SUPPLEMENTARY INFORMATION

Methods

Study samples and phenotypes. Each of the 46 participating studies in the primary meta-analysis is described in **Supplementary Table 1** and in further detail below. In most studies, total cholesterol, HDL-C, and triglycerides were measured at fasting in subjects. Direct measurements of LDL-C were available for individuals in the Baltimore Longitudinal Study of Aging and Women's Genome Health Study and for a subset of individuals in the Health2000 GenMets Study; otherwise, LDL-C was calculated using the Friedewald formula, with missing values assigned to individuals with triglycerides >400 mg/dL. Individuals known to be on lipid-lowering therapy were excluded from analysis for all studies except the Fenland, EPIC Norfolk, and EPIC Norfolk Obese cohorts; fewer than 2% of individuals in each of these studies were known to be on lipid-lowering medication, and no exclusions or adjustments were made. All individuals in each of these 46 studies were reported to be of European descent. All participants provided informed consent, and local ethical committees at participating institutions approved individual study protocols.

Study descriptions.

I. **Primary Analysis: Community-based cohorts**

a. **Age, Gene/Environment Susceptibility (AGES) Study.** The AGES study has been described previously[21]. The study was initiated in 2002 to examine genetic susceptibility and gene/environment interactions related to disease and disability in old age. The AGES study is comprised of approximately 2,500 samples drawn from the Reykjavik Study, a population-based cohort comprised of individuals born between 1907 and 1935 and followed since 1967 by the Icelandic Heart Association.

b. **Atherosclerosis Risk in Communities (ARIC) Study.** The ARIC study has been described in detail previously[22]. The ARIC Study is a multi-center prospective investigation of atherosclerotic disease. White and African American men and women aged 45-64 years at baseline were recruited from four communities: Forsyth County, North Carolina; Jackson, Mississippi; suburban areas of Minneapolis, Minnesota; and Washington County, Maryland. A total of 15,792 individuals participated in the baseline examination in 1987-1989, with three triennial follow-up examinations. 7,841 white subjects were included in this analysis. Individuals known to be taking lipid-lowering medications and/or to have type 2 diabetes were excluded. Prevalent type 2 diabetes was defined as the presence of any of the following: a fasting blood glucose level of ≥126 mg/dL (7.0 mmol/L); a nonfasting blood glucose level of ≥200 mg/dL (11.1 mmol/L); self-reported physician diagnosis of type 2 diabetes; or pharmacologic treatment of diabetes in the past two weeks.

c. **Australian, Danish, Dutch, Finnish, Swedish Twin Cohorts and TwinsUK.** Twin samples were drawn from the GenomEUtwin project[23], which is comprised of the Danish, Dutch, Finnish, Italian, Norwegian, and Swedish national twin cohorts, an Australian twin cohort, and the UK-based TwinsUK cohort. The current study included monozygotic twin pairs from the Australian (MZGWA-AUS; 449 pairs), Danish (MZGWA-DK; 142 pairs), Dutch (MZGWA-NLD; 289 pairs), Finnish (MZGWA-FIN; 137 pairs), Swedish (MZGWA-SWE; 297 pairs), and UK (MZGWA-UK; 457 pairs) cohorts. In each of the six twin cohorts, female monozygotic twin pairs were identified, lipid measurements were averaged for each pair, and genotype data for one of the individuals was used in the analysis.

d. **Baltimore Longitudinal Study of Aging (BLSA).** This study has been described in detail previously[24]. The BLSA is an on-going prospective study that began in

1958 to investigate changes that occur with normal aging. The study consists of volunteers recruited primarily from the Washington, DC, and Baltimore, MD, areas. Genome-wide data were available for 1,230 participants. The analysis was restricted to 713 Caucasian individuals with lipid measurements.

e. **British 1958 Birth Cohort – Wellcome Trust Case Control Consortium (B58C-WTCCC).** This study was part of the Wellcome Trust Case Control Consortium (WTCCC) and has been described previously[25, 26]. The British 1958 Birth Cohort is a national population sample followed periodically from birth to age 44-45 years. The current analysis included 1,459 individuals that passed quality control criteria and had lipid measurements available.

f. **Cardiovascular Health Study (CHS).** The CHS has been described in detail previously[27]. The CHS is a population-based cohort study of risk factors for coronary heart disease and stroke in adults ≥65 years conducted across four field centers. The original predominantly Caucasian cohort of 5,201 persons was recruited in 1989-1990 from random samples of the Medicare eligibility lists, and an additional 687 African-Americans were enrolled subsequently for a total sample of 5,888. DNA was extracted from blood samples drawn on all participants at their baseline examination in 1989-90. In 2007-2008, genotyping was performed at the General Clinical Research Center's Phenotyping/Genotyping Laboratory at Cedars-Sinai on 3,980 CHS participants who were free of cardiovascular disease at baseline, consented to genetic testing, and had DNA available for genotyping. To limit the possibility of confounding due to population structure, these analyses were limited to the 3,121 white participants with genotype data and lipid measurements.

g. **The Cohorte Lausannoise (CoLaus) Study.** The CoLaus study has been described in detail previously[28]. Participants were randomly selected from a list of 56,694 individuals aged 35 to 75 years who were permanent residents of the City of Lausanne, Switzerland. Only individuals with four grandparents of European origin were included in the study. The CoLaus study was sponsored in part by GlaxoSmithKline, and all participants were duly informed about this sponsorship. Principal components were computed to adjust for population stratification using EIGENSOFT (http://genepath.med.harvard.edu/~reich/Software.htm). After using the Akaike Information Criterion (AIC) based stepwise model selection, the 3 principal components significant at $P < 0.05$ were included as covariates in the association analyses. A total of 5,253 participants with lipids measurements were included in this analysis.

h. **KORA - Cooperative Health Research in the Region of Augsburg (KORA).** The KORA surveys have been described in detail previously[29, 30]. The third KORA survey (KORA S3, n=3,996) is a population-based sample from the general population of the South-German city of Augsburg and surrounding counties from 1994/1995. A subsample of 1,644 individuals from this survey with 10-year followup (KORA F3) information available was successfully genotyped (the KORA S3/F3 500K Study). All participants had a German passport and were of European origin. A total of 1,405 participants not on lipid-lowering therapy and with lipid measurements were included in this analysis.

i. **The European Prospective Investigation of Cancer-Norfolk Subcohort (EPIC-N-SUBCOH).** The EPIC-Norfolk studies have been described previously[31, 32]. EPIC-Norfolk is an ongoing prospective cohort study of chronic diseases comprising 25,663 Norfolk residents, an ethnically homogenous European origin population aged 39-79 who were recruited from general practice

registers between 1993 and 1997 for a first health examination. A total of 2,346 non-obese subjects were included in this analysis.

j. **Fenland Study.** The Fenland Study is a community-based cohort of individuals born between 1950 and 1975 and residing in East Cambridgeshire or Fenland, UK. The goal of the Fenland Study is to study the interactions between diet, lifestyle, and genetic factors and risk of diabetes and obesity. A total of 1,401 individuals with genotype data and lipid measurements were included in the current analysis.

k. **Invecchiare in Chianti (InCHIANTI) Study.** InCHIANTI, described in detail previously[33], is an epidemiological study of risk factors contributing to the decline in physical functioning in late life. Individuals were selected from the population registries of two small towns in Tuscany, Italy. Participants, all of white European origin, were invited to a clinic visit for evaluation of health status as described in detail previously[34]. Genotype data and lipid measurements were available for 1,134 individuals.

l. **London Life Sciences Prospective Population Study (LOLIPOP).** LOLIPOP is an ongoing community cohort of approximately 30,000 individuals aged 35-75 years, recruited in West London, UK[35] to study the environmental and genetic factors that contribute to cardiovascular disease among UK Indian Asians. The study includes both European and Indian Asian subjects. Indian Asian participants reported having all four grandparents born on the Indian subcontinent, while European participants are self-classified whites born in Europe. For the current study, genotypes and lipid measurements were available for 1,599 European white individuals included in the primary meta-analysis.

m. **National FINRISK Study.** The FINRISK study is a population survey of risk factors for chronic, non-communicable diseases carried out in Finland. Since 1972, the survey has been performed every five years using independent, random and representative population samples from different parts of the country[36]. Participants complete a questionnaire and undergo a physical examination, including measurement of anthropometric traits and blood draw. The current analysis included 910 healthy individuals from the Helsinki area, who participated in a FINRISK survey and had genotype data and lipid measurements available.

n. **Northern Finland Birth Cohort 1966 (NFBC1966).** The NFBC1966 has been described in detail previously[37]. The study was originally designed to study factors affecting pre-term birth, low birth weight, and subsequent morbidity and mortality. Mothers living in the two northern-most provinces of Finland were invited to participate if they had expected delivery dates during 1966. A total of 12,058 live-births were included in the study. At age 31, 5,923 individuals still living in the Helsinki area or Northern Finland were asked to participate in a detailed biological and medical examination as well as a questionnaire. Genotypes and lipid measurements were available for 5,138 individuals included in this analysis.

o. **Pharmacogenomics and Risk of Cardiovascular Disease Study (PARC).** There were two clinical populations in the PARC study, which has been described in detail previously[38]. The first was derived from the Cholesterol Atherosclerosis Pharmacogenetics (CAP) Study. CAP subjects were recruited from two clinical sites located in Los Angeles and San Francisco, California. Participants were Caucasians, aged 30 and above, who received open label 40 mg simvastatin daily for 6 weeks. They were recruited on the basis of having serum total cholesterol levels of 4.14-10.36 mmol/L (160-400 mg/dL). The second population was

derived from the Pravastatin Inflammation CRP Evaluation (PRINCE). These subjects were enrolled from 1,143 sites representing 49 states and the District of Columbia, with no single site enrolling more than 4 patients. Participants were Caucasians, aged 21 and older, who received 40 mg daily pravastatin for 12 weeks. They were recruited for having an LDL-cholesterol concentration ≥3.5 mmol/L (>135 mg/dL) or a history of myocardial infarction, stroke, or coronary revascularization regardless of their baseline LDL-cholesterol. Subjects were excluded for baseline use of statins or other lipid lowering agents, pregnancy, lactation, alcohol or drug abuse, liver disease, known statin intolerance, uncontrolled diabetes, uncontrolled thyroid disease or abnormal thyroid function, or <90% compliance with the study medication during a two-week run-in period. A total of 1,939 individuals were available for analysis.

p. **Rotterdam Baseline Study and Rotterdam Extension of Baseline Study.** The Rotterdam Study is an ongoing prospective population-based cohort study, focused on chronic disabling conditions of the elderly. The study comprises an outbred ethnically homogenous population of Dutch Caucasian origin. The rationale of the study has been described in detail elsewhere[39, 40]. In summary, 7,983 men and women aged 55 years or older, living in Ommoord, a suburb of Rotterdam, the Netherlands, were invited to participate. A total of 5,701 individuals from the initial study were included in the current study. In 2000-2001, a second cohort was established with approximately 3,000 individuals, 1,628 of whom were included in this study.

q. **Supplementation en Vitamines et Mineraux Antioxydants (SUVIMAX) Study.** The SUVIMAX study has been described previously[41, 42]. SUVIMAX was a controlled randomized primary prevention trial to study the effects of supplemented vitamins and minerals on cardiovascular disease and cancers in

French men and women between 45-60 and 35-60 years of age, respectively. A total of 1,813 individuals with lipid measurements were included in the current analysis.

r. **Women's Genome Health Study (WGHS).** The WGHS has been described previously[43]. Participants were drawn from the Women's Health Study, where they had been followed over a 12-year period and monitored for serious health-related events, including myocardial infarction, stroke, and diabetes. Genome-wide genotyping was performed on individuals within the WGHS, and 22,041 participants with lipid measurements were included in the current analysis.

II. Primary Analysis: Case-control samples

a. **British Genetics of Hypertension (BRIGHT) Study.** The BRIGHT study has been described previously[44]. Individuals diagnosed with hypertension before age 60 were recruited to study hypertension, an important risk factor for coronary artery and cerebrovascular diseases. All individuals reported having four grandparents of white British ancestry. A total of 1,615 hypertensive cases with lipid measurements were included in the current analysis.

b. **British 1958 Birth Cohort Type 1 Diabetes Genetics Consortium (B58C-T1DGC).** The B58C-T1DGC is a sample from the national population-based 1958 Birth Cohort collected in the UK and sampled periodically from birth to age 44-45 years[26]. Samples are distinct from those included in the B58C-WTCCC cohort described above. A total of 2,534 individuals with lipids measurements were included in the current analysis.

c. **Diabetes Genetics Initiative (DGI).** The DGI study has been described in detail previously[45, 46]. The DGI study is a type 2 diabetes case-control study that

includes 1,588 T2D cases and 1,523 matched controls of European ancestry from Sweden and Finland. A total of 1,528 cases and 1,508 controls with lipid measurements were included in the current analysis.

d. **The European Prospective Investigation of Cancer-Norfolk Obese Cohort (EPIC-N-OBSET).** The EPIC-Norfolk studies have been described previously[31, 32]. EPIC-Norfolk is an ongoing prospective cohort study of chronic diseases comprising 25,663 Norfolk residents, an ethnically homogenous European origin population aged 39-79 years who were recruited from general practice registers between 1993 and 1997 for a first health examination. A subcohort of 1,078 obese (BMI $\geq$ 30 $kg \cdot m^{-2}$) individuals with lipid measurements was included in the current analysis.

e. **The Family Heart Study (FHS).** The FHS is a multicenter study of the genetic and non-genetic risk factors for coronary heart disease and has been described in detail previously[47]. A total of 356 individuals with coronary heart disease and 394 controls with lipid measurements were available for the current analysis.

f. **Finland-United States Investigation of NIDDM Genetics (FUSION) Study.** The FUSION study has been described in detail previously[48, 49]. The FUSION GWAS is a type 2 diabetes (T2D) case-control study that includes 1,161 Finnish T2D cases and 1,174 normal glucose tolerant (NGT) controls. A total of 772 cases and 982 controls with lipid measurements were included in the current analysis.

g. **Health2000 GenMets Study.** The GenMets sample has been described in detail previously[50]. Individuals are metabolic syndrome cases and matched controls drawn from the Finnish Health2000 study. A total of 867 metabolic syndrome cases and 892 controls with genotype data and lipid measurements were included in the current analysis.

h. **MedSTAR Study.** MedSTAR is a cross-sectional study of coronary atherosclerosis that has been described in detail previously[51]. 1,500 subjects who underwent cardiac catheterization at the Washington Hospital Center between August 2004 and March 2007 were recruited to participate. The cohort is comprised of 874 cases with history of coronary artery disease (CAD) and 447 controls without history of CAD. A total of 716 CAD cases and 393 controls with genotype data and lipid measurements were included in the present study.

i. **PennCATH Study.** PennCATH is an angiographic study based at the University of Pennsylvania Medical Center that has been described previously[52]. Individuals who underwent cardiac catheterization at Penn between July 1998 and March 2003 were invited to participate. The cohort is comprised of 933 CAD cases and 468 controls with no history of CAD. The current analysis included 892 CAD cases and 454 controls with genotype data and lipid measurements available.

III. Primary Analysis: Family-based samples

a. **Erasmus Rucphen Family (ERF) Study.** The ERF study has been described in detail previously[53]. A total of approximately 3,000 participants descend from 22 couples who lived in the Rucphen region in The Netherlands in the 19th century. A total of 1,108 individuals with genotype data and lipid measurements were included in the current analysis.

b. **Framingham Heart Study (FramHS).** The FramHS is a three generational prospective cohort that has been described in detail previously[54]. Individuals were initially recruited in 1948 in Framingham, USA to evaluate cardiovascular disease risk factors. The second generation cohort (5,124 offspring of the original cohort) was recruited between 1971 and 1975, and multiple lipid measurements were available and have been averaged. The third generation cohort (4,095 grand-

children of the original cohort) was collected between 2002 and 2005, and a single lipid measurement was available. The current analysis includes 7,132 individuals for whom genotypes and lipid measurements were available.

c. **MICROS Study of Population Microisolates in South Tyrol.** The MICROS study has been described in detail previously[55]. As part of the genomic healthcare program "GenNova," an extensive survey was carried out during 2001–2003 in three villages of the Val Venosta (South Tyrol, Italy) on the populations of Stelvio, Vallelunga, and Martello. The current analysis includes 1,037 individuals for whom genotype data and lipid measurements were available.

d. **Northern Swedish Population Health Study (NSPHS).** The NSPHS is a family-based prospective population study in Sweden. The parish of Karesuando, in the subartic region of the County of Norrbotten, has about 1,500 inhabitants, 740 of whom participated in the study. The region has experienced little immigration during the last 200 years. The current analysis included 593 individuals for whom genotypes and lipid measurements were available.

e. **Orkney Complex Disease Study (ORCADES).** ORCADES is an ongoing family-based genetic epidemiology collection in the isolated Scottish archipelago of Orkney. The current analysis included 633 individuals from a subgroup of the Orkney islands who had genotype data and lipid measurements available for study.

f. **SardiNIA Study of Aging.** The SardiNIA study has been described in detail previously[56]. The study includes 4,301 related individuals from the Ogliastra region of Sardinia, Italy who have been studied longitudinally for age-related quantitative traits. The current study included 4,184 individuals with genotype data and lipid measurements available.

g. **Vis Study.** The Vis study has been described in detail previously[57]. Croatians aged 18-93 years were recruited from the villages of Vis and Komiza on the Dalmation island of Vis between 2003 and 2004. The current analysis included 771 individuals for whom genotype data and lipid measurements were available.

IV. Replication (European and non-European) groups

a. East Asian cohorts

i. **Cebu Longitudinal Health and Nutritional Survey (CLHNS). The** CLHNS is part of an ongoing study of a cohort of Filipino women who gave birth between 1983 and 1984 and has been described previously[58]. The four lipid traits were measured using blood plasma from the 2005 survey, and 1,789 women who were not taking lipid-lowering medication were included in this study. Samples were genotyped with the Affymetrix Genome-Wide Human SNP Array 5.0[59], and HapMap SNPs polymorphic in both the 60 HapMap CEU founders and the 89 combined HapMap CHB+JPT samples were imputed using MACH version 1.0. Residuals were adjusted for age, age^2, measures of socioeconomic status (total assets, natural log-transformed income), number of previous pregnancies, menopausal status, and seven principal components of variation representing population substructure.

ii. **Korea Association Resource (KARE) Project.** The KARE project was initiated in 2007 to perform large-scale genome-wide association analyses of the Ansung and Ansan population-based cohorts in Korea[60]. The cohorts were collected as part of the Korean Genome Epidemiology Study and included 5,018 Ansung and 5,020 Ansan inhabitants between 40 and 69 years of age. Individuals were collected in the Gyeonggi Province,

close to Seoul, Republic of Korea. All participants have been examined every two years since baseline, and more than 260 traits have been examined. Genotypes were obtained using the Affymetrix Genome-Wide Human SNP array 5.0, and a total of 352,228 markers were successfully genotyped in 8,842 individuals. A total of 8,801 subjects with lipid measurements and not taking lipid-lowering medications were included in the current analysis.

iii. **Singapore Malay Eye Study (SiMES).** The Singapore Malay Eye Study (SiMES) is a population-based cross-sectional epidemiological study of 3,280 individuals from one of the three major ethnic groups residing in Singapore[61, 62]. All subjects were Malay and aged 40-80 years. In summary, an age-stratified random sample comprised of 1,400 people from each decade of 40-49, 50-59, 60-69 and 70-79 was drawn from a computer-generated list of 15 residential districts provided by the Singapore Ministry of Home Affairs. Of the 5,600 names generated, a door to door household visit was made to confirm eligibility. Among the 4,168 eligible individuals, 3,280 participated in the study. In total, there are 2,542 Malays with genotypes on 557,824 autosomal SNPs from the Illumina610quad genotyping array. The 2,231 individuals not taking lipid-lowering drugs were included in the current analysis.

iv. **Singapore Prospective Study Program (SP2).** The SP2 is a population-based study of diabetes and cardiovascular disease in Singapore that has been described previously[63]. The SP2 has recruited 10,633 Chinese, Malay, and Indian subjects from four cross-sectional studies that were conducted in Singapore between 1984 and 1998. Subjects were aged 18-69 at baseline and represented a random sample of the Singapore

population, with over-sampling of the minority Malay and Indian ethnic groups to achieve a ratio of 60:20:20 in the overall sample. From 2003 to 2007, 7,772 subjects were re-contacted and interviewed, 5,094 of whom provided blood and other clinical data. In total, there are 2,434 Chinese individuals with genotypes on 489,028 common SNPs combined from three Illumina genotyping arrays, namely Illumina610quad, Illumina1Mduo and Illumina550v3. The 2,225 individuals not taking lipid-lowering drugs were included in the current analysis.

b. South Asian cohort

i. **London Life Sciences Prospective Population Study (LOLIPOP).** LOLIPOP is an ongoing community cohort of approximately 30,000 individuals aged 35-75 years, recruited in West London, UK[35] to study the environmental and genetic factors that contribute to cardiovascular disease among UK Indian Asians. The study includes both European and Indian Asian subjects; Indian Asian participants reported having all four grandparents born on the Indian subcontinent, while European participants are self-classified whites born in Europe. For the current study, genotypes and lipid measurements were available for 9,705 Indian Asian individuals included in the cross-ethnic analysis.

c. African American cohorts

i. **National Heart, Lung, and Blood Institute Candidate Gene Association Resource (NHLBI CARe).** These cohorts, including ARIC study, the Coronary Artery Risk Development in Young Adults study, the Cleveland Family Study, the Jackson Heart Study, and the Multi-Ethnic Study of Atherosclerosis, have previously been described[64]. For the

current study, genotypes and lipid measurements were available for 8,061 African American individuals included in the cross-ethnic analysis.

d. European cohorts

i. **deCODE.** The deCODE lipid study includes lipid measurements from Icelanders recruited through various genetic studies at deCODE, primarily cardiovascular studies[65]. The measurements were done between the years 1987 and 2008. For the current analysis we included individuals born after 1935 and excluded those using lipid lowering drugs. Genotypes and lipid measurements were thus available for 7,063 Icelanders included in the cross-ethnic analysis. The study was approved by the Icelandic Data Protection Commission and the National Bioethics Committee. All study participants signed informed consent and donated blood samples. Personal identities were encrypted by a third party system provided by the Icelandic Data Protection Commission.

ii. **Malmö Diet and Cancer Study – Cardiovascular Cohort (MDC-CC).** The Malmö Diet and Cancer Study, a community-based prospective epidemiologic cohort of 28,449 persons recruited for a baseline examination between 1991 and 1996[66]. From this cohort, 6,103 persons were randomly selected to participate in the cardiovascular cohort, which sought to investigate risk factors for cardiovascular disease. All participants underwent a medical history assessment and a physical examination. Of the participants in the cardiovascular cohort, 4,991 had DNA samples available for this analysis and data available for at least one lipoprotein or lipid phenotype.

iii. **National FINRISK 1997 Study (FINRISK97).** FINRISK97 was a population-based cross-sectional survey designed to study the prevalence of cardiovascular risk factors in Finland[67]. Surveys are conducted every 5 years, and the 1997 survey included 8,389 Finnish men and women aged 25–74. Participants underwent a physical examination and completed a questionnaire regarding cardiovascular risk factors. Of these FINRISK97 participants, 7,026 had DNA samples available for this analysis and data available for at least one lipoprotein or lipid phenotype.

