

SUPPLEMENTS

Supplementary Table 1: Genome-wide significant hits for total cholesterol (TC), high-density lipoprotein (HDL), low-density lipoprotein (LDL) and triglycerides (TG)

Genome-wide significant hits for TC												
SNP	Chromosome	Pos, Mb	Gene	Allele 1	Allele 2	Effect allele	Effect allele frequency	N	Beta	SE(Beta)	P-value	R2
rs873308	1	25,50	TMEM57	A	G	G	0,456	17473	-0,066	0,011	4,64E-09	0,196
rs10903129	1	25,51	TMEM57	A	G	G	0,544	22550	0,061	0,010	5,45E-10	0,171
rs1167998	1	62,64	DOCK7	A	C	C	0,334	17346	-0,073	0,012	6,39E-10	0,220
rs10889353	1	62,83	DOCK7	A	C	C	0,321	19099	-0,079	0,011	3,72E-12	0,253
rs585362	1	109,50	SARS/CELSR2/MYBPHL	A	G	G	0,138	17454	-0,093	0,016	7,97E-09	0,191
rs611917	1	109,53	SARS/CELSR2/MYBPHL	A	G	G	0,327	17445	-0,084	0,012	9,63E-13	0,292
rs646776	1	109,53	SARS/CELSR2/MYBPHL	A	G	G	0,224	17441	-0,128	0,013	8,53E-22	0,528
rs4970834	1	109,62	SARS/CELSR2/MYBPHL	A	G	G	0,804	7465	0,120	0,021	9,53E-09	0,441
rs10198175	2	21,06	APOB	A	G	G	0,902	17471	-0,104	0,019	2,38E-08	0,178
rs693	2	21,14	APOB	A	G	G	0,523	22500	-0,096	0,010	8,70E-23	0,429
rs541041	2	21,15	APOB	A	G	G	0,156	5873	-0,146	0,026	1,46E-08	0,547
rs1713222	2	21,18	APOB	A	G	G	0,855	17439	0,135	0,016	3,18E-17	0,408
rs1429974	2	21,21	APOB	A	C	C	0,690	19055	-0,090	0,011	4,93E-15	0,322
rs754524	2	21,22	APOB	A	C	C	0,265	17469	0,084	0,013	3,48E-11	0,251
rs754523	2	21,22	APOB	A	G	G	0,312	19051	0,092	0,011	1,25E-15	0,336
rs312985	2	21,29	APOB	A	G	G	0,788	17456	0,087	0,014	1,69E-10	0,234
rs506585	2	21,31	APOB	A	G	G	0,210	19112	-0,085	0,013	6,33E-11	0,224
rs949790	2	21,36	APOB	A	G	G	0,772	17452	-0,079	0,013	2,37E-09	0,204
rs13398007	2	21,38	APOB	A	G	G	0,871	17468	0,103	0,017	6,74E-10	0,218

rs6756629	2	43,98	ABCG5	A	G	G	0,928	17472	0,145	0,022	1,49E-11	0,261
rs7714420	5	74,38	GCNT4/HMGCR/POLK	A	C	C	0,297	19086	0,065	0,012	3,10E-08	0,161
rs7700965	5	74,39	GCNT4/HMGCR/POLK	A	G	G	0,353	17467	0,070	0,012	1,66E-09	0,208
rs3923323	5	74,41	GCNT4/HMGCR/POLK	A	G	G	0,176	19101	0,097	0,014	3,88E-12	0,252
rs4345300	5	74,41	GCNT4/HMGCR/POLK	A	G	G	0,647	17439	-0,070	0,012	1,64E-09	0,208
rs2035191	5	74,45	GCNT4/HMGCR/POLK	A	G	G	0,188	17472	0,099	0,014	3,42E-12	0,277
rs1422698	5	74,48	GCNT4/HMGCR/POLK	A	G	G	0,648	22496	-0,067	0,010	3,46E-11	0,195
rs6866661	5	74,57	GCNT4/HMGCR/POLK	A	G	G	0,360	17473	0,069	0,012	1,92E-09	0,206
rs1551894	5	74,61	GCNT4/HMGCR/POLK	A	G	G	0,760	17465	-0,101	0,013	1,05E-14	0,342
rs2335418	5	74,64	GCNT4/HMGCR/POLK	A	G	G	0,570	7509	-0,095	0,017	1,51E-08	0,427
rs10474433	5	74,65	GCNT4/HMGCR/POLK	A	G	G	0,340	9316	0,086	0,016	3,25E-08	0,328
rs3761740	5	74,67	GCNT4/HMGCR/POLK	A	C	C	0,898	19051	-0,104	0,018	3,22E-09	0,184
rs3846662	5	74,69	GCNT4/HMGCR/POLK	A	G	G	0,440	20873	0,092	0,010	2,52E-19	0,387
rs4385188	5	74,77	GCNT4/HMGCR/POLK	A	G	G	0,234	17471	0,072	0,013	4,30E-08	0,172
rs6872314	5	74,77	GCNT4/HMGCR/POLK	A	C	C	0,234	17473	0,072	0,013	4,48E-08	0,171
rs6896136	5	74,82	GCNT4/HMGCR/POLK	A	G	G	0,405	20884	0,086	0,010	7,87E-17	0,333
rs10055011	5	74,83	GCNT4/HMGCR/POLK	A	G	G	0,861	17415	-0,094	0,016	3,56E-09	0,200
rs1051795	5	74,93	GCNT4/HMGCR/POLK	A	G	G	0,792	17473	-0,078	0,014	9,99E-09	0,188
rs904743	5	74,95	GCNT4/HMGCR/POLK	A	G	G	0,143	20904	0,093	0,014	9,25E-11	0,201
rs34358	5	75,00	GCNT4/HMGCR/POLK	A	G	G	0,357	17468	0,065	0,012	2,23E-08	0,179
rs6987702	8	126,57	TRIB1/FAM84B	A	G	G	0,288	17413	0,073	0,012	3,28E-09	0,201
rs174570	11	61,35	FADS3/FADS2	A	G	G	0,834	20916	0,088	0,014	1,48E-10	0,196
rs11668477	19	11,06	...LDLR	A	G	G	0,194	17390	-0,137	0,014	2,74E-22	0,542
rs6511720	19	11,06	LDLR	A	C	C	0,878	9310	0,198	0,023	6,84E-18	0,798
rs2228671	19	11,07	LDLR	A	G	G	0,883	20910	0,158	0,016	9,33E-24	0,483

rs2228603	19	19,19	NCAN...ZNF101	A	G	G	0,933	17246	0,160	0,022	6,86E-13	0,299
rs2238675	19	19,20	NCAN...ZNF102	A	G	G	0,887	17465	0,097	0,018	4,84E-08	0,171
rs12610185	19	19,58	NCAN...ZNF103	A	G	G	0,924	18994	0,138	0,020	4,74E-12	0,252
rs2304128	19	19,61	NCAN...ZNF104	A	C	C	0,919	17470	0,149	0,020	2,64E-13	0,306
rs2304130	19	19,65	NCAN...ZNF104	A	G	G	0,075	20914	-0,153	0,019	2,00E-15	0,302
rs2965101	19	49,93	CEACAM16...TOMM40	A	G	G	0,309	17468	-0,070	0,012	6,58E-09	0,193
rs4803750	19	49,94	CEACAM16...TOMM40	A	G	G	0,058	17468	-0,179	0,024	7,81E-14	0,320
rs10402271	19	50,02	CEACAM16...TOMM40	A	C	C	0,350	22536	0,079	0,010	1,26E-14	0,264
rs6859	19	50,07	CEACAM16...TOMM40	A	G	G	0,577	17413	-0,068	0,011	1,64E-09	0,209
rs157580	19	50,09	CEACAM16...TOMM40	A	G	G	0,341	20903	-0,090	0,011	5,14E-17	0,336
rs2075650	19	50,09	CEACAM16...TOMM40	A	G	G	0,152	17463	0,138	0,015	2,88E-19	0,461

Genome-wide significant hits for HDL

SNP	Chromosome	Pos, Mb	Gene	Allele 1	Allele 2	Effect allele	Effect allele frequency	N	Beta	SE(Beta)	P-value	R2
rs6754295	2	21,12	APOB	A	C	C	0,254	17915	0,068	0,012	4,43E-08	0,167
rs264	8	19,86	LPL/SLC18A1	A	G	G	0,865	17923	-0,102	0,016	1,74E-10	0,227
rs10096633	8	19,88	LPL/SLC18A1	A	G	G	0,878	16286	-0,141	0,017	6,08E-16	0,401
rs4523270	8	19,90	LPL/SLC18A1	A	G	G	0,281	16271	0,073	0,013	7,79E-09	0,205
rs2083637	8	19,91	LPL/SLC18A1	A	G	G	0,259	17922	0,107	0,012	5,50E-18	0,417
rs2410630	8	19,92	LPL/SLC18A1	A	G	G	0,587	16280	-0,079	0,012	8,98E-12	0,286
rs3847303	9	104,73	ABCA1	A	G	G	0,881	16285	0,123	0,018	3,43E-12	0,297
rs3905000	9	104,74	ABCA1	A	G	G	0,865	17913	0,113	0,016	8,65E-13	0,285
rs1051006	11	47,26	MADD...FOLH1	A	G	G	0,794	21388	-0,078	0,012	1,72E-10	0,191
rs4752979	11	47,30	MADD...FOLH1	A	G	G	0,252	19747	0,065	0,012	4,26E-08	0,152
rs747782	11	47,90	MADD...FOLH1	A	G	G	0,202	17869	0,086	0,013	1,73E-10	0,228
rs7946766	11	47,96	MADD...FOLH1	A	G	G	0,840	16251	-0,084	0,015	4,03E-08	0,185

rs2270994	11	48,11	MADD...FOLH1	A	G	G	0,613	16223	-0,066	0,012	1,98E-08	0,194
rs10838852	11	48,24	MADD...FOLH1	A	G	G	0,446	21377	0,058	0,010	5,57E-09	0,159
rs7395662	11	48,48	MADD...FOLH1	A	G	G	0,605	17917	-0,073	0,011	6,05E-11	0,239
rs7120743	11	48,88	MADD...FOLH1	A	G	G	0,402	17772	0,069	0,011	5,56E-10	0,216
rs1809986	11	48,94	MADD...FOLH1	A	C	C	0,402	17921	0,070	0,011	2,92E-10	0,222
rs4775041	15	56,46	LIPC	G	C	C	0,309	3464	0,156	0,026	1,77E-09	1,045
rs10468017	15	56,47	LIPC	A	G	G	0,702	9299	-0,137	0,016	1,63E-17	0,780
rs166358	15	56,47	LIPC	A	G	G	0,850	16272	-0,092	0,016	7,12E-09	0,206
rs2043085	15	56,47	LIPC	T	C	C	0,604	3464	-0,160	0,024	3,97E-11	1,259
rs1532085	15	56,47	LIPC	A	G	G	0,588	19736	-0,130	0,010	9,72E-36	0,789
rs415799	15	56,48	LIPC	A	G	G	0,546	19723	0,111	0,010	4,61E-27	0,588
rs397923	15	56,48	LIPC	A	T	T	0,570	3464	-0,135	0,024	2,55E-08	0,895
rs487766	15	56,48	LIPC	A	G	G	0,235	16264	0,084	0,013	4,58E-10	0,239
rs11856159	15	56,49	LIPC	A	G	G	0,799	19742	-0,089	0,013	4,44E-12	0,243
rs473224	15	56,52	LIPC	A	C	C	0,859	16210	-0,108	0,016	2,89E-11	0,273
rs261336	15	56,53	LIPC	A	G	G	0,185	16282	0,094	0,015	9,09E-11	0,258
rs2241770	16	55,42	NUP93/HERPUD1/CETP	A	G	G	0,099	16282	-0,107	0,019	1,40E-08	0,198
rs16962767	16	55,43	NUP93/HERPUD1/CETP	A	G	G	0,100	10954	-0,123	0,023	4,82E-08	0,272
rs2217332	16	55,53	NUP93/HERPUD1/CETP	A	G	G	0,855	19745	0,090	0,015	6,77E-10	0,193
rs247615	16	55,54	NUP93/HERPUD1/CETP	A	G	G	0,210	16273	-0,089	0,014	1,81E-10	0,250
rs9989419	16	55,54	NUP93/HERPUD1/CETP	A	G	G	0,611	21359	0,147	0,010	3,07E-48	0,997
rs12448528	16	55,54	NUP93/HERPUD1/CETP	A	G	G	0,773	3464	0,175	0,029	1,94E-09	1,040
rs247616	16	55,55	NUP93/HERPUD1/CETP	T	C	C	0,679	3464	-0,209	0,026	2,80E-16	1,932
rs3764261	16	55,55	NUP93/HERPUD1/CETP	A	C	C	0,683	16253	-0,245	0,012	2,59E-89	2,470
rs1800775	16	55,55	NUP93/HERPUD1/CETP	A	C	C	0,521	5840	-0,187	0,019	2,25E-23	1,699

rs711752	16	55,55	NUP93 /HERPUD1/CETP	A	G	G	0,568	3464	-0,194	0,025	3,12E-15	1,795
rs1864163	16	55,55	NUP93 /HERPUD1/CETP	A	G	G	0,752	5806	0,181	0,022	4,16E-17	1,218
rs7203984	16	55,56	NUP93 /HERPUD1/CETP	A	C	C	0,187	3464	-0,193	0,031	2,67E-10	1,152
rs7205804	16	55,56	NUP93 /HERPUD1/CETP	A	G	G	0,562	3464	-0,201	0,024	7,69E-17	2,006
rs1532624	16	55,56	NUP93 /HERPUD1/CETP	A	C	C	0,568	19674	-0,213	0,010	9,45E-94	2,144
rs7499892	16	55,56	NUP93 /HERPUD1/CETP	A	G	G	0,826	16266	0,232	0,015	1,69E-54	1,46
rs4784744	16	55,57	NUP93 /HERPUD1/CETP	A	G	G	0,650	19747	0,106	0,011	6,66E-23	0,492
rs5882	16	55,57	NUP93 /HERPUD1/CETP	A	G	G	0,337	19742	0,085	0,011	6,37E-15	0,308
rs6499137	16	66,23	CTCF...PRMT8	A	C	C	0,095	16282	0,124	0,019	1,47E-10	0,252
rs2271293	16	66,46	CTCF...PRMT8	A	G	G	0,869	17910	-0,129	0,016	8,34E-16	0,362
rs10468274	16	66,48	CTCF...PRMT8	A	G	G	0,831	16281	-0,100	0,015	2,64E-11	0,273
rs9932251	16	66,69	CTCF...PRMT8	A	G	G	0,855	16286	-0,108	0,016	1,40E-11	0,280
rs2418736	16	66,71	CTCF...PRMT8	A	G	G	0,816	16278	-0,088	0,015	1,57E-09	0,224
rs4359427	16	66,76	CTCF...PRMT8	A	G	G	0,856	16263	-0,109	0,016	1,38E-11	0,281
rs1975802	16	66,84	CTCF...PRMT8	A	G	G	0,168	16283	0,084	0,015	2,28E-08	0,192
rs8058517	16	66,94	CTCF...PRMT8	A	G	G	0,862	17927	-0,097	0,016	6,92E-10	0,212
rs4939883	18	45,42	LIPG/ACCA2	A	G	G	0,832	16258	0,103	0,015	1,59E-11	0,279

Genome-wide significant hits for LDL

SNP	Chromosome	Pos, Mb	Gene	Allele 1	Allele 2	Effect allele	Effect allele frequency	N	Beta	SE(Beta)	P-value	R2
rs611917	1	109,53	SARS/CELSR2/MYBPHL	A	G	G	0,327	12681	-0,091	0,014	4,73E-11	0,341
rs629301	1	109,53	SARS/CELSR2/MYBPHL	T	G	G	0,223	3445	-0,162	0,029	2,01E-08	0,914
rs646776	1	109,53	SARS/CELSR2/MYBPHL	A	G	G	0,220	12685	-0,155	0,016	7,76E-23	0,763
rs10198175	2	21,06	APOB	A	G	G	0,904	12704	-0,135	0,022	9,11E-10	0,295
rs10495712	2	21,11	APOB	A	G	G	0,744	14335	-0,081	0,014	1,15E-08	0,227
rs693	2	21,14	APOB	A	G	G	0,533	16112	-0,098	0,012	3,56E-17	0,441

rs1713222	2	21,18	APOB	A	G	G	0,853	12683	0,131	0,019	2,15E-12	0,389
rs1429974	2	21,21	APOB	A	C	C	0,694	14289	-0,098	0,013	2,87E-13	0,373
rs754524	2	21,22	APOB	A	C	C	0,263	12705	0,098	0,015	3,96E-11	0,343
rs754523	2	21,22	APOB	A	G	G	0,309	14283	0,099	0,013	1,03E-13	0,387
rs6756629	2	43,98	ABCG5	A	G	G	0,924	12706	0,157	0,025	2,59E-10	0,315
rs3846662	5	74,69	GCNT4/ HMGR/ POLK	A	G	G	0,443	16135	0,079	0,012	1,49E-11	0,282
rs6896136	5	74,82	GCNT4 /HMGR/ POLK	A	G	G	0,410	16124	0,071	0,012	1,55E-09	0,226
rs12670798	7	21,38	DNAH11	A	G	G	0,243	12695	0,089	0,015	6,09E-09	0,266
rs174570	11	61,35	FADS3/FADS2	A	G	G	0,821	16153	0,110	0,015	4,39E-13	0,325
rs2851682	11	61,37	FADS3/FADS2	A	G	G	0,155	12700	-0,112	0,018	1,39E-09	0,289
rs11668477	19	11,06	LDLR	A	G	G	0,184	12638	-0,117	0,017	5,23E-12	0,377
rs2228671	19	11,07	LDLR	A	G	G	0,886	16148	0,136	0,018	4,22E-14	0,353
rs2965101	19	49,93	CEACAM16...TOMM40	A	G	G	0,308	12702	-0,091	0,014	1,61E-10	0,322
rs4803750	19	49,94	CEACAM16...TOMM40	A	G	G	0,053	12707	-0,251	0,029	9,59E-18	0,579
rs1871045	19	50,02	CEACAM16...TOMM40	A	G	G	0,645	17788	0,063	0,011	3,40E-08	0,171
rs10402271	19	50,02	CEACAM16...TOMM40	A	C	C	0,354	16147	0,096	0,012	1,68E-15	0,393
rs6859	19	50,07	CEACAM16...TOMM40	A	G	G	0,575	12668	-0,077	0,013	5,44E-09	0,269
rs157580	19	50,09	CEACAM16...TOMM40	A	G	G	0,333	16142	-0,111	0,012	2,06E-19	0,503
rs2075650	19	50,09	CEACAM16...TOMM40	A	G	G	0,152	12697	0,160	0,018	9,26E-19	0,616
rs405509	19	50,10	CEACAM16...TOMM40	A	C	C	0,545	12705	-0,082	0,013	5,19E-10	0,304

