1.52	1.40	1.24	-0.08	3.06E-11	8.09E-03	
rs3735964	8	19868325	*LPL*	C	A	0.12	1.48	1.31	1.17	-0.10	9.09E-09	6.18E-03	
rs13702	8	19868772	*LPL*	A	G	0.30	1.52	1.40	1.24	-0.08	2.85E-11	8.21E-03	
rs3916027	8	19869148	*SLC18A1*	G	A	0.27	1.51	1.40	1.24	-0.08	1.04E-10	7.43E-03	

rsID	Chr	Position	Gene	A1	A2	Freq					P1	P2	
rs2197089	8	19870653	SLC18A1	A	G	0.45	1.35	1.45	1.57	0.06	5.03E-09	7.37E-03	
rs17482753	8	19876926	SLC18A1	C	A	0.11	1.48	1.31	1.07	-0.11	3.20E-09	6.76E-03	
rs10503669	8	19891970	SLC18A1	C	A	0.11	1.48	1.30	1.08	-0.11	1.05E-09	7.28E-03	
rs17410962	8	19892360	SLC18A1	G	A	0.13	1.49	1.31	1.13	-0.10	4.64E-09	7.01E-03	
rs17489268	8	19896325	SLC18A1	A	T	0.27	1.51	1.40	1.24	-0.08	1.78E-10	7.48E-03	
rs17411031	8	19896590	SLC18A1	C	G	0.27	1.51	1.40	1.24	-0.08	2.90E-10	7.27E-03	
rs17489282	8	19896798	SLC18A1	G	A	0.27	1.51	1.40	1.24	-0.08	2.13E-10	7.33E-03	
rs17411126	8	19899552	SLC18A1	A	G	0.27	1.51	1.40	1.24	-0.08	1.74E-10	7.27E-03	
rs765547	8	19910554	SLC18A1	G	A	0.27	1.51	1.40	1.24	-0.08	2.02E-10	7.20E-03	
rs11986942	8	19911725	SLC18A1	G	C	0.31	1.51	1.41	1.28	-0.06	4.79E-08	5.47E-03	
rs1919484	8	19913956	SLC18A1	G	A	0.27	1.51	1.40	1.24	-0.08	1.46E-10	7.33E-03	
rs6586891	8	19958878	SLC18A1	A	C	0.34	1.41	1.45	1.56	0.05	4.17E-06	3.54E-03	
rs2001844	8	126547927	TRIB1	A	G	0.47	1.52	1.43	1.38	-0.05	8.89E-06	3.86E-03	
rs17321515	8	126555591	TRIB1	A	G	0.47	1.53	1.43	1.37	-0.05	3.47E-06	4.25E-03	
rs2980869	8	126557432	TRIB1	G	A	0.47	1.53	1.43	1.38	-0.05	6.88E-06	3.86E-03	
rs17108993	10	95354023	RBP4	C	G	0.03	1.42	1.72	1.53	0.14	8.04E-06	4.22E-03	0.06
rs499790	11	116024949	BUD13	G	A	0.10	1.41	1.55	2.06	0.09	3.24E-07	5.34E-03	0.09
rs480823	11	116030940	BUD13	A	G	0.08	1.41	1.59	2.29	0.11	1.07E-08	6.75E-03	
rs481843	11	116031077	BUD13	G	A	0.08	1.41	1.59	2.32	0.11	1.48E-08	6.57E-03	
rs4938303	11	116090197	BUD13	A	G	0.27	1.39	1.49	1.59	0.06	3.47E-06	4.64E-03	
rs28927680	11	116124283	BUD13	C	G	0.07	1.42	1.62	1.90	0.13	4.24E-09	7.63E-03	
rs180327	11	116128869	BUD13	A	G	0.36	1.31	1.52	1.57	0.08	3.09E-12	1.02E-02	
rs11820589	11	116139072	BUD13	G	A	0.06	1.42	1.62	1.99	0.13	2.58E-09	7.80E-03	
rs6589565	11	116145447	BUD13	G	A	0.07	1.39	1.81	1.92	0.19	4.49E-20	1.63E-02	
rs12286037	11	116157417	ZNF259	G	A	0.06	1.42	1.64	1.83	0.13	1.55E-09	7.96E-03	
rs2075290	11	116158506	ZNF259	A	G	0.07	1.39	1.80	1.92	0.19	6.55E-20	1.60E-02	
rs603446	11	116159645	ZNF259	G	A	0.45	1.52	1.45	1.31	-0.05	8.78E-06	4.26E-03	
rs12285095	11	116163241	ZNF259	A	C	0.06	1.42	1.63	1.85	0.13	7.29E-09	7.18E-03	
rs2266788	11	116165896	APOA5	A	G	0.07	1.39	1.81	1.88	0.19	1.16E-19	1.59E-02	
rs2072560	11	116167036	APOA5	G	A	0.06	1.39	1.81	2.04	0.21	1.92E-20	1.62E-02	
rs12287066	11	116167541	APOA5	C	A	0.06	1.42	1.64	1.85	0.13	3.13E-09	7.70E-03	
rs651821	11	116167789	APOA5	A	G	0.06	1.39	1.81	2.04	0.21	8.89E-21	1.64E-02	
rs662799	11	116168917	APOA4	A	G	0.06	1.39	1.81	2.04	0.21	2.91E-20	1.62E-02	
rs10750097	11	116169250	APOA4	A	G	0.21	1.38	1.53	1.70	0.09	1.26E-10	8.11E-03	
rs7396835	11	116189238	APOA4	G	A	0.13	1.40	1.56	1.79	0.09	1.38E-08	6.27E-03	

rs7396851	11	116189374	*APOA4*	G	A	0.13	1.40	1.56	1.80	0.09	4.66E-09	6.67E-03	
rs33989105	11	116205352	*APOC3*	G	A	0.25	1.40	1.47	1.67	0.07	1.75E-07	5.44E-03	
rs5142	11	116207060	*APOA1*	G	A	0.09	1.41	1.61	1.88	0.11	1.26E-08	6.14E-03	
rs5072	11	116212793	*APOA1;NCAN*	G	A	0.08	1.41	1.60	1.84	0.11	1.74E-07	5.50E-03	
rs3794991	19	19471596	*PBX4*	G	A	0.09	1.47	1.32	1.08	-0.09	4.41E-06	4.37E-03	0.06
rs16996148	19	19519472	*PBX4*	C	A	0.08	1.47	1.31	1.09	-0.09	1.69E-06	4.76E-03	
rs12610185	19	19582722	*PBX4*	G	A	0.09	1.47	1.31	1.09	-0.10	5.64E-07	5.22E-03	
rs10500212	19	19584215	*GMIP*	G	A	0.09	1.47	1.31	1.09	-0.10	6.79E-07	5.12E-03	
rs2304128	19	19607151	*GMIP*	C	A	0.09	1.47	1.31	0.99	-0.10	3.15E-07	5.29E-03	