V. Coronary artery disease cohorts

a. **Coronary ARtery DIsease Genome-wide Replication And Meta-analysis (CARDIoGRAM) study.** CARDIoGRAM combines data from all published and several unpublished GWAS including individuals with European ancestry, includes >22,000 cases with CAD and/or MI and >60,000 controls, and unifies samples from Atherosclerotic Disease VAscular functioN and genetiC Epidemiology study, CADomics, Cohorts for Heart and Aging Research in Genomic Epidemiology, deCODE, the German Myocardial Infarction Family Studies I, II, and III, Ludwigshafen Risk and Cardiovascular Heath Study/AtheroRemo, MedStar, Myocardial Infarction Genetics Consortium, Ottawa Heart Genomics Study, PennCath, and the Wellcome Trust Case Control Consortium[68]. CAD was defined as: 1) coronary artery stenosis > 50% in at least one major epicardial artery; 2) fatal MI; 3) non-fatal MI based on ECG and cardiac biomarkers; 4) angina with positive stress testing; 5) percutaneous transluminal angioplasty; or 6) coronary artery bypass surgery. The control definition varied by study and ranged from population-based controls to self-reported freedom from CAD to lack of obstructive lesions on coronary angiography. Genotyping platforms and quality control criteria have been described[68].

b. **COROGENE.** The COROGENE study includes individuals who underwent coronary angiography in Helsinki University Hospital, Finland and matched controls. Cases (n = 2,172) were individuals admitted to the Helsinki University Hospital for acute coronary syndrome (unstable angina pectoris or acute myocardial infarction). Controls (n = 1,579) were age- and sex- and area of residence matched individuals from the FINRISK 1997, 2002, or 2007 studies. Genotype and quality control criteria have been described[69].

VI. Extreme lipids case-control cohorts

a. **High HDL-C.** For the study of the cumulative effects of common variants in individuals at the extremes of the HDL distribution, cases with high HDL (>90th percentile for age, gender, and race) were selected from the University of Pennsylvania High HDL Cholesterol Study (HHDL) and controls with low HDL (<30th percentile for age, gender, and race) were selected from the University of Pennsylvania Catheterization cohort (PennCATH). HHDL is a cross-sectional study of genetic factors contributing to elevated HDL-C levels. Probands with elevated HDL-C (>75th percentile for age and gender) were identified by physician referrals or through the Hospital of the University of Pennsylvania clinical laboratory[70]. Relatives of HHDL probands were also invited to participate in the study. Subjects completed a lifestyle questionnaire and provided a blood sample for the measurement of HDL and other lipid-related traits. Genotyping was performed at the Center for Applied Genomics (Children's Hospital of Pennsylvania) following manufacturer specifications for amplification and hybridization to the Affymetrix Genome-Wide Human SNP Array 6.0. Quality control measures to exclude unreliable SNPs and eliminate SNPs with genotype call rate < 95%, with minor allele frequency (MAF) < 1% or if there was significant departure from Hardy-Weinberg equilibrium ($P < 1 \times 10^{-6}$ in combined

cases and controls) were performed. Imputation was conducted using a Hidden Markov Model algorithm as implemented in MACH.

b. **High LDL-C.** Blood samples of unrelated hypercholesterolemic patients were collected from 64 Dutch Lipid Clinics. Based on clinical criteria, all patients were suspected for familial hypercholesterolemia by cardiologists and internists using a uniform protocol and internationally accepted criteria[71, 72]. All patients were routinely analysed for the presence of mutations by direct sequencing of the complete *LDLR* and the LDL-receptor binding region of *APOB* (amino acids 3414 to 3588). For the identification of large rearrangements in the *LDLR* gene, a multiplex ligation-dependent probe (MLPA) technique with the Salsa P062 LDLR Exon Deletion Test Kit (MRC-Holland, Amsterdam, the Netherlands) was used, according to the manufacturer's instructions. For this analysis, we considered only the 344 patients in whom a functional *LDLR* or *APOB* mutation was *not* identified. After an overnight fast, blood was sampled, and plasma concentrations of total cholesterol, HDL-C, and triglycerides were measured by commercially available kits (Boehringer Mannheim, Mannheim, Germany). LDL-C concentrations were calculated by the Friedewald formula only when the triglyceride concentration was below 4.5 mmol/L. Genomic DNA was prepared from 10 ml whole blood on an AutopureLS apparatus according to a protocol provided by the manufacturer (Gentra Systems, Minneapolis, MI, USA).

c. **High triglycerides.** In total, 344 unrelated adult subjects of European ancestry with hypertriglyceridemia, defined as having untreated 12 h fasting plasma triglyceride concentrations >3 mmol/L on at least two occasions, were studied[73]. Patients were ascertained through a single tertiary referral lipid clinic, and had undergone complete medical history and examination, together with collection of demographic, clinical, and biochemical variables. Low triglyceride control

subjects were comprised of 144 unrelated adult subjects of European ancestry with fasting plasma triglyceride concentrations < 2.4 mmol/L, including both healthy population-based controls from Ontario and subjects with molecularly confirmed familial hypercholesterolemia. Study subjects were genotyped using the Affymetrix Genome-Wide Human SNP Array 6.0 platform (Affymetrix, Santa Clara, CA), according to protocols of the London Regional Genomics Centre (www.lrgc.ca). Genotypes were called using Affymetrix Genotyping Console, setting quality control thresholds for SNP call rate (95%), Hardy-Weinberg equilibrium ($P > 0.0001$) and minor allele frequency (>1%). SNP imputation was subsequently conducted using phased haplotypes from the European HapMap cohort in MACH.

Genotyping and imputation. All cohorts were genotyped using commercially available Affymetrix or Illumina genotyping arrays, or custom Perlegen arrays. Quality control was performed independently for each study. To facilitate meta-analysis, each group performed genotype imputation using BIMBAM, IMPUTE, or MACH, with reference to the Phase II CEU HapMap[74]. Study-specific details are presented in **Supplementary Table 3**.

Genome-wide association analyses. Within each study, residual lipoprotein concentrations were determined after regression adjustment. To calculate residuals, each study included as covariates age, age^2, and sex. Each group was given the option to include additional covariates (e.g., principal components, study site) to account for population structure; study-specific covariates are detailed in **Supplementary Table 3**. Residuals were normalized to have mean 0 and standard deviation 1, and normalized residuals were used as phenotypes to test for genotype-phenotype association. In each of the six twin cohorts (Australian, Danish National, Dutch National, Finnish National, TwinsUK, and Swedish National) monozygotic twin pairs were identified, lipid measurements were averaged for each pair, and a single individual with this average value was used to represent the pair.

In each study, each genotyped or imputed SNP was tested for association with each of the lipid traits, assuming an additive genetic model. Linear regression was employed for studies of unrelated individuals, and linear mixed effects models were used to account for family structure in the family-based studies. For the six case-control studies of type 2 diabetes (Diabetes Genetic Initiative, FUSION), myocardial infarction (MedSTAR, PennCATH), coronary heart disease (Family Heart Study), and metabolic syndrome (Health2000 GenMets), cases and controls were analysed separately to avoid confounding effects due to disease status. Each study excluded SNPs with MAF < 0.01 and SNPs with poor imputation quality: Rsq < 0.3 (BIMBAM and MACH) or proper info < 0.3 (IMPUTE/SNPTEST). Since BIMBAM does not output an imputation quality score, Rsq was calculated manually as the ratio of observed to expected variance: $var/[2p(1-p)]$, where p is the minor allele frequency, and var is the sample variance of the estimated dosages.

Meta-analysis of directly typed and imputed SNPs. To combine association results across the 46 studies, we performed a fixed-effects meta-analysis using METAL for each of the four lipid traits. For each SNP, in each study, a Z-statistic was calculated that summarized the magnitude and direction of effect relative to a randomly selected reference allele. The overall Z-statistic was calculated from the weighted sum of the individual study statistics; weights were proportional to the square root of the sample size of each study and scaled so that squared weights summed to one. Each study was subjected to genomic control correction before inclusion in the meta-analysis to account for P-value inflation due to residual population structure or other confounding factors. For each of the six case-control studies, cases and controls were meta-analysed together to create a single dataset and genomic control correction was applied to each case-control dataset. Finally, the results of the overall meta-analysis were subjected to a second round of genomic control correction. As a result, the final genomic control lambda for each of the four sets of association results was exactly 1.0. Genomic control factors for the individual contributing studies and for the overall meta-analysis prior to genomic control correction are

provided in **Supplementary Table 4**. The pre-specified statistical significance threshold for heterogeneity (calculated in METAL) was $P < 0.0005$ to account for multiple testing (102 SNPs in 95 loci tested).

To determine whether spurious associations arose as a result of imputation artifact, SNPs with $r^2 \geq 0.8$ with the most highly associated SNP ("best SNP") in the locus were identified, and from these the SNP directly genotyped on the greatest number of Illumina genotyping arrays and having the highest r^2 with the best SNP was chosen as the "Proxy Illumina SNP." The "Proxy Affymetrix SNP" was chosen in the same manner. **Supplementary Table 5** shows meta-analysis *P*-values for the best Illumina and Affymetrix proxy SNPs.

To ensure that the results were robust to whether or not principal components analysis (PCA) correction was used, we performed separate meta-analyses for cohorts in which principal components analysis (PCA) had been used ($n = 47,782$) and cohorts in which PCA had not been used ($n = 52,408$). We then calculated heterogeneity *P*-values between the groups for all SNPs well represented in each group (typed in >10,000 individuals). We present the full results of this analysis in **Supplementary Table 19**. Overall, there was minimal evidence of heterogeneity between studies that used PCA to account for population structure and those that did not.

Estimation of effect sizes. To estimate regression coefficients in clinically interpretable units, we repeated the variance-weighted meta-analysis (using METAL) on untransformed HDL-C, LDL-C, TC, and log-transformed TG values (owing to skewness in the data) with exclusion criteria and covariates as before.

Conditional analysis of top signals. To identify additional lipid-associated SNPs at each of the reported loci and genome-wide, we repeated the primary association analysis for each trait, including genotypes or imputed dosages for the lead SNPs of genome-wide significant association signals as additional covariates. When data for a lead SNP were unavailable, high-

LD proxies were included instead. Association results for each study were again combined by fixed-effects meta-analysis. Genomic control correction was performed before meta-analysis on each study, and after meta-analysis on the meta-analysis results.

Sex-specific analysis. To detect loci that exhibit different effects in males and females, we repeated the primary analysis for each trait, analyzing males and females separately. For each trait, residuals were calculated separately for males and females, including covariates as described for the primary analysis. For each sex, residuals were normalized to have mean 0 and standard deviation 1, and normalized residuals were used as phenotypes to test for genotype-phenotype association. For both males and females, association results for each study were combined by fixed-effects meta-analysis. Genomic control correction was performed before meta-analysis on each study, and after meta-analysis on the meta-analysis results. For each SNP, heterogeneity of effect size between males and females was determined using the *T* statistic:

$$\left(b_m - b_w\right) \Big/ \sqrt{se_m^2 + se_w^2 - 2 \cdot r \cdot se_m \cdot se_w},$$

where b_m and b_w are the estimates of effect sizes for men and women, respectively, se_m and se_w are the standard errors estimated for men and women, respectively, and r is the Pearson's correlation between effect size estimates for males and females, across all SNPs. The pre-specified statistical significance threshold for heterogeneity was $P < 0.0005$ to account for multiple testing (102 SNPs in 95 loci tested).

***Cis*-expression quantitative trait locus analysis.** To determine whether lipid-associated SNPs might act as *cis*-regulators of nearby genes, we profiled expression levels of 39,280 transcripts in 960 human liver samples, 741 human omental fat samples, and 609 human subcutaneous fat samples. Tissue samples were collected postmortem or during surgical resection from donors; tissue collection, DNA and RNA isolation, expression profiling, and genotyping were performed as described[75]. MACH was used to obtain imputed genotypes for ~2.5 million SNPs in the

HapMap release 22 for each of the samples. We examined the correlation between each SNP and all transcripts within 500 kb of the SNP position, performing association analyses as previously described[75].

Analysis of lipid-associated SNPs in samples of European and non-European groups. To investigate the relevance of our findings in non-European populations, lead SNPs reported in **Figure 1** were analysed in 9,705 South Asian, 15,046 East Asian, and 8,061 African American samples, as well as 7,063 separate European samples as a control cohort. Association testing was performed for each SNP-trait pair from **Figure 1**, using the same association testing strategy applied to the primary European samples. The pre-specified statistical significance threshold for heterogeneity between each of the non-European groups and the primary European samples was $P < 0.0005$ to account for multiple testing (102 SNPs in 95 loci tested) (**Supplementary Table 11**).

To assess whether the observed concordance between effect directions in each replication group and the primary meta-analysis cohort was due to chance, we tested the overall number of concordant SNPs, regardless of *P*-value in the group, via a binomial draw with a null expectation of $P = 0.5$. To investigate whether the observed number of nominally significant, concordant associations in each group would be expected by chance, we performed the same test on SNPs with $P < 0.05$ in the group, with a null expectation of $P = 0.05$.

For the additional European replication cohorts (MDC-CC and FINRISK97), with a total of 12,017 samples, a subset of the lead SNPs were directly genotyped using either the iPLEX Sequenom MassARRAY platform or allelic discrimination on an ABI 7900 instrument (Applied Biosystems). All reported SNPs had a genotyping call rate >95% on the replication samples and had a Hardy-Weinberg equilibrium $P > 0.001$. Association testing was performed using the same strategy applied to the primary European samples.

Analyses of lipid-associated SNPs in individuals with and without coronary artery disease. Lead SNPs associated with LDL-C, HDL-C, TG, and/or TC levels were queried in each of the CARDIoGRAM and COROGENE consortium samples for association with coronary artery disease (CAD), with a total of 24,607 individuals with CAD and 66,197 without CAD. The pooled test of association was determined by a weighted fixed-effects meta-analysis of these cohorts using METAL.

Analysis of associated SNPs in patients with extreme LDL-C, HDL-C and TG levels. Lead SNPs associated with LDL-C, HDL-C, and/or TG levels were tested in case-control cohorts ascertained based on extreme LDL-C, HDL-C, or TG concentrations, respectively. Logistic regression was used to test for association between dichotomous extreme status and genotypes for each SNP; age and sex were included as covariates in the model. In addition, for each individual, we constructed a genetic risk score statistic, given by the sum of risk allele counts, weighted by effect size, and adjusted for the number of SNPs genotyped. Weighted risk scores were adjusted for age and sex, by multiplying each covariate by the parameter estimate obtained by linear regression, and summed with the uncorrected, weighted risk score. Corrected/weighted risk scores were subsequently ranked by increasing score and divided into quartiles. Quartile 1 was the reference quartile, originating from the lowest risk scores. The number of cases and controls in each quartile were counted, and subsequently compared using chi-square analysis, generating odds ratios and *P*-values that correspond to each quartile's comparison to the reference. The significance of increasing odds ratios between quartiles was assessed using the Cochran-Armitage test for trend.

Simulation studies to assess overlap between GWAS signals and Mendelian disease loci. To estimate the overlap between the 95 loci identified in our GWAS and loci previously implicated in Mendelian dyslipidemias, we examined the proportion of lead SNPs falling within 0, 10, 20, 50 and 100 kb of a Mendelian dyslipidemia locus. To account for the fact that lead SNPs were located near genes more often than expected by chance and for bias in allele frequency due to

SNP ascertainment, we first organized all SNPs examined in our GWAS into a series of bins, each including SNPs with the same minor allele frequency (MAF) (rounded to the nearest 0.01) and the same number of flanking RefSeq genes (not rounded). Next, we counted the number of GWAS lead SNPs within each bin and sampled an appropriate number of SNPs from that bin. As an example, suppose that there were 10,000 analysed SNPs with MAF = 0.10 examined and which lie within 10 kb of at least one RefSeq gene; further, suppose two of these corresponded to GWAS lead SNPs. Our resampling scheme would ensure that every permuted dataset would also include exactly two SNPs from this bin. After generating 1,000,000 SNP sets, we tallied the average number of Mendelian loci hit per simulation and the maximum number of Mendelian loci hit in a single simulation. None of the simulations hit more Mendelian disease loci than that observed in our original GWAS.

Mouse studies. We created adeno-associated virus 8 (AAV8) vectors encoding the mouse orthologues of the *Galnt2* and *Ppp1r3b* genes, driven by the liver-specific thyroxine-binding globulin (TBG) promoter. We generated an AAV8 vector encoding an shRNA targeting the endogenous mouse *Galnt2* gene (sequence of hairpin: GAACTTGGAGATCTCATTCTTCAAGAGAGAATGAGATCTCCAAGTTC) driven by the U6 polymerase III promoter. We generated an adenoviral vector encoding an shRNA targeting the endogenous mouse *Ttc39b* gene (sequence of hairpin: GCACAGTTGTCGAGTCTTTCTCTTCCTGTCAAGAAAGACTCGACAACTGTGC) driven by the U6 polymerase III promoter. Viral vectors encoding shRNAs with scrambled sequence were used as controls.

Separate groups of wild-type C57BL/6J mice (six per group for *Galnt2*, seven per group for *Ppp1r3b*) were injected via the peritoneal route with 1×10^{12} vector genomes/mouse of the relevant vectors. Plasma samples were taken immediately before vector administration, 14 days, and 28 days following vector administration for analysis of lipids. Lipid measurements were

performed on a Cobas Fara II autoanalyzer (Roche Diagnostic Systems Inc, Nutley, NJ) using Wako Chemicals (Richmond, VA) reagents. Upon sacrifice, livers were harvested and perfused with cold phosphate-buffered saline (PBS). Liver RNA was isolated using the mirVana microRNA isolation kit (Ambion, Inc., Austin, TX). Taqman Gene Expression Assays (Applied Biosystems, Foster City, California) were used to perform quantitative real-time polymerase chain reaction (qRT-PCR) measurements of transcript levels. Fast protein liquid chromatography (FPLC) was used to fractionate mouse plasma samples, followed by measurement of the cholesterol content. Cholesterol was measured enzymatically using the Cholesterol E kit from Wako Chemicals (Richmond, VA).