Genome-wide significant hits for TG

SNP	Chromosome	Pos, Mb	Gene	Allele 1	Allele 2	Effect allele	Effect allele frequency	N	Beta	SE(Beta)	P-value	R2
rs1167998	1	62,64	DOCK7	A	C	C	0,322	14268	-0,091	0,013	1,95E-12	0,347
rs10889353	1	62,83	DOCK7	A	C	C	0,307	14337	-0,085	0,013	8,23E-11	0,294
rs6754295	2	21,12	APOB	A	C	C	0,255	14338	-0,077	0,014	2,45E-08	0,217

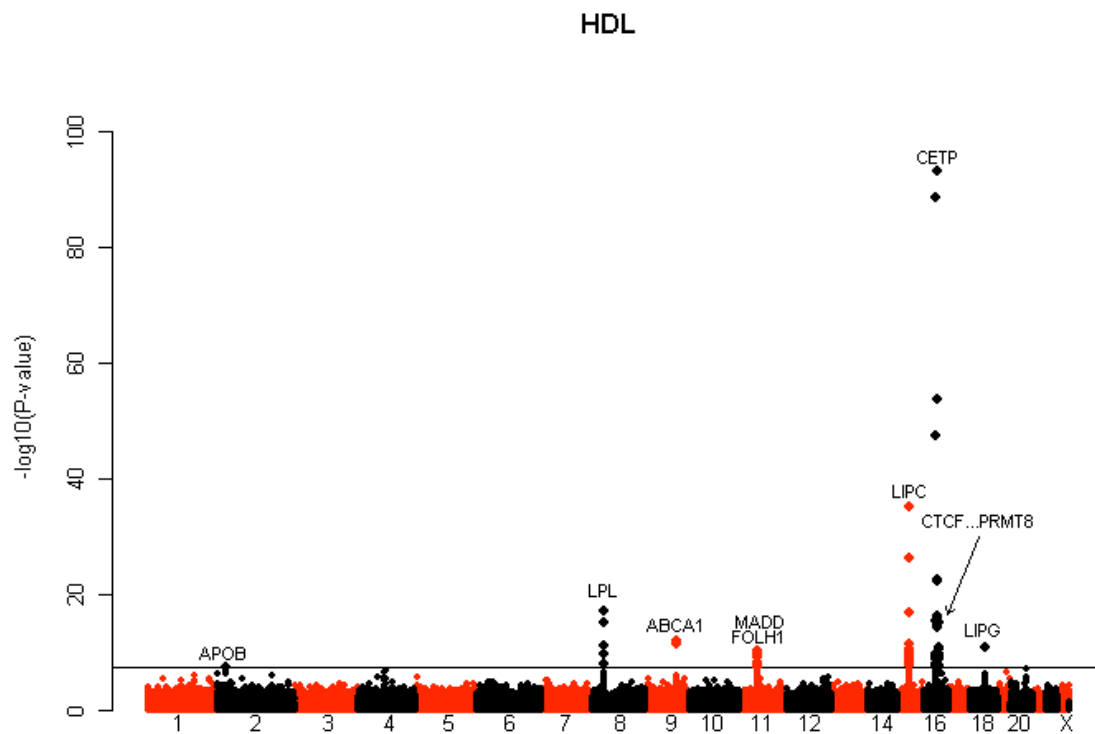
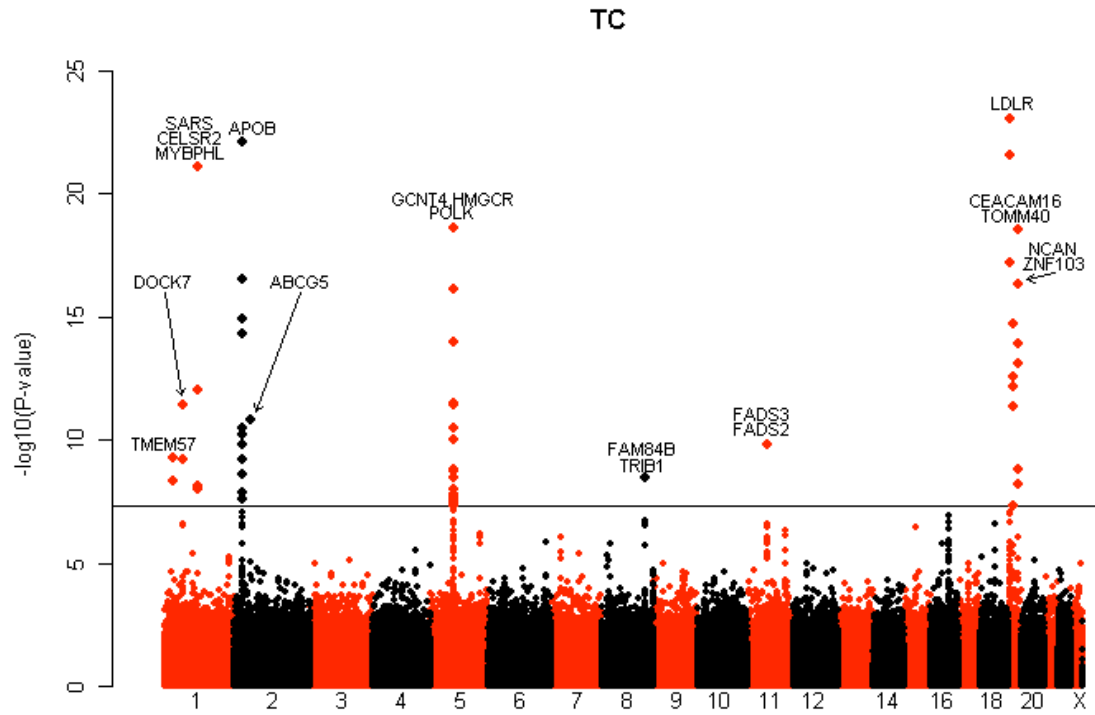
rs673548	2	21,15	APOB	A	G	G	0,760	12694	0,086	0,015	1,10E-08	0,257
rs1260326	2	27,64	GCKR	A	G	G	0,632	12435	-0,112	0,013	5,17E-17	0,565
rs780094	2	27,65	GCKR	A	G	G	0,629	17790	-0,103	0,011	3,06E-20	0,478
rs1919127	2	27,71	GCKR	A	G	G	0,266	14339	0,078	0,014	1,24E-08	0,226
rs2240466	7	72,30	BAZ1B/BCL7B/TBL2/MLXIPL	A	G	G	0,874	12680	0,137	0,019	1,11E-12	0,399
rs714052	7	72,31	BAZ1B/BCL7B/TBL2/MLXIPL	A	G	G	0,127	12704	-0,136	0,019	1,61E-12	0,393
rs2286276	7	72,43	BAZ1B/BCL7B/TBL2/MLXIPL	A	G	G	0,740	12688	0,087	0,015	3,03E-09	0,277
rs11974409	7	72,43	BAZ1B/BCL7B/TBL2/MLXIPL	A	G	G	0,184	12705	-0,105	0,017	2,13E-10	0,318
rs10096633	8	19,88	LPL/SLC18A1	A	G	G	0,879	12708	0,174	0,020	1,89E-18	0,604
rs4523270	8	19,90	LPL/SLC18A1	A	G	G	0,278	12694	-0,082	0,014	1,30E-08	0,255
rs2083637	8	19,91	LPL/SLC18A1	A	G	G	0,258	14344	-0,107	0,014	1,04E-14	0,417
rs2410630	8	19,92	LPL/SLC18A1	A	G	G	0,594	12701	0,080	0,013	1,32E-09	0,290
rs480878	11	116,03	BUD13/APO(A1/A4/A5/C3)...	A	G	G	0,863	16160	-0,097	0,017	7,99E-09	0,206
rs12272004	11	116,11	BUD13/APO(A1/A4/A5/C3)...	A	C	C	0,926	12622	-0,181	0,025	5,38E-13	0,412
rs28927680	11	116,12	BUD13/APO(A1/A4/A5/C3)...	G	C	C	0,927	3465	-0,274	0,046	3,86E-09	1,001
rs12292921	11	116,13	BUD13/APO(A1/A4/A5/C3)...	A	C	C	0,072	12691	0,181	0,025	9,06E-13	0,402
rs35120633	11	116,16	BUD13/APO(A1/A4/A5/C3)...	A	G	G	0,934	3465	-0,309	0,049	2,29E-10	1,160
rs3135506	11	116,17	BUD13/APO(A1/A4/A5/C3)...	G	C	C	0,065	3465	0,307	0,050	7,44E-10	1,094
rs2075292	11	116,24	BUD13/APO(A1/A4/A5/C3)...	A	C	C	0,132	16163	0,116	0,017	5,68E-12	0,293
rs588918	11	116,36	BUD13/APO(A1/A4/A5/C3)...	A	G	G	0,866	14345	-0,097	0,018	4,92E-08	0,207
rs1351452	11	116,45	BUD13/APO(A1/A4/A5/C3)...	A	C	C	0,862	12706	-0,116	0,019	7,41E-10	0,298
rs157580	19	50,09	CEACAM16...TOMM40	A	G	G	0,333	16160	-0,069	0,012	1,19E-08	0,201
rs439401	19	50,11	CEACAM16...TOMM40	A	G	G	0,681	11885	0,086	0,014	1,78E-09	0,305

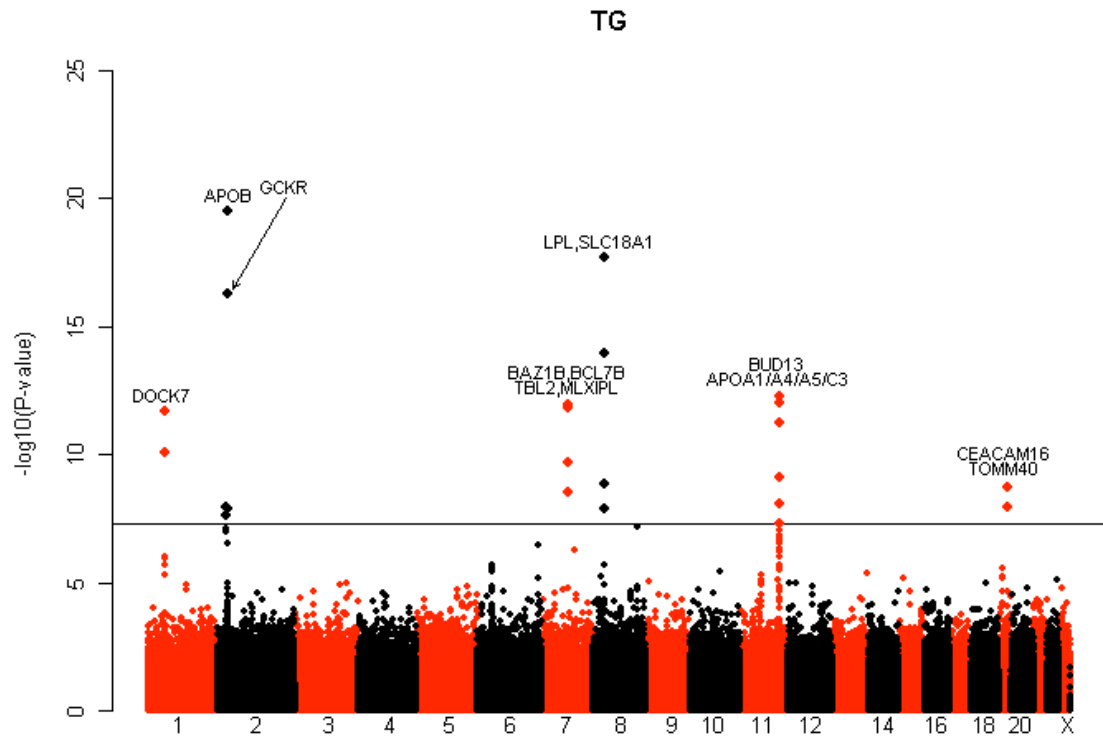
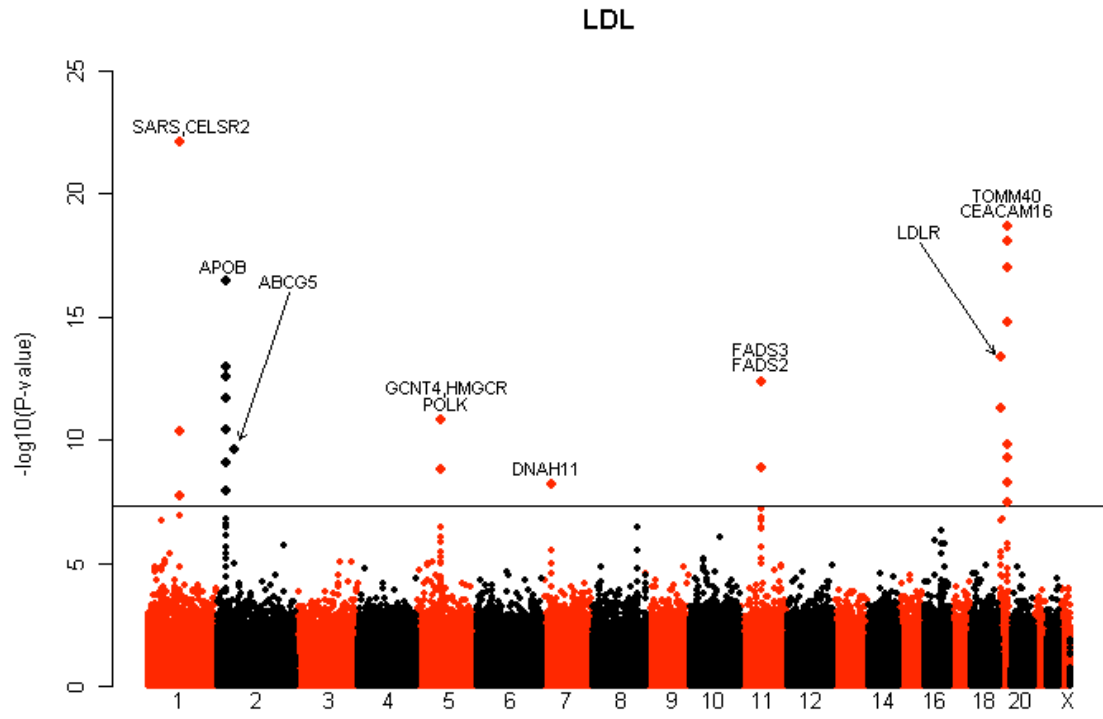
Supplementary Table 2: Most strongly associated pathways from the GWANA analyses for total cholesterol (TC), high-density lipoprotein (HDL), low-density lipoprotein (LDL) and triglycerides (TG)

TC pathways		
Pathway	Score	Marker rank permuted score
Cholesterol metabolic process	9.88×10^{-8}	0.0001
Sterol metabolic process	2.67×10^{-7}	0.0001
Lipid transporter activity	2.50×10^{-6}	0.0001
Response to nutrient	2.33×10^{-5}	0.0001
Regulation of protein transport	3.94×10^{-5}	0.0001
Response to nutrient levels	1.55×10^{-4}	0.0002
Lipid transport	8.23×10^{-7}	0.0003
Steroid metabolic process	2.00×10^{-5}	0.0003
Response to extracellular stimulus	2.34×10^{-4}	0.0003
Humoral immune response	1.81×10^{-4}	0.0010
Glycosaminoglycan binding	1.34×10^{-4}	0.0035
Transcriptional activator activity	3.67×10^{-4}	0.0037
Polysaccharide binding	2.03×10^{-4}	0.0046
Heparin binding	3.59×10^{-4}	0.0046
Endopeptidase activity	3.75×10^{-4}	0.0073
Regulation of hydrolase activity	4.67×10^{-4}	0.0074
Pattern binding	3.82×10^{-4}	0.0079
HDL pathways		
Pathway	Score	Marker rank permuted score
Lipid transport	4.70×10^{-9}	0.0001
Cholesterol metabolic process	2.01×10^{-8}	0.0001
Sterol metabolic process	4.67×10^{-8}	0.0001
Monocarboxylic acid metabolic process	7.22×10^{-6}	0.0001
Alcohol metabolic process	1.86×10^{-5}	0.0001
Lipid transporter activity	4.98×10^{-7}	0.0002
Steroid metabolic process	2.01×10^{-6}	0.0003
Lipid catabolic process	7.51×10^{-5}	0.0003
Fatty acid metabolic process	6.29×10^{-5}	0.0004
Solute: cation antiporter activity	3.74×10^{-4}	0.0007
Solute: hydrogen antiporter activity	3.74×10^{-4}	0.0007