HMZ, homozygote ; HTZ, heterozygote

Table S3d. All SNPs significantly associated with HDL-C

| SNP | CHR | BP | GENE | Alleles | | MAF | Common HMZ mean mmol/l | HTZ mean mmol/l | Rare HMZ mean mmol/l | Beta | P-value | R2 (univariate) | Chr R2 |
				1	2								
rs285	8	19859469	LPL	G	A	0.47	1.41	1.42	1.49	0.03	1.61E-06	4.94E-03	0.17
rs301	8	19861214	LPL	A	G	0.25	1.41	1.46	1.52	0.04	9.25E-11	6.87E-03	
rs320	8	19863357	LPL	A	C	0.28	1.41	1.45	1.50	0.03	3.61E-09	5.21E-03	
rs327	8	19863816	LPL	A	C	0.29	1.41	1.45	1.50	0.03	6.71E-09	5.22E-03	
rs328	8	19864004	LPL	C	G	0.11	1.42	1.49	1.51	0.05	3.17E-08	5.53E-03	
rs331	8	19864685	LPL	G	A	0.27	1.41	1.45	1.50	0.04	2.83E-10	5.89E-03	
rs12679834	8	19864713	LPL	A	G	0.11	1.42	1.49	1.51	0.05	5.39E-08	5.51E-03	
rs3208305	8	19867928	LPL	A	T	0.30	1.41	1.45	1.51	0.04	5.35E-10	5.87E-03	
rs3735964	8	19868325	LPL	C	A	0.12	1.42	1.49	1.47	0.04	1.17E-07	4.80E-03	
rs13702	8	19868772	LPL	A	G	0.30	1.41	1.45	1.51	0.04	7.49E-10	5.87E-03	
rs3916027	8	19869148	SLC18A1	G	A	0.27	1.41	1.45	1.51	0.04	5.39E-10	5.64E-03	
rs2197089	8	19870653	SLC18A1	A	G	0.45	1.48	1.41	1.41	-0.03	2.68E-06	4.58E-03	
rs17482753	8	19876926	SLC18A1	C	A	0.11	1.42	1.49	1.51	0.05	5.31E-08	5.38E-03	
rs10503669	8	19891970	SLC18A1	C	A	0.11	1.42	1.49	1.51	0.05	6.00E-08	5.42E-03	
rs17410962	8	19892360	SLC18A1	G	A	0.13	1.42	1.48	1.52	0.04	1.31E-07	5.52E-03	
rs17489268	8	19896325	SLC18A1	A	T	0.27	1.41	1.45	1.51	0.04	1.19E-09	5.73E-03	
rs17411031	8	19896590	SLC18A1	C	G	0.27	1.41	1.45	1.51	0.04	1.09E-09	5.80E-03	
rs17489282	8	19896798	SLC18A1	G	A	0.27	1.41	1.45	1.51	0.04	7.54E-10	5.75E-03	
rs17411126	8	19899552	SLC18A1	A	G	0.27	1.41	1.45	1.51	0.04	7.77E-10	5.65E-03	
rs765547	8	19910554	SLC18A1	G	A	0.27	1.41	1.45	1.51	0.04	5.55E-10	5.69E-03	
rs11986942	8	19911725	SLC18A1	G	C	0.31	1.41	1.45	1.49	0.03	4.01E-08	4.44E-03	
rs1919484	8	19913956	SLC18A1	G	A	0.27	1.41	1.45	1.51	0.04	9.68E-10	5.59E-03	
rs180327	11	116128869	BUD13	A	G	0.36	1.45	1.43	1.38	-0.03	3.81E-06	4.31E-03	0.17
rs11820589	11	116139072	BUD13	G	A	0.06	1.44	1.39	1.14	-0.05	7.66E-06	4.19E-03	
rs6589565	11	116145447	BUD13	G	A	0.07	1.44	1.37	1.40	-0.05	4.40E-07	4.25E-03	
rs2075290	11	116158506	ZNF259	A	G	0.07	1.44	1.37	1.40	-0.05	4.24E-07	4.11E-03	
rs2266788	11	116165896	APOA5	A	G	0.07	1.44	1.37	1.41	-0.05	4.82E-07	4.19E-03	
rs2072560	11	116167036	APOA5	G	A	0.06	1.44	1.37	1.28	-0.06	7.39E-08	4.63E-03	
rs651821	11	116167789	APOA5	A	G	0.06	1.44	1.38	1.28	-0.06	1.03E-07	4.36E-03	