Separate groups of wild-type C57Bl/6 mice (six per group for *Ttc39b*) were injected with 4×10^9 pfu of adenovirus in 0.2 mL via tail vein. Mice were sacrificed after four days or seven days, and blood samples were collected from the mice after six hours of fasting. Plasma HDL-C levels were measured by precipitation and an enzymatic procedure (Wako Chemicals, Richmond, VA).

URLs. Bayesian Imputation Based Association Mapping, BIMBAM, http://quartus.uchicago.edu/~yguan/bimbam/index.html; genotype imputation program, IMPUTE, http://www.stats.ox.ac.uk/~marchini/software/gwas/impute.html; Markov chain haplotyping package, MACH, http://www.sph.umich.edu/csg/abecasis/MACH; MACH2QTL, http://www.sph.umich.edu/csg/abecasis/MACH/download; pedigree analysis package, MERLIN, http://www.sph.umich.edu/csg/abecasis/Merlin; meta-analysis tool for GWASs, METAL, http://www.sph.umich.edu/csg/abecasis/Metal/index.html; whole-genome association analysis package, PLINK, http://pngu.mgh.harvard.edu/~purcell/plink; whole-genome association analysis of imputed data, ProbABEL, http://mga.bionet.nsc.ru/~yurii/ABEL; whole-genome association analysis software, QUICKTEST, http://toby.freeshell.org/software/quicktest.shtml;

statistical computer software, R, http://www.r-project.org; whole-genome association analysis package, SNPTEST, http://www.stats.ox.ac.uk/~marchini/software/gwas/snptest.html.

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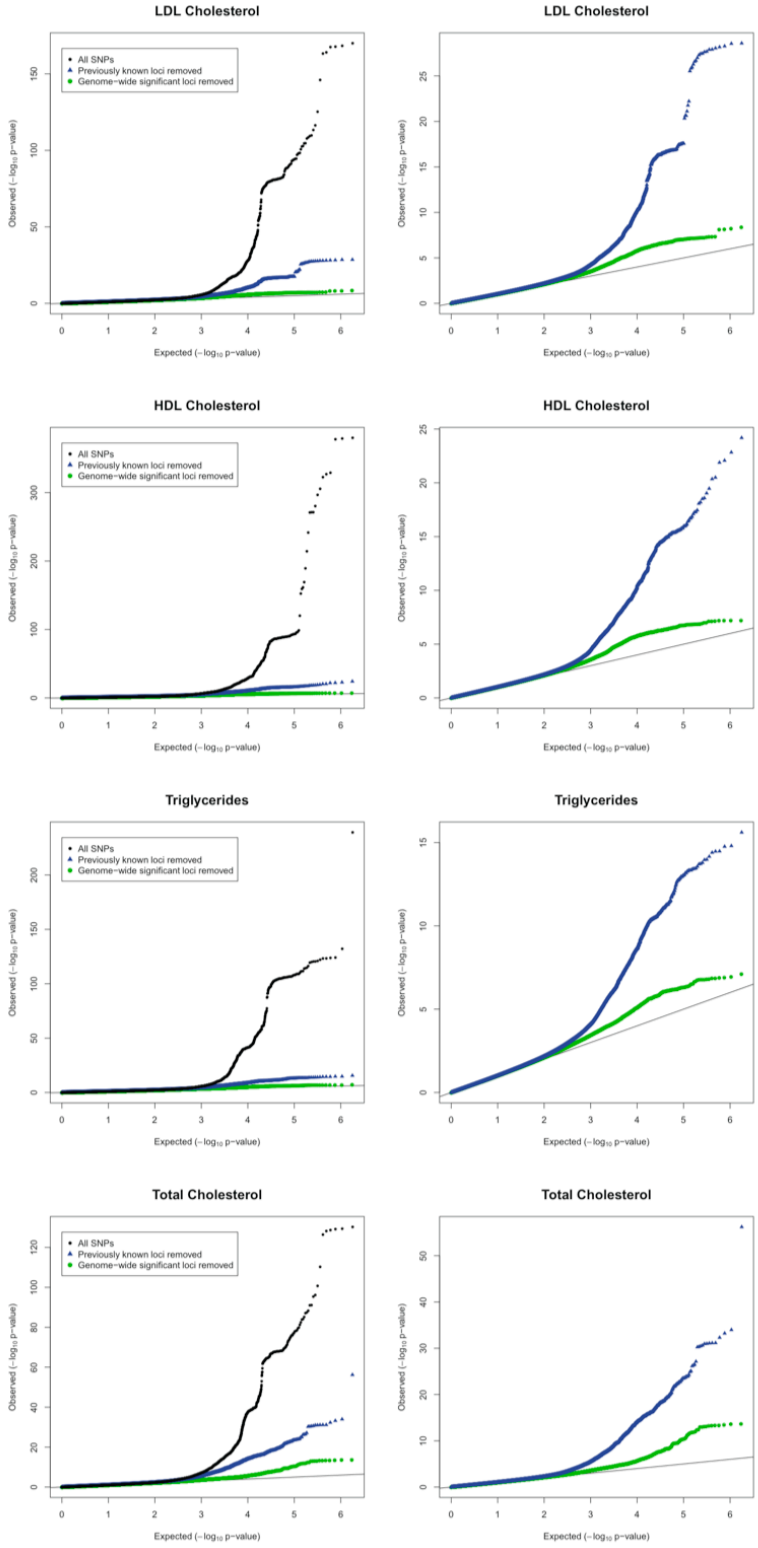
Supplementary Figure Legends

Supplementary Figure 1. Quantile-quantile plots for test statistics, with observed association *P*-values plotted as a function of expected *P*-values. For each trait, the same data is presented with two differing y-axis scales. Black line, all test statistics; blue line, previously reported loci excluded; green line, genome-wide significant loci confirmed or identified in this study excluded.

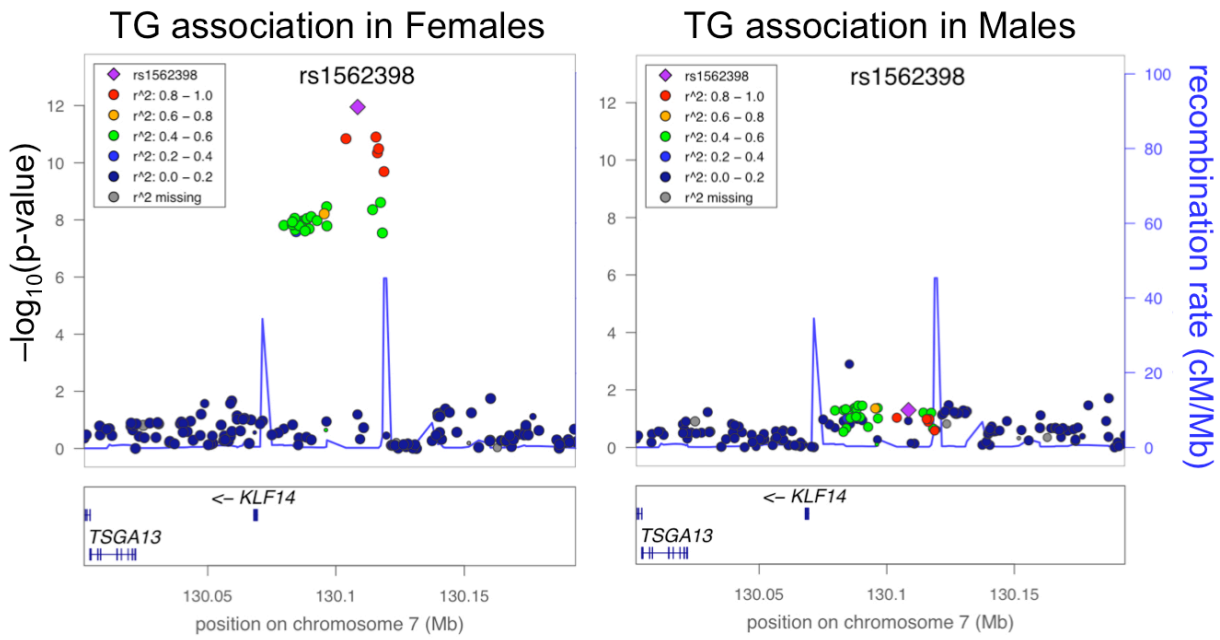
Supplementary Figure 2. Sex-specific effect of rs1562398 on serum TG levels. Regional plots of the *KLF14* locus. Purple diamonds indicate rs1562398, which in women has the strongest association evidence in the locus. Each circle indicates a SNP with the color of the circle indicating the linkage disequilibrium (r^2) between that SNP and rs1562398. Blue lines indicate estimated recombination rates in HapMap. The bottom panels show the relative position and the transcribed strand of each gene in the locus.

Supplementary Figure 3. Analysis of genotype scores in patients with extreme lipid levels. Genotype scores were calculated for LDL-C, HDL-C, and TG in each case (high lipid level) or control (low lipid level) individual. For each analysis, individuals were stratified into quartiles of the genotype score. Quartile 1 (Q1) is the reference quartile, originating from the lowest scores. Shown are odds ratios for case status for each quartile in comparison to Q1. Bars indicate 95% confidence intervals.

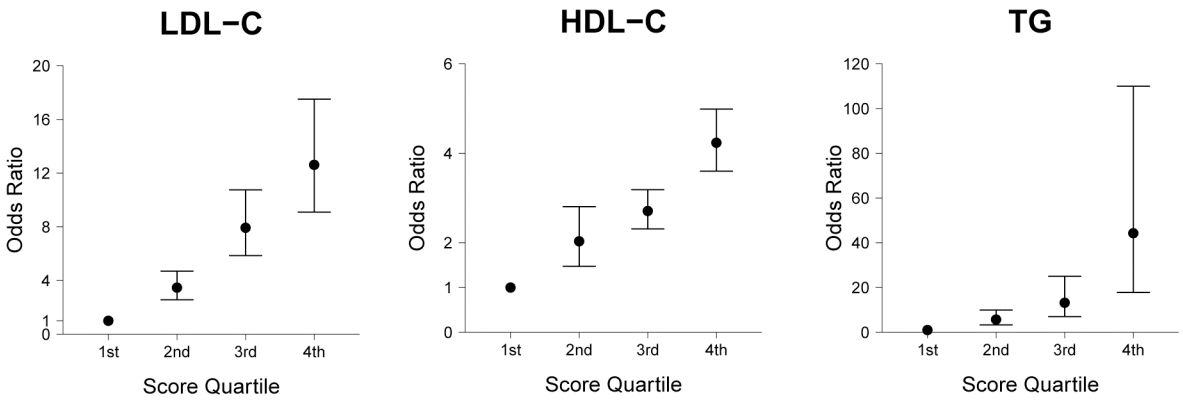
Supplementary Figure 1.



Supplementary Figure 2.



Supplementary Figure 3.



Supplementary Table 1. Cohort characteristics.

	Study	*n*	Country of origin	Mean age, years	% Female	Total cholesterol (TC), mg/dL	LDL cholesterol, mg/dL	HDL cholesterol, mg/dL	Triglycerides (TG), mg/dL
				Community-based cohorts					
AGES	Age, Gene/Environment Susceptibility Reykjavik Study	2,485	Iceland	76.6 ± 5.7	61.6	230 ± 40	147 ± 36	62 ± 17	103 ± 48
ARIC	Atherosclerosis Risk in Communities Study	7,841	US	54.3 ± 5.7	53.0	214 ± 40	137 ± 37	51 ± 17	135 ± 88
MZGWA-AUS	Australian Twin Cohort	449	Australia	46.8 ± 12.5	100.0	220 ± 39	133 ± 37	61 ± 10	139 ± 82
BLSA	Baltimore Longitudinal Study of Aging	713	US	68.9 ± 17.4	56.0	188 ± 37	110 ± 32	56 ± 17	112 ± 86
B58C-WTCCC	British 1958 Birth Cohort – Wellcome Trust Case Control Consortium	1,459	UK	44.9 ± 0.4	49.9	227 ± 42	131 ± 35	60 ± 15	186 ± 134
CHS	Cardiovascular Health Study	3,121	US	72.4 ± 5.4	60.4	212 ± 39	130 ± 35	55 ± 16	139 ± 75
CoLaus	The Cohorte Lausannoise Study	5,253	Switzerland	53.2 ± 10.8	52.3	217 ± 40	148 ± 42	63 ± 17	124 ± 107
KORA	KORA - Cooperative Health Research in the Region of Augsburg	1,405	Germany	62.5 ± 10.1	51.0	225 ± 39	134 ± 32	59 ± 17	168 ± 116
MZGWA-DK	Danish Twins Registry	142	Denmark	44.2 ± 19.2	100.0	210 ± 46	121 ± 35	63 ± 15	103 ± 34
MZGWA-NLD	Dutch Twins Registry	289	Netherlands	33.8 ± 11.9	100.0	189 ± 36	109 ± 33	60 ± 14	100 ± 43
EPIC-N-SUBCOH	EPIC-Norfolk Subcohort	2,346	UK	59.3 ± 9.0	53.2	239 ± 44	170 ± 42	55 ± 16	161 ± 98
FENLAND	Fenland Study	1,401	UK	45.0	56.1	208 ± 39	130 ± 34	57 ± 15	107 ± 74
MZGWA-FIN	Finnish National Twin Cohort	137	Finland	60.8 ± 15.4	100.0	208 ± 31	134 ± 33	62 ± 17	106 ± 58
InCHIANTI	Invecchiare in Chianti Study†	1,134	Italy	68.2 ± 15.9	55.6	213 ± 40	132 ± 35	56 ± 15	123 ± 75
LOLIPOP	London Life Sciences Prospective Population Study	1,599	UK	54.4	12.8	205 ± 43	124 ± 37	51 ± 14	152 ± 118
FINRISK	National FINRISK Study	910	Finland	59.6 ± 10.7	34.7	219 ± 40	135 ± 34	55 ± 16	142 ± 87
NFBC66	Northern Finland Birth Cohort 1966	5,138	Finland	31 ± 0.0	51.9	196 ± 39	116 ± 34	60 ± 15	105 ± 63
PARC	Pharmacogenomics and Risk of Cardiovascular Disease Study*	1,939	US	61.6 ± 13.7	30.6	214 ± 38	138 ± 32	42 ± 15	178 ± 118
RS-I	Rotterdam Study Baseline	5,701	Netherlands	69.5 ± 9.1	59.3	255 ± 47	145 ± 34	52 ± 14	135 ± 65
RS-II	Rotterdam Study Extension of Baseline	1,628	Netherlands	64.7 ± 8.1	55.0	227 ± 38	146 ± 35	54 ± 14	139 ± 79
MZGWA-UK	Twins UK	457	UK	51.9 ± 11.2	100.0	205 ± 41	130 ± 36	58 ± 15	86 ± 68
SUVIMAX	Supplementation en Vitamines et Mineraux Antioxydants Study	1,813	France	50.1 ± 6.3	62.0	225 ± 32	138 ± 32	63 ± 15	92 ± 47
MZGWA-SWE	Swedish National Twin Cohort	297	Sweden	71.9 ± 5.9	100.0	233 ± 34	149 ± 31	60 ± 15	127 ± 60

WGHS	Women's Genome Health Study*	22,041	US	54.6 ± 7.1	100.0	211 ± 41	124 ± 34	54 ± 15	142 ± 89
Case-control samples									
BRIGHT	British Genetics of Hypertension Study Cases	1,615	UK	56.4 ± 11.3	61.5	216 ± 40	148 ± 37	52 ± 15	191 ± 134
B58C-T1DGC	British 1958 Birth Cohort T1D Controls	2,534	UK	45.3 ± 0.3	51.3	228 ± 42	132 ± 35	60 ± 15	186 ± 153
DGI	Diabetes Genetics Initiative T2D Cases†	1,528	Finland, Sweden	64.3 ± 10.5	49.7	224 ± 46	146 ± 40	45 ± 12	175 ± 124
DGI	Diabetes Genetics Initiative Controls†	1,508	Finland, Sweden	58.8 ± 10.4	51.5	229 ± 42	155 ± 39	51 ± 13	118 ± 61
EPIC-N-OBSET	EPIC-Norfolk Obese Cases	1,078	UK	59.3 ± 8.8	56.9	246 ± 44	179 ± 41	49 ± 15	205 ± 110
FHS	Family Heart Study CHD Cases	356	US	55.1 ± 11.6	54.5	213 ± 43	132 ± 38	49 ± 13	158 ± 77
FHS	Family Heart Study Controls	394	US	54.9 ± 11.1	50.3	202 ± 36	123 ± 32	52 ± 16	134 ± 68
FUSION	Finland-United States Investigation of NIDDM Genetics T2D Cases	772	Finland	62.7 ± 7.7	41.2	221 ± 44	140 ± 38	47 ± 13	180 ± 114
FUSION	Finland-United States Investigation of NIDDM Genetics T2D Controls	982	Finland	63.1 ± 7.5	49.2	227 ± 38	146 ± 35	58 ± 16	120 ± 59
GENMETS	Health2000 GenMets MS Cases	867	Finland	49.9 ± 11.1	51.2	240 ± 45	153 ± 42	45 ± 12	187 ± 103
GENMETS	Health2000 GenMets Controls	892	Finland	49.9 ± 11.0	51.2	228 ± 38	141 ± 37	57 ± 14	109 ± 51
MedSTAR	MedSTAR MI Cases	716	US	54.7 ± 7.3	28.2	170 ± 44	101 ± 39	43 ± 16	155 ± 110
MedSTAR	MedSTAR Controls	393	US	59.7 ± 8.9	48.8	180 ± 39	106 ± 33	50 ± 16	127 ± 79
PennCATH	PennCATH MI Cases	892	US	56.9 ± 9.2	24.3	179 ± 43	107 ± 9	42 ± 11	179 ± 43
PennCATH	PennCATH Controls	454	US	61.7 ± 9.5	51.7	179 ± 39	108 ± 32	49 ± 15	114 ± 83
Family-based samples									
ERF	Erasmus Rucphen Family Study	1,108	Netherlands	47.1 ± 14.7	60.8	219 ± 43	148 ± 38	50 ± 14	115 ± 68
FramHS	Framingham Heart Study	7,132	US	44.8 ± 10.6	54.0	198 ± 36	122 ± 33	53 ± 15	117 ± 84
MICROS	MICROS Study of Population Microisolates in South Tyrol	1,037	Austria	44.4 ± 15.8	56.5	227 ± 47	137 ± 43	65 ± 14	125 ± 90
NSPHS	Northern Swedish Population Health Study	593	Sweden	44.8 ± 20.4	54.0	228 ± 52	138 ± 42	62 ± 16	192 ± 138
ORCADES	Orkney Complex Disease Study	633	UK	51.9 ± 16.7	54.5	227 ± 43	141 ± 41	66 ± 15	115 ± 58
SardiNIA	SardiNIA Study of Aging	4,184	Italy	43.6 ± 17.6	56.0	208 ± 31	127 ± 29	64 ± 15	86 ± 54
Vis	Vis Study	771	Croatia	56.5 ± 15.4	58.0	197 ± 39	125 ± 37	43 ± 6	151 ± 82

* PARC is a pharmacogenetic genetic study; WGHS is a prospective clinical trial

† The DGI and InCHIANTI studies each included a small number of related individuals.

Supplementary Table 2. Findings of the primary meta-analysis.