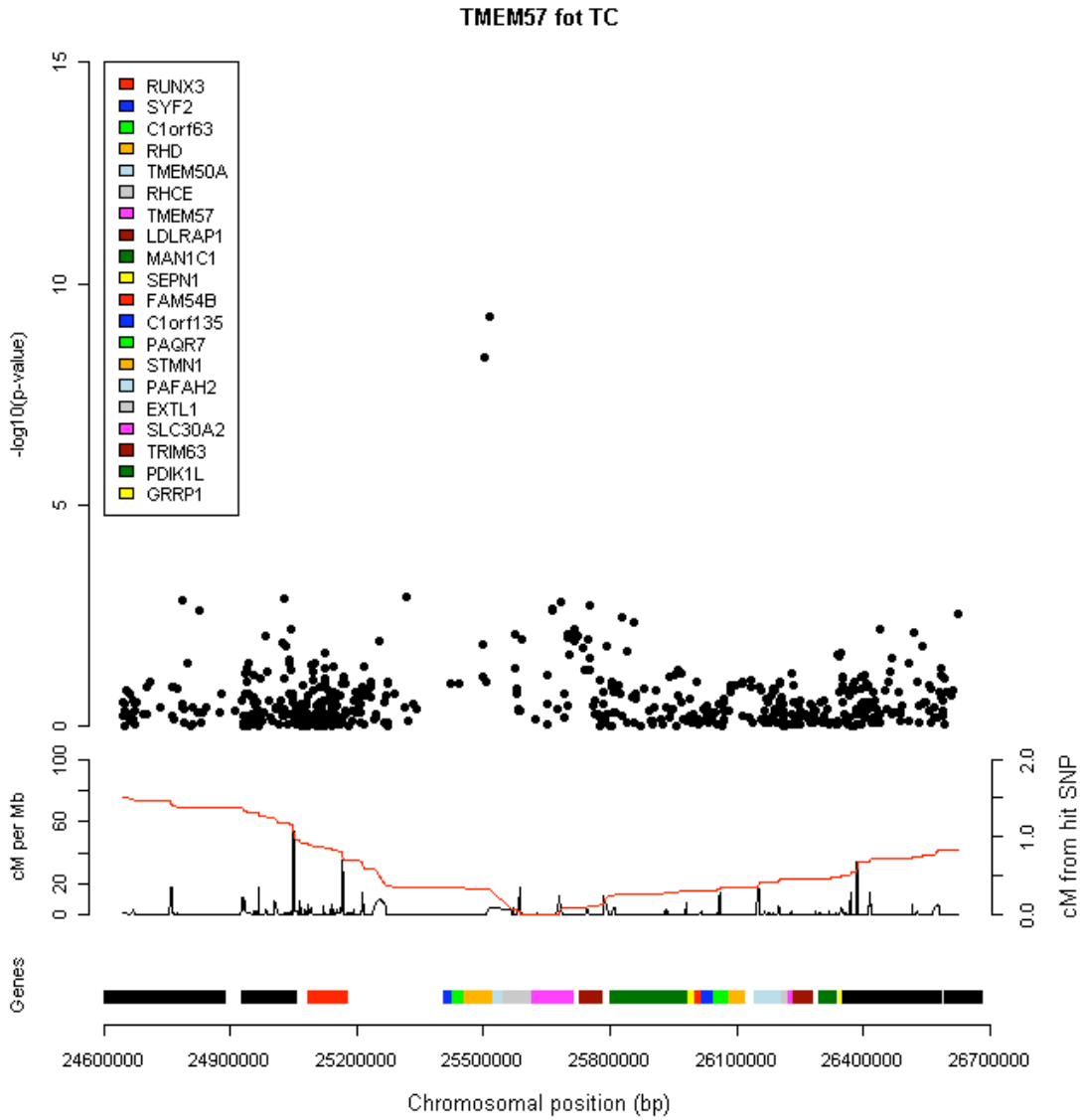
Lipid binding	2.94×10^{-7}	0.0036
Lipid biosynthetic process	4.23×10^{-4}	0.0036
Carbohydrate biosynthetic process	5.55×10^{-5}	0.0038
Carboxylic ester hydrolase activity	1.89×10^{-4}	0.0041
Circulation	1.41×10^{-4}	0.0052
Carbohydrate binding	4.65×10^{-4}	0.0290
Phospholipid binding	3.28×10^{-5}	0.0316
GPI anchor binding	7.34×10^{-5}	0.0384
Glycerolipid metabolism	2.07×10^{-4}	0.0025
LDL pathways		
Pathway	Score	Marker rank permuted score
Sterol metabolic process	9.19×10^{-9}	0.0001
Cholesterol metabolic process	9.46×10^{-8}	0.0001
Steroid biosynthetic process	4.73×10^{-5}	0.0001
Steroid metabolic process	4.86×10^{-6}	0.0002
Lipid biosynthetic process	2.66×10^{-4}	0.0017
TG pathways		
Pathway	Score	Marker rank permuted score
Lipid catabolic process	1.68×10^{-4}	0.0006
Transcription coactivator activity	1.99×10^{-4}	0.0008
Transcription cofactor activity	9.72×10^{-5}	0.0010
Transcription factor binding	4.51×10^{-4}	0.0033

Supplementary Figure 1: Manhattan-plots for total cholesterol (TC), high-density lipoprotein (HDL), low-density lipoprotein (LDL) and triglycerides (TG)

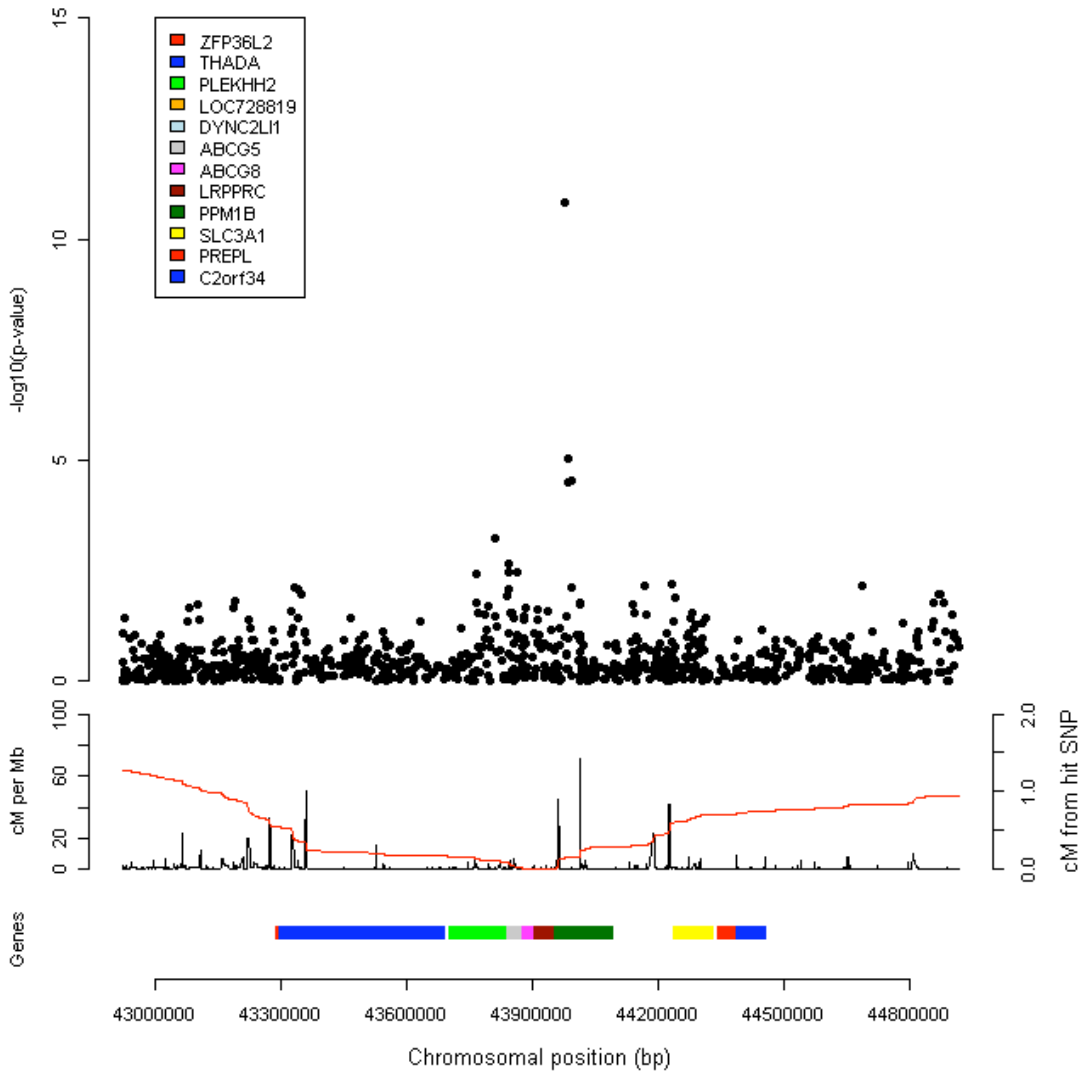




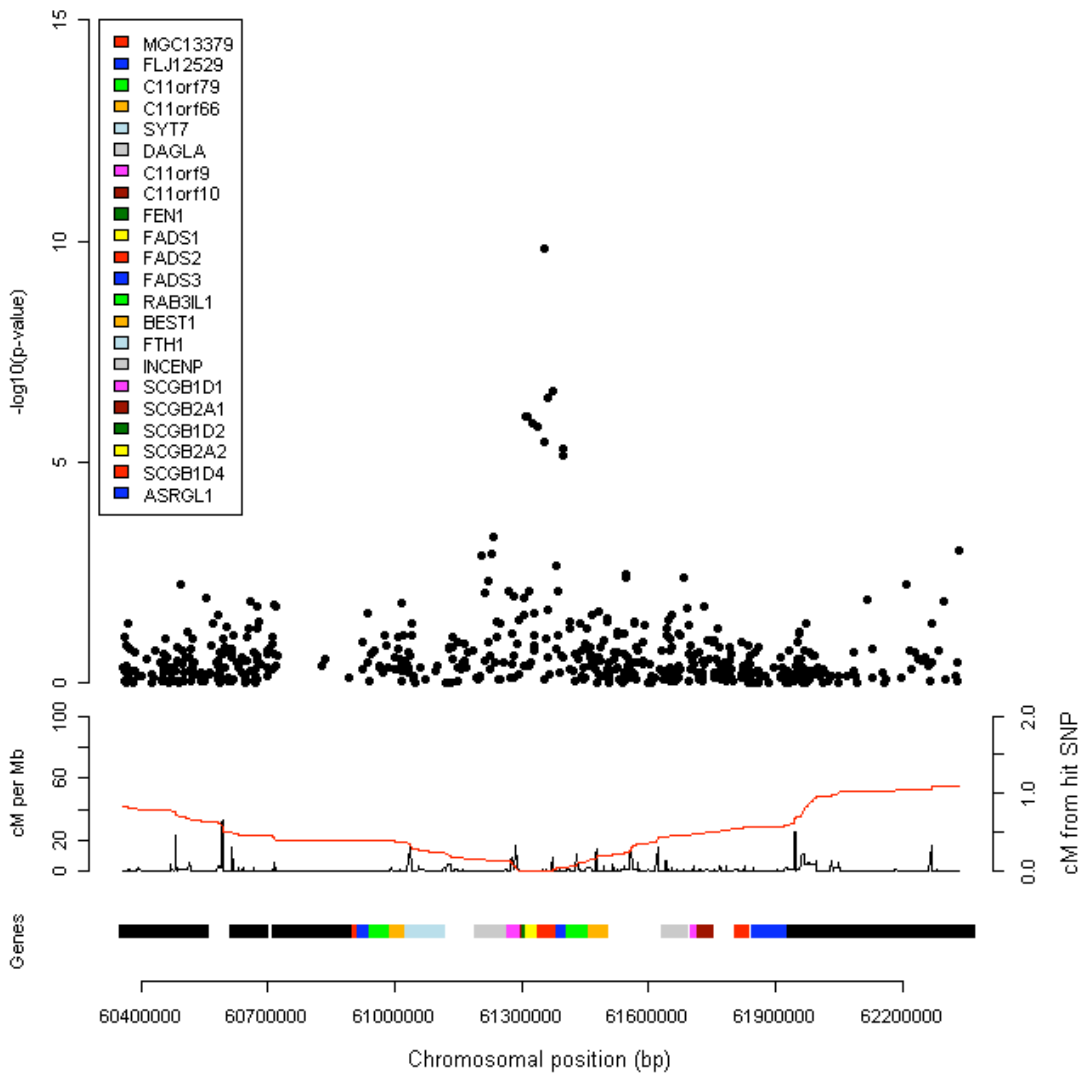
Supplementary Figure 2: 2Mb window around the newly identified regions shaded grey in Supplementary table 1. In the second section of the picture red line represents the cM from the SNP having lowest p-value and black line represents the linkage structure with cM/Mb