rs662799	11	116168917	*APOA4*	A	G	0.06	1.44	1.37	1.28	-0.06	6.52E-08	4.70E-03	
rs10750097	11	116169250	*APOA4*	A	G	0.21	1.45	1.41	1.37	-0.03	1.33E-07	4.41E-03	
rs4775041	15	56461987	*LIPC*	C	G	0.30	1.41	1.43	1.53	0.03	2.05E-07	4.51E-03	0.18
rs1800588	15	56510967	*LIPC*	G	A	0.21	1.41	1.45	1.54	0.03	3.85E-07	4.87E-03	
rs2070895	15	56511231	*LIPC*	G	A	0.22	1.41	1.45	1.54	0.03	2.38E-07	5.08E-03	
rs261332	15	56514617	*LIPC*	G	A	0.21	1.41	1.45	1.55	0.03	1.92E-07	5.14E-03	
rs588136	15	56517790	*LIPC*	A	G	0.21	1.41	1.46	1.53	0.03	7.02E-07	4.94E-03	
rs261342	15	56518445	*LIPC*	C	G	0.22	1.41	1.45	1.54	0.03	6.28E-08	5.48E-03	
rs9989419	16	55542640	*CETP*	G	A	0.40	1.49	1.42	1.34	-0.05	9.76E-21	1.58E-02	0.21
rs12708967	16	55550712	*CETP*	A	G	0.19	1.47	1.38	1.29	-0.06	8.79E-23	1.71E-02	
rs3764261	16	55550825	*CETP*	C	A	0.33	1.37	1.47	1.56	0.07	6.80E-36	2.60E-02	
rs12720918	16	55551713	*CETP*	A	G	0.28	1.47	1.40	1.37	-0.05	1.00E-15	1.03E-02	
rs17231506	16	55552029	*CETP*	G	A	0.32	1.37	1.47	1.56	0.07	2.21E-36	2.62E-02	
rs1800775	16	55552737	*CETP*	C	A	0.49	1.35	1.44	1.52	0.06	2.63E-29	2.21E-02	
rs711752	16	55553712	*CETP*	G	A	0.43	1.35	1.45	1.52	0.06	6.48E-32	2.36E-02	
rs708272	16	55553789	*CETP*	G	A	0.43	1.35	1.45	1.52	0.06	1.87E-32	2.41E-02	
rs1864163	16	55554734	*CETP*	G	A	0.26	1.48	1.38	1.32	-0.06	2.80E-27	2.07E-02	
rs7203984	16	55556759	*CETP*	A	C	0.19	1.47	1.37	1.31	-0.06	1.08E-20	1.51E-02	
rs11508026	16	55556829	*CETP*	G	A	0.43	1.35	1.45	1.52	0.06	9.92E-30	2.15E-02	
rs708273	16	55557450	*CETP*	G	A	0.30	1.46	1.41	1.37	-0.03	1.00E-06	4.51E-03	
rs12720922	16	55558386	*CETP*	G	A	0.18	1.47	1.37	1.30	-0.06	1.34E-21	1.60E-02	
rs12597002	16	55559905	*CETP*	C	A	0.30	1.46	1.41	1.37	-0.03	1.31E-06	4.40E-03	
rs9939224	16	55560233	*CETP*	C	A	0.20	1.47	1.38	1.30	-0.06	5.81E-23	1.71E-02	
rs1532625	16	55562802	*CETP*	G	A	0.44	1.35	1.45	1.52	0.06	2.91E-31	2.25E-02	
rs1532624	16	55562980	*CETP*	C	A	0.44	1.35	1.45	1.52	0.06	4.96E-31	2.23E-02	
rs11076175	16	55563879	*CETP*	A	G	0.17	1.47	1.37	1.29	-0.07	5.58E-23	1.76E-02	
rs7499892	16	55564091	*CETP*	G	A	0.17	1.47	1.36	1.30	-0.07	7.14E-24	1.83E-02	
rs5883	16	55564854	*CETP*	G	A	0.06	1.42	1.51	1.54	0.05	5.92E-06	4.31E-03	
rs11076176	16	55564947	*CETP*	A	C	0.16	1.45	1.39	1.31	-0.05	4.62E-12	8.18E-03	
rs289714	16	55564952	*CETP*	A	G	0.17	1.45	1.39	1.35	-0.04	2.56E-10	6.91E-03	
rs289716	16	55566877	*CETP*	A	T	0.31	1.40	1.45	1.51	0.03	1.22E-09	7.35E-03	
rs289717	16	55566889	*CETP*	G	A	0.35	1.46	1.42	1.36	-0.03	6.89E-10	6.54E-03	
rs289718	16	55567433	*CETP*	A	G	0.32	1.40	1.44	1.52	0.04	2.55E-10	8.36E-03	
rs289719	16	55567442	*CETP*	G	A	0.31	1.40	1.44	1.51	0.03	1.27E-09	7.19E-03	
rs4784744	16	55568686	*CETP*	G	A	0.35	1.46	1.42	1.36	-0.03	5.37E-10	6.40E-03	

rs291044	16	55568953	CETP	G	A	0.35	1.46	1.42	1.36	-0.03	9.67E-10	6.23E-03	
rs12720889	16	55570064	CETP	T	A	0.30	1.40	1.45	1.51	0.03	1.33E-09	7.23E-03	
rs4784745	16	55572376	CETP	A	G	0.35	1.46	1.43	1.36	-0.03	5.13E-09	5.75E-03	
rs5880	16	55572592	CETP	G	C	0.05	1.44	1.34	1.20	-0.08	6.90E-12	7.02E-03	
rs5882	16	55573593	CETP	A	G	0.32	1.41	1.44	1.50	0.03	2.78E-07	4.91E-03	
rs1800777	16	55574820	CETP	G	A	0.04	1.44	1.33	1.23	-0.09	8.46E-11	6.19E-03	
rs289743	16	55575297	NLRC5	A	G	0.31	1.41	1.44	1.51	0.03	8.62E-09	6.38E-03	