Nearby genes*	Lead SNP	Trait	Best SNP	Chr	Position†	*n*	Major allele, minor allele (MAF)‡	Effect size (SE) mg/dL§	*P*-value	Previous GWAS finding?
LDLRAP1	rs12027135	TC	rs12027135	1	25,648,320	100,184	T, A (0.47)	-1.22 (0.19)	4.12×10^{-11}	Y
		LDL	rs12027135	1	25,648,320	95,454	T, A (0.47)	-1.10 (0.18)	1.24×10^{-10}	N
PABPC4	rs4660293	HDL	rs4660293	1	39,800,767	99,855	A, G (0.23)	-0.48 (0.09)	3.99×10^{-10}	N
PCSK9	rs2479409	TC	rs2479409	1	55,277,238	100,164	A, G (0.30)	1.96 (0.24)	3.84×10^{-24}	N
		LDL	rs2479409	1	55,277,238	95,435	A, G (0.30)	2.01 (0.22)	1.93×10^{-28}	Y
ANGPTL3	rs2131925	TC	rs3850634	1	62,823,186	97,148	T, G (0.32)	-2.60 (0.20)	4.90×10^{-41}	Y
		LDL	rs3850634	1	62,823,186	92,503	T, G (0.32)	-1.59 (0.19)	2.63×10^{-18}	N
		TG	rs2131925	1	62,798,530	96,598	T, G (0.32)	-4.94 (0.40)	8.84×10^{-43}	Y
EVI5	rs7515577	TC	rs7515577	1	92,782,026	100,165	A, C (0.21)	-1.18 (0.24)	2.78×10^{-08}	N
SORT1	rs629301	TC	rs629301	1	109,619,829	100,184	T, G (0.22)	-5.41 (0.24)	5.77×10^{-131}	Y
		LDL	rs629301	1	109,619,829	95,454	T, G (0.22)	-5.65 (0.21)	9.70×10^{-171}	Y
ZNF648	rs1689800	HDL	rs1689800	1	180,435,508	99,900	A, G (0.35)	-0.47 (0.08)	3.18×10^{-10}	N
MOSC1	rs2642442	TC	rs2807834	1	219,037,216	100,098	G, T (0.32)	-1.38 (0.22)	4.90×10^{-13}	N
		LDL	rs2807834	1	219,037,216	95,372	G, T (0.32)	-1.09 (0.20)	5.62×10^{-11}	N
GALNT2	rs4846914	HDL	rs4846914	1	228,362,314	99,881	A, G (0.40)	-0.61 (0.07)	3.66×10^{-21}	Y
		TG	rs1321257	1	228,371,935	92,418	A, G (0.39)	2.76 (0.38)	2.09×10^{-14}	Y
IRF2BP2	rs514230	TC	rs514230	1	232,925,220	100,184	T, A (0.48)	-1.36 (0.20)	5.37×10^{-14}	N
		LDL	rs514230	1	232,925,220	95,454	T, A (0.48)	-1.13 (0.18)	9.38×10^{-12}	N
APOB	rs1367117	TC	rs1367117	2	21,117,405	100,176	G, A (0.30)	4.16 (0.22)	4.08×10^{-96}	Y
		LDL	rs1367117	2	21,117,405	95,446	G, A (0.30)	4.05 (0.19)	4.48×10^{-114}	Y
	rs1042034	HDL	rs1042034	2	21,078,786	99,892	T, C (0.22)	0.90 (0.09)	1.22×10^{-30}	Y
		TG	rs1042034	2	21,078,786	96,590	T, C (0.22)	-5.99 (0.45)	1.36×10^{-45}	Y
GCKR	rs1260326	TC	rs1260326	2	27,584,444	100,176	C, T (0.41)	1.91 (0.19)	7.31×10^{-27}	N
		TG	rs1260326	2	27,584,444	96,590	C, T (0.41)	8.76 (0.40)	5.68×10^{-133}	Y
ABCG5/8	rs4299376	TC	rs4299376	2	43,926,080	95,992	T, G (0.30)	3.01 (0.22)	4.03×10^{-45}	Y
		LDL	rs4299376	2	43,926,080	91,285	T, G (0.30)	2.75 (0.20)	1.73×10^{-47}	Y
RAB3GAP1	rs7570971	TC	rs6759321	2	136,039,146	95,242	G, T (0.31)	1.18 (0.22)	1.39×10^{-08}	N
COBLL1	rs12328675	HDL	rs12328675	2	165,249,046	99,892	T, C (0.13)	0.68 (0.12)	2.72×10^{-10}	Y
	rs10195252	TG	rs10195252	2	165,221,337	96,590	T, C (0.40)	-2.01 (0.38)	1.63×10^{-10}	N
IRS1	rs2972146	HDL	rs1515100	2	226,837,161	96,875	A, C (0.37)	0.46 (0.08)	2.01×10^{-09}	N

IRS1		TG	rs2943645	2	226,807,424	93,554	T, C (0.37)	-1.89 (0.38)	2.35×10^{-08}	N
RAF1	rs2290159	TC	rs2290159	3	12,603,920	99,434	G, C (0.22)	-1.42 (0.23)	4.21×10^{-09}	N
MSL2L1	rs645040	TG	rs645040	3	137,409,312	96,597	T, G (0.22)	-2.22 (0.45)	2.52×10^{-08}	N
KLHL8	rs442177	TG	rs442177	4	88,249,285	96,598	T, G (0.41)	-2.25 (0.38)	8.65×10^{-12}	N
SLC39A8	rs13107325	HDL	rs13107325	4	103,407,732	92,059	C, T (0.07)	-0.84 (0.16)	7.20×10^{-11}	N
ARL15	rs6450176	HDL	rs6450176	5	53,333,782	99,900	G, A (0.26)	-0.49 (0.09)	4.98×10^{-08}	N
MAP3K1	rs9686661	TG	rs9686661	5	55,897,543	95,848	C, T (0.20)	2.57 (0.49)	1.32×10^{-10}	N
HMGCR	rs12916	TC	rs12916	5	74,692,295	100,184	T, C (0.39)	2.84 (0.20)	8.79×10^{-47}	Y
		LDL	rs12916	5	74,692,295	95,454	T, C (0.39)	2.45 (0.18)	5.12×10^{-45}	Y
TIMD4	rs6882076	TC	rs6882076	5	156,322,875	100,184	C, T (0.35)	-1.98 (0.20)	7.46×10^{-28}	N
		LDL	rs6882076	5	156,322,875	95,454	C, T (0.35)	-1.67 (0.19)	1.89×10^{-22}	Y
		TG	rs1553318	5	156,411,901	96,598	C, G (0.36)	-2.63 (0.39)	3.68×10^{-12}	N
MYLIP	rs3757354	TC	rs3757354	6	16,235,386	96,000	C, T (0.22)	-1.46 (0.24)	2.78×10^{-09}	N
		LDL	rs3757354	6	16,235,386	91,293	C, T (0.22)	-1.43 (0.21)	1.16×10^{-11}	N
HFE	rs1800562	TC	rs1800562	6	26,201,120	98,550	G, A (0.06)	-2.16 (0.43)	2.49×10^{-08}	N
		LDL	rs1800562	6	26,201,120	93,821	G, A (0.06)	-2.22 (0.39)	6.07×10^{-10}	N
HLA	rs3177928	TC	rs3177928	6	32,520,413	100,151	G, A (0.16)	2.31 (0.27)	3.96×10^{-19}	N
		LDL	rs3177928	6	32,520,413	95,425	G, A (0.16)	1.83 (0.24)	2.40×10^{-15}	N
	rs2247056	TG	rs2247056	6	31,373,469	96,598	C, T (0.25)	-2.99 (0.42)	1.60×10^{-15}	Y
C6orf106	rs2814982	TC	rs2814982	6	34,654,538	100,184	C, T (0.11)	-1.86 (0.33)	4.68×10^{-11}	N
	rs2814944	HDL	rs2814944	6	34,660,775	99,811	G, A (0.16)	-0.49 (0.10)	3.81×10^{-09}	N
FRK	rs9488822	TC	rs9488822	6	116,419,586	100,184	A, T (0.35)	-1.18 (0.20)	1.69×10^{-10}	N
		LDL	rs11153594	6	116,461,284	95,367	C, T (0.41)	-0.89 (0.18)	2.95×10^{-9}	N
CITED2	rs605066	HDL	rs605066	6	139,871,359	99,900	T, C (0.42)	-0.39 (0.08)	2.55×10^{-08}	N
LPA	rs1564348	TC	rs1564348	6	160,498,850	100,168	T, C (0.17)	2.18 (0.27)	9.71×10^{-17}	N
		LDL	rs1564348	6	160,498,850	95,439	T, C (0.17)	1.95 (0.24)	1.70×10^{-17}	N
	rs1084651	HDL	rs1084651	6	161,009,807	99,900	G, A (0.16)	-0.56 (0.10)	2.97×10^{-08}	N
DNAH11	rs12670798	TC	rs2285942	7	21,549,442	100,184	C, T (0.15)	1.70 (0.28)	6.55×10^{-10}	N
		LDL	rs12670798	7	21,573,877	95,454	T, C (0.23)	1.26 (0.20)	6.88×10^{-10}	Y
NPC1L1	rs2072183	TC	rs2072183	7	44,545,705	97,063	G, C (0.25)	2.01 (0.29)	3.22×10^{-11}	N
		LDL	rs217386	7	44,567,220	95,454	G, A (0.43)	-1.17 (0.19)	4.25×10^{-11}	N
TYW1B	rs13238203	TG	rs13238203	7	71,767,603	78,797	C, T (0.04)	-7.91 (1.34)	1.13×10^{-09}	N
MLXIPL	rs17145738	HDL	rs17145738	7	72,620,810	99,898	C, T (0.12)	0.57 (0.12)	1.19×10^{-09}	N
		TG	rs7811265	7	72,572,446	96,598	A, G (0.19)	-7.91 (0.50)	9.06×10^{-59}	Y
KLF14	rs4731702	HDL	rs4731702	7	130,083,924	99,900	C, T (0.48)	0.59 (0.07)	1.21×10^{-15}	N
PPP1R3B	rs9987289	TC	rs2126259	8	9,222,556	100,184	C, T (0.10)	-3.14 (0.32)	8.98×10^{-24}	N

PPP1R3B		LDL	rs2126259	8	9,222,556	95,454	C, T (0.10)	-2.22 (0.29)	7.43×10^{-15}	N
		HDL	rs9987289	8	9,220,768	99,900	G, A (0.09)	-1.21 (0.13)	6.40×10^{-25}	N
PINX1	rs11776767	TG	rs11776767	8	10,721,339	96,598	G, C (0.37)	2.01 (0.39)	1.30×10^{-08}	Y
NAT2	rs1495741	TC	rs1961456	8	18,299,989	100,184	A, G (0.32)	1.07 (0.21)	1.68×10^{-09}	N
		TG	rs1495743	8	18,317,580	96,580	C, G (0.22)	2.97 (0.42)	4.11×10^{-14}	N
LPL	rs12678919	HDL	rs12678919	8	19,888,502	99,900	A, G (0.12)	2.25 (0.12)	9.71×10^{-98}	Y
		TG	rs12678919	8	19,888,502	96,598	A, G (0.12)	-13.64 (0.65)	1.50×10^{-115}	Y
CYP7A1	rs2081687	TC	rs1030431	8	59,474,251	100,184	G, A (0.35)	1.26 (0.20)	8.79×10^{-13}	N
		LDL	rs1030431	8	59,474,251	95,454	G, A (0.35)	0.95 (0.18)	3.86×10^{-09}	N
TRPS1	rs2737229	TC	rs2737229	8	116,717,740	100,184	A, C (0.30)	-1.11 (0.21)	2.45×10^{-08}	N
	rs2293889	HDL	rs2293889	8	116,668,374	99,900	G, T (0.41)	-0.44 (0.08)	5.77×10^{-11}	N
TRIB1	rs2954029	TC	rs2954022	8	126,551,803	100,184	C, A (0.46)	-2.30 (0.19)	5.02×10^{-36}	Y
		LDL	rs2954022	8	126,551,803	95,454	C, A (0.46)	-1.84 (0.17)	2.59×10^{-29}	N
		HDL	rs10808546	8	126,565,000	99,900	C, T (0.44)	0.61 (0.07)	6.35×10^{-19}	N
		TG	rs2954029	8	126,560,154	96,598	A, T (0.47)	-5.64 (0.39)	3.29×10^{-55}	Y
PLEC1	rs11136341	TC	rs11136341	8	145,115,531	93,052	A, G (0.40)	1.34 (0.24)	8.96×10^{-10}	N
		LDL	rs11136341	8	145,115,531	88,376	A, G (0.40)	1.40 (0.21)	4.44×10^{-13}	N
TTC39B	rs581080	TC	rs581080	9	15,295,378	100,184	C, G (0.18)	-1.57 (0.26)	3.08×10^{-09}	N
		HDL	rs643531	9	15,286,034	99,889	A, C (0.14)	-0.72 (0.10)	1.30×10^{-13}	Y
ABCA1	rs1883025	TC	rs1883025	9	106,704,122	99,463	C, T (0.25)	-2.24 (0.24)	3.39×10^{-27}	N
		HDL	rs1883025	9	106,704,122	99,179	C, T (0.25)	-0.94 (0.09)	1.75×10^{-33}	Y
ABO	rs9411489	TC	rs651007	9	135,143,696	98,535	C, T (0.21)	2.30 (0.25)	8.66×10^{-21}	N
		LDL	rs649129	9	135,144,125	95,454	C, T (0.22)	2.05 (0.21)	7.85×10^{-22}	Y
JMJD1C	rs10761731	TG	rs10761731	10	64,697,616	96,598	A, T (0.43)	-2.38 (0.38)	3.48×10^{-12}	N
CYP26A1	rs2068888	TG	rs2068888	10	94,829,632	96,598	G, A (0.47)	-2.28 (0.38)	2.38×10^{-08}	N
GPAM	rs2255141	TC	rs2255141	10	113,923,876	100,184	G, A (0.30)	1.14 (0.20)	2.03×10^{-10}	N
		LDL	rs1129555	10	113,900,711	95,438	G, A (0.29)	1.08 (0.20)	2.14×10^{-09}	N
AMPD3	rs2923084	HDL	rs2923084	11	10,345,358	99,898	A, G (0.17)	-0.41 (0.10)	4.62×10^{-08}	N
SPTY2D1	rs10128711	TC	rs10832963	11	18,620,817	100,184	G, T (0.29)	-1.06 (0.22)	2.52×10^{-08}	N
LRP4	rs3136441	HDL	rs3136441	11	46,699,823	99,900	T, C (0.15)	0.78 (0.10)	3.48×10^{-18}	N
FADS1–2–3	rs174546	TC	rs174550	11	61,328,054	100,184	T, C (0.34)	-1.78 (0.20)	2.08×10^{-22}	Y
		LDL	rs174583	11	61,366,326	95,443	C, T (0.35)	-1.71 (0.19)	1.17×10^{-21}	Y
		HDL	rs174601	11	61,379,716	99,900	C, T (0.36)	-0.73 (0.08)	1.50×10^{-22}	Y
		TG	rs174546	11	61,326,406	96,598	C, T (0.34)	3.82 (0.38)	5.41×10^{-24}	Y
APOA1–C3–A4–A5	rs964184	TC	rs964184	11	116,154,127	100,162	C, G (0.13)	4.68 (0.29)	6.21×10^{-57}	N
		LDL	rs964184	11	116,154,127	95,432	C, G (0.13)	2.85 (0.27)	1.47×10^{-26}	N

APOA1–C3–A4–A5		HDL	rs964184	11	116,154,127	99,878	C, G (0.13)	-1.50 (0.11)	5.21×10^{-47}	Y
		TG	rs964184	11	116,154,127	96,576	C, G (0.13)	16.95 (0.48)	6.71×10^{-240}	Y
UBASH3B	rs7941030	TC	rs7941030	11	122,027,585	100,184	T, C (0.38)	0.97 (0.19)	1.52×10^{-10}	N
		HDL	rs7115089	11	122,035,801	99,900	C, G (0.37)	0.31 (0.08)	2.66×10^{-08}	N
ST3GAL4	rs11220462	TC	rs11220463	11	125,753,421	100,184	A, T (0.11)	2.01 (0.33)	2.12×10^{-11}	N
		LDL	rs11220462	11	125,749,162	95,454	G, A (0.14)	1.95 (0.26)	1.20×10^{-15}	N
PDE3A	rs7134375	HDL	rs7134375	12	20,365,025	99,900	C, A (0.42)	0.40 (0.08)	3.84×10^{-08}	N
LRP1	rs11613352	HDL	rs3741414	12	56,130,316	99,900	C, T (0.24)	0.46 (0.09)	1.64×10^{-08}	N
		TG	rs11613352	12	56,078,847	96,598	C, T (0.23)	-2.70 (0.43)	4.43×10^{-10}	N
MVK	rs7134594	HDL	rs7134594	12	108,484,576	99,900	T, C (0.47)	-0.44 (0.07)	6.88×10^{-15}	Y
BRAP	rs11065987	TC	rs11065987	12	110,556,807	100,184	A, G (0.42)	-0.96 (0.20)	6.77×10^{-12}	N
		LDL	rs11065987	12	110,556,807	95,454	A, G (0.42)	-0.97 (0.18)	1.51×10^{-09}	N
HNF1A	rs1169288	TC	rs1169288	12	119,901,033	100,184	A, C (0.33)	1.45 (0.20)	1.48×10^{-14}	N
		LDL	rs1169288	12	119,901,033	95,454	A, C (0.33)	1.42 (0.19)	1.13×10^{-15}	Y
SBNO1	rs4759375	HDL	rs4759375	12	122,362,191	99,900	C, T (0.06)	0.86 (0.16)	7.50×10^{-09}	N
ZNF664	rs4765127	HDL	rs4765127	12	123,026,120	99,787	G, T (0.34)	0.44 (0.08)	2.89×10^{-10}	N
		TG	rs12310367	12	123,052,631	96,598	A, G (0.34)	-2.42 (0.41)	1.21×10^{-08}	Y
SCARB1	rs838880	HDL	rs838880	12	123,827,546	80,428	T, C (0.31)	0.61 (0.09)	2.58×10^{-14}	N
NYNRIN	rs8017377	LDL	rs2332328	14	23,952,898	95,454	C, T (0.48)	1.17 (0.19)	4.41×10^{-11}	N
CAPN3	rs2412710	TG	rs2412710	15	40,471,079	86,707	G, A (0.02)	7.00 (1.49)	1.87×10^{-08}	N
FRMD5	rs2929282	TG	rs2929282	15	42,033,223	95,070	A, T (0.05)	5.13 (0.86)	1.63×10^{-11}	N
LIPC	rs1532085	TC	rs1532085	15	56,470,658	98,656	G, A (0.39)	1.54 (0.20)	8.83×10^{-20}	N
		HDL	rs1532085	15	56,470,658	98,409	G, A (0.39)	1.45 (0.08)	2.92×10^{-96}	Y
		TG	rs261342	15	56,518,445	95,070	C, G (0.22)	2.99 (0.45)	2.42×10^{-13}	N
LACTB	rs2652834	HDL	rs2652834	15	61,183,920	98,409	G, A (0.20)	-0.39 (0.10)	8.75×10^{-09}	N
CTF1	rs11649653	TG	rs11649653	16	30,825,988	95,034	C, G (0.40)	-2.13 (0.39)	3.35×10^{-08}	N
CETP	rs3764261	TC	rs3764261	16	55,550,825	94,472	C, A (0.32)	1.67 (0.23)	6.67×10^{-14}	N
		LDL	rs247616	16	55,547,091	89,838	C, T (0.32)	-1.45 (0.20)	9.25×10^{-13}	N
		HDL	rs3764261	16	55,550,825	94,225	C, A (0.32)	3.39 (0.09)	7.10×10^{-380}	Y
		TG	rs7205804	16	55,562,390	95,070	G, A (0.45)	-2.88 (0.38)	1.15×10^{-12}	Y
LCAT	rs16942887	HDL	rs16942887	16	66,485,543	98,409	G, A (0.12)	1.27 (0.11)	8.39×10^{-33}	Y
HPR	rs2000999	TC	rs2000999	16	70,665,594	98,656	G, A (0.20)	2.34 (0.24)	3.22×10^{-24}	N
		LDL	rs2000999	16	70,665,594	93,999	G, A (0.20)	2.00 (0.22)	1.75×10^{-22}	N
CMIP	rs2925979	HDL	rs2925979	16	80,092,291	98,409	C, T (0.30)	-0.45 (0.08)	2.09×10^{-11}	N
STARD3	rs11869286	HDL	rs881844	17	35,063,744	98,409	G, C (0.34)	-0.51 (0.08)	2.84×10^{-14}	N
OSBPL7	rs7206971	TC	rs7206971	17	42,780,114	90,614	G, A (0.49)	1.01 (0.20)	1.05×10^{-08}	N