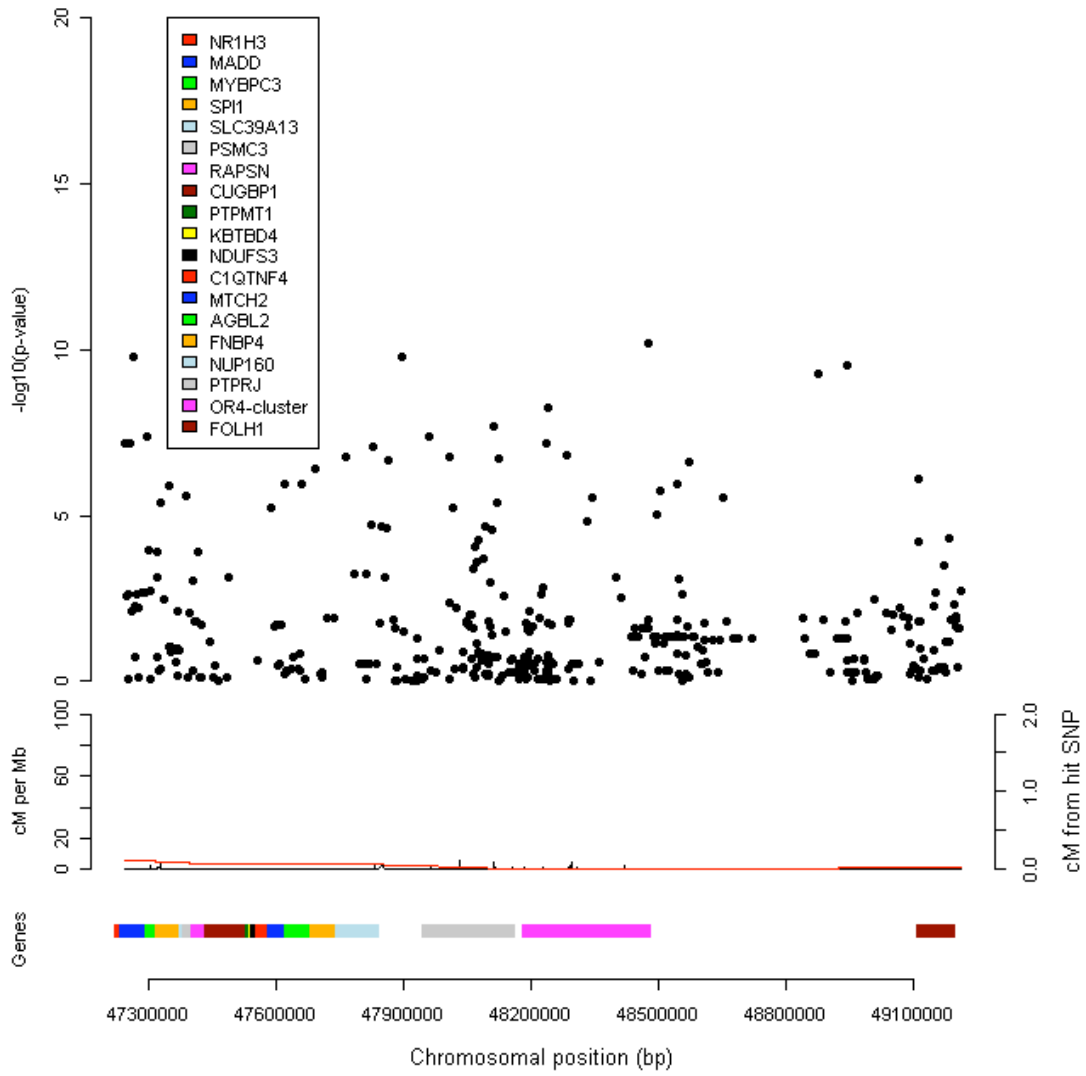
ABCG5 for TC



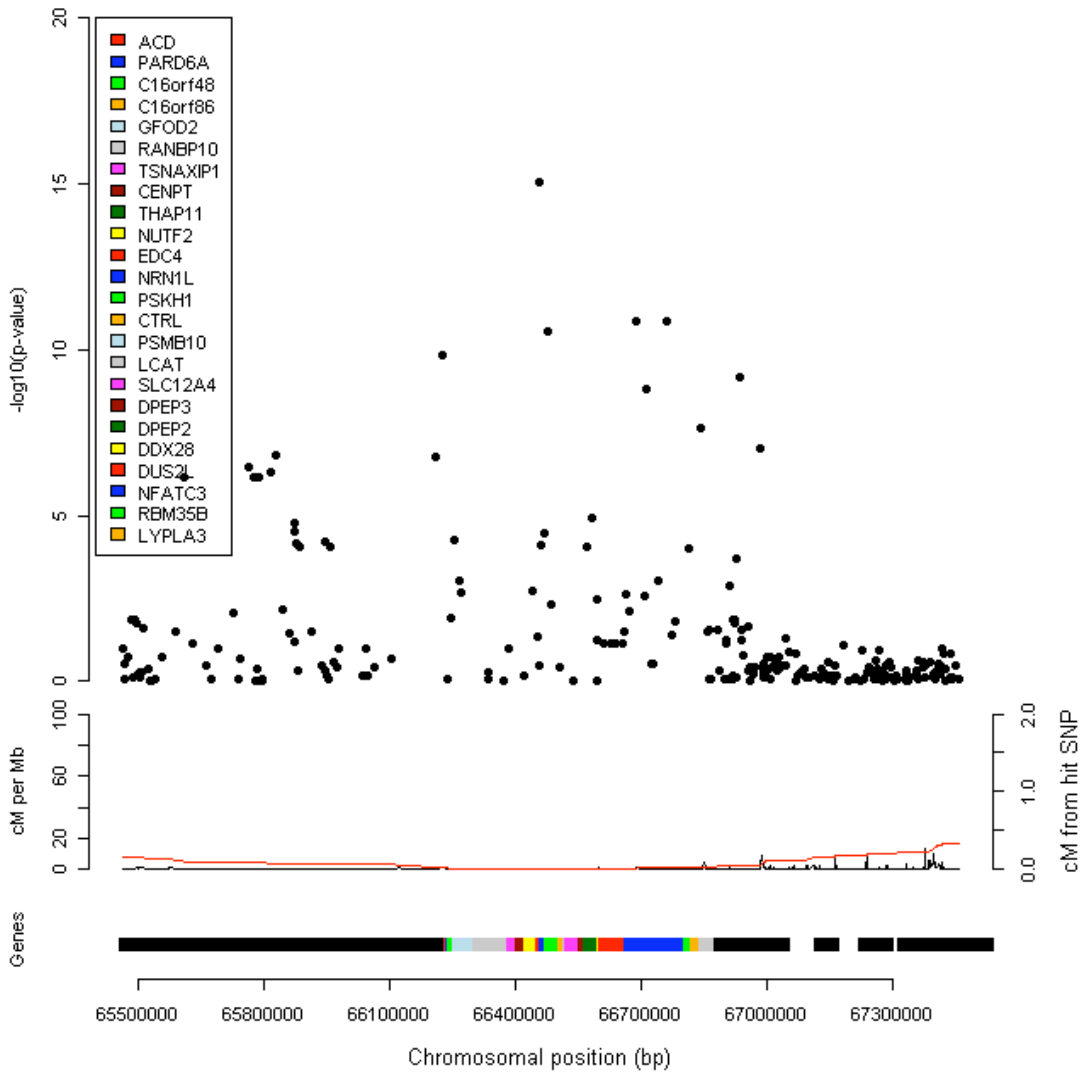
FADS2/FADS3 for TC



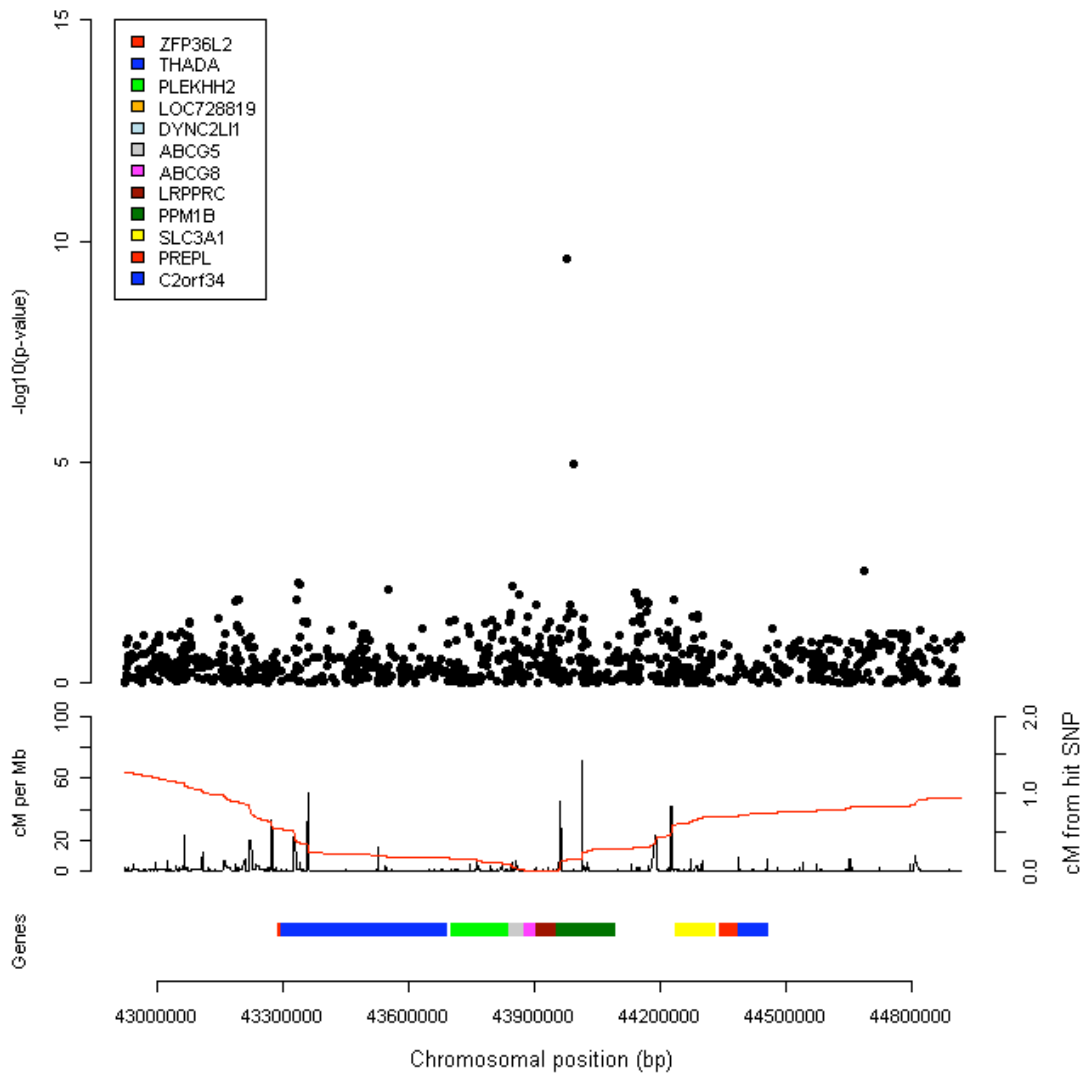
MADD-FOLH1 for HDL



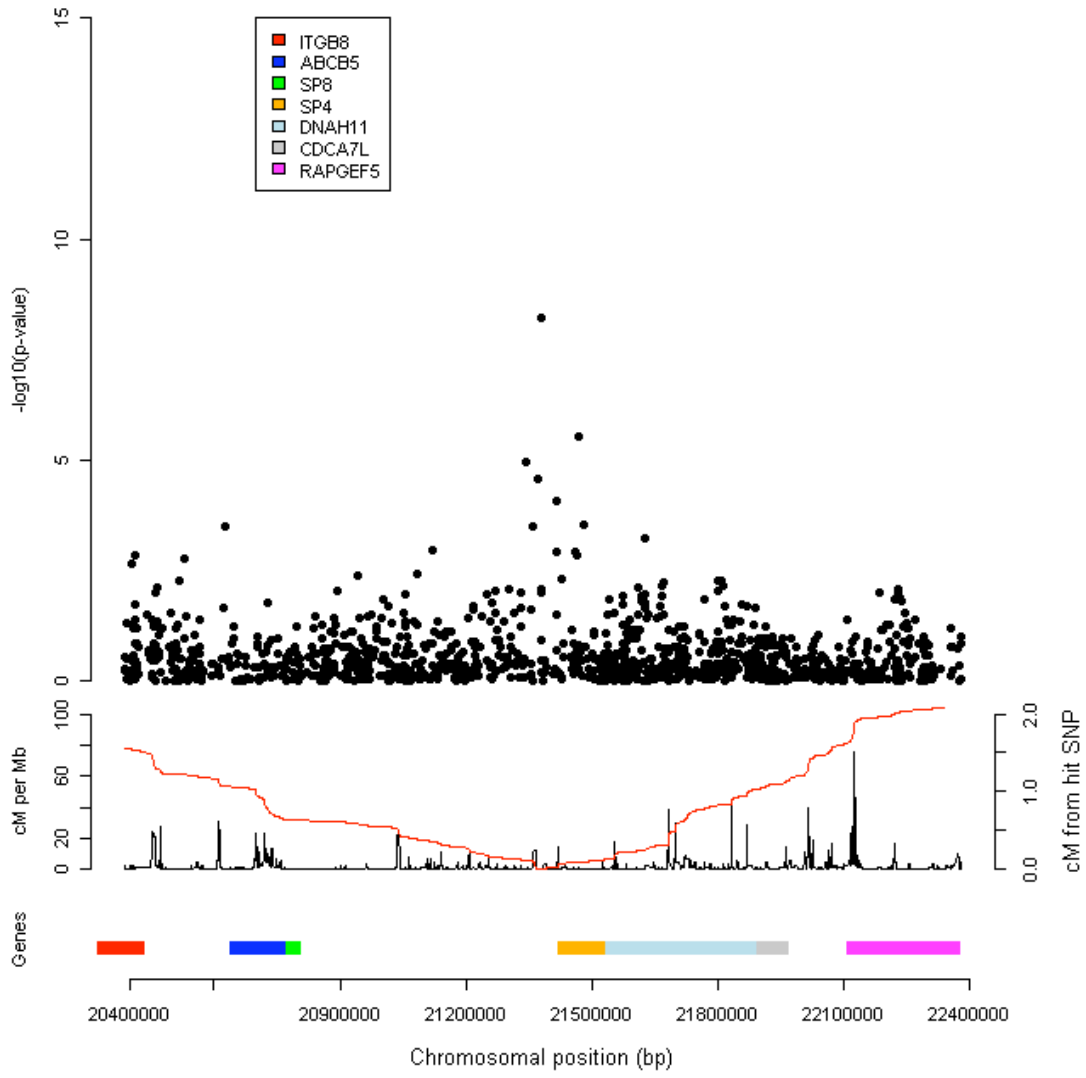
CTCF-PRMT8 for HDL



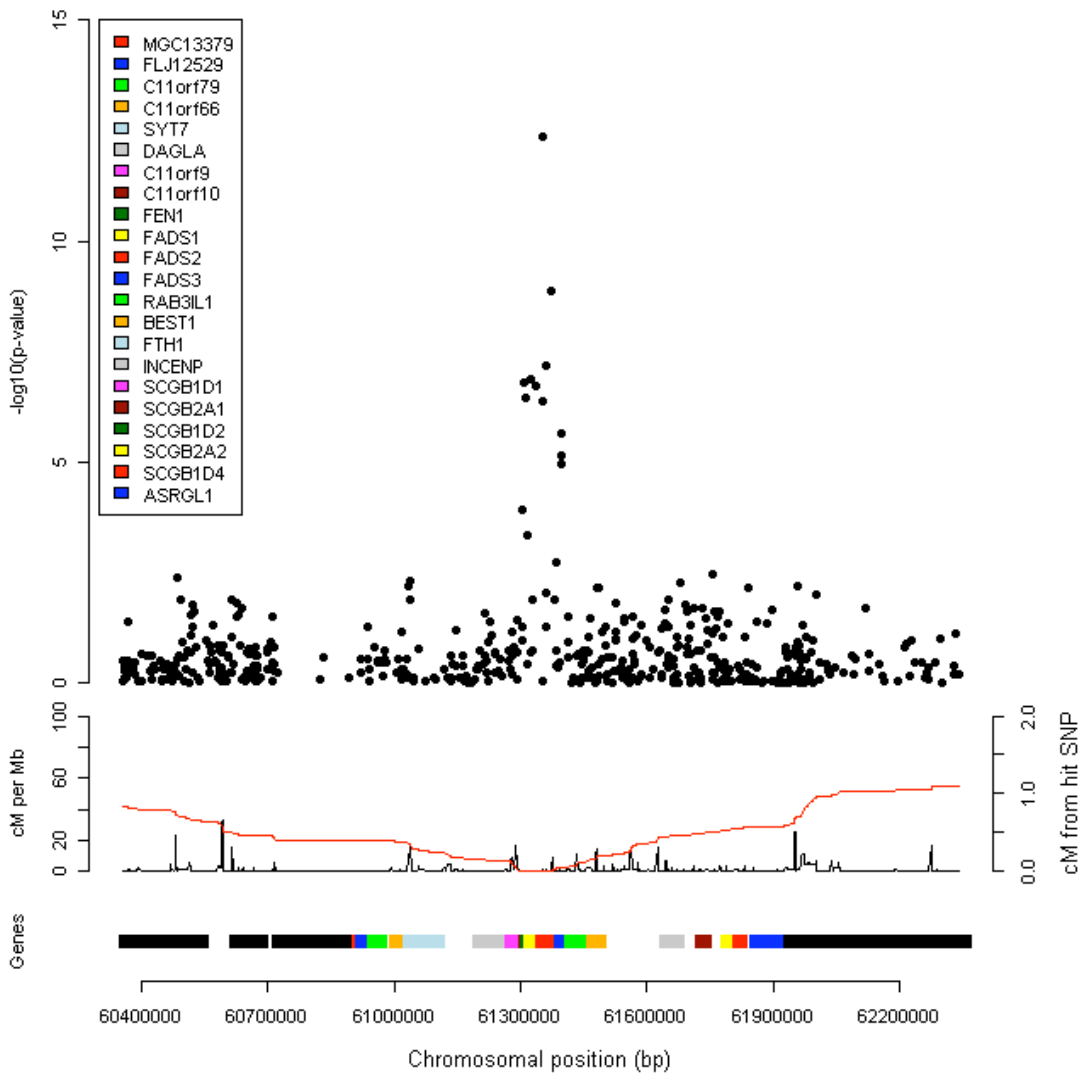
ABCG5 for LDL



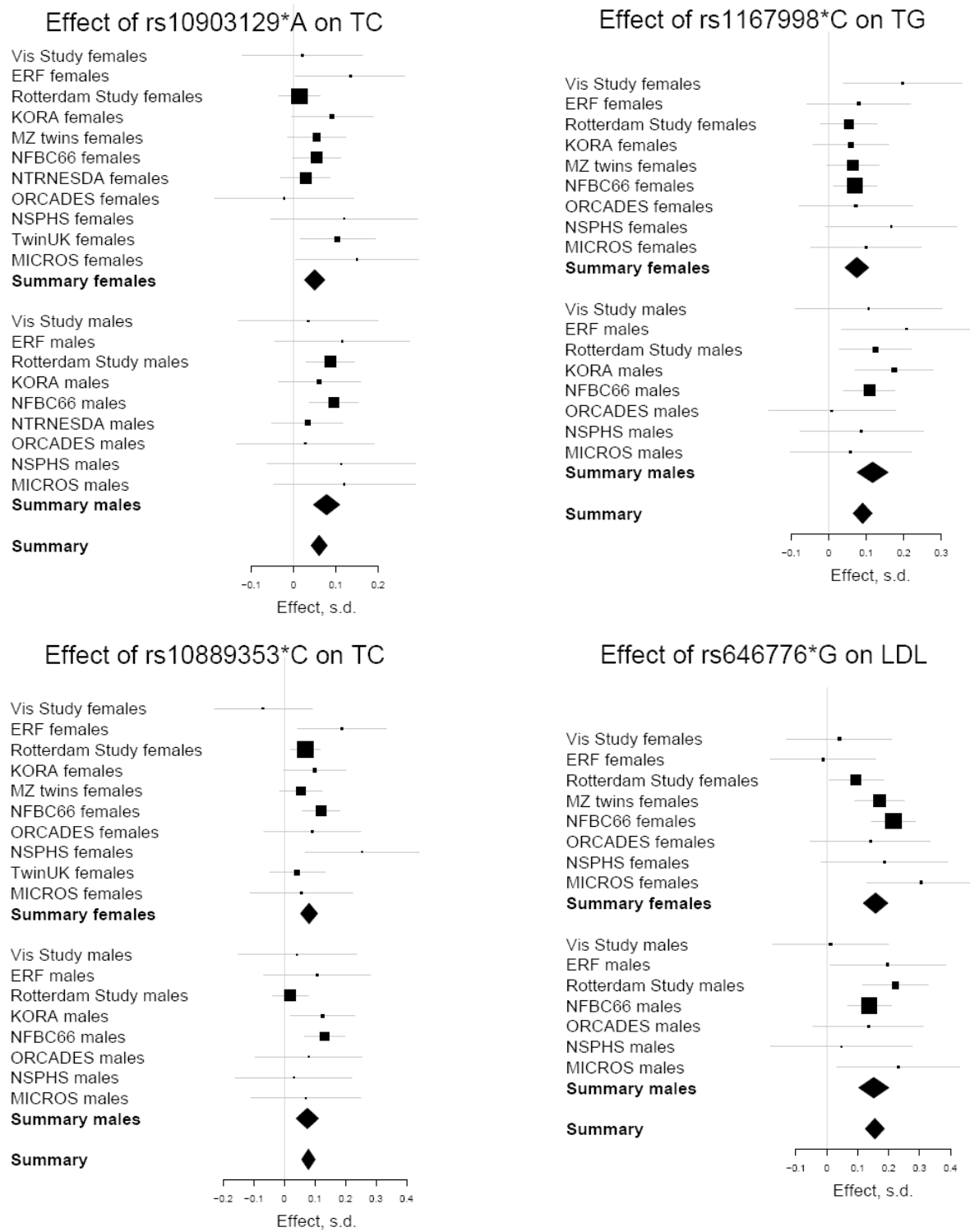
DNAH11 for LDL



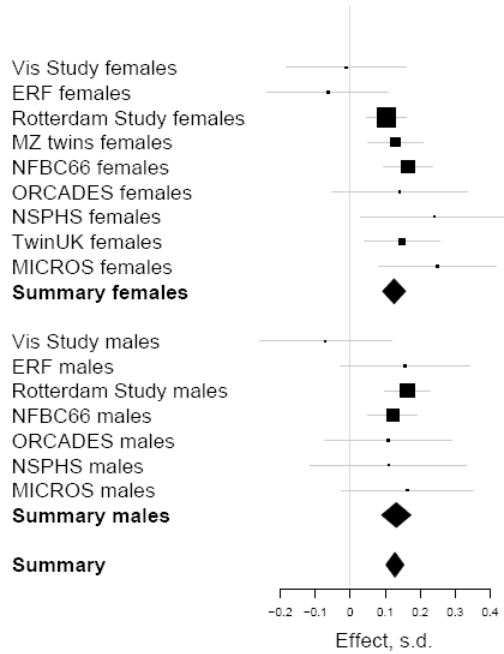
FADS2/FADS3 for LDL



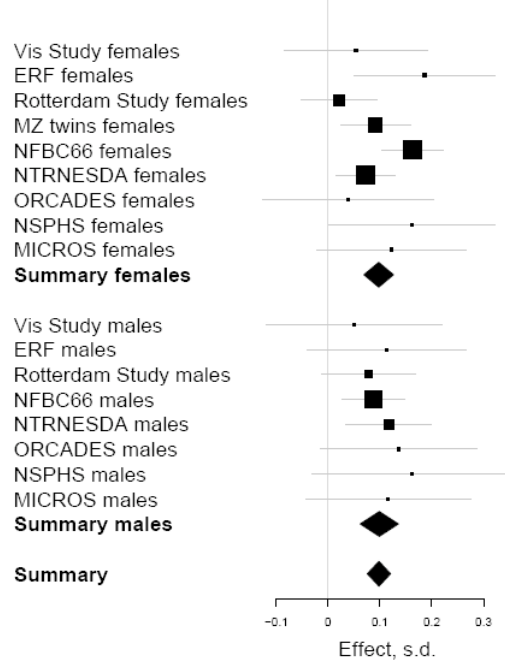
Supplementary Figure 3: Effect of SNPs specified in Supplementary table 1 on the associated trait separately for different cohorts and sexes