HMZ, homozygote ; HTZ, heterozygote

Table S3e. All SNPs significantly associated with ApoAI

SNP	CHR	BP	GENE	Alleles		MAF	Common HMZ mean g/l	HTZ mean g/l	Rare HMZ mean g/l	Beta	P-value	R2 (univariate)	Chr R2
				1	2								
rs301	8	19861214	*LPL*	A	G	0.25	2.12	2.15	2.21	0.04	4.16E-06	3.60E-03	0.14
rs1883025	9	106704122	*ABCA1*	G	A	0.26	2.16	2.12	2.09	-0.04	4.81E-06	4.29E-03	0.14
rs4775041	15	56461987	*LIPC*	C	G	0.30	2.12	2.14	2.22	0.04	2.39E-08	5.48E-03	0.15
rs11635491	15	56507033	*LIPC*	G	A	0.27	2.12	2.16	2.20	0.04	2.00E-07	5.34E-03	
rs1800588	15	56510967	*LIPC*	G	A	0.21	2.12	2.16	2.26	0.05	5.38E-10	7.47E-03	
rs2070895	15	56511231	*LIPC*	G	A	0.22	2.12	2.16	2.26	0.05	4.54E-10	7.55E-03	
rs8034802	15	56512084	*LIPC*	T	A	0.28	2.11	2.16	2.20	0.04	1.50E-08	6.52E-03	
rs8033940	15	56512134	*LIPC*	G	A	0.29	2.11	2.16	2.20	0.04	1.02E-08	6.60E-03	
rs261332	15	56514617	*LIPC*	G	A	0.21	2.12	2.16	2.27	0.05	6.48E-10	7.38E-03	
rs588136	15	56517790	*LIPC*	A	G	0.21	2.12	2.16	2.26	0.05	9.75E-10	7.51E-03	
rs261342	15	56518445	*LIPC*	C	G	0.22	2.12	2.16	2.26	0.06	2.85E-11	8.44E-03	
rs261341	15	56518859	*LIPC*	G	A	0.29	2.11	2.15	2.20	0.04	4.05E-08	5.85E-03	
rs261338	15	56522297	*LIPC*	G	A	0.17	2.12	2.16	2.27	0.04	1.73E-06	4.24E-03	
rs485671	15	56528426	*LIPC*	C	A	0.17	2.13	2.16	2.23	0.04	7.88E-06	3.51E-03	
rs485538	15	56528469	*LIPC*	A	G	0.17	2.12	2.16	2.23	0.04	4.32E-06	3.81E-03	
rs572410	15	56528676	*LIPC*	G	C	0.24	2.12	2.15	2.22	0.04	2.69E-06	4.24E-03	
rs261336	15	56529710	*LIPC*	A	G	0.16	2.12	2.16	2.24	0.04	2.64E-06	4.02E-03	
rs9989419	16	55542640	*CETP*	G	A	0.40	2.18	2.13	2.08	-0.05	2.59E-12	9.33E-03	0.16
rs12708967	16	55550712	*CETP*	A	G	0.19	2.16	2.10	2.02	-0.06	1.60E-13	9.84E-03	
rs3764261	16	55550825	*CETP*	C	A	0.33	2.10	2.16	2.21	0.06	6.19E-19	1.35E-02	
rs12720918	16	55551713	*CETP*	A	G	0.28	2.16	2.12	2.09	-0.04	1.15E-08	5.23E-03	
rs17231506	16	55552029	*CETP*	G	A	0.32	2.09	2.17	2.21	0.07	1.41E-19	1.39E-02	
rs1800775	16	55552737	*CETP*	C	A	0.49	2.08	2.14	2.19	0.05	8.75E-16	1.15E-02	
rs711752	16	55553712	*CETP*	G	A	0.43	2.08	2.15	2.20	0.06	2.19E-18	1.33E-02	
rs708272	16	55553789	*CETP*	G	A	0.43	2.08	2.15	2.20	0.06	1.02E-18	1.37E-02	
rs1864163	16	55554734	*CETP*	G	A	0.26	2.17	2.10	2.06	-0.06	8.48E-16	1.17E-02	
rs7203984	16	55556759	*CETP*	A	C	0.19	2.16	2.10	2.05	-0.06	1.19E-12	8.74E-03	

rs11508026	16	55556829	*CETP*	G	A	0.43	2.08	2.15	2.20	0.06	7.52E-18	1.26E-02	
rs12720922	16	55558386	*CETP*	G	A	0.18	2.16	2.09	2.05	-0.06	8.69E-13	8.97E-03	
rs9939224	16	55560233	*CETP*	C	A	0.20	2.16	2.10	2.03	-0.06	5.63E-14	1.01E-02	
rs1532625	16	55562802	*CETP*	G	A	0.44	2.08	2.15	2.20	0.06	2.61E-18	1.29E-02	
rs1532624	16	55562980	*CETP*	C	A	0.44	2.08	2.15	2.20	0.06	4.69E-18	1.26E-02	
rs11076175	16	55563879	*CETP*	A	G	0.17	2.16	2.09	2.04	-0.06	5.66E-13	9.44E-03	
rs7499892	16	55564091	*CETP*	G	A	0.17	2.16	2.09	2.04	-0.07	1.27E-13	9.97E-03	
rs11076176	16	55564947	*CETP*	A	C	0.16	2.15	2.11	2.06	-0.05	2.07E-07	4.56E-03	
rs289714	16	55564952	*CETP*	A	G	0.17	2.15	2.11	2.08	-0.04	1.14E-06	4.05E-03	
rs289716	16	55566877	*CETP*	A	T	0.31	2.11	2.14	2.22	0.04	1.06E-08	6.69E-03	
rs289717	16	55566889	*CETP*	G	A	0.35	2.16	2.13	2.09	-0.04	1.65E-07	4.94E-03	
rs289718	16	55567433	*CETP*	A	G	0.32	2.11	2.14	2.23	0.04	2.45E-09	7.60E-03	
rs289719	16	55567442	*CETP*	G	A	0.31	2.11	2.14	2.22	0.04	1.01E-08	6.58E-03	
rs4784744	16	55568686	*CETP*	G	A	0.35	2.16	2.13	2.09	-0.04	2.17E-07	4.69E-03	
rs291044	16	55568953	*CETP*	G	A	0.35	2.16	2.13	2.09	-0.04	2.62E-07	4.65E-03	
rs12720889	16	55570064	*CETP*	T	A	0.30	2.11	2.15	2.22	0.04	3.91E-09	6.97E-03	
rs4784745	16	55572376	*CETP*	A	G	0.35	2.16	2.13	2.08	-0.04	4.07E-07	4.53E-03	
rs5880	16	55572592	*CETP*	G	C	0.05	2.15	2.07	1.97	-0.08	6.81E-08	4.39E-03	
rs5882	16	55573593	*CETP*	A	G	0.32	2.12	2.14	2.21	0.04	5.42E-07	4.79E-03	
rs1800777	16	55574820	*CETP*	G	A	0.04	2.14	2.06	2.00	-0.09	1.79E-07	3.97E-03	
rs1801706	16	55575163	*CETP*	G	A	0.18	2.12	2.16	2.24	0.04	6.98E-06	4.25E-03	
rs289743	16	55575297	*NLRC5*	A	G	0.31	2.12	2.14	2.22	0.04	1.54E-08	6.30E-03	

HMZ, homozygote ; HTZ, heterozygote

Table S4. SNPs from published GWASs (Kathiresan, 2008 and Willer, 2008) that did not reach significance in the WHII study.