OSBPL7		LDL	rs7225700	17	42,746,803	93,999	C, T (0.35)	-0.87 (0.18)	3.92×10^{-09}	N
ABCA8	rs4148008	HDL	rs4148008	17	64,386,889	98,409	C, G (0.32)	-0.42 (0.08)	1.79×10^{-10}	N
PGS1	rs4129767	HDL	rs4082919	17	73,889,077	98,409	T, G (0.48)	-0.40 (0.08)	4.98×10^{-09}	N
LIPG	rs7241918	TC	rs7239867	18	45,418,715	98,656	G, A (0.17)	-1.94 (0.26)	2.03×10^{-19}	N
		HDL	rs7241918	18	45,414,951	98,409	T, G (0.17)	-1.31 (0.10)	2.73×10^{-49}	Y
MC4R	rs12967135	HDL	rs12967135	18	56,000,003	98,409	G, A (0.23)	-0.42 (0.09)	6.58×10^{-09}	N
ANGPTL4	rs7255436	HDL	rs7255436	19	8,339,196	98,409	A, C (0.47)	-0.45 (0.08)	3.25×10^{-08}	Y
LDLR	rs6511720	TC	rs6511720	19	11,063,306	97,764	G, T (0.11)	-7.09 (0.34)	6.65×10^{-97}	Y
		LDL	rs6511720	19	11,063,306	93,131	G, T (0.11)	-6.99 (0.30)	4.28×10^{-117}	Y
LOC55908	rs737337	HDL	rs737337	19	11,208,493	98,409	T, C (0.08)	-0.64 (0.14)	3.10×10^{-09}	N
CILP2	rs10401969	TC	rs10401969	19	19,268,718	98,640	T, C (0.07)	-4.74 (0.42)	2.90×10^{-38}	Y
		LDL	rs10401969	19	19,268,718	93,983	T, C (0.07)	-3.11 (0.38)	6.69×10^{-22}	Y
		TG	rs10401969	19	19,268,718	95,054	T, C (0.07)	-7.83 (0.82)	1.61×10^{-29}	Y
APOE–C1–C2	rs4420638	TC	rs4420638	19	50,114,786	87,766	A, G (0.17)	6.83 (0.32)	5.20×10^{-111}	Y
		LDL	rs4420638	19	50,114,786	83,209	A, G (0.17)	7.14 (0.29)	8.72×10^{-147}	Y
		HDL	rs4420638	19	50,114,786	87,520	A, G (0.17)	-1.06 (0.12)	4.40×10^{-21}	Y
	rs439401	TG	rs439401	19	50,106,291	65,871	C, T (0.36)	-5.50 (0.44)	1.14×10^{-30}	Y
FLJ36070	rs492602	TC	rs492602	19	53,898,229	97,148	A, G (0.49)	1.27 (0.21)	2.01×10^{-10}	N
LILRA3	rs386000	HDL	rs386000	19	59,484,573	86,430	G, C (0.20)	0.83 (0.11)	4.29×10^{-16}	N
ERGIC3	rs2277862	TC	rs2277862	20	33,616,196	98,656	C, T (0.15)	-1.19 (0.27)	3.82×10^{-10}	N
MAFB	rs2902940	TC	rs2902940	20	38,524,901	98,656	A, G (0.29)	-1.38 (0.21)	6.08×10^{-11}	N
		LDL	rs2902941	20	38,524,928	93,999	A, G (0.33)	-0.98 (0.19)	1.11×10^{-08}	Y
TOP1	rs6029526	TC	rs4297946	20	39,244,689	98,588	G, C (0.47)	1.52 (0.19)	2.76×10^{-17}	N
		LDL	rs909802	20	39,370,229	93,999	C, T (0.47)	1.41 (0.17)	3.18×10^{-19}	N
HNF4A	rs1800961	TC	rs1800961	20	42,475,778	70,383	C, T (0.03)	-4.73 (0.66)	5.72×10^{-13}	N
		HDL	rs1800961	20	42,475,778	71,749	C, T (0.03)	-1.88 (0.24)	1.05×10^{-15}	Y
PLTP	rs6065906	HDL	rs6065906	20	43,987,422	98,409	T, C (0.18)	-0.93 (0.10)	1.90×10^{-22}	Y
		TG	rs4810479	20	43,978,455	95,070	T, C (0.24)	3.32 (0.42)	4.69×10^{-18}	Y
UBE2L3	rs181362	HDL	rs181362	22	20,262,068	96,905	C, T (0.20)	-0.46 (0.09)	1.11×10^{-08}	N
PLA2G6	rs5756931	TG	rs5756931	22	36,875,979	95,067	T, C (0.40)	-1.54 (0.38)	3.82×10^{-08}	N

* When possible, plausible biological candidate genes have been listed; otherwise, the nearest gene(s) is indicated.

† Positions are relative to Human Genome NCBI Build 36, except for rs9411489, which is Build 35.

‡ Alleles are designated with respect to the "+" strand.

§ Effect sizes for HDL, LDL, and total cholesterol were estimated directly. Effect sizes for triglycerides were estimated as percent changes due to a single copy of the minor allele; effect in mg/dL was determined at mean triglyceride level 137.9 mg/dL.

Supplementary Table 3. SNP genotyping platforms, imputation details, and association testing methods.

Study	Genotyping platform(s)	Imputation method	NCBI Build	Study-specific covariates	Association testing method
Age, Gene/Environment Susceptibility Reykjavik Study	Illumina 370K	MACH 1.0.16	36		ProbABEL 0.0.5c
Atherosclerosis Risk in Communities Study	Affymetrix 1M	MACH 1.0	35	PCs	MACH2QTL
Australian Twin Cohort	Illumina 318K	MACH 1.0.10	36	None, but samples excluded based on PCs	PLINK 1.04
Baltimore Longitudinal Study of Aging	Illumina 550K	MACH 1.0	35	PCs	MERLIN
British 1958 Birth Cohort T1D Controls	Illumina 550K	MACH	35		ProbABEL 0.0.5b
British 1958 Birth Cohort – Wellcome Trust Case Control Consortium	Affymetrix 500K	IMPUTE 0.2.0	35	None, but samples excluded based on PCs	SNPTEST 1.1.3
British Genetics of Hypertension Study	Affymetrix 500K	IMPUTE	35	None, but samples excluded based on PCs	QUICKTEST 0.94
Cardiovascular Health Study	Illumina 370CNV	BIMBAM 0.99	36	Study site	R
The Cohorte Lausannoise Study	Affymetrix 500K	IMPUTE 0.3.0	35	PCs	QUICKTEST 0.9
KORA - Cooperative Health Research in the Region of Augsburg	Affymetrix 500K	MACH	35		MACH2QTL
Danish Twins Registry	Illumina 318K	MACH 1.0.10	36	None, but samples excluded based on PCs	PLINK 1.04
Diabetes Genetics Initiative T2D Cases and Controls*	Affymetrix 500K	MACH 1.0	35	Study site	MACH2QTL
Dutch National Twin Cohort	Illumina 318K	MACH 1.0.10	36	None, but samples excluded based on PCs	PLINK 1.04
EPIC-Norfolk Obese Cases	Affymetrix 500K	IMPUTE 0.3.1	35		SNPTEST 1.1.5
EPIC-Norfolk Subcohort	Affymetrix 500K	IMPUTE 0.3.1	35		SNPTEST 1.1.5
Erasmus Rucphen Family Study	Illumina 300K, 370K; Affymetrix Nsp 250K	MACH 1.0.15	36		ProbABEL
Family Heart Study CHD Cases and Controls	Illumina 550K	MACH 1.0.15	36	Field center and PCs	Mixed model regression to account for family structure
Fenland Study	Affymetrix 500K	IMPUTE 0.4.2	35		SNPTEST 1.1.5
Finnish National Twin Cohort	Illumina 318K	MACH 1.0.10	36	None, but samples excluded based on PCs	PLINK 1.04
Framingham Heart Study	Affymetrix 500K; MIPS 50K	MACH 1.0	36	PCs	GWAF (R package) linear mixed effects model
Finland-United States Investigation of NIDDM Genetics T2D Cases and Controls	Illumina 317K	MACH	35	Birth province	R

Health2000 GenMets MS Cases and Controls	Illumina 610K	MACH 1.0.10	36	None, but samples excluded based on PCs	ProbABEL
Invecchiare in Chianti Study*	Illumina 550K	MACH 1.0	35		MERLIN
London Life Sciences Population Study	Affymetrix 500K; Perlegen custom array	MACH	35	PCs	MACH2QTL
MedSTAR MI Cases and Controls	Affymetrix 1M	MACH 1.0	36	PCs	SNPTEST 1.1.5
MICROS Study of Population Microisolates in South Tyrol	Illumina 300K	MACH 1.0.15	36		ProbABEL
National FINRISK Study	Illumina 610K	MACH 1.0.10	36	None, but samples excluded based on PCs	ProbABEL
Northern Finland Birth Cohort 1966	Illumina 370K	MACH 1.0.10	36	None, but samples excluded based on PCs	PLINK 1.04
Northern Swedish Population Health Study	Illumina 300K	MACH 1.0.15	36		ProbABEL
Orkney Complex Disease Study	Illumina 300K	MACH 1.0.15	36		ProbABEL
PennCATH MI Cases and Controls	Affymetrix 1M	MACH 1.0	36	PCs	SNPTEST 1.1.5
Pharmacogenomics and Risk of Cardiovascular Disease Study	Illumina 317K; Illumina 610K	BIMBAM 0.9.5	36	Study site	SNPTEST 1.1.5
Rotterdam Study Baseline	Illumina 550K	MACH 1.0.15	36		ProbABEL
Rotterdam Study Extension of Baseline	Illumina 550K	MACH 1.0.15	36		ProbABEL
SardiNIA Study of Aging	Affymetrix 500K	MACH	35		
Twins UK	Illumina 318K	MACH 1.0.10	36	None, but samples excluded based on PCs	PLINK 1.04
Supplementation en Vitamines et Mineraux Antioxydants Study	Illumina 317K	MACH	35		
Swedish National Twin Cohort	Illumina 318K	MACH 1.0.10	36	None, but samples excluded based on PCs	PLINK 1.04
Vis Study	Illumina 300K	MACH 1.0.15	36		ProbABEL
Women's Genome Health Study	Illumina 300K Duo "+"	MACH 1.0.16	35	Eigenvectors (EIGENSTRAT)	MACH2QTL

PCs = principal components.

* Contained a small number of related individuals.

Supplementary Table 4. Genomic control inflation factors.

Study	HDL	LDL	TG	TC
Age, Gene/Environment Susceptibility Reykjavik Study	1.077	1.045	1.049	1.052
Atherosclerosis Risk in Communities Study	1.013	1.025	1.042	1.026
Baltimore Longitudinal Study of Aging	1.013	1.016	1.057	1.044
British 1958 Birth Cohort – Wellcome Trust Case Control Consortium	1.004	1.004	1.006	1.004
British 1958 Birth Cohort T1D Controls	1.021	1.02	1.01	1.014
British Genetics of Hypertension Study	0.991	1.013	1.007	1
Cardiovascular Health Study	1.038	1.021	1.023	1.023
The Cohorte Lausannoise Study	1.016	0.996	1.038	0.999
KORA - Cooperative Health Research in the Region of Augsburg	1.01	1.007	1.004	1.012
Diabetes Genetics Initiative T2D Cases and Controls*†	1.477	1.266	1.077	1.134
ENGAGE‡	1.046	1.043	1.031	0.989
EPIC-Norfolk Obese Cases	1.009	1.003	1.007	1.009
EPIC-Norfolk Subcohort	1.008	1.013	1.021	1.005
Family Heart Study CHD Cases and Controls	1.113	1.074	1.082	1.084
Fenland Study	1.024	1.016	1.015	1.034
Framingham Heart Study	1.022	1.02	1.03	1.031
Finland-United States Investigation of NIDDM Genetics T2D Cases and Controls*	1.006	1.016	1.007	1.016
Invecchiare in Chianti Study†	1	1.015	1.021	1.014
London Life Sciences Population Study	1.018	1.008	1.011	1.009
MedSTAR MI Cases and Controls*	1.037	1.024	1.015	1.015
PennCATH MI Cases and Controls*	1.004	1.007	1.024	1
Pharmacogenomics and Risk of Cardiovascular Disease Study	1.008	1.013	1.016	1.001
SardiNIA Study of Aging	1.119	1.133	1.129	1.147
Supplementation en Vitamines et Mineraux Antioxydants Study	1	1	1	1.047
Women's Genome Health Study	1.064	1.034	1.084	1.040
Overall meta-analysis	1.14	1.097	1.121	1.105

* The cohort's case and control sets were meta-analysed and genomic control correction was applied before the combined cohort was meta-analysed with the remaining studies.

† The DGI and InCHIANTI studies each included a small number of related individuals.

‡ Meta-analysis of: Australian Twin Cohort, Danish Twins Registry, Dutch National Twin Cohort, Erasmus Rucphen Family Study, Finnish National Twin Cohort, Health2000 GenMets MS, MICROS Study of Population Microisolates in South Tyrol, National FINRISK Study, Northern Finland Birth Cohort 1966, Northern Swedish Population Health Study, Orkney Complex Disease Study, Rotterdam Study Baseline, Rotterdam Study Extension of Baseline, TwinsUK, Swedish National Twin Cohort, Vis Study.

Supplementary Table 5. Evidence of association for best proxies directly genotyped on Affymetrix and Illumina arrays.

					Proxy Illumina SNP*								Proxy Affymetrix SNP*					
Lead SNP	Trait	Best SNP	*n*	*P*-value	SNP	r^2	*P*-value	A	B	C	D	Approx. typed *n*	SNP	r^2	*P*-value	E	F	Approx. typed *n*
rs12027135	LDL	rs12027135	95,454	1E-10	rs10903129	1.00	2E-10	Y	Y	Y	Y	59,333	rs11802413	1.00	2E-10	Y	Y	41,912
rs12027135	TC	rs12027135	100,184	4E-11	rs10903129	1.00	7E-11	Y	Y	Y	Y	59,333	rs11802413	1.00	5E-11	Y	Y	41,912
rs4660293	HDL	rs4660293	99,855	4E-10	rs4660293	1.00	4E-10	Y	Y	Y	Y	59,333	rs4660293	1.00	4E-10	Y	Y	41,912
rs2479409	LDL	rs2479409	95,435	2E-28									rs2479409	1.00	2E-28	Y	Y	41,912
rs2479409	TC	rs2479409	100,164	4E-24									rs2479409	1.00	4E-24	Y	Y	41,912
rs2131925	LDL	rs3850634	92,503	3E-18	rs10889353	1.00	2E-17	Y	Y	Y	Y	59,333	rs995000	1.00	5E-17	Y	Y	41,912
rs2131925	TC	rs3850634	97,148	5E-41	rs10889353	1.00	1E-40	Y	Y	Y	Y	59,333	rs995000	1.00	1E-39	Y	Y	41,912
rs2131925	TG	rs2131925	96,598	9E-43	rs1167998	1.00	5E-41	Y	Y	Y	Y	59,333	rs7539035	1.00	3E-42	Y	Y	41,912
rs7515577	TC	rs7515577	100,165	3E-8	rs2025607	0.90	4E-8	Y	Y	Y	Y	59,333	rs4970712	0.95	3E-8	Y	Y	41,912
rs629301	LDL	rs629301	95,454	1E-172	rs646776	1.00	5E-169	Y	Y	Y	Y	59,333	rs599839	0.89	3E-168	Y	Y	41,912
rs629301	TC	rs629301	100,184	6E-131	rs646776	1.00	7E-130	Y	Y	Y	Y	59,333	rs599839	0.89	4E-130	Y	Y	41,912
rs1689800	HDL	rs1689800	99,900	3E-10	rs1689803	0.86	4E-9	Y	Y	Y	Y	59,333	rs1689802	0.83	9E-10	Y	Y	41,912
rs2642442	LDL	rs2807834	95,372	6E-11									rs2807834	1.00	6E-11	Y	Y	41,912
rs2642442	TC	rs2807834	100,098	5E-13									rs2807834	1.00	5E-13	Y	Y	41,912
rs4846914	HDL	rs4846914	99,881	4E-21	rs10779835	0.97	6E-20	Y	Y	Y	Y	59,333	rs2144300	1.00	5E-20	Y	Y	41,912
rs4846914	TG	rs1321257	92,418	2E-14	rs10779835	0.97	1E-13	Y	Y	Y	Y	59,333	rs2281719	0.97	1E-13	Y	Y	41,912
rs514230	LDL	rs514230	95,454	9E-12	rs822928	0.84	2E-9	Y	Y	Y	Y	59,333	rs553427	1.00	3E-10	Y	Y	41,912
rs514230	TC	rs514230	100,184	5E-14	rs822928	0.84	3E-10	Y	Y	Y	Y	59,333	rs553427	1.00	5E-12	Y	Y	41,912
rs1042034	HDL	rs1042034	99,892	1E-30	rs673548	1.00	4E-30	Y	Y	Y	Y	59,333	rs6544366	0.86	2E-27	Y	Y	41,912
rs1367117	LDL	rs1367117	95,446	4E-114									rs7575840	0.85	2E-98	Y	Y	41,912
rs1367117	TC	rs1367117	100,176	4E-96									rs7575840	0.85	3E-79	Y	Y	41,912
rs1042034	TG	rs1042034	96,590	1E-45	rs673548	1.00	3E-45	Y	Y	Y	Y	59,333	rs6544366	0.86	5E-42	Y	Y	41,912
rs1260326	TC	rs1260326	100,176	7E-27	rs1260326	1.00	7E-27	Y	Y	Y	Y	59,333	rs780094	0.93	1E-24	Y	Y	41,912
rs1260326	TG	rs1260326	96,590	6E-133	rs1260326	1.00	6E-133	Y	Y	Y	Y	59,333	rs780094	0.93	7E-125	Y	Y	41,912
rs4299376	LDL	rs4299376	91,285	2E-47	rs4299376	1.00	2E-47			Y	Y	17,068	rs4245791	1.00	3E-45	Y	Y	41,912
rs4299376	TC	rs4299376	95,992	4E-45	rs4299376	1.00	4E-45			Y	Y	17,068	rs4245791	1.00	2E-43	Y	Y	41,912
rs7570971	TC	rs6759321	95,242	1E-8	rs1561277	0.95	3E-7	Y	Y	Y	Y	59,333						
rs12328675	HDL	rs12328675	99,892	3E-10	rs10490694†	1.00	7E-3	Y	Y	Y	Y	59,333	rs7607980	1.00	4E-10		Y	10,296
rs10195252	TG	rs10195252	96,590	2E-10	rs10195252	1.00	2E-10	Y	Y	Y	Y	59,333	rs6717858	0.94	3E-9	Y	Y	41,912
rs2972146	HDL	rs1515100	96,875	2E-9	rs2943645	0.93	5E-9	Y	Y	Y	Y	59,333	rs2943658	1.00	5E-8	Y	Y	41,912
rs2972146	TG	rs2943645	93,554	2E-8	rs2943645	1.00	2E-8	Y	Y	Y	Y	59,333	rs2972147	1.00	1E-7	Y	Y	41,912