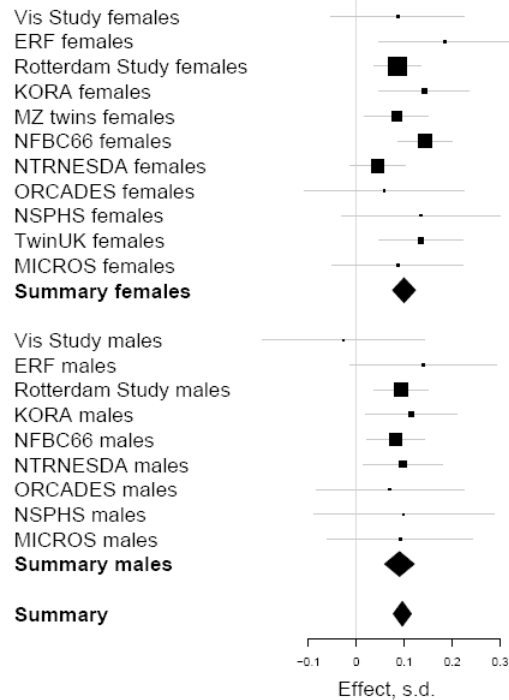
Effect of rs646776*G on TC



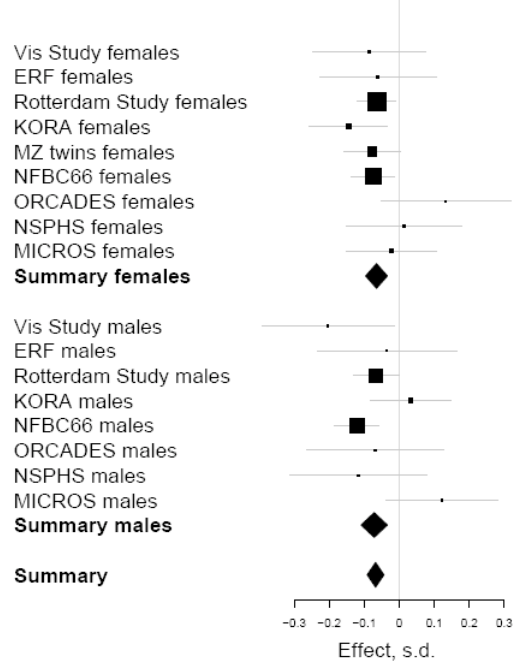
Effect of rs693*A on LDL



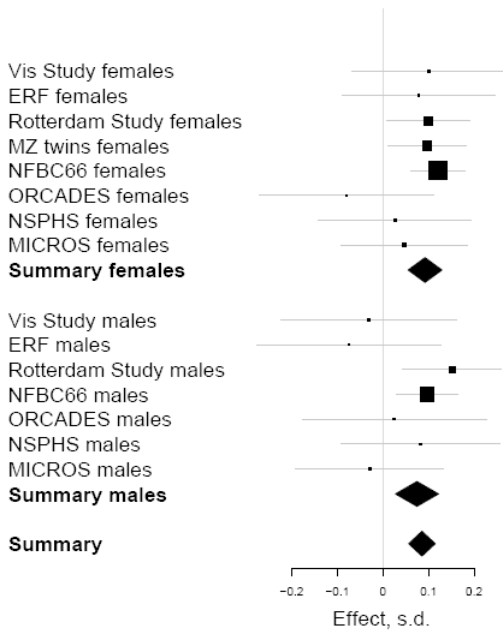
Effect of rs693*A on TC



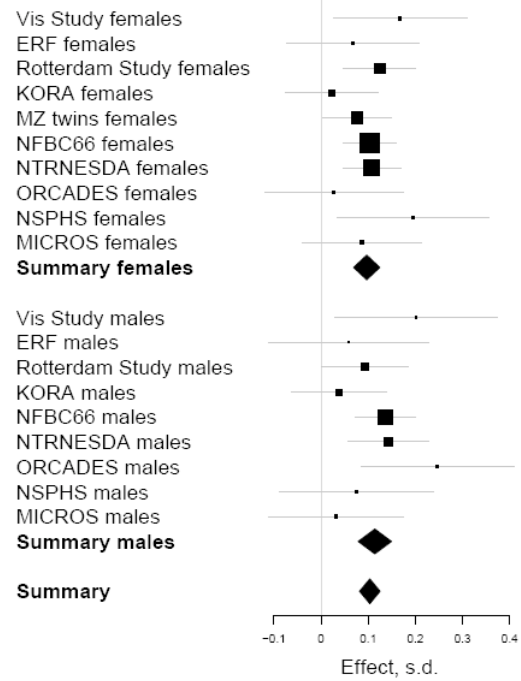
Effect of rs6754295*C on HDL



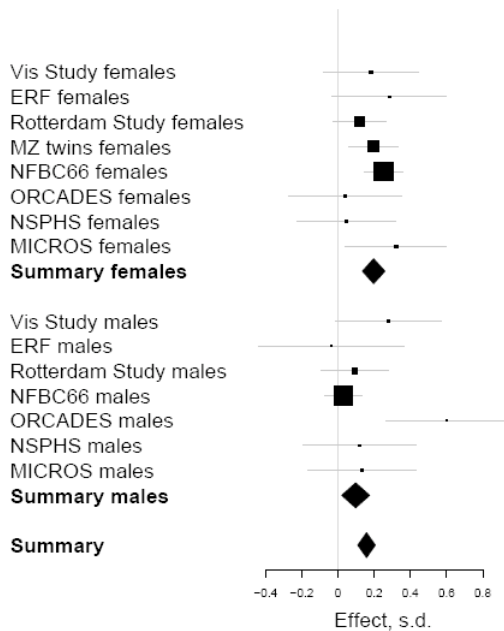
Effect of rs673548*A on TG



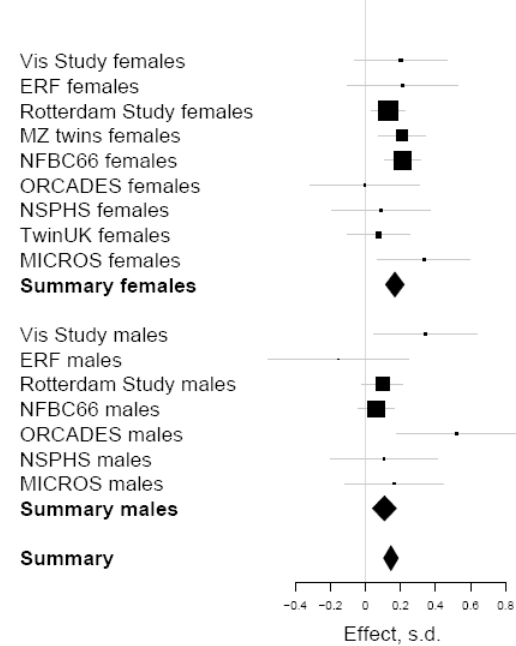
Effect of rs780094*A on TG



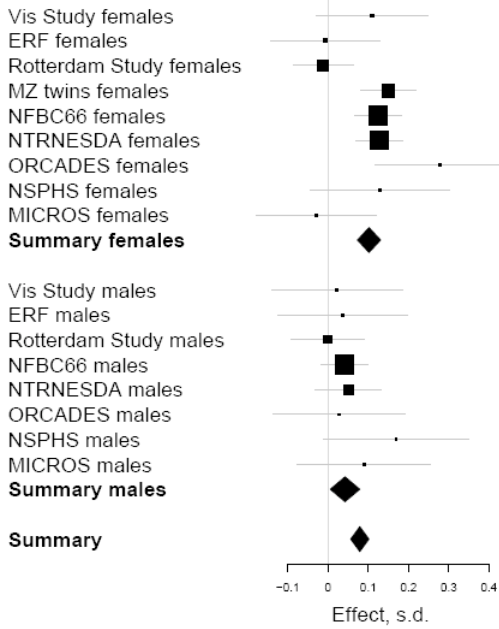
Effect of rs6756629*A on LDL



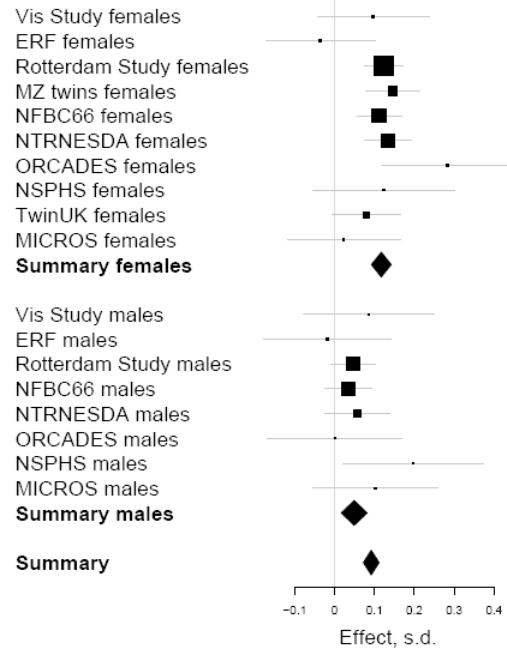
Effect of rs6756629*A on TC



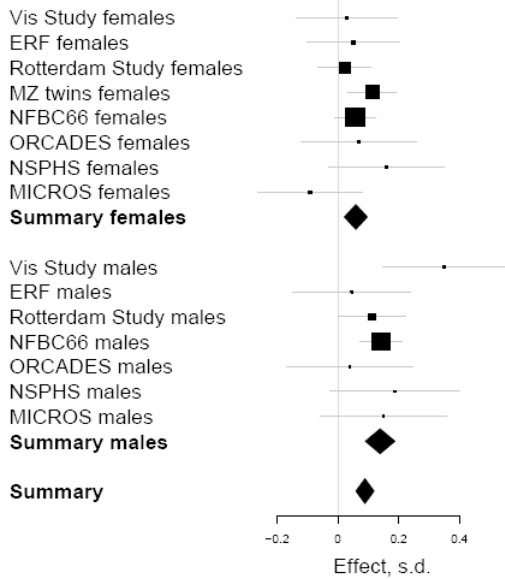
Effect of rs3846662*G on LDL



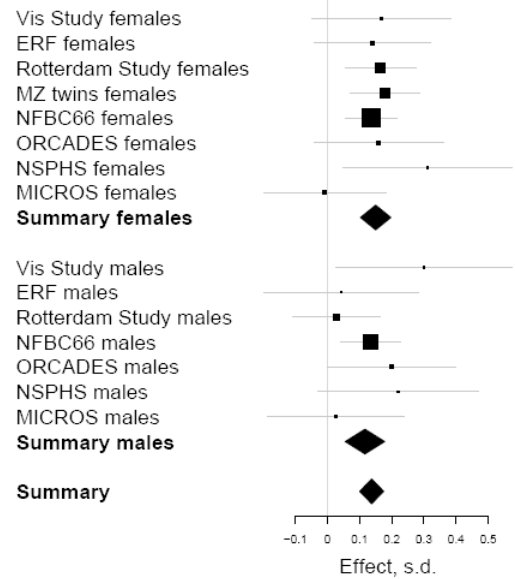
Effect of rs3846662*G on TC



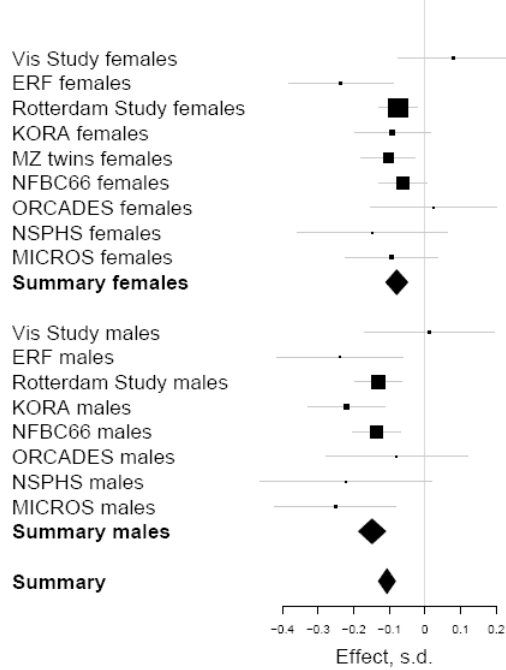
Effect of rs12670798*G on LDL



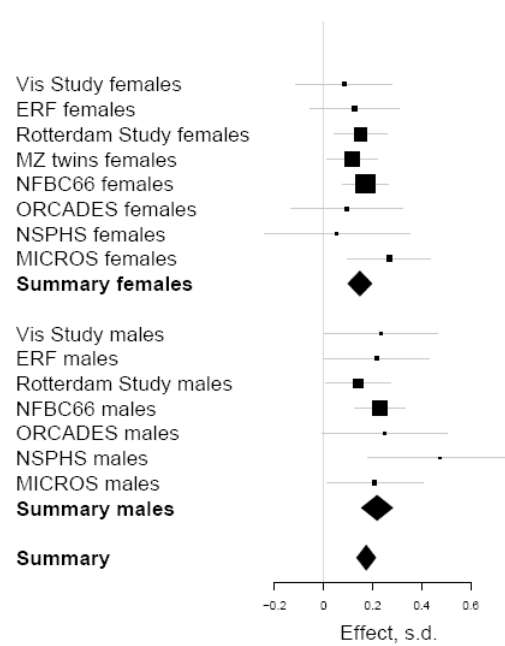
Effect of rs2240466*A on TG



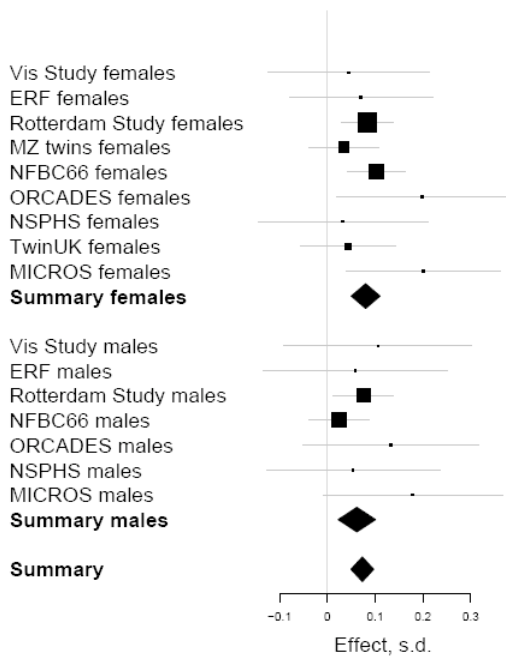