GWAS	Trait	Chr	Gene	SNP	Reported β (sem) (meta-analysis)	Reported p-value (meta-analysis)	Reported β (sem) (initial GWAS)	Reported p-value (initial GWAS)	p-value in WHII
Kathiresan, 2008, Nat Genet	LDL	19q13.32	APOE, APOC1, APOC4, APOC2	rs4420638	0.19 (0.02)	1.00E-60	0.25 (0.03)	3.00E-13	not in chip
	LDL	1p32.3	PCSK9	rs11591147	−0.47 (0.03)	2.00E-44	not typed		not in chip
	LDL	19p13	CILP2,PBX4	rs16996148	−0.10 (0.02)	3.00E-08	−0.10 (0.05)	4.00E-02	6.01E-04
	HDL	1q42.13	GALNT2	rs4846914	−0.07 (0.01)	2.00E-13	−0.10 (0.03)	3.00E-04	not in chip
	HDL	9q31	ABCA1	rs3890182	−0.10 (0.02)	3.00E-10	−0.17 (0.04)	3.00E-05	1.71E-02
	HDL	11q23	APOA1-C3-A4-A5, ZNF259, BUD13	rs28927680	−0.13 (0.03)	2.00E-05	−0.06 (0.05)	3.10E-01	1.58E-04
	HDL	18q21	LIPG, ACAA2	rs2156552	−0.07 (0.01)	2.00E-07	−0.09 (0.03)	2.00E-02	1.44E-02
	Triglycerides	1q42.13	GALNT2	rs4846914	0.08 (0.01)	7.00E-15	0.11 (0.03)	9.00E-05	not in chip
	Triglycerides	1p31.3	ANGPTL3, DOCK7, ATG4C	rs12130333	−0.11 (0.02)	2.00E-08	−0.12 (0.03)	6.00E-04	not in chip
	Triglycerides	7q11	BCL7B,TBL2,MLXIPL	rs17145738	−0.14 (0.02)	7.00E-22	−0.12 (0.03)	3.00E-03	1.04E-05
Willer, 2008, Nat Genet*	LDL	19q13.32	APOE, APOC1, APOC4, APOC2	rs4420638	6.61mg/dl	3.00E-43	8.02mg/dl	3.20E-21	not in chip
	LDL	19	NCAN	rs2228603			6.46mg/dl	1.80E-07	1.53E-05
	HDL	9	GRIN3A, PPP3R2	rs1323432	-0.03mg/dl	7.70E-04	1.93mg/dl	2.50E-08	1.98E-01
	HDL	9q31	ABCA1	rs4149274	0.82mg/dl	1.20E-10	1.51mg/dl	7.40E-08	not in chip
	HDL	18q21	LIPG	rs4939883			1.87mg/dl	1.40E-07	not in chip
	HDL	1q42.13	GALNT2	rs4846914			1.15mg/dl	2.90E-07	1.26E-02
	Triglycerides	11q23	APOA5	rs964184			18.12mg/dl	1.50E-16	not in chip
	Triglycerides	8p21	LPL	rs6993414			14.2mg/dl	1.40E-13	not in chip
	Triglycerides	8	TRIB1	rs2954029			6.42mg/dl	2.80E-08	1.54E-05
	Triglycerides	19	NCAN	rs10401969			12.28mg/dl	2.30E-07	not in chip

*Data reported as per-allele change in mean lipid value (mg/dl).

References

(1) Kathiresan S, Melander O, Guiducci C, Surti A, Burtt NP, Rieder MJ et al. Six new loci associated with blood low-density lipoprotein cholesterol, high-density lipoprotein cholesterol or triglycerides in humans. Nat Genet 2008; 40:189-197.

(2) Willer CJ, Sanna S, Jackson AU, Scuteri A, Bonnycastle LL, Clarke R et al. Newly identified loci that influence lipid concentrations and risk of coronary artery disease. Nat Genet 2008; 40:161-169

Table S5. Mean lipid values and gene count score for approximate quintiles of WHII individuals.

Traits	Number of individuals	Mean genescore	Trait mean	95CI-	95CI+
LDL-C mmol/l					
1	1,022	22.33	3.96	3.90	4.02
2	842	25.54	4.25	4.18	4.32
3	991	27.50	4.40	4.34	4.46
4	876	29.44	4.59	4.52	4.65
5	798	32.21	4.79	4.72	4.86
ApoB g/l					
1	1,031	23.47	1.12	1.10	1.14
2	975	26.54	1.21	1.19	1.23
3	1,114	28.50	1.27	1.25	1.28
4	948	30.45	1.30	1.28	1.32
5	540	32.96	1.38	1.36	1.41
TG mmol/l					
1	1,046	8.744741	1.05	1.01	1.08
2	1,155	11.5645	1.16	1.12	1.19
3	699	13	1.22	1.17	1.27
4	1,007	14.43694	1.30	1.26	1.35
5	701	17.28103	1.52	1.46	1.59
HDL-C mmol/l					
1	1,360	8.87	1.26	1.25	1.28
2	654	11.00	1.33	1.30	1.36
3	1,373	12.48	1.40	1.38	1.42
4	527	14.00	1.48	1.44	1.51
5	679	15.79	1.54	1.51	1.57
ApoAI g/l					
1	1,159	6.98	2.04	2.02	2.06
2	745	9.00	2.09	2.07	2.11
3	1,625	10.50	2.15	2.14	2.17
4	626	12.00	2.21	2.19	2.24
5	453	13.48	2.29	2.26	2.33
ApoB/ApoAI ratio					
1	1,221	20.39	0.54	0.53	0.55
2	1,012	23.51	0.58	0.57	0.59
3	560	25.00	0.61	0.60	0.62
4	976	26.45	0.64	0.63	0.65
5	839	29.05	0.67	0.66	0.69

Table S6. SNPs independently associating with lipid and apolipoprotein traits in genes/regions previously detected by GWASs or candidate gene studies in the WH-II study.