rs2290159	TC	rs2290159	99,434	4E-9	rs11128607	0.86	1E-8	Y	Y	Y	Y	59,333	rs7956	1.00	4E-8	Y	Y	41,912
rs645040	TG	rs645040	96,597	3E-8	rs684773	1.00	1E-7	Y	Y	Y	Y	59,333	rs684773	1.00	1E-7	Y	Y	41,912
rs442177	TG	rs442177	96,598	9E-12	rs236996	0.96	2E-10	Y	Y	Y	Y	59,333	rs3775214	0.96	4E-11	Y	Y	41,912
rs13107325	HDL	rs13107325	92,059	7E-11	rs13107325	1.00	7E-11	Y	Y	Y	Y	59,333	rs13107325	1.00	7E-11		Y	10,296
rs6450176	HDL	rs6450176	99,900	5E-8	rs4311394	0.91	1E-7	Y	Y	Y	Y	59,333	rs6886510	0.91	2E-7	Y	Y	41,912
rs9686661	TG	rs9686661	95,848	1E-10	rs3843467	1.00	1E-9	Y	Y	Y	Y	59,333	rs3843467	1.00	1E-9	Y	Y	41,912
rs12916	LDL	rs12916	95,454	5E-45	rs3846662	0.84	2E-35	Y	Y	Y	Y	59,333	rs3846663	0.97	2E-42	Y	Y	41,912
rs12916	TC	rs12916	100,184	9E-47	rs3846662	0.84	1E-37	Y	Y	Y	Y	59,333	rs3846663	0.97	3E-43	Y	Y	41,912
rs6882076	LDL	rs6882076	95,454	2E-22	rs1363232	0.96	4E-19	Y	Y	Y	Y	59,333	rs1501908	1.00	6E-20	Y	Y	41,912
rs6882076	TC	rs6882076	100,184	7E-28	rs1363232	0.96	3E-24	Y	Y	Y	Y	59,333	rs1501908	1.00	8.E-26	Y	Y	41,912
rs6882076	TG	rs1553318	96,598	4E-12														
rs3757354	LDL	rs3757354	91,293	1E-11	rs3757354	1.00	1E-11	Y	Y	Y	Y	59,333						
rs3757354	TC	rs3757354	96,000	3E-9	rs3757354	1.00	3E-9	Y	Y	Y	Y	59,333						
rs1800562	LDL	rs1800562	93,821	6E-10	rs1800562	1.00	6E-10	Y	Y	Y	Y	59,333	rs1800562	1.00	6E-10	Y	Y	41,912
rs1800562	TC	rs1800562	98,550	2E-8	rs1800562	1.00	2E-8	Y	Y	Y	Y	59,333	rs1800562	1.00	2E-8	Y	Y	41,912
rs3177928	LDL	rs3177928	95,425	2E-15	rs13209234	0.94	2E-14	Y	Y	Y	Y	59,333	rs9391858	1.00	2E-13	Y	Y	41,912
rs3177928	TC	rs3177928	100,151	4E-19	rs13209234	0.94	3E-18	Y	Y	Y	Y	59,333	rs9391858	1.00	2E-16	Y	Y	41,912
rs2247056	TG	rs2247056	96,598	2E-15	rs6457374	1.00	2E-15	Y	Y	Y	Y	59,333						
rs2814944	HDL	rs2814944	99,811	4E-9	rs2814944	1.00	4E-9	Y	Y	Y	Y	59,333	rs2814944	1.00	4E-9	Y	Y	41,912
rs2814982	TC	rs2814982	100,184	5E-11	rs2814982	1.00	5E-11	Y	Y	Y	Y	59,333						
rs9488822	LDL	rs11153594	95,367	3E-9	rs6909746	1.00	3E-9	Y	Y	Y	Y	59,333	rs10456902	1.00	3E-9	Y	Y	41,912
rs9488822	TC	rs9488822	100,184	2E-10	rs3798236	1.00	3E-10	Y	Y	Y	Y	59,333						
rs605066	HDL	rs605066	99,900	3E-8	rs668459	1.00	1E-7	Y	Y	Y	Y	59,333	rs634869	1.00	5E-8	Y	Y	41,912
rs1084651	HDL	rs1084651	99,900	3E-8	rs783149	1.00	1E-7	Y	Y	Y	Y	59,333	rs1652507	0.93	5E-7	Y	Y	41,912
rs1564348	LDL	rs1564348	95,439	2E-17	rs1564348	1.00	2E-17	Y	Y	Y	Y	59,333	rs1564348	1.00	2E-17		Y	10,296
rs1564348	TC	rs1564348	100,168	1E-16	rs1564348	1.00	1E-16	Y	Y	Y	Y	59,333	rs1564348	1.00	1E-16		Y	10,296
rs12670798	LDL	rs12670798	95,454	7E-10	rs12670798	1.00	7E-10	Y	Y	Y	Y	59,333						
rs12670798	TC	rs2285942	100,184	7E-10														
rs2072183	LDL	rs217386	95,454	4E-11	rs217369	0.84	7E-9	Y	Y	Y	Y	59,333	rs217381	0.90	5E-11	Y	Y	41,912
rs2072183	TC	rs2072183	97,063	3E-11														
rs13238203	TG	rs13238203	78,797	1E-9														
rs17145738	HDL	rs17145738	99,898	1E-9	rs2240466	1.00	4E-9	Y	Y	Y	Y	59,333	rs17145738	1.00	1E-9	Y	Y	41,912
rs17145738	TG	rs7811265	96,598	9E-59	rs11974409	1.00	1E-58	Y	Y	Y	Y	59,333	rs1178977	1.00	3E-55	Y	Y	41,912
rs4731702	HDL	rs4731702	99,900	1E-15	rs4731702	1.00	1E-15	Y	Y	Y	Y	59,333	rs13230111	1.00	4E-15	Y	Y	41,912
rs9987289	HDL	rs9987289	99,900	6E-25	rs2126259	0.80	1E-22	Y	Y	Y	Y	59,333	rs1461729	0.80	9E-20		Y	10,296
rs9987289	LDL	rs2126259	95,454	7E-15	rs2126259	1.00	7E-15	Y	Y	Y	Y	59,333	rs1461729	1.00	1E-12		Y	10,296

rs9987289	TC	rs2126259	100,184	9E-24	rs2126259	1.00	9E-24	Y	Y	Y	Y	59,333	rs1461729	1.00	8E-20		Y	10,296
rs11776767	TG	rs11776767	96,598	1E-8	rs6992366	0.87	1E-5	Y	Y	Y	Y	59,333	rs2278335	0.80	2E-5	Y	Y	41,912
rs1495741	TC	rs1961456	100,184	2E-9														
rs1495741	TG	rs1495743	96,580	4E-14	rs1495741	1.00	5E-14	Y	Y	Y	Y	59,333	rs1495743	1.00	4E-14	Y	Y	41,912
rs12678919	HDL	rs12678919	99,900	1E-97	rs10096633	0.86	1E-83	Y	Y	Y	Y	59,333	rs10503669	0.93	5E-92	Y	Y	41,912
rs12678919	TG	rs12678919	96,598	2E-115	rs10096633	0.86	1E-97	Y	Y	Y	Y	59,333	rs10503669	0.93	2E-108	Y	Y	41,912
rs2081687	LDL	rs1030431	95,454	4E-9	rs4738679	0.93	1E-8	Y	Y	Y	Y	59,333	rs13277801	1.00	7E-9	Y	Y	41,912
rs2081687	TC	rs1030431	100,184	9E-13	rs4738679	0.93	3E-12	Y	Y	Y	Y	59,333	rs13277801	1.00	2E-12	Y	Y	41,912
rs2293889	HDL	rs2293889	99,900	6E-11	rs3808439	0.93	4E-9	Y	Y	Y	Y	59,333	rs3808461	0.96	1E-10	Y	Y	41,912
rs2737229	TC	rs2737229	100,184	2E-8	rs2737229	1.00	2E-8	Y	Y	Y	Y	59,333	rs3808477	0.85	1E-7	Y	Y	41,912
rs2954029	HDL	rs10808546	99,900	6E-19	rs10808546	1.00	6E-19	Y	Y	Y	Y	59,333	rs2980875	0.97	4E-17	Y	Y	41,912
rs2954029	LDL	rs2954022	95,454	3E-29	rs10808546	0.97	1E-26	Y	Y	Y	Y	59,333	rs2980875	1.00	3E-29	Y	Y	41,912
rs2954029	TC	rs2954022	100,184	5E-36	rs10808546	0.97	2E-32	Y	Y	Y	Y	59,333	rs2980875	1.00	6E-36	Y	Y	41,912
rs2954029	TG	rs2954029	96,598	3E-55	rs10808546	0.97	4E-54	Y	Y	Y	Y	59,333	rs2980875	1.00	7E-54	Y	Y	41,912
rs11136341	LDL	rs11136341	88,376	4E-13														
rs11136341	TC	rs11136341	93,052	9E-10														
rs581080	HDL	rs643531	99,889	1E-13	rs686030	0.95	3E-13	Y	Y	Y	Y	59,333	rs643531	1.00	1E-13	Y	Y	41,912
rs581080	TC	rs581080	100,184	3E-9														
rs1883025	HDL	rs1883025	99,179	2E-33	rs2575876†	0.90	6E-17				Y	4,608						
rs1883025	TC	rs1883025	99,463	3E-27	rs2575876†	0.90	1E-9				Y	4,608						
rs9411489	LDL	rs649129	95,454	8E-22	rs495828	1.00	2E-21			Y	Y	17,068	rs651007	0.95	5E-21	Y	Y	41,912
rs9411489	TC	rs651007	98,535	9E-21	rs495828	0.95	4E-20			Y	Y	17,068	rs651007	1.00	9E-21	Y	Y	41,912
rs10761731	TG	rs10761731	96,598	3E-12	rs10509186	0.88	3E-10	Y	Y	Y	Y	59,333	rs10761739	1.00	9E-12	Y	Y	41,912
rs2068888	TG	rs2068888	96,598	2E-8	rs2068888	1.00	2E-8	Y	Y	Y	Y	59,333						
rs2255141	LDL	rs1129555	95,438	2E-9	rs2419604	1.00	4E-9	Y	Y	Y	Y	59,333	rs1129555	1.00	2E-9	Y	Y	41,912
rs2255141	TC	rs2255141	100,184	2E-10	rs2419604	1.00	5E-10	Y	Y	Y	Y	59,333	rs1129555	1.00	3E-10	Y	Y	41,912
rs2923084	HDL	rs2923084	99,898	5E-8	rs2923084	1.00	5E-8	Y	Y	Y	Y	59,333	rs1349326	0.81	2E-5	Y	Y	41,912
rs10128711	TC	rs10832963	100,184	3E-8	rs4757676	0.96	6E-8	Y	Y	Y	Y	59,333	rs11024739	0.96	2E-7	Y	Y	41,912
rs3136441	HDL	rs3136441	99,900	3E-18	rs5896	1.00	7E-16	Y	Y	Y	Y	59,333	rs2290883	1.00	4E-15	Y	Y	41,912
rs174546	HDL	rs174601	99,900	2E-22	rs102275	0.86	2E-22	Y	Y	Y	Y	59,333	rs174547	0.86	1E-21	Y	Y	41,912
rs174546	LDL	rs174583	95,443	1E-21	rs102275	1.00	5E-21	Y	Y	Y	Y	59,333	rs174547	1.00	1E-19	Y	Y	41,912
rs174546	TC	rs174550	100,184	2E-22	rs1535	1.00	4E-22	Y	Y	Y	Y	59,333	rs174547	1.00	2E-20	Y	Y	41,912
rs174546	TG	rs174546	96,598	5E-24	rs1535	1.00	5E-23	Y	Y	Y	Y	59,333	rs174547	1.00	6E-23	Y	Y	41,912
rs964184	HDL	rs964184	99,878	5E-47	rs964184	1.00	5E-47				Y	4,608	rs964184	1.00	5E-47		Y	10,296
rs964184	LDL	rs964184	95,432	1E-26	rs964184	1.00	1E-26				Y	4,608	rs964184	1.00	1E-26		Y	10,296
rs964184	TC	rs964184	100,162	6E-57	rs964184	1.00	6E-57				Y	4,608	rs964184	1.00	6E-57		Y	10,296

rs964184	TG	rs964184	96,576	7E-240	rs964184	1.00	7E-240				Y	4,608	rs964184	1.00	7E-240		Y	10,296
rs7941030	HDL	rs7115089	99,900	3E-8	rs7941030	0.87	3E-8	Y	Y	Y	Y	59,333	rs10892873	1.00	4E-8	Y	Y	41,912
rs7941030	TC	rs7941030	100,184	2E-10	rs7941030	1.00	2E-10	Y	Y	Y	Y	59,333	rs7123220	0.90	5E-10	Y	Y	41,912
rs11220462	LDL	rs11220462	95,454	1E-15	rs7940893	1.00	2E-14	Y	Y	Y	Y	59,333						
rs11220462	TC	rs11220463	100,184	2E-11														
rs7134375	HDL	rs7134375	99,900	4E-8	rs7134375	1.00	4E-8	Y	Y	Y	Y	59,333						
rs11613352	HDL	rs3741414	99,900	2E-8	rs3741414	1.00	2E-8			Y	Y	17,068	rs11614506	0.84	1E-7	Y	Y	41,912
rs11613352	TG	rs11613352	96,598	4E-10	rs11172147	1.00	1E-9			Y	Y	17,068	rs11614506	1.00	2E-9	Y	Y	41,912
rs7134594	HDL	rs7134594	99,900	7E-15	rs7134594	1.00	7E-15	Y	Y	Y	Y	59,333	rs10161126	1.00	8E-13	Y	Y	41,912
rs11065987	LDL	rs11065987	95,454	2E-9	rs11065987	1.00	2E-9			Y	Y	17,068						
rs11065987	TC	rs11065987	100,184	7E-12	rs11065987	1.00	7E-12			Y	Y	17,068						
rs1169288	LDL	rs1169288	95,454	1E-15	rs2650000	0.92	3E-14	Y	Y	Y	Y	59,333	rs2650000	0.92	3E-14		Y	10,296
rs1169288	TC	rs1169288	100,184	1E-14	rs2650000	0.92	5E-14	Y	Y	Y	Y	59,333	rs2650000	0.92	5E-14		Y	10,296
rs4759375	HDL	rs4759375	99,900	8E-9														
rs4765127	HDL	rs4765127	99,787	3E-10	rs12298484	0.97	1E-9	Y	Y	Y	Y	59,333	rs1187415	1.00	1E-9	Y	Y	41,912
rs4765127	TG	rs12310367	96,598	1E-8	rs12298484	0.97	8E-8	Y	Y	Y	Y	59,333	rs1187415	1.00	2E-8	Y	Y	41,912
rs838880	HDL	rs838880	80,428	3E-14	rs838878	0.96	6E-14	Y	Y	Y	Y	59,333	rs838880	1.00	3E-14		Y	10,296
rs8017377	LDL	rs2332328	95,454	4E-11	rs8017377	1.00	5E-11	Y	Y	Y	Y	59,333						
rs2412710	TG	rs2412710	86,707	2E-8														
rs2929282	TG	rs2929282	95,070	2E-11	rs2929275	1.00	3E-11			Y	Y	17,068	rs2918952	1.00	9E-11	Y	Y	41,912
rs1532085	HDL	rs1532085	98,409	3E-96	rs1532085	1.00	3E-96	Y	Y	Y	Y	59,333						
rs1532085	TC	rs1532085	98,656	9E-20	rs1532085	1.00	9E-20	Y	Y	Y	Y	59,333						
rs1532085	TG	rs261342	95,070	2E-13	rs261341	0.85	4E-8	Y	Y	Y	Y	59,333	rs261332	0.88	5E-12	Y	Y	41,912
rs2652834	HDL	rs2652834	98,409	9E-9														
rs11649653	TG	rs11649653	95,034	3E-8									rs11649653	1.00	3E-8	Y	Y	41,912
rs3764261	HDL	rs3764261	94,225	7E-380	rs3764261	1.00	7E-380	Y	Y	Y	Y	59,333						
rs3764261	LDL	rs247616	89,838	9E-13	rs3764261	1.00	2E-12	Y	Y	Y	Y	59,333						
rs3764261	TC	rs3764261	94,472	7E-14	rs3764261	1.00	7E-14	Y	Y	Y	Y	59,333						
rs3764261	TG	rs7205804	95,070	1E-12	rs1532624	1.00	1E-12	Y	Y	Y	Y	59,333						
rs16942887	HDL	rs16942887	98,409	8E-33	rs2271293	1.00	5E-32	Y	Y	Y	Y	59,333	rs2292316	1.00	2E-32	Y	Y	41,912
rs2000999	LDL	rs2000999	93,999	2E-22	rs2000999	1.00	2E-22	Y	Y	Y	Y	59,333						
rs2000999	TC	rs2000999	98,656	3E-24	rs2000999	1.00	3E-24	Y	Y	Y	Y	59,333						
rs2925979	HDL	rs2925979	98,409	2E-11	rs2925979	1.00	2E-11	Y	Y	Y	Y	59,333						
rs11869286	HDL	rs881844	98,409	3E-14	rs931992	1.00	9E-14	Y	Y	Y	Y	59,333	rs11869286	1.00	1E-13	Y	Y	41,912
rs7206971	LDL	rs7225700	93,999	4E-9	rs6504833	1.00	6E-9	Y	Y	Y	Y	59,333	rs11650072	1.00	1E-8		Y	10,296
rs7206971	TC	rs7206971	90,614	1E-8	rs11079784	0.94	9E-7	Y	Y	Y	Y	59,333	rs7206971	1.00	1E-8	Y	Y	41,912

rs4148008	HDL	rs4148008	98,409	2E-10	rs4148005	1.00	2E-10	Y	Y	Y	Y	59,333	rs1373068	0.92	4E-10	Y	Y	41,912
rs4129767	HDL	rs4082919	98,409	5E-9	rs4129767	0.97	8E-9	Y	Y	Y	Y	59,333	rs4969183	0.94	1E-8	Y	Y	41,912
rs7241918	HDL	rs7241918	98,409	3E-49	rs4939883	1.00	4E-49	Y	Y	Y	Y	59,333	rs4939883	1.00	4E-49	Y	Y	41,912
rs7241918	TC	rs7239867	98,656	2E-19	rs4939883	1.00	5E-19	Y	Y	Y	Y	59,333	rs4939883	1.00	5E-19	Y	Y	41,912
rs12967135	HDL	rs12967135	98,409	7E-9	rs12970134	0.81	1E-5	Y	Y	Y	Y	59,333	rs17782313	1.00	1E-8	Y	Y	41,912
rs7255436	HDL	rs7255436	98,409	3E-8	rs2278236	1.00	4E-8	Y	Y	Y	Y	59,333	rs7254882	1.00	2E-7		Y	10,296
rs6511720	LDL	rs6511720	93,131	4E-117	rs6511720	1.00	4E-117			Y	Y	17,068						
rs6511720	TC	rs6511720	97,764	7E-97	rs6511720	1.00	7E-97			Y	Y	17,068						
rs737337	HDL	rs737337	98,409	3E-9	rs737337	1.00	3E-9	Y	Y	Y	Y	59,333						
rs10401969	LDL	rs10401969	93,983	7E-22	rs12610185	0.80	2E-16	Y	Y	Y	Y	59,333	rs16996148	0.89	6E-21	Y	Y	41,912
rs10401969	TC	rs10401969	98,640	3E-38	rs12610185	0.80	3E-30	Y	Y	Y	Y	59,333	rs16996148	0.89	7E-36	Y	Y	41,912
rs10401969	TG	rs10401969	95,054	2E-29	rs12610185	0.80	9E-24	Y	Y	Y	Y	59,333	rs16996148	0.89	3E-26	Y	Y	41,912
rs4420638	HDL	rs4420638	87,520	4E-21									rs4420638	1.00	4E-21	Y	Y	41,912
rs4420638	LDL	rs4420638	83,209	9E-147									rs4420638	1.00	9E-147	Y	Y	41,912
rs4420638	TC	rs4420638	87,766	5E-111									rs4420638	1.00	5E-111	Y	Y	41,912
rs439401	TG	rs439401	65,871	1E-30	rs439401	1.00	1E-30	Y	Y	Y	Y	59,333						
rs492602	TC	rs492602	97,148	2E-10	rs504963	0.82	3E-7	Y	Y	Y	Y	59,333	rs632111	0.82	8E-9		Y	10,296
rs386000	HDL	rs386000	86,430	4E-16	rs103294	0.83	1E-15	Y	Y	Y	Y	59,333	rs798887	0.89	6E-14		Y	10,296
rs2277862	TC	rs2277862	98,656	4E-10	rs2104417	1.00	5E-10	Y	Y	Y	Y	59,333	rs6119625	1.00	1E-9	Y	Y	41,912
rs2902940	LDL	rs2902941	93,999	1E-8	rs2902941	1.00	1E-8	Y	Y	Y	Y	59,333	rs2143877	0.89	8E-8	Y	Y	41,912
rs2902940	TC	rs2902940	98,656	6E-11	rs2902941	0.92	1E-10	Y	Y	Y	Y	59,333	rs2143877	0.96	3E-10	Y	Y	41,912
rs6029526	LDL	rs909802	93,999	3E-19	rs2235367	0.97	1E-18	Y	Y	Y	Y	59,333	rs2866611	0.97	6E-19	Y	Y	41,912
rs6029526	TC	rs4297946	98,588	3E-17	rs2235367	0.94	2E-16	Y	Y	Y	Y	59,333	rs4297946	1.00	3E-17	Y	Y	41,912
rs1800961	HDL	rs1800961	71,749	1E-15	rs1800961	1.00	1E-15	Y	Y	Y	Y	59,333	rs1800961	1.00	1E-15		Y	10,296
rs1800961	TC	rs1800961	70,383	6E-13	rs1800961	1.00	6E-13	Y	Y	Y	Y	59,333	rs1800961	1.00	6E-13		Y	10,296
rs6065906	HDL	rs6065906	98,409	2E-22	rs6065906	1.00	2E-22	Y	Y	Y	Y	59,333	rs7679	0.94	1E-21	Y	Y	41,912
rs6065906	TG	rs4810479	95,070	5E-18	rs4810479	1.00	5E-18	Y	Y	Y	Y	59,333						
rs181362	HDL	rs181362	96,905	1E-8	rs5754217	1.00	3E-8	Y	Y	Y	Y	59,333	rs181359	1.00	4E-8	Y	Y	41,912
rs5756931	TG	rs5756931	95,067	4E-8	rs2284060	0.83	2E-6	Y	Y	Y	Y	59,333	rs2284060	0.83	2E-6	Y	Y	41,912

* The four Illumina arrays utilized in this study were: (A) HumanHap300, *n* = 31,521 samples; (B) Human370CNV, *n* = 10,744; (C) HumanHap550, *n* = 12,460; and (D) HumanHap610, *n* = 4,608. The two Affymetrix arrays utilized were: (E) Affymetrix 500K, *n* = 31,616; and (F) Affymetrix 6.0, *n* = 10,296. Selected proxy SNPs were directly genotyped on all arrays with a "Y" in columns A-F. The "Approx typed *n*" is the total number of samples genotyped on the arrays indicated in columns A-D or E-F; actual samples sizes for proxy SNPs vary slightly. r^2 indicates linkage disequilibrium between proxy SNPs and the best SNP at each locus, based on HapMap Phase II CEU samples.