Effect of rs2083637*G on HDL



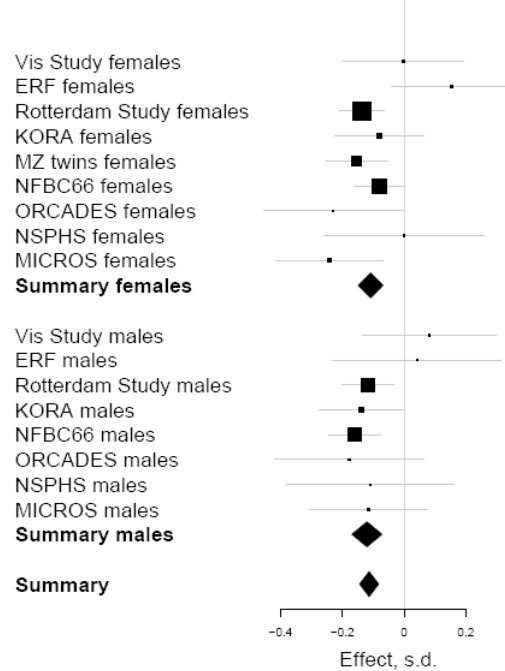
Effect of rs10096633*A on TG



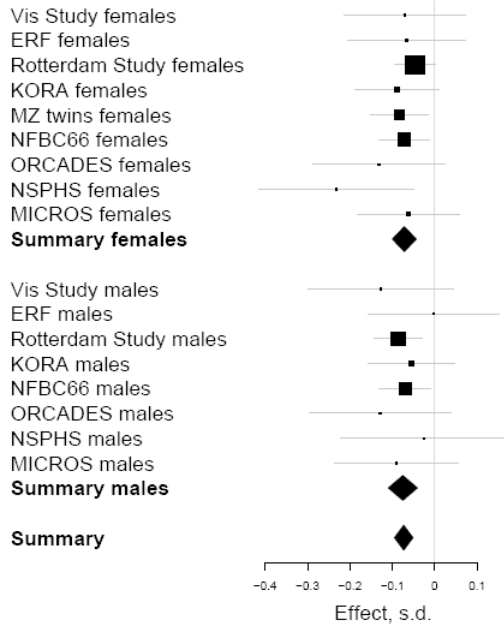
Effect of rs6987702*G on TC



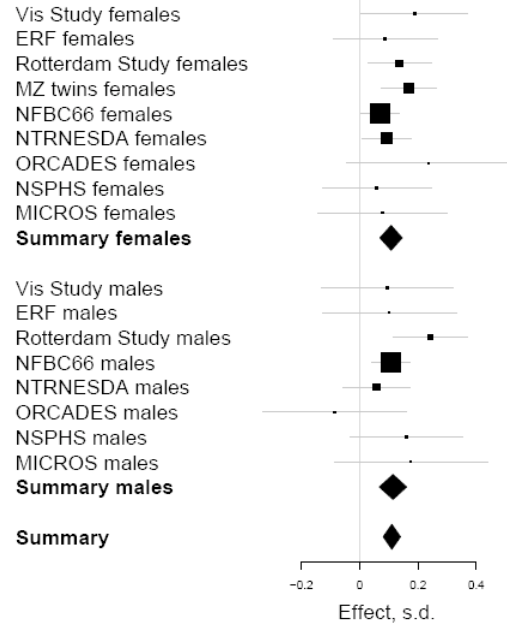
Effect of rs3905000*A on HDL



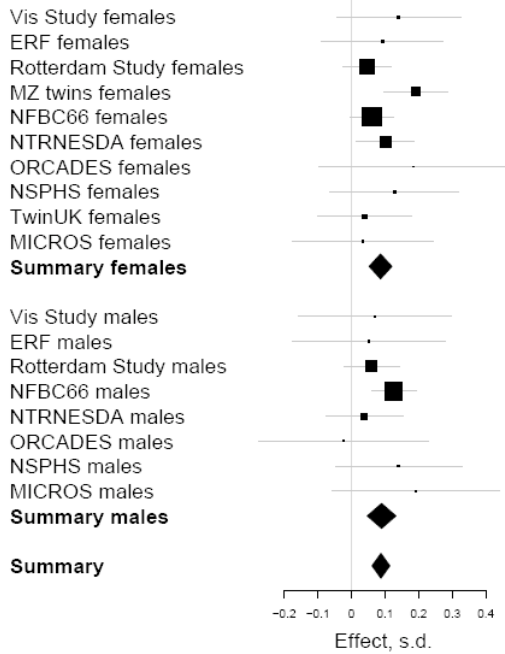
Effect of rs7395662*A on HDL



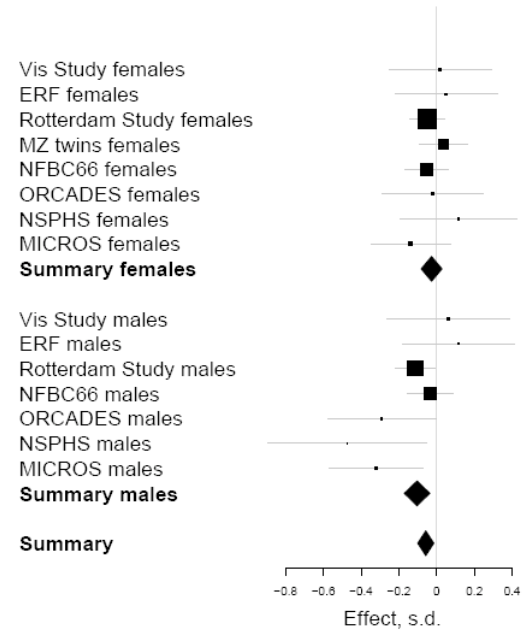
Effect of rs174570*A on LDL



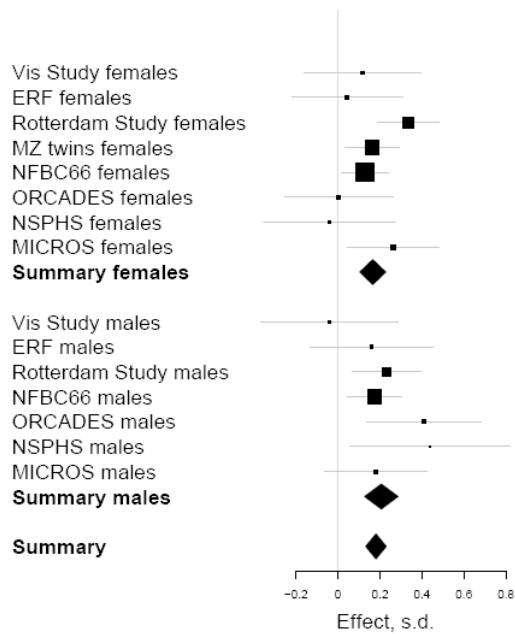
Effect of rs174570*A on TC



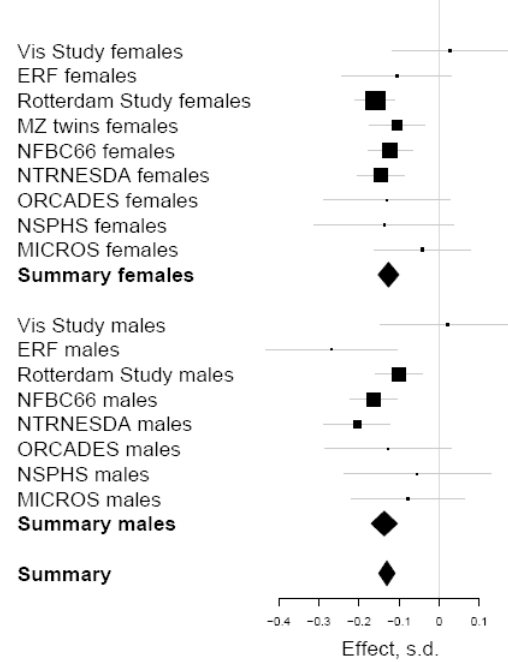
Effect of rs12272004*A on HDL



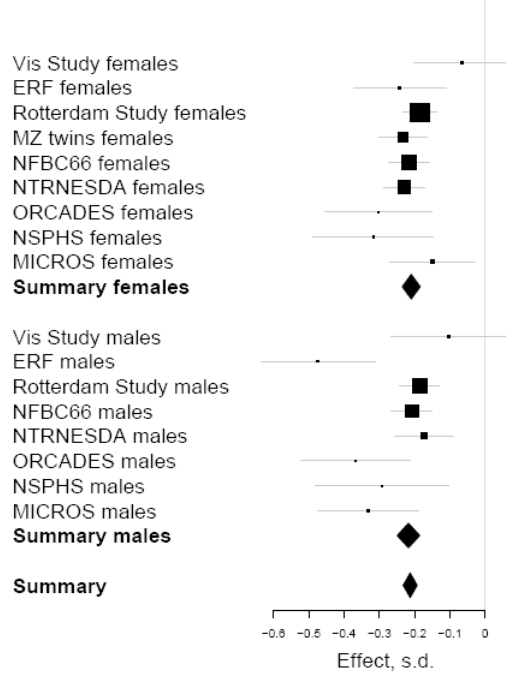
Effect of rs12272004*A on TG



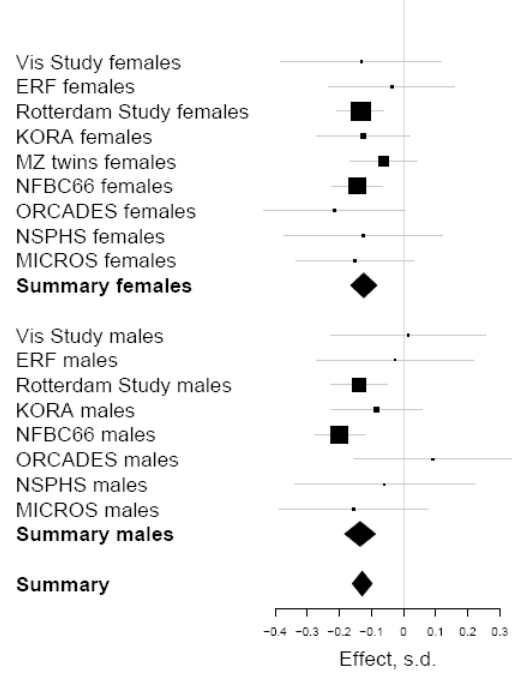
Effect of rs1532085*A on HDL



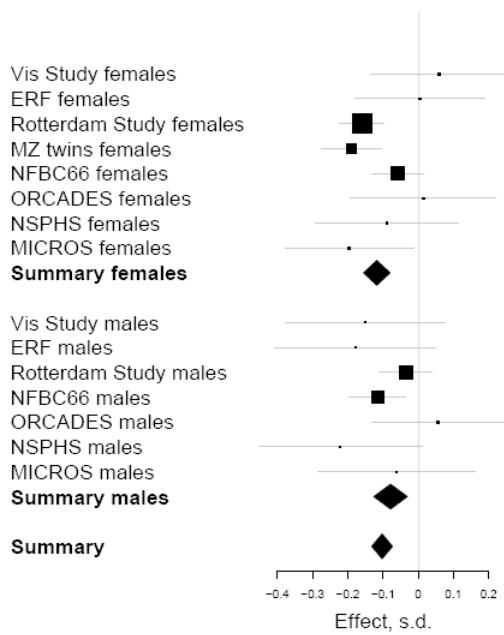
Effect of rs1532624*A on HDL



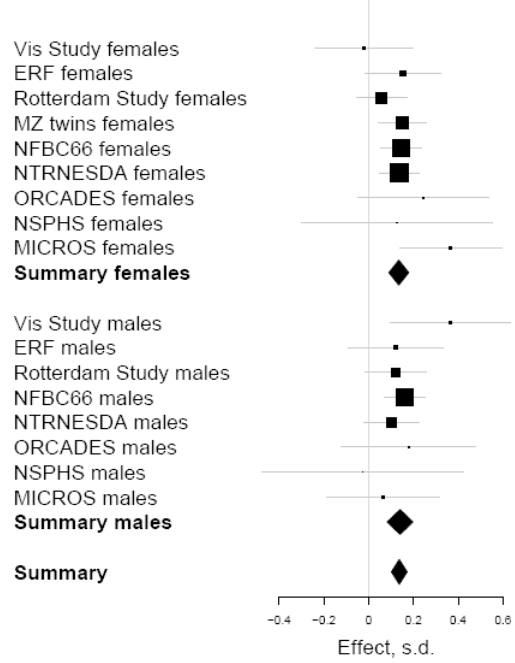
Effect of rs2271293*A on HDL



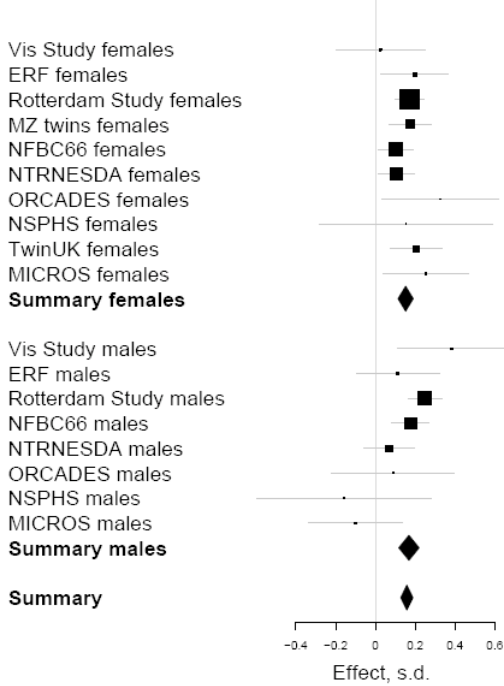