SNP	Chr	Basepairs	Gene	cSNPs	MAF	Previous GWAS	Common HMZ[c] mean	HTZ[d] mean	Rare HMZ[c] mean	Beta	p-value[a]	StepAIC[b]*
LDL-C												
rs11591147	1	55278235	PCSK9	L46R	0.02	[1]	4.38	3.84	2.98	-0.55	9.28E-12	4.95E-12
rs4970834	1	109616403	CELSR2		0.18		4.42	4.27	4.08	-0.16	5.18E-09	1.16E-01
rs12740374	1	109619113	CELSR2		0.21	[2]; LD with rs646776 from [3]	4.43	4.28	4.12	-0.15	1.82E-09	4.73E-04
rs629301	1	109619829	CELSR2		0.21	LD with rs12740374 from [2]	4.43	4.28	4.14	-0.15	6.50E-09	1.24E-03
rs693	2	21085700	APOB	T2488T	0.48		4.48	4.34	4.27	-0.11	3.86E-08	1.00E-01
rs934197	2	21120966	APOB		0.33		4.30	4.40	4.53	0.12	3.43E-08	1.16E-02
rs562338	2	21141826	APOB		0.18	[4],[5]; LD with rs515135 from [2]; LD with rs506585 from [3]	4.43	4.24	4.16	-0.18	1.21E-11	8.86E-07
rs4299376	2	43926080	ABCG8		0.32	LD with rs6544713 from [2]	4.28	4.42	4.53	0.13	8.70E-10	1.33E-09
rs12916	5	74692295	HMGCR		0.41	LD with rs3846663 from [2]; LD with rs12654264 [1]	4.26	4.39	4.51	0.12	6.66E-09	2.22E-05
rs3804231	5	74732535	HMGCR		0.13		4.33	4.46	4.62	0.14	5.15E-06	2.59E-02
rs2072560	11	116167036	APOA5		0.06		4.34	4.51	5.33	0.22	2.36E-07	2.39E-07
rs17231506	16	55552029	CETP		0.32		4.44	4.33	4.22	-0.11	5.02E-07	4.63E-07
rs1529729	19	11024562	LDLR		0.45		4.28	4.39	4.44	0.09	6.71E-06	1.13E-01
rs17248720	19	11059187	LDLR		0.13		4.45	4.14	3.81	-0.31	7.86E-25	2.00E-16
rs8110695	19	11067530	LDLR		0.22		4.43	4.27	4.21	-0.14	1.12E-08	1.51E-01
rs2228671	19	11071912	LDLR	C27C	0.13	[6]	4.42	4.21	4.18	-0.18	6.52E-10	1.08E-04
rs1531517	19	49934013	BCL3		0.07		4.40	4.17	4.08	-0.22	6.26E-08	1.23E-02
rs10402271	19	50021054	BCL3/PVRL2		0.33		4.26	4.44	4.53	0.15	2.06E-12	9.72E-06
rs519113	19	50068124	PVRL2		0.24		4.42	4.31	4.18	-0.12	9.37E-07	1.42E-02
rs6859	19	50073874	PVRL2		0.41		4.27	4.38	4.52	0.12	3.53E-08	2.95E-03
rs283813	19	50081014	PVRL2		0.07		4.39	4.23	3.70	-0.19	2.51E-06	6.49E-05
rs2075650	19	50087459	TOMM40		0.14	[6]	4.31	4.51	4.87	0.23	1.14E-14	2.45E-02
rs12721046	19	50113094	APOC1		0.15		4.30	4.51	4.74	0.21	7.58E-14	1.16E-01
rs12721109	19	50139061	APOC4		0.02		4.39	3.82	4.32	-0.54	5.06E-14	9.44E-08
ApoB												
rs11591147	1	55278235	PCSK9	L46R	0.02	[1],[3]	1.28	1.14	0.94	-0.12	1.89E-10	1.08E-10
rs4970834	1	109616403	CELSR2		0.18		1.29	1.25	1.18	-0.04	2E-08	1.46E-01
rs12740374	1	109619113	CELSR2		0.21	[2]	1.29	1.25	1.19	-0.03	4.7E-09	2.13E-04
rs629301	1	109619829	CELSR2		0.21		1.29	1.25	1.19	-0.03	1.76E-08	6.14E-04
rs562338	2	21141826	APOB		0.18	[5],[4]	1.29	1.24	1.19	-0.05	6E-13	4.77E-09
rs754523	2	21165196	APOB		0.33		1.25	1.27	1.32	0.02	1.11E-06	1.22E-02
rs4299376	2	43926080	ABCG8		0.32		1.25	1.28	1.32	0.03	7.6E-08	1.03E-07

SNP	Chr	Position	Gene	AA	Freq	Notes					
rs12916	5	74692295	*HMGCR*		0.41		1.25	1.27	1.31	0.02	3.34E-06	2.42E-06
rs180327	11	116128869	*BUD13*		0.36		1.24	1.29	1.29	0.02	7.7E-07	4.45E-02
rs2072560	11	116167036	*APOA5*		0.06		1.26	1.34	1.58	0.07	1.4E-12	8.65E-09
rs9804646	11	116170289	*APOA4*		0.09		1.28	1.22	1.22	-0.04	1.25E-06	2.29E-04
rs3764261	16	55550825	*CETP*		0.33	[7, 4]	1.29	1.26	1.23	-0.02	1.52E-06	1.12E-06
rs17248720	19	11059187	*LDLR*		0.13		1.29	1.22	1.14	-0.06	2.1E-15	3.31E-13
rs2228671	19	11071912	*LDLR*		0.13	[6]	1.28	1.24	1.23	-0.03	5E-06	1.27E-03
rs1531517	19	49934013	*BCL3*		0.07		1.28	1.20	1.15	-0.07	1.96E-13	2.15E-03
rs10402271	19	50021054	*BCL3/PVRL2*		0.33		1.24	1.29	1.32	0.04	7.05E-13	1.69E-05
rs519113	19	50068124	*PVRL2*		0.24		1.29	1.25	1.22	-0.03	2.14E-08	4.99E-02
rs6859	19	50073874	*PVRL2*		0.41		1.24	1.28	1.32	0.03	1.49E-10	2.88E-03
rs283813	19	50081014	*PVRL2*		0.07		1.28	1.23	1.09	-0.05	2.61E-08	8.63E-07
rs157580	19	50087106	*TOMM40*		0.40	[6]	1.30	1.26	1.23	-0.02	6.55E-07	4.66E-07
rs405509	19	50100676	*APOE*		0.48		1.25	1.27	1.30	0.03	1.89E-08	2.80E-10
rs12721109	19	50139061	*APOC4*		0.02		1.28	1.10	1.05	-0.15	3.88E-19	9.28E-07
HDL-C												
rs301	8	19861214	*LPL*		0.25		1.41	1.46	1.52	0.04	9.25E-11	4.75E-06
rs17410962	8	19892360	*LPL*		0.13	LD with rs12678919 from [2]	1.42	1.48	1.52	0.04	1.31E-07	2.55E-02
rs11820589	11	116139072	*BUD13*	L148P	0.06		1.44	1.39	1.14	-0.05	7.66E-06	1.54E-06
rs662799	11	116168917	*APOA5*		0.06		1.44	1.37	1.28	-0.06	6.52E-08	1.07E-08
rs4775041	15	56461987	*LIPC*		0.30	[4]	1.41	1.43	1.53	0.03	2.05E-07	6.63E-08
rs261342	15	56518445	*LIPC*		0.22		1.41	1.45	1.54	0.04	6.28E-08	2.12E-08
rs9989419	16	55542640	*CETP*		0.40	[4]	1.49	1.42	1.34	-0.05	9.76E-21	1.11E-02
rs12708967	16	55550712	*CETP*		0.19		1.47	1.38	1.29	-0.06	8.79E-23	5.02E-05
rs17231506	16	55552029	*CETP*		0.32	LD with rs173539 from [2]; LD with rs3764261 from [3]	1.37	1.47	1.56	0.07	2.21E-36	1.52E-06
rs711752	16	55553712	*CETP*		0.43		1.35	1.45	1.52	0.06	6.48E-32	6.86E-03
rs5883	16	55564854	*CETP*	F287F	0.06		1.42	1.51	1.54	0.05	5.92E-06	2.46E-15
rs5880	16	55572592	*CETP*	P309A	0.05		1.44	1.34	1.20	-0.08	6.90E-12	1.93E-03
ApoAI												
rs301	8	19861214	*LPL*		0.25	LD with rs331 from [3]	2.12	2.15	2.21	0.04	4.16E-06	2.41E-06
rs1883025	9	106704122	*ABCA1*		0.26	[2]	2.16	2.12	2.09	-0.04	4.81E-06	7.15E-06
rs4775041	15	56461987	*LIPC*		0.30	[4]	2.12	2.14	2.22	0.04	2.39E-08	5.80E-09
rs261342	15	56518445	*LIPC*		0.22		2.12	2.16	2.26	0.06	2.85E-11	7.93E-12
rs12708967	16	55550712	*CETP*		0.19		2.16	2.10	2.02	-0.06	1.6E-13	2.46E-02
rs17231506	16	55552029	*CETP*		0.32		2.09	2.17	2.21	0.07	1.41E-19	8.78E-12
rs1864163	16	55554734	*CETP*		0.26		2.17	2.10	2.06	-0.06	8.48E-16	1.57E-01
rs5880	16	55572592	*CETP*	P390A	0.05		2.15	2.07	1.97	-0.08	6.81E-08	6.69E-03
rs1801706	16	55575163	*CETP*		0.18		2.12	2.16	2.24	0.04	6.98E-06	1.20E-06
Triglycerides												