† For two proxy SNPs (rs10490694 and rs2575876), meta-analysis sample size is ~38,000; these SNPs consequently have less significant *P*-values. All other proxy SNPs were meta-analysed in >65,000 individuals.

Supplementary Table 6. Genome-wide significant SNPs after conditioning upon lead SNPs from primary GWAS analysis.

Locus	SNP	Trait	Chr	Position*	*n*	Allele 1, Allele 2†	*P*-value	Effect	Conditioned SNP in locus	D' ‡	r^2 ‡
PABPC4	rs4660808	TG	1	39,791,096	90,819	T, C	2.96×10^{-08}	+			
PCSK9	rs1998013	TC	1	55,670,051	40,265	T, C	3.93×10^{-17}	-	rs2479409	1	0.004
		LDL	1	55,730,618	36,329	T, C	1.97×10^{-20}	-	rs2479409	1	0.004
EVI5	rs531514	HDL	1	93,412,233	97,559	T, C	7.46×10^{-09}	+	rs7515577	0.71	0.052
APOB	rs515135	TC	2	21,197,709	97,140	T, C	6.38×10^{-52}	-	rs1367117	1	0.11
		LDL	2	21,139,562	93,223	T, C	1.32×10^{-56}	-	rs1367117	1	0.11
	rs668948	TG	2	21,145,034	91,483	A, G	4.31×10^{-10}	+	rs1042034	0.61	0.026
ABCG5/8	rs4953023	TC	2	43,985,651	90,564	A, G	1.18×10^{-19}	-	rs4299376	1	0.032
		LDL	2	43,927,504	86,105	A, G	1.11×10^{-23}	-	rs4299376	1	0.032
RAB3GAP1	rs10445686	LDL	2	135,609,842	93,223	A, G	3.82×10^{-08}	-	rs7570971	1	0.15
KLHL8	rs442177	HDL	4	88,387,440	97,559	T, G	1.84×10^{-08}	-			
HLA	rs12660719	TG	6	32,683,961	83,173	A, G	1.13×10^{-08}	-	rs2247056	1	0.0056
C6orf106	rs3800406	LDL	6	35,241,052	86,867	A, G	1.69×10^{-08}	+			
CITED2	rs636202	TG	6	139,885,276	93,855	T, C	2.56×10^{-08}	+			
LPA	rs10455872	TC	6	160,980,529	90,193	A, G	2.67×10^{-23}	-	rs1564348	0.04	0
		LDL	6	160,930,108	86,418	A, G	3.55×10^{-21}	-	rs1564348	0.04	0
	rs486359	TG	6	160,694,431	93,855	C, G	3.64×10^{-09}	-			
KLF14	rs1562398	TG	7	130,108,471	93,855	C, G	2.37×10^{-08}	-			
LPL	rs7016529	HDL	8	19,850,911	84,515	T, C	6.38×10^{-37}	+	rs12678919	1	0.004
		TG	8	19,850,911	81,126	T, C	1.74×10^{-29}	-	rs12678919	1	0.004
TRIB1	rs12677676	TC	8	126,571,708	68,665	A, G	2.04×10^{-09}	-	rs2954029	0.73	0.045
ABCA1	rs4149311	TC	9	104,668,332	92,064	T, C	2.30×10^{-10}	+	rs1883025	0.14	0.012
	rs1800978	LDL	9	106,705,799	92,510	C, G	3.77×10^{-08}	+			
	rs11789603	HDL	9	104,726,574	94,899	T, C	4.49×10^{-14}	+	rs1883025	0.22	0.014
SPTY2D1	rs10128711	LDL	11	18,589,560	88,177	T, C	2.66×10^{-08}	-			
APOA1-C3-A4-A5	rs9804646	TC	11	116,170,289	90,646	T, C	6.70×10^{-12}	-	rs964184	0.065	0.002
	rs12225230	HDL	11	116,233,840	97,559	C, G	6.77×10^{-33}	+	rs964184	0.54	0.19
ZNF664	rs11057244	HDL	12	122,298,143	93,375	C, G	4.58×10^{-09}	+	rs4765127	0.34	0.0062
	rs838880	HDL	12	123,786,473	80,113	T, C	8.54×10^{-15}	-	rs4765127	0.26	0.018
NYNRIN	rs6573778	TC	14	23,942,049	97,148	T, C	1.99×10^{-08}	+			
LIPC	rs261342	TC	15	56,518,445	97,148	C, G	1.27×10^{-21}	-	rs1532085	0.06	0.001
	rs2070895	HDL	15	56,511,231	97,559	A, G	1.53×10^{-80}	+	rs1532085	0.15	0.005
	rs261334	TG	15	56,514,036	93,855	C, G	1.56×10^{-13}	-	rs1532085	0.03	0
CETP	rs9939224	HDL	16	55,560,233	92,366	T, G	3.98×10^{-120}	-	rs3764261	1	0.12

LIPG	rs2040293	HDL	18	45,532,343	97,559	A, G	4.20×10^{-08}	+	rs7241918	0.41	0.023
LDLR	rs688	TC	19	11,088,602	92,775	T, C	2.60×10^{-27}	+	rs6511720	0.19	0.003
	rs5930	LDL	19	11,085,265	93,231	A, G	2.62×10^{-39}	-	rs6511720	0.19	0.004
APOE-C1-C2	rs395908	TC	19	50,065,405	97,148	A, G	2.85×10^{-47}	-	rs4420638	0.005	0
	rs445925	LDL	19	50,107,480	23,783	A, G	1.57×10^{-86}	-	rs4420638	0.27	0.002
	rs5167	HDL	19	50,140,305	97,559	T, G	1.19×10^{-08}	-	rs4420638	0.10	0.005
	rs4803770	TG	19	50,119,193	74,315	C, G	2.88×10^{-12}	+	rs439401	0.87	0.25
FLJ36070	rs492602	LDL	19	53,898,229	90,280	A, G	4.69×10^{-08}	-			
MAFB	rs6016382	TC	20	38,614,660	97,148	A, T	3.86×10^{-11}	-	rs2902940	0.12	0.011
		LDL	20	38,614,660	93,231	A, T	5.11×10^{-10}	-	rs2902940	0.12	0.011

* Positions are relative to Human Genome NCBI Build 36.

† Alleles are designated with respect to the "+" strand.

‡ D' or r^2 between the post-conditioning best genome-wide significant SNP and, if this SNP was in one of the original genome-wide significant loci for the trait, the lead SNP in the locus (on which the analysis was conditioned). D' and r^2 estimated in HapMap Phase II CEU individuals.

Supplementary Table 7. Loci exhibiting sex heterogeneity.

Locus*	SNP	Chr	Position†	Trait	Allele1, Allele2‡	Female *n*	Female *P*-value	Female Effect (SE)§	Male *n*	Male *P*-value	Male Effect (SE)§	Heterogeneity *P*-value
Loci identified in primary analysis that also demonstrate heterogeneity of effect size in men and women‖												
LPL	rs12678919	8	19,888,502	HDL	A, G	62,816	4×10^{-37}	-0.133 (0.01)	37,745	5×10^{-50}	-0.196 (0.012)	3×10^{-5}
ZNF664	rs12310367	12	123,052,631	TG	A, G	59,473	4×10^{-10}	0.043 (0.007)	35,288	0.61	0.002 (0.008)	5×10^{-5}
CILP2	rs10401969	19	19,268,718	TC	T, C	62,932	5×10^{-11}	0.095 (0.013)	37,873	2×10^{-21}	0.177 (0.017)	3×10^{-5}
CILP2	rs10401969	19	19,268,718	LDL	T, C	60,529	0.03	0.030 (0.013)	35,734	9×10^{-15}	0.149 (0.017)	4×10^{-9}
APOE	rs4420638	19	50,114,786	TC	A, G	57,292	1×10^{-72}	-0.188 (0.01)	32,624	6×10^{-20}	-0.124 (0.012)	2×10^{-5}
Loci with $P < 5 \times 10^{-8}$ in only one sex												
LRPAP1	rs762861	4	3,411,809	TG	C, G	53,412	4×10^{-8}	0.045 (0.009)	29,868	0.07	0.020 (0.011)	0. 07
DHX16	rs9262145	6	30,762,510	LDL	C, G	61,803	0.80	-0.003 (0.007)	36,840	4×10^{-8}	0.048 (0.009)	1×10^{-6}
VEGFA	rs998584	6	43,865,874	TG	A, C	55,289	0.007	0.020 (0.008)	31,104	1×10^{-8}	0.053 (0.009)	0.004
KLF14	rs1562398	7	13,010,8471	TG	C, G	59,473	2×10^{-12}	-0.046 (0.007)	35,288	0.05	-0.012 (0.008)	7×10^{-4}
SOX17	rs10102164	8	55,584,167	TC	A, G	64,235	0.01	0.019 (0.007)	39,104	4×10^{-10}	0.059 (0.009)	4×10^{-4}
ABCA8	rs740516	17	64,594,557	LDL	C, G	61,233	7×10^{-9}	0.062 (0.011)	35,156	0.24	0.027 (0.016)	0.05
C20orf152	rs7265718	20	34,098,855	TC	T, G	64,235	0.02	0.022 (0.009)	39,104	2×10^{-8}	0.062 (0.011)	0.003

* Bold indicates locus already identified as genome-wide significant in primary analysis.
† Positions are relative to Human Genome NCBI Build 36.
‡ Alleles are designated with respect to the "+" strand.
§ Effect sizes and standard errors are in s.d. units.
‖ Pre-specified statistical threshold of $P < 0.0005$ to account for multiple testing of 102 lead SNPs in 95 loci.

Supplementary Table 8. *Cis*-acting associations of SNPs with transcript levels in human liver.

Lead SNP	Chr	Position*	Transcript gene symbol	# of samples	Major, minor alleles†	Mean expression			Transcript *P*-value	Trait	Lipid effect (modeled on minor allele)
						Homo. major	Hetero.	Homo. minor			
rs12027135	1	25,648,320	*RHCE*	948	T, A	-0.064	0.005	0.068	7E-54	LDL	-
										TC	-
			RHD	953	T, A	-0.030	-0.008	0.027	4E-8	LDL	-
										TC	-
			TMEM50A	955	T, A	-0.028	-0.010	0.024	4E-8	LDL	-
										TC	-
			TMEM57	954	T, A	-0.088	0.004	0.081	2E-145	LDL	-
										TC	-
rs2131925	1	62,798,530	*ANGPTL3*	924	T, G	0.033	-0.031	-0.104	1E-13	TG	-
										LDL	-
										TC	-
			DOCK7	952	T, G	-0.018	0.018	0.068	1E-22	TG	-
										LDL	-
										TC	-
rs629301	1	109,619,829	*CELSR2*	951	T, G	-0.053	0.114	0.268	5E-94	TC	-
										LDL	-
			PSMA5	955	T, G	-0.025	0.024	0.037	9E-17	LDL	-
										TC	-
			PSRC1	949	T, G	-0.170	0.291	0.531	2E-271	LDL	-
										TC	-
			SORT1	951	T, G	-0.182	0.286	0.537	2E-300	LDL	-
										TC	-
			SYPL2	955	T, G	-0.039	0.041	0.129	1E-23	TC	-
										LDL	-
rs1260326	2	27,584,444	*IFT172*	944	C, T	0.037	0.002	-0.050	7E-32	TC	+
										TG	+
rs13107325	4	103,407,732	*SLC39A8*	952	C, T	0.009	-0.075	-0.167	3E-19	HDL	-
rs3177928	6	32,520,413	*HLA-DQB1*	955	G, A	0.026	-0.043	-0.110	2E-13	TC	+
			HLA-DRB1	918	G, A	-0.052	0.171	0.257	7E-44	TC	+
rs9488822	6	116,419,586	*FRK*	953	A, T	0.030	-0.010	-0.068	4E-12	LDL	-
										TC	-
rs9987289	8	9,220,768	*PPP1R3B*	955	G, A	-0.030	0.134	0.264	1E-14	LDL	-
										TC	-
										HDL	-
rs518080	9	15,295,378	*TTC39B*	953	C, G	-0.025	0.036	0.076	2E-15	HDL	-
rs10128711	11	18,589,560	*SPTY2D1*	952	C, T	-0.036	0.019	0.069	1E-16	TC	-
rs174546	11	61,326,406	*FADS1*	944	C, T	0.085	-0.017	-0.197	5E-18	TG	+
										HDL	-
										LDL	-
										TC	-
rs11220462	11	125,749,162	*ST3GAL4*	951	G, A	-0.019	0.062	0.098	2E-22	LDL	+
										TC	+
rs7134594	12	108,484,576	*MMAB*	955	T, C	-0.106	0.019	0.111	2E-44	HDL	-
rs8017377	14	23,953,727	*NYNRIN*	954	G, A	-0.098	0.023	0.088	3E-46	LDL	+
rs2929282	15	42,033,223	*CKMT1A*	954	T, A	-0.003	0.072	0.132	8E-28	TG	+
rs1532085	15	56,470,658	*ALDH1A2*	949	G, A	0.020	0.001	-0.026	5E-8	HDL	+
										TC	+
										TG	+
			LIPC	953	G, A	0.067	-0.034	-0.129	7E-23	TG	+
										HDL	+
										TC	+
rs11649653	16	30,825,988	*VKORC1*	950	C, G	0.076	-0.016	-0.150	7E-47	TG	-
rs16942887	16	66,485,543	*NFATC3*	954	G, A	0.009	-0.048	-0.090	3E-15	HDL	+
rs11869286	17	35,067,382	*PERLD1*	950	C, G	-0.037	0.021	0.085	9E-24	HDL	-
rs7206971	17	42,780,114	*TBKBP1*	952	G, A	0.023	0.004	-0.025	6E-10	TC	+
										LDL	-
rs7241918	18	45,414,951	*LIPG*	938	T, G	-0.031	0.040	0.132	4E-10	HDL	-
										TC	-
rs7255436	19	83,39,196	*ANGPTL4*	902	A, C	0.058	-0.037	-0.107	4E-8	HDL	-
rs439401	19	50,106,291	*APOC4*	920	C, T	0.037	-0.018	-0.054	4E-9	TG	-
rs386000	19	59,484,573	*LILRA3*	953	G, C	0.021	-0.014	-0.044	9E-12	HDL	+
rs2277862	20	33,616,196	*CEP250*	949	C, T	-0.009	0.058	0.072	3E-8	TC	-
			CPNE1	954	C, T	0.018	-0.039	-0.080	7E-41	TC	-
rs6065906	20	43,987,422	*PLTP*	913	T, C	0.041	-0.049	-0.142	3E-18	TG	+
										HDL	-
rs181362	22	20,262,068	*UBE2L3*	954	C, T	-0.013	0.030	0.028	6E-13	HDL	-

* Positions are relative to Human Genome NCBI Build 36.

† Alleles are designated with respect to the "+" strand.

Supplementary Table 9. *Cis*-acting associations of SNPs with transcript levels in human omental fat.

Lead SNP	Chr	Position*	Transcript gene symbol	# of samples	Major, minor alleles†	Mean expression			Transcript *P*-value	Trait	Lipid effect (modeled on minor allele)
						Homo. major	Hetero.	Homo. minor			
rs12027135	1	25648320	*RHCE*	730	T, A	0.025	0.002	-0.026	3E-55	LDL	-
										TC	-
			RHD	736	T, A	-0.025	-0.003	0.032	5E-10	LDL	-
										TC	-
			TMEM50A	739	T, A	0.030	0.004	-0.035	2E-29	TC	-
										LDL	-
			TMEM57	740	T, A	0.056	0.004	-0.063	3E-115	TC	-
										LDL	-
rs4660293	1	39800767	*OXCT2*	740	A, G	0.074	0.041	-0.051	2E-37	HDL	-
rs2131925	1	62798530	*DOCK7*	738	T, G	0.126	0.032	-0.069	3E-91	LDL	-
										TC	-
										TG	-
rs1260326	2	27584444	*IFT172*	705	C, T	-0.107	0.000	0.075	2E-65	TG	+
										TC	+
rs10195252	2	165221337	*GRB14*	734	T, C	-0.079	-0.008	0.040	1E-13	TG	-
rs2972146	2	226808942	*IRS1*	714	T, G	0.047	0.009	-0.026	2E-8	TG	-
										HDL	+
rs3177928	6	32520413	*HLA-DOA1*	740	G, A	0.171	0.275	-0.051	2E-11	TC	+
			HLA-DOA2	737	G, A	-0.048	-0.036	0.008	9E-13	TC	+
			HLA-DRB1	728	G, A	0.264	0.274	-0.058	1E-15	TC	+
			HLA-DRB5	728	G, A	0.516	0.271	-0.089	7E-12	TC	+
rs2814944	6	34660775	*UHRF1BP1*	725	G, A	0.102	0.044	-0.023	3E-25	HDL	-
rs9488822	6	116419586	*FRK*	740	A, T	-0.083	-0.014	0.058	6E-33	TC	-
										LDL	-
			NT5DC1	735	A, T	-0.013	-0.007	0.018	1E-8	LDL	-
										TC	-
rs3136441	11	46699823	*ARHGAP1*	739	T, C	0.015	-0.018	-0.003	1E-9	HDL	+
rs174546	11	61326406	*FADS1*	727	C, T	-0.098	-0.027	0.045	2E-8	HDL	-
										LDL	-
										TC	-
										TG	+
rs7134594	12	108484576	*MMAB*	738	T, C	0.093	0.022	-0.082	1E-72	HDL	-
rs2652834	15	61183920	*LACTB*	732	G, A	0.000	-0.031	0.017	2E-11	HDL	-
rs16942887	16	66485543	*ACD*	721	G, A	-0.011	-0.016	0.004	1E-8	HDL	+
			NFATC3	741	G, A	-0.068	-0.032	0.008	4E-10	HDL	+
			PRMT7	729	G, A	0.034	0.025	-0.006	5E-9	HDL	+
rs11869286	17	35067382	*CRKRS*	691	C, G	0.020	-0.012	-0.056	3E-18	HDL	-
			PERLD1	737	C, G	-0.014	0.007	0.038	1E-10	HDL	-
rs2277862	20	33616196	*CEP250*	737	C, T	-0.027	0.043	0.103	8E-37	TC	-
			CPNE1	732	C, T	0.030	-0.051	-0.114	1E-73	TC	-
			ERGIC3	731	C, T	0.014	-0.015	-0.062	2E-11	TC	-

***** Positions are relative to Human Genome NCBI Build 36.

† Alleles are designated with respect to the "+" strand.

Supplementary Table 10. *Cis*-acting association of SNPs with transcript levels in human subcutaneous fat.

Lead SNP	Chr	Position*	Transcript gene symbol	# of samples	Major, minor alleles†	Mean expression			Transcript *P*-value	Trait	Lipid effect (modeled on minor allele)
						Homo. major	Hetero.	Homo. minor			
rs12027135	1	25648320	*RHCE*	607	T, A	0.038	0.001	-0.038	1E-41	LDL	-
										TC	-
			TMEM50A	609	T, A	0.040	0.005	-0.041	2E-29	LDL	-
										TC	-
			TMEM57	609	T, A	0.080	0.004	-0.082	1E-99	LDL	-
										TC	-
rs4660293	1	39800767	*OXCT2*	609	A, G	0.037	0.038	-0.040	1E-17	HDL	-
rs2131925	1	62798530	*DOCK7*	608	T, G	0.188	0.054	-0.110	6E-80	TG	-
										LDL	-
										TC	-
rs1260326	2	27584444	*IFT172*	582	C, T	-0.102	0.000	0.071	8E-54	TC	+
										TG	+
rs3177928	6	32520413	*HLA-DQA1*	609	G, A	0.229	0.287	-0.064	2E-10	TC	+
			HLA-DQA2	605	G, A	-0.067	-0.082	0.017	6E-13	TC	+
			HLA-DRB1	605	G, A	-0.138	-0.145	0.034	7E-13	TC	+
			HLA-DRB5	604	G, A	0.517	0.315	-0.103	2E-9	TC	+
rs2814944	6	34660775	*UHRF1BP1*	589	G, A	0.095	0.041	-0.024	2E-18	HDL	-
rs9488822	6	116419586	*FRK*	607	A, T	-0.073	-0.007	0.052	3E-18	LDL	-
										TC	-
rs17145738	7	72620810	*MLXIPL*	539	C, T	-0.020	0.018	-0.035	2E-8	HDL	+
										TG	-
rs7134594	12	108484576	*MMAB*	606	T, C	0.093	0.026	-0.079	4E-53	HDL	-
rs11869286	17	35067382	*CRKRS*	588	C, G	0.024	-0.018	-0.042	3E-11	HDL	-
			GSDM1	607	C, G	0.080	-0.016	-0.311	3E-8	HDL	-
rs2277862	20	33616196	*CEP250*	609	C, T	-0.029	0.047	0.138	6E-31	TC	-
			CPNE1	607	C, T	0.031	-0.050	-0.138	1E-47	TC	-
			ERGIC3	583	C, T	0.011	-0.022	-0.038	2E-8	TC	-

* Positions are relative to Human Genome NCBI Build 36.