Effect of rs4939883*A on HDL



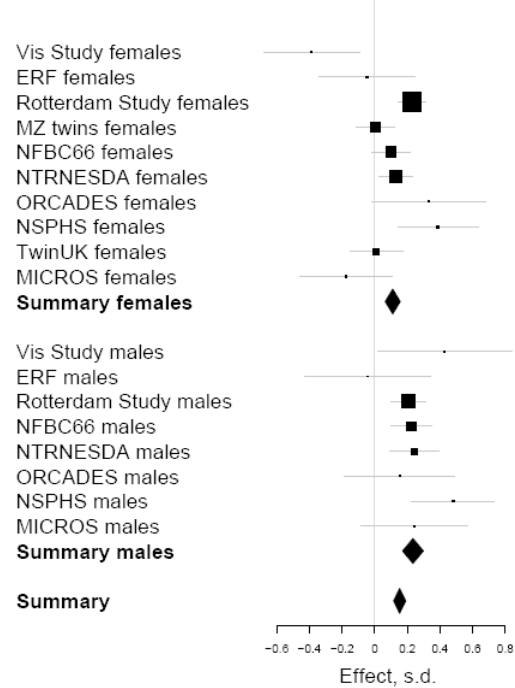
Effect of rs2228671*A on LDL



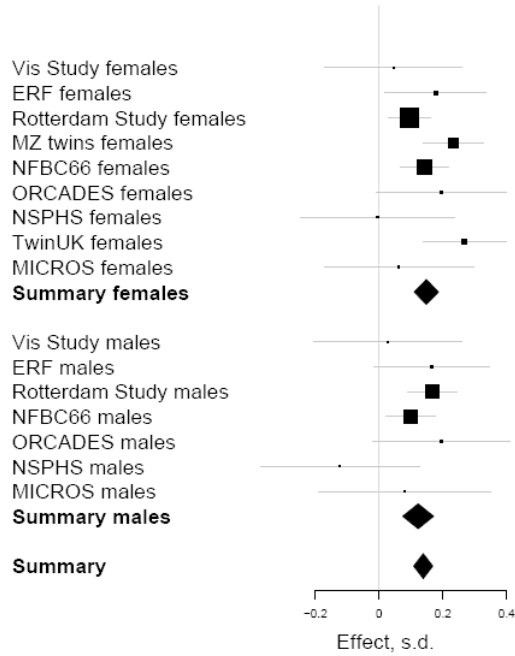
Effect of rs2228671*A on TC



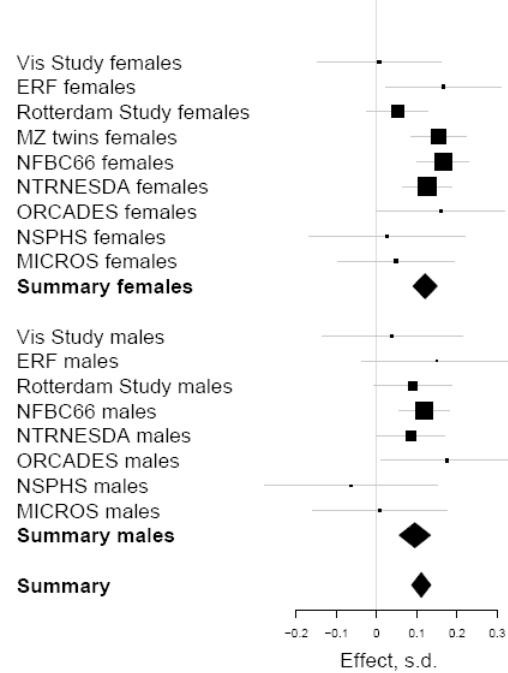
Effect of rs2304130*G on TC



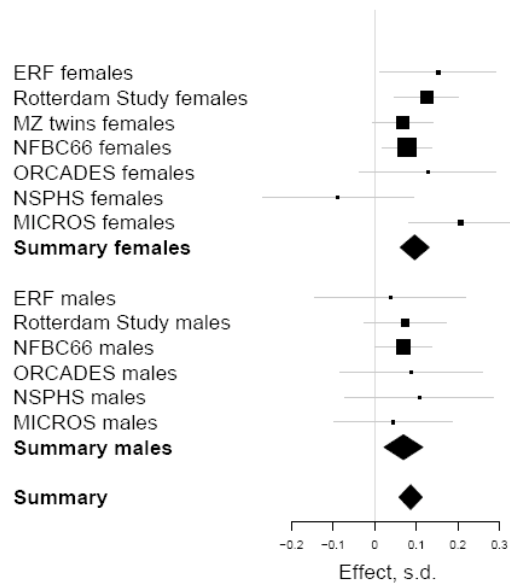
Effect of rs2075650*G on TC



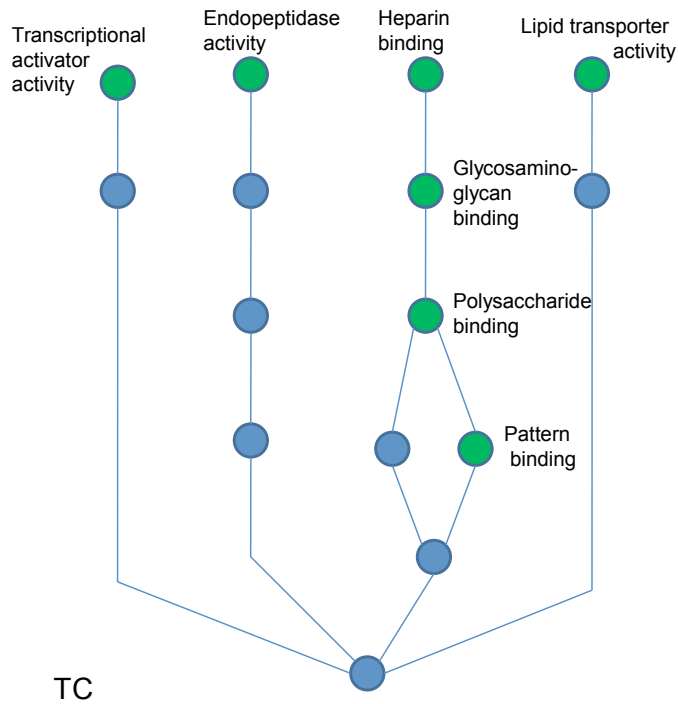
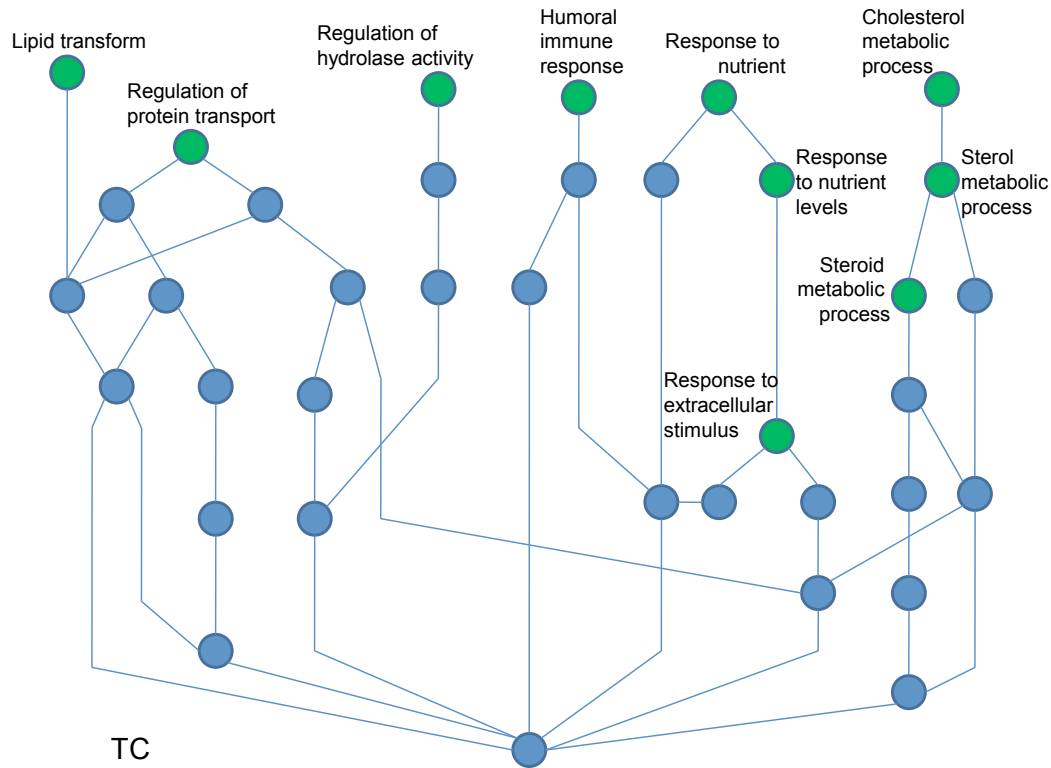
Effect of rs157580*G on LDL

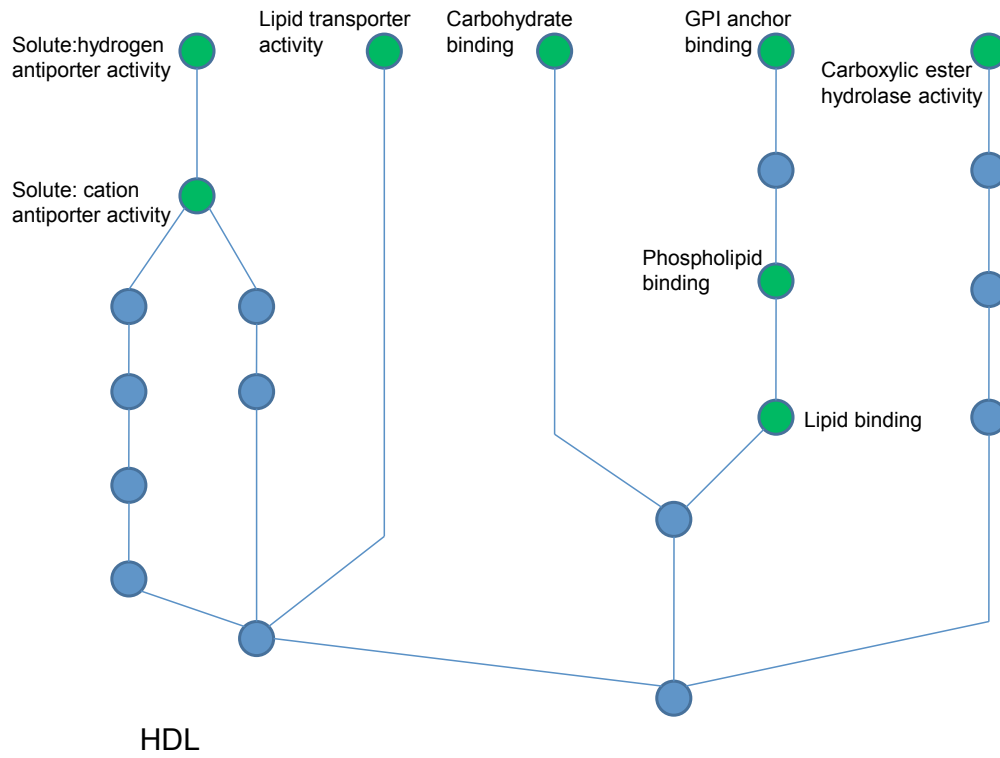
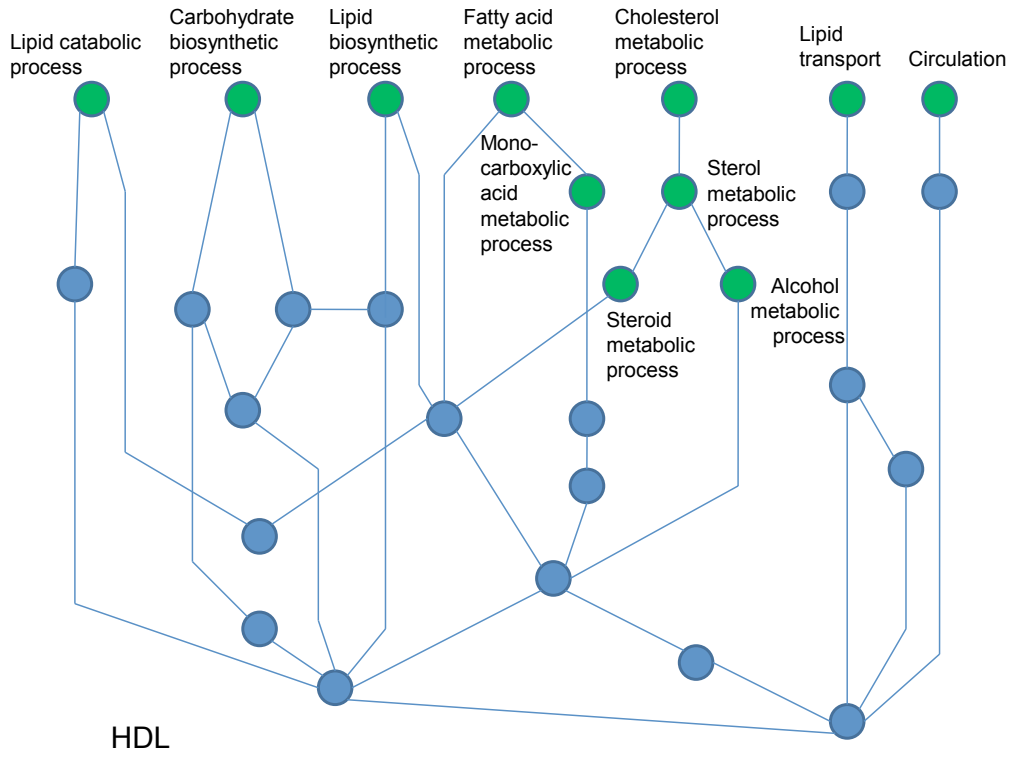


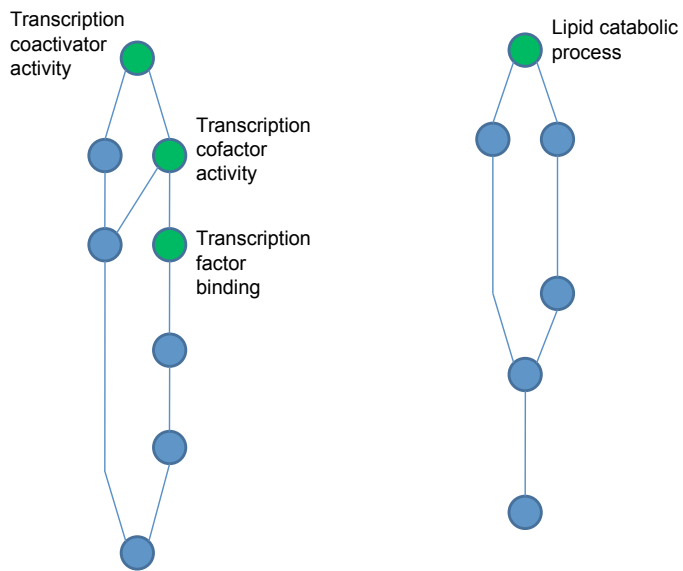
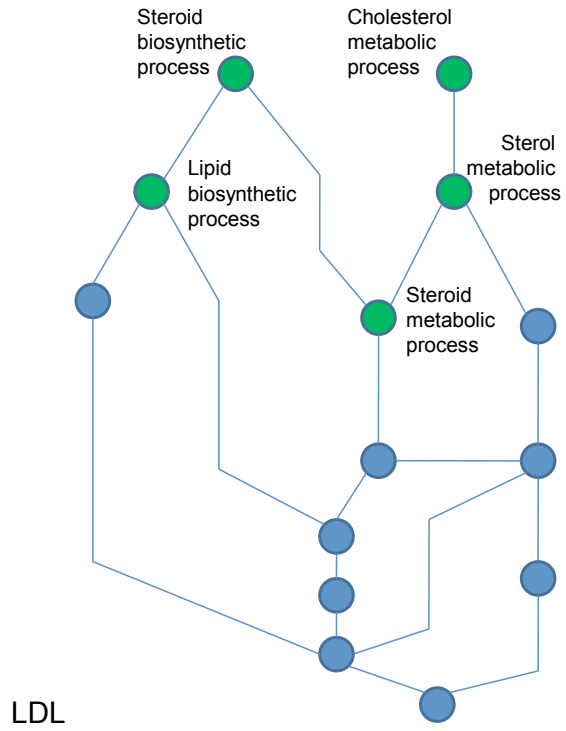
Effect of rs439401*A on TG



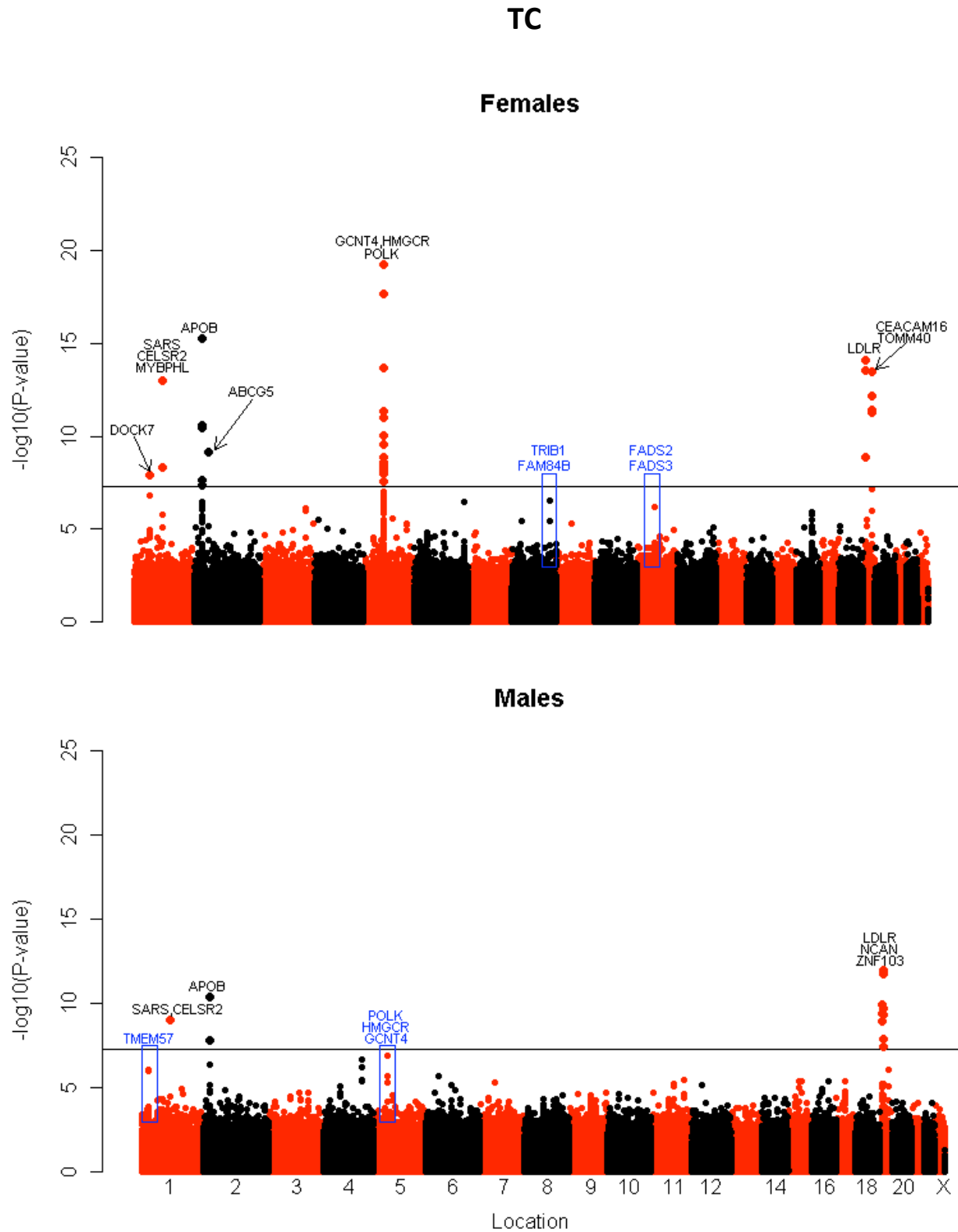
Supplementary Figure 4: Most strongly associated pathways (green dots) and their connecting pathways for total cholesterol (TC), high-density lipoprotein (HDL), low-density lipoprotein (LDL) and triglycerides (TG)