rs1260326	2	27584444	GCKR	P446L	0.40	[2,7,3]	1.38	1.43	1.63	0.06	1.83E-07	2.21E-07
rs17145713	7	72542746	BAZ1B		0.20		1.50	1.36	1.25	-0.09	5.29E-10	6.05E-10
rs285	8	19859469	LPL		0.47		1.54	1.45	1.31	-0.07	2.65E-09	6.15E-05
rs331	8	19864685	LPL		0.27	LD with rs326 from [8]	1.51	1.39	1.24	-0.08	1.73E-11	1.40E-02
rs3289	8	19867472	LPL		0.03		1.43	1.70	1.04	0.16	3.16E-06	5.58E-06
rs3916027	8	19869148	LPL		0.27	LD with rs326 from [8]	1.51	1.40	1.24	-0.08	1.04E-10	2.55E-02
rs10503669	8	19891970	LPL		0.11	[4], LD with rs10096633 from [6], LD with rs12678919 from [2], LD with rs328 from [3]	1.48	1.30	1.08	-0.11	1.05E-09	1.61E-02
rs17321515	8	126555591	TRIB1		0.47	[4]	1.53	1.43	1.37	-0.05	3.47E-06	4.62E-06
rs17108993	10	95354023	RBP4		0.03		1.42	1.72	1.53	0.14	8.04E-06	8.04E-06
rs6589565	11	116145447	BUD13		0.07		1.39	1.81	1.92	0.19	4.49E-20	5.73E-02
rs12286037	11	116157417	ZNF259		0.06	[4]; LD with rs12272004 from [6]; LD with rs28927680 from [1]	1.42	1.64	1.83	0.13	1.55E-09	1.01E-12
rs651821	11	116167789	APOA5		0.06	LD with rs662799 from [3]	1.39	1.81	2.04	0.21	8.89E-21	3.35E-03
rs10750097	11	116169250	APOA4		0.21		1.38	1.53	1.70	0.09	1.26E-10	5.46E-03
rs33989105	11	116205352	APOC3		0.25		1.40	1.47	1.67	0.07	1.75E-07	1.72E-03
rs5072	11	116212793	APOA1/ NCAN		0.08		1.41	1.60	1.84	0.11	1.74E-07	1.21E-01
rs2304128	19	19607151	GMIP		0.09		1.47	1.31	0.99	-0.10	3.15E-07	3.74E-07

[a]P-value for association adjusted for age and gender.

[b]P-value for the specified SNP in the final stepwise regression model, i.e. adjusted for age, gender and all other SNPs in this final model

[c]HMZ, homozygote ; [d] HTZ, heterozygote

LDL-C, low density lipoprotein –cholesterol; ApoB, apolipoprotein B; HDL-C, high density lipoprotein –cholesterol; ApoAI, apolipoprotein AI;

LD, linkage disequilibrium; StepAI.C, stepwise selection scheme using the Akaike's Information Criterion (AIC)[9].

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Table S7. Results from the meta-analysis of SNPs with MAF>0.01and p-value cut off of 10^{-5} and their association with lipid and apolipoprotein traits

SNP	Chr	BP	Nearest gene	Alleles 1	Alleles 2	MAF	Common HMZ[c] mean	HTZ[d] mean	Rare HMZ[c] mean	Beta	P-value	R2 (univariate)	Meta-analysis P-value
LDL-C													
rs822430	1	155168883	C1orf92	A	G	0.48	4.48	4.33	4.31	-0.09	2.76E-05	0.004	2.66E-02
rs12467409	2	203102593	BMPR2	C	A	0.12	4.34	4.45	4.71	0.13	7.50E-05	0.003	2.65E-06
rs3184504	12	110368991	SH2B3	G	A	0.48	4.42	4.38	4.26	-0.08	6.90E-05[a]	0.003	7.52E-06
rs4568	14	23829849	DHRS1	G	A	0.24	4.33	4.37	4.66	0.10	2.03E-05	0.003	1.57E-03
rs17184682	14	23863602	ADCY4	A	C	0.11	4.34	4.43	4.84	0.13	5.27E-05	0.003	7.35E-04
rs987644	14	78313798	NRXN3	G	A	0.19	4.41	4.29	4.20	-0.11	2.40E-05	0.004	2.30E-03
rs1529729	19	11024562	SMARCA4	A	G	0.45	4.28	4.39	4.44	0.09	6.71E-06	0.004	4.52E-08
rs1531517	19	49934013	BCL3	G	A	0.07	4.40	4.17	4.08	-0.22	6.26E-08[††]	0.006	2.22E-16
rs10402271	19	50021054	PVRL2	A	C	0.33	4.26	4.44	4.53	0.15	2.06E-12[b]	0.010	0.00E+00
rs4803763	19	50049131	PVRL2	G	C	0.26	4.29	4.43	4.58	0.15	2.20E-10[b]	0.008	0.00E+00
rs519113	19	50068124	PVRL2	C	G	0.24	4.42	4.31	4.18	-0.12	9.37E-07[b]	0.005	1.25E-11
rs387976	19	50070900	PVRL2	A	C	0.35	4.43	4.34	4.22	-0.10	5.98E-06[a]	0.004	1.33E-08
rs6859	19	50073874	PVRL2	G	A	0.41	4.27	4.38	4.52	0.12	3.53E-08[a]	0.007	7.83E-10
rs283813	19	50081014	PVRL2	T	A	0.07	4.39	4.23	3.70	-0.19	2.51E-06	0.004	1.85E-08
rs17836542	19	60241198	GP6	C	G	0.05	4.38	4.21	3.70	-0.19	9.56E-05	0.004	2.13E-02
ApoB													