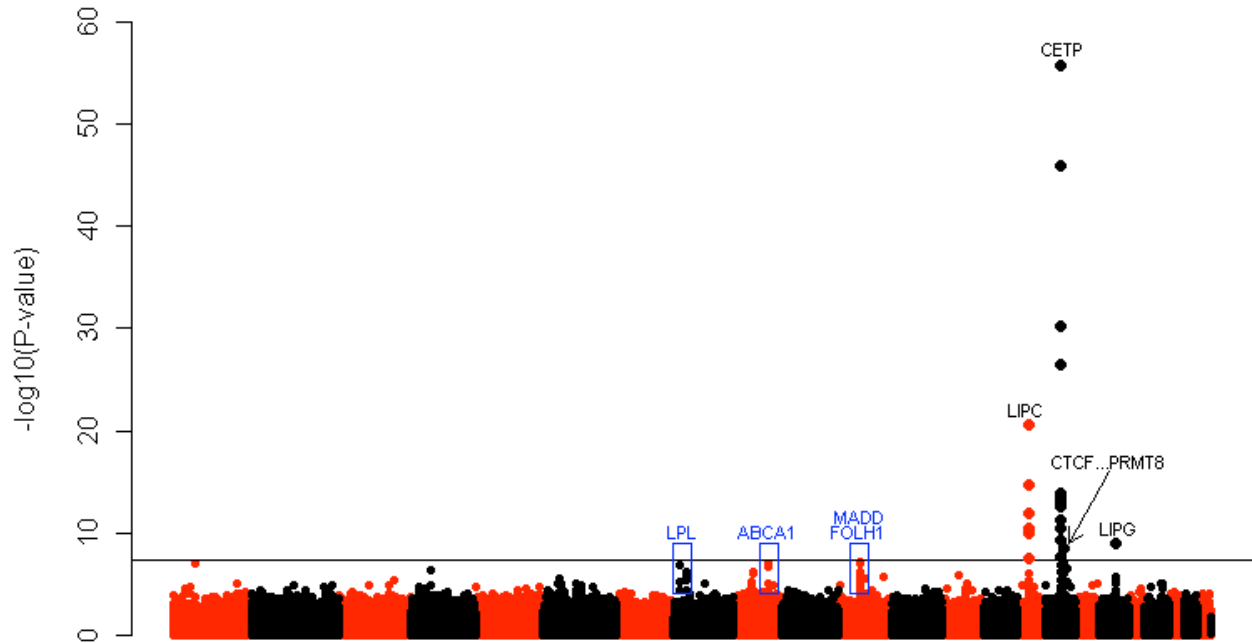


Supplementary Figure 5: Sex specific Manhattan-plots for total cholesterol (TC), high-density lipoprotein (HDL), low-density lipoprotein (LDL) and triglycerides (TG)

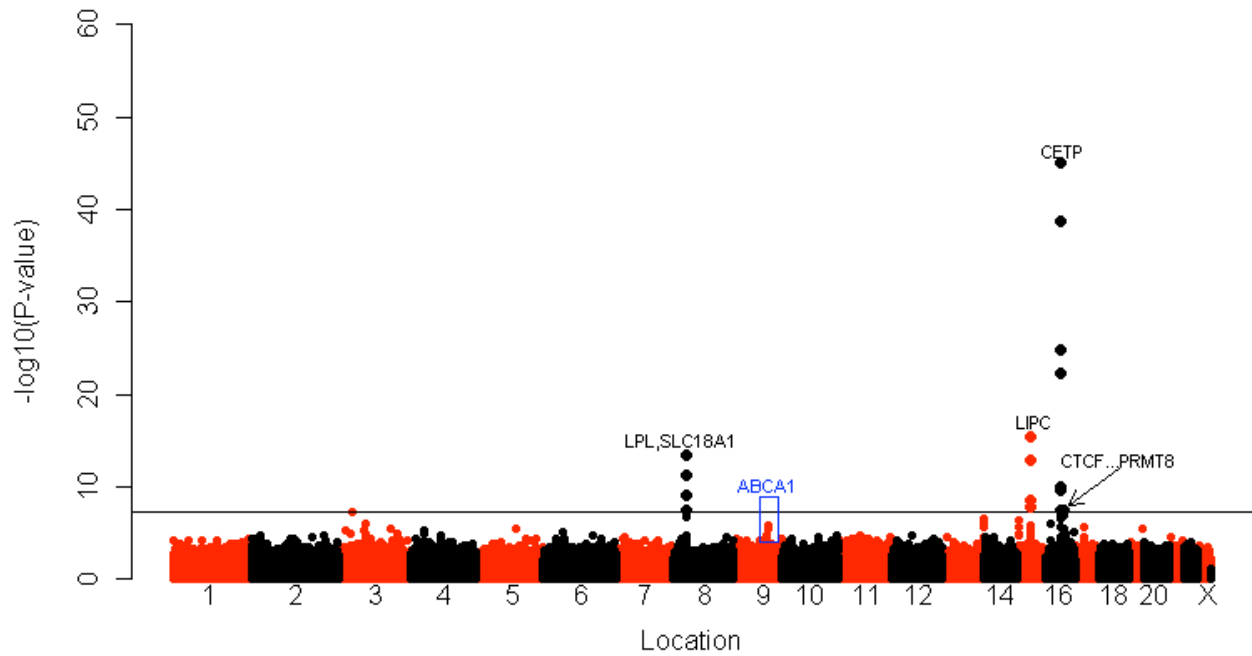


HDL

Females

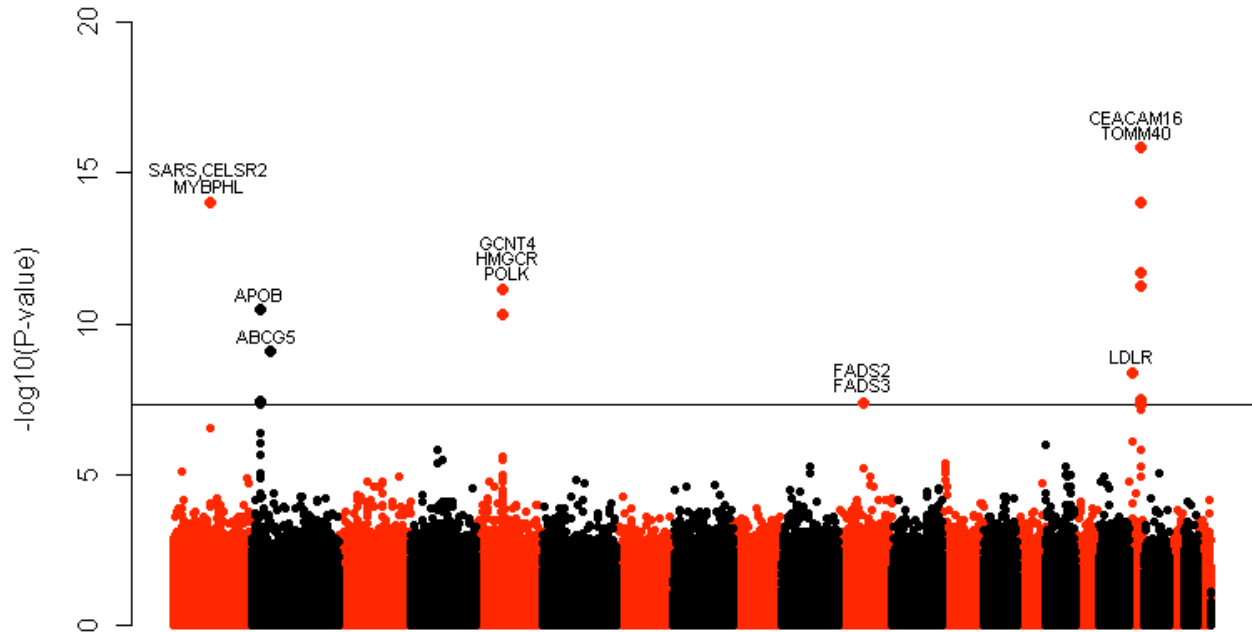


Males

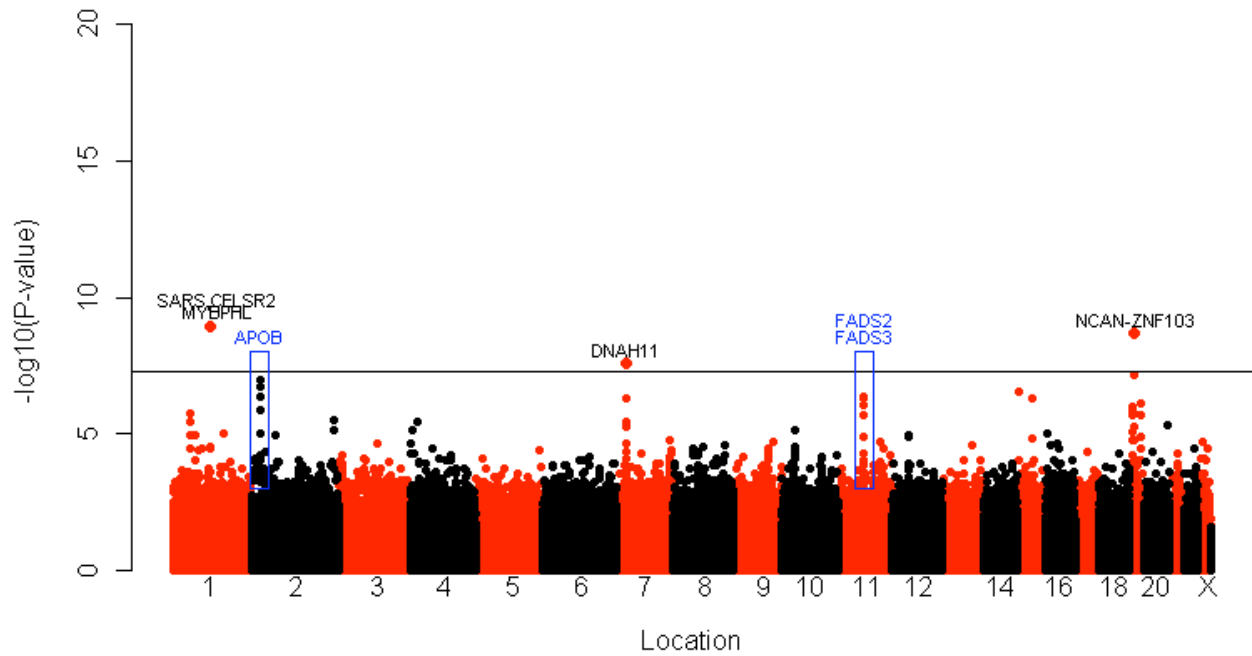


LDL

Females

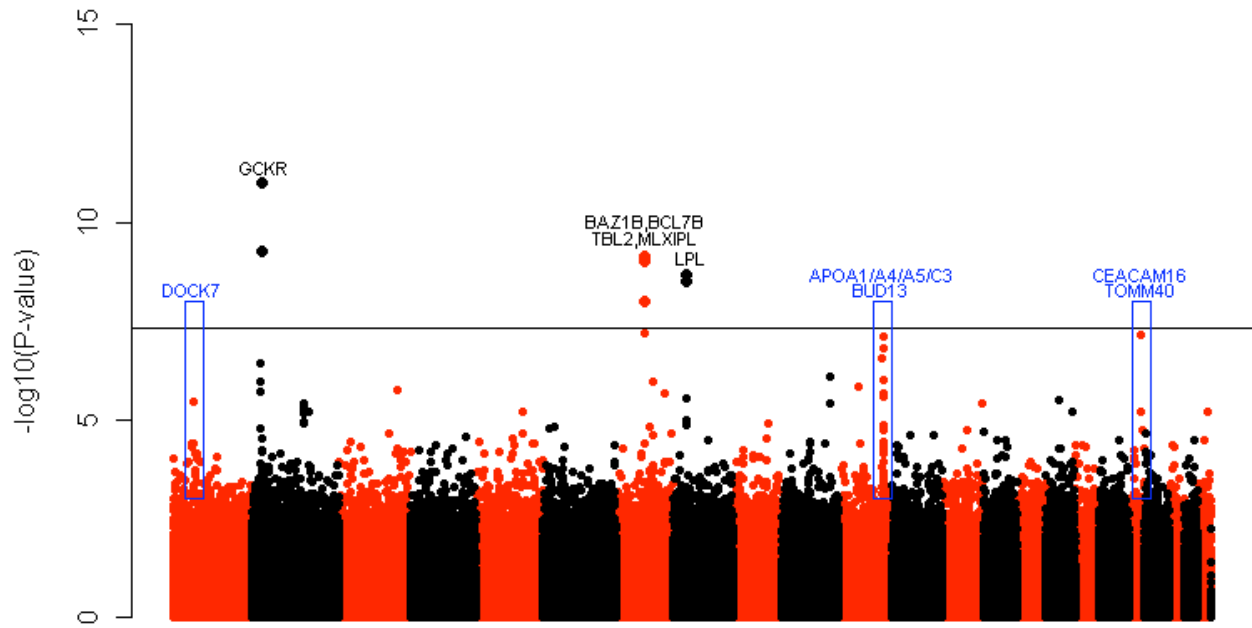


Males

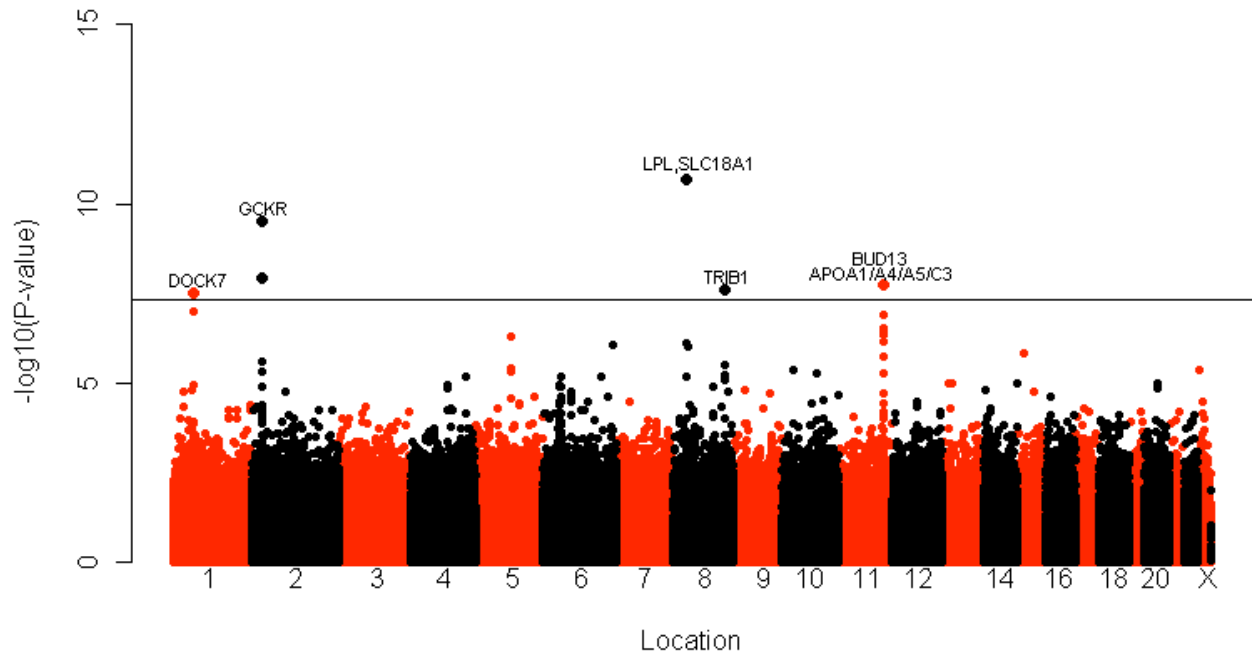


TG

Females



Males



Supplementary Figure 6: Proportion of variance explained in the NFBC and MZ-twin cohorts calculated separately for both sexes. Red bar shows the proportion of variance explained by the known and novel loci and blue bar shows the proportion explained by BMI. The stack of bars shows the total variances for NFBC, and after age adjustment for combined MZ-twin cohorts