rs	Chr	Pos	Gene	A1	A2	Freq							
rs4299376	2	43926080	*ABCG8*	A	C	0.32	1.25	1.28	1.32	0.03	7.60E-08	0.006	-
rs1459047	6	21308369	*CDKAL1*	A	G	0.07	1.26	1.31	1.33	0.04	6.06E-05	0.003	-
rs4568	14	23829849	*DHRS1*	G	A	0.24	1.26	1.27	1.36	0.02	2.41E-05	0.003	-
rs1531517	19	49934013	*BCL3*	G	A	0.07	1.28	1.20	1.15	-0.07	1.96E-13	0.010	-
rs10402271	19	50021054	*PVRL2*	A	C	0.36	1.24	1.29	1.32	0.04	7.05E-13	0.010	-
rs4803763	19	50049131	*PVRL2*	G	C	0.26	1.25	1.29	1.34	0.04	2.75E-12	0.009	-
rs519113	19	50068124	*PVRL2*	C	G	0.24	1.29	1.25	1.22	-0.03	2.14E-08	0.006	-
rs387976	19	50070900	*PVRL2*	A	C	0.35	1.29	1.26	1.22	-0.03	1.54E-07	0.006	-
rs6859	19	50073874	*PVRL2*	G	A	0.41	1.24	1.28	1.32	0.03	1.49E-10	0.009	-
rs283813	19	50081014	*PVRL2*	T	A	0.07	1.28	1.23	1.09	-0.05	2.61E-08	0.005	-
HDL-C													
rs6546578	2	70346714	*PCYOX1*	G	A	0.32	1.42	1.43	1.49	0.02	6.47E-05	0.003	1.21E-02
rs6546579	2	70346786	*PCYOX1*	A	C	0.32	1.42	1.43	1.50	0.02	7.84E-05	0.003	1.33E-02
rs3088063	19	40529916	*CD22*	G	A	0.06	1.42	1.50	1.58	0.04	9.55E-05	0.003	1.10E-03
rs6018424	20	45420391	*RPL35AP*	G	A	0.19	1.42	1.45	1.54	0.03	7.73E-05	0.004	1.67E-03
ApoAI													
rs4953019	2	43896897	*ABCG5*	G	A	0.07	2.15	2.09	2.05	-0.05	5.99E-05	0.003	-
rs4437632	8	69014046	*PREX2*	A	C	0.27	2.12	2.15	2.20	0.03	6.52E-05	0.004	-
rs838878	12	123826598	*SCARB1*	G	A	0.30	2.12	2.15	2.17	0.03	5.05E-05	0.003	-
rs12580803	12	123883200	*SCARB1*	A	G	0.17	2.13	2.16	2.21	0.04	7.40E-05	0.003	-
rs3088063	19	40529916	*CD22*	G	A	0.06	2.13	2.19	2.24	0.06	6.31E-05	0.004	-
rs10426830	19	40530818	*CD22*	C	A	0.06	2.13	2.19	2.40	0.06	4.87E-05	0.003	-
Triglycerides													

rs1049817	2	27404471	GTF3C2	A	G	0.39	1.51	1.43	1.33	-0.05	5.67E-05[#]	0.004	1.45E-06
rs3134947	6	32253183	RNF5	G	A	0.22	1.47	1.40	1.35	-0.05	5.08E-05	0.003	6.21E-03
rs2854275	6	32736406	HLA-DQB1	C	A	0.14	1.47	1.38	1.33	-0.07	4.24E-05	0.004	8.33E-04
rs2781659	6	131933513	ARG1;MED3	A	G	0.32	1.49	1.43	1.30	-0.05	4.40E-05	0.003	3.81E-03
rs17108993	10	95354023	RBP4	C	G	0.03	1.42	1.72	1.53	0.14	8.04E-06	0.004	1.62E-03
rs163182	11	2800792	KCNQ1	C	G	0.45	1.38	1.43	1.56	0.05	4.32E-05	0.004	7.37E-03
rs163184	11	2803645	KCNQ1	A	C	0.47	1.37	1.44	1.55	0.05	2.91E-05	0.004	1.13E-02
rs2228603	19	19190924	GATAD2A	G	A	0.08	1.47	1.33	1.00	-0.09	1.53E-05	0.004	-
rs3794991	19	19471596	PBX4	G	A	0.09	1.47	1.32	1.08	-0.09	4.41E-06	0.004	8.48E-05
rs16996148	19	19519472	PBX4	C	A	0.08	1.47	1.31	1.09	-0.09	1.69E-06	0.005	4.92E-05
rs12610185	19	19582722	PBX4	G	A	0.09	1.47	1.31	1.09	-0.10	5.64E-07	0.005	2.31E-05
rs10500212	19	19584215	GMIP	G	A	0.09	1.47	1.31	1.09	-0.10	6.79E-07	0.005	2.53E-05
rs2304128	19	19607151	GMIP	C	A	0.09	1.47	1.31	0.99	-0.10	3.15E-07	0.005	4.23E-06

[a] P-value in replication study <0.05 [b] P-value in replication study <1x10^{-3} [†] P-value in replication study <1x10^{-5}

[c] HMZ, homozygote ; [d] HTZ, heterozygote   Highlighted in bold are those SNPs which showed significant replication in the meta-analyses

LDL-C, low density lipoprotein –cholesterol; ApoB, apolipoprotein B, HDL-C, high density lipoprotein –cholesterol, ApoAI, apolipoprotein AI;

Chr, chromosome , BP, base pair; MAF, minor allele frequency