† Alleles are designated with respect to the "+" strand.

Supplementary Table 11. Associations of lead SNPs in European and non-European groups.

Locus	Lead SNP	Trait	Major Allele*	Minor Allele*	Primary meta-analysis (*n* = 100,184)			European (*n* = 7,063)			East Asian (*n* =15,046)			South Asian (*n* = 9,705)			African American (*n* =8,061)		
					Dir.	*P*-value	Het.†	Dir.	*P*-value	Het.‡	Dir.	*P*-value	Het.‡	Dir.	P-value	Het.‡	Dir.	P-value	Het.‡
LDLRAP1	rs12027135	LDL	T	A	-	1E-10	N	-	1E-1	-	-	7E-5	Y	-	3E-1	N	-	4E-1	N
		TC	T	A	-	4E-11	N	-	2E-1	-	-	3E-3	N	-	2E-1	N	n.d.	n.d.	
PABPC4	rs4660293	HDL	A	G	-	4E-10	N	-	2E-3	-	-	6E-3	N	-	3E-1	N	-	8E-1	N
PCSK9	rs2479409	LDL	A	G	+	2E-28	N	+	1E-1	+	+	4E-1	Y	+	4E-2	N	+	3E-3	N
		TC	A	G	+	4E-24	N	+	5E-2	+	+	5E-1	Y	+	1E-1	N	n.d.	n.d.	
ANGPTL3	rs2131925	TG	T	G	-	9E-43	N	-	3E-4	-	-	2E-7	N	-	3E-7	N	-	1E-3	N
		LDL	T	G	-	2E-17	N	-	2E-3	+	+	7E-1	N	-	9E-1	N	-	1E-2	N
		TC	T	G	-	3E-40	N	-	9E-5	-	-	6E-3	N	-	1E-2	N	n.d.	n.d.	
EVI5	rs7515577	TC	A	C	-	3E-8	N	-	4E-3	-	-	2E-2	N	-	9E-1	N	n.d.	n.d.	
SORT1	rs629301	LDL	T	G	-	1E-170	Y	-	2E-11	-	-	5E-13	N	-	6E-18	N	-	2E-14	N
		TC	T	G	-	6E-131	N	-	8E-10	-	-	6E-11	N	-	2E-11	N	n.d.	n.d.	
ZNF648	rs1689800	HDL	A	G	-	3E-10	N	-	2E-1	-	-	7E-4	N	-	4E-1	N	+	6E-1	N
MOSC1	rs2642442	LDL	T	C	-	1E-10	N	+	9E-1	-	-	2E-2	N	-	1E-1	N	-	2E-1	N
		TC	T	C	-	6E-13	N	-	3E-1	-	-	2E-1	N	-	2E-1	N	n.d.	n.d.	
GALNT2	rs4846914	HDL	A	G	-	4E-21	N	-	4E-1	-	-	2E-1	N	-	2E-5	N	-	4E-3	N
		TG	A	G	+	8E-14	N	+	3E-3	+	+	3E-1	N	+	9E-1	N	+	3E-1	N
IRF2BP2	rs514230	LDL	T	A	-	9E-12	N	-	2E-1	-	-	5E-2	Y	-	8E-3	N	-	4E-1	N
		TC	T	A	-	5E-14	N	-	2E-2	-	-	4E-3	N	-	8E-3	N	n.d.	n.d.	
APOB	rs1042034	HDL	T	C	+	1E-30	N	+	3E-3	+	+	4E-1	Y	+	4E-4	N	+	1E-2	N
		TG	T	C	-	1E-45	N	-	4E-4	+	+	9E-1	Y	-	2E-5	N	-	5E-4	N
	rs1367117	LDL	G	A	+	5E-114	N	+	8E-6	+	+	2E-3	N	+	2E-6	N	+	2E-2	N
		TC	G	A	+	4E-96	N	+	5E-7	+	+	5E-4	N	+	4E-8	N	n.d.	n.d.	
GCKR	rs1260326	TC	C	T	+	7E-27	N	+	4E-3	+	+	3E-8	N	+	8E-7	N	n.d.	n.d.	
		TG	C	T	+	6E-133	Y	+	5E-14	+	+	1E-17	N	+	7E-16	N	+	2E-5	N
ABCG5/8	rs4299376	LDL	T	G	+	2E-47	Y	+	3E-3	+	+	3E-2	Y	+	2E-1	N	+	4E-2	N
		TC	T	G	+	4E-45	N	+	3E-3	+	+	3E-1	N	+	1E-1	N	n.d.	n.d.	
RAB3GAP1	rs7570971	TC	C	A	+	2E-8	N	+	7E-1	-	-	6E-1	N	n.d.	n.d.		n.d.	n.d.	
COBLL1	rs10195252	TG	T	C	-	2E-10	N	-	3E-2	-	-	8E-1	N	-	2E-2	N	-	2E-2	N
	rs12328675	HDL	T	C	+	3E-10	N	+	5E-3	+	+	7E-2	N	n.d.	n.d.		+	4E-3	N
IRS1	rs2972146	TG	T	G	-	3E-8	N	-	1E-1	-	-	2E-3	N	-	1E-1	N	+	1	N
		HDL	T	G	+	3E-9	N	+	3E-1	+	+	5E-3	N	+	2E-3	N	+	8E-1	N
RAF1	rs2290159	TC	G	C	-	4E-9	N	-	8E-2	-	-	4E-1	N	-	8E-1	N	n.d.	n.d.	
MSL2L1	rs645040	TG	T	G	-	3E-8	N	-	3E-1	-	-	5E-1	N	+	8E-1	N	-	4E-2	N
KLHL8	rs442177	TG	T	G	-	9E-12	N	-	5E-1	-	-	5E-3	N	-	5E-4	N	-	5E-1	N
SLC39A8	rs13107325	HDL	C	T	-	7E-11	N	-	7E-1	+	+	8E-1	N	n.d.	n.d.		+	5E-1	N
ARL15	rs6450176	HDL	G	A	-	5E-8	N	+	6E-1	n.d.	n.d			n.d.	n.d.		-	8E-2	N
MAP3K1	rs9686661	TG	C	T	+	1E-10	N	+	7E-1	+	+	4E-2	N	+	3E-1	N	+	6E-1	N
HMGCR	rs12916	LDL	T	C	+	5E-45	N	+	1E-4	+	+	2E-15	N	+	1E-4	N	+	2E-1	N
		TC	T	C	+	9E-47	N	+	2E-3	+	+	5E-12	N	+	9E-4	N	n.d.	n.d.	

TIMD4	rs6882076	LDL	C	T	-	2E-22	N	-	2E-2	-	3E-2	N	-	1E-1	N	-	2E-1	N
		TC	C	T	-	8E-28	N	-	1E-3	-	4E-3	N	-	8E-3	N	n.d.	n.d.	
		TG	C	T	-	1E-10	N	-	7E-2	-	4E-2	N	-	6E-4	N	-	3E-1	N
MYLIP	rs3757354	LDL	C	T	-	1E-11	N	-	1E-2	+	5E-1	Y	+	2E-1	Y	-	4E-2	N
		TC	C	T	-	3E-9	N	-	3E-1	+	8E-1	N	+	4E-1	N	n.d.	n.d.	
HFE	rs1800562	LDL	G	A	-	6E-10	N	-	1E-2	-	2E-1	N	n.d.	n.d.		-	8E-1	N
		TC	G	A	-	3E-8	N	-	1E-2	-	3E-1	N	n.d.	n.d.		n.d.	n.d.	
HLA	rs2247056	TG	C	T	-	2E-15	N	-	2E-3	-	1E-1	Y	-	8E-3	N	+	9E-1	N
	rs3177928	LDL	G	A	+	2E-15	N	+	3E-2	+	6E-2	N	+	1E-1	N	+	2E-3	N
		TC	G	A	+	4E-19	N	+	6E-2	+	8E-3	N	+	2E-1	N	n.d.	n.d.	
C6orf106	rs2814982	TC	C	T	-	5E-11	N	+	2E-1	+	9E-1	N	-	1E-1	N	n.d.	n.d.	
	rs2814944	HDL	G	A	-	4E-9	N	-	5E-1	-	9E-1	N	-	6E-1	N	+	3E-1	N
FRK	rs9488822	TC	A	T	-	2E-10	N	-	2E-1	-	6E-1	N	-	3E-2	N	n.d.	n.d.	
		LDL	A	T	-	4E-8	N	-	2E-1	-	6E-1	N	-	1E-2	N	-	9E-1	N
CITED2	rs605066	HDL	T	C	-	3E-8	N	-	1E-2	-	6E-2	N	+	5E-1	N	-	1	N
LPA	rs1564348	LDL	T	C	+	2E-17	N	+	2E-4	+	9E-1	N	n.d.	n.d.		+	6E-2	N
		TC	T	C	+	1E-16	N	+	2E-3	+	9E-1	N	n.d.	n.d.		n.d.	n.d.	
	rs1084651	HDL	G	A	-	3E-8	N	-	1E-2	-	1E-1	N	n.d.	n.d.		-	3E-1	N
DNAH11	rs12670798	TC	T	C	+	9E-10	N	+	1E-2	+	4E-1	Y	+	5E-2	N	n.d.	n.d.	
		LDL	T	C	+	7E-10	N	+	1E-2	+	1	Y	+	1E-1	N	-	6E-1	N
NPC1L1	rs2072183	TC	G	C	+	3E-11	N	+	3E-1	-	7E-1	Y	+	5E-2	N	n.d.	n.d.	
		LDL	G	C	+	7E-11	N	+	1	-	8E-1	Y	+	2E-2	N	+	4E-1	N
TYW1B	rs13238203	TG	C	T	-	1E-9	N	-	6E-1	n.d.	n.d.		n.d.	n.d.		n.d.	n.d.	
MLXIPL	rs17145738	TG	C	T	-	6E-58	N	-	2E-5	-	2E-6	N	-	3E-11	N	-	2E-1	N
		HDL	C	T	+	1E-9	N	+	1E-1	+	1	Y	+	3E-1	N	-	2E-2	Y
KLF14	rs4731702	HDL	C	T	+	1E-15	N	+	2E-1	+	2E-1	N	+	3E-3	N	+	2E-1	N
PPP1R3B	rs9987289	HDL	G	A	-	6E-25	Y	-	2E-2	-	4E-2	Y	-	4E-6	N	-	4E-5	N
		LDL	G	A	-	2E-14	N	-	9E-2	-	2E-1	N	-	3E-3	N	-	7E-2	N
		TC	G	A	-	7E-23	N	-	9E-2	-	1E-1	N	-	8E-3	N	n.d.	n.d.	
PINX1	rs11776767	TG	G	C	+	1E-8	N	-	8E-1	+	5E-1	N	+	5E-3	N	+	3E-1	N
NAT2	rs1495741	TC	A	G	+	3E-8	N	-	1	+	6E-1	N	+	8E-1	N	n.d.	n.d.	
		TG	A	G	+	5E-14	N	-	7E-1	+	8E-2	Y	+	4E-2	N	+	4E-1	N
LPL	rs12678919	HDL	A	G	+	1E-97	N	+	4E-7	+	7E-17	N	+	2E-7	N	+	1E-3	N
		TG	A	G	-	2E-115	Y	-	1E-11	-	6E-18	N	-	7E-15	N	-	5E-3	N
CYP7A1	rs2081687	LDL	C	T	+	2E-8	N	+	1E-1	+	1	N	+	7E-1	N	+	8E-1	N
		TC	C	T	+	2E-12	N	+	2E-1	+	5E-1	Y	+	4E-1	N	n.d.	n.d.	
TRPS1	rs2293889	HDL	G	T	-	6E-11	N	-	6E-2	-	2E-3	N	-	9E-2	N	-	3E-1	N
		TC	A	C	-	3E-8	N	-	5E-2	-	2E-3	N	+	9E-1	N	n.d.	n.d.	
TRIB1	rs2954029	LDL	A	T	-	5E-29	N	-	7E-2	-	2E-4	N	-	2E-2	N	-	6E-1	N
		TC	A	T	-	1E-35	N	-	4E-4	-	4E-8	N	-	3E-4	N	n.d.	n.d.	
		TG	A	T	-	3E-55	N	-	8E-6	-	1E-9	N	-	3E-6	N	-	3E-1	N
		HDL	A	T	+	5E-18	N	+	3E-2	-	7E-1	Y	+	2E-1	N	+	2E-1	N
PLEC1	rs11136341	LDL	A	G	+	4E-13	N	+	7E-1	+	1E-2	N	+	5E-1	N	+	5E-2	N
		TC	A	G	+	9E-10	N	+	9E-1	+	5E-3	N	+	8E-1	N	n.d.	n.d.	
TTC39B	rs581080	HDL	C	G	-	3E-12	N	-	1E-1	+	4E-1	N	-	6E-2	N	-	5E-1	N

TTC39B		TC	C	G	-	3E-9	N	+	6E-1	-	7E-1	Y	-	6E-1	N	n.d.	n.d.	
ABCA1	rs1883025	HDL	C	T	-	2E-33	Y	-	9E-2	-	2E-12	N	-	2E-5	N	-	3E-1	N
		TC	C	T	-	3E-27	N	-	5E-5	-	5E-7	Y	-	2E-2	N	n.d.	n.d.	
ABO	rs9411489	TC	C	T	+	5E-10	N	n.d.	n.d.	n.d.	n.d.		n.d.	n.d.		n.d.	n.d.	
		LDL	C	T	+	6E-13	N	n.d.	n.d.	n.d.	n.d.		n.d.	n.d.		n.d.	n.d.	
JMJD1C	rs10761731	TG	A	T	-	4E-12	N	-	4E-3	-	4E-4	N	-	5E-1	N	-	8E-1	N
CYP26A1	rs2068888	TG	G	A	-	2E-8	N	-	5E-1	-	8E-2	N	-	6E-1	N	-	7E-1	N
GPAM	rs2255141	LDL	G	A	+	2E-9	N	+	1E-1	+	8E-3	N	+	2E-1	N	+	5E-2	N
		TC	G	A	+	2E-10	N	+	3E-1	+	3E-3	N	+	2E-1	N	n.d.	n.d.	
AMPD3	rs2923084	HDL	A	G	-	5E-8	N	-	8E-1	-	4E-1	N	+	5E-1	N	-	4E-2	N
SPTY2D1	rs10128711	TC	C	T	-	3E-8	N	-	6E-2	+	4E-1	Y	-	5E-1	N	n.d.	n.d.	
LRP4	rs3136441	HDL	T	C	+	4E-18	N	+	5E-4	+	2E-1	N	+	3E-3	N	n.d.	n.d.	
FADS1–2–3	rs174546	TG	C	T	+	5E-24	N	+	2E-1	+	2E-3	N	+	3E-5	N	+	3E-5	N
		TC	C	T	-	3E-22	N	-	2E-5	-	2E-2	N	-	2E-2	N	n.d.	n.d.	
		LDL	C	T	-	2E-21	N	-	1E-3	-	4E-3	N	-	8E-3	N	-	2E-1	N
		HDL	C	T	-	3E-22	N	-	3E-2	-	6E-2	N	-	5E-5	N	-	1E-1	N
APOC3	rs964184	HDL	C	G	-	5E-47	N	-	2E-2	-	1E-23	N	-	3E-5	N	-	3E-1	Y
		LDL	C	G	+	2E-26	Y	+	2E-3	-	2E-1	Y	-	3E-1	Y	+	9E-1	Y
		TC	C	G	+	6E-57	Y	+	2E-9	+	2E-2	Y	+	1E-4	N	n.d.	n.d.	
		TG	C	G	+	7E-240	Y	+	4E-28	+	2E-50	N	+	9E-52	Y	+	2E-1	Y
UBASH3B	rs7941030	TC	T	C	+	2E-10	N	+	4E-1	+	3E-2	N	+	5E-2	N	n.d.	n.d.	
		HDL	T	C	+	3E-8	N	-	6E-1	-	9E-1	Y	+	8E-2	N	+	1E-2	N
ST3GAL4	rs11220462	LDL	G	A	+	1E-15	N	+	8E-2	+	4E-2	N	+	2E-1	N	+	4E-1	N
		TC	G	A	+	6E-11	N	+	4E-1	+	1E-1	N	+	3E-1	N	n.d.	n.d.	
PDE3A	rs7134375	HDL	C	A	+	4E-8	N	+	8E-1	+	1E-1	N	+	8E-1	N	+	3E-1	N
LRP1	rs11613352	TG	C	T	-	4E-10	N	-	6E-2	-	3E-1	N	n.d.	n.d.		-	2E-2	N
		HDL	C	T	+	4E-8	N	+	5E-3	+	2E-1	N	n.d.	n.d.		+	1E-1	N
MVK	rs7134594	HDL	T	C	-	7E-15	N	-	7E-3	-	2E-1	N	n.d.	n.d.		-	2E-1	N
BRAP	rs11065987	LDL	A	G	-	2E-9	N	-	9E-1	-	3E-1	N	n.d.	n.d.		-	2E-1	N
		TC	A	G	-	7E-12	N	-	6E-1	-	2E-1	N	n.d.	n.d.		n.d.	n.d.	
TCF1	rs1169288	LDL	A	C	+	1E-15	N	+	6E-3	+	9E-2	N	+	2E-1	N	+	4E-1	N
		TC	A	C	+	2E-14	N	+	1E-3	+	2E-1	N	+	2E-1	N	n.d.	n.d.	
SBNO1	rs4759375	HDL	C	T	+	8E-9	N	+	3E-1	n.d.	n.d.		n.d.	n.d.		+	3E-1	N
ZNF664	rs4765127	HDL	G	T	+	3E-10	N	-	9E-1	+	4E-1	Y	-	9E-1	N	+	9E-3	N
		TG	G	T	-	2E-8	N	+	9E-1	-	6E-1	N	-	8E-1	N	-	9E-1	N
SCARB1	rs838880	HDL	T	C	+	3E-14	N	+	3E-2	+	9E-1	N	-	7E-1	N	n.d.	n.d.	
KIAA1305	rs8017377	LDL	G	A	+	5E-11	N	+	3E-1	-	1	N	+	8E-2	N	+	5E-2	N
CAPN3	rs2412710	TG	G	A	+	2E-8	N	+	5E-1	n.d.	n.d.		n.d.	n.d.		-	5E-1	N
FRMD5	rs2929282	TG	A	T	+	2E-11	N	+	7E-2	-	3E-1	N	-	6E-1	N	-	5E-1	Y
LIPC	rs1532085	HDL	G	A	+	3E-96	Y	+	5E-12	+	4E-30	N	+	9E-3	N	+	5E-3	N
		TC	G	A	+	9E-20	N	+	1E-1	+	6E-8	N	+	2E-1	N	n.d.	n.d.	
		TG	G	A	+	2E-11	N	+	4E-1	+	1E-4	N	+	2E-1	N	+	2E-3	N
LACTB	rs2652834	HDL	G	A	-	9E-9	N	-	7E-1	n.d.	n.d.		n.d.	n.d.		n.d.	n.d.	
CTF1	rs11649653	TG	C	G	-	3E-8	N	-	2E-1	n.d.	n.d.		n.d.	n.d.		+	5E-1	N
CETP	rs3764261	LDL	C	A	-	2E-12	N	-	4E-5	+	4E-1	N	-	8E-3	N	-	2E-1	N

CETP		HDL	C	A	+	7e-380	Y	+	6E-36	+	6E-19	N	+	4E-38	N	+	3E-18	N
		TC	C	A	+	7E-14	N	+	9E-1	+	5E-3	N	+	2E-1	N	n.d.	n.d.	
		TG	C	A	-	6E-12	N	-	3E-3	-	5E-3	N	+	1	N	-	7E-1	N
LCAT	rs16942887	HDL	G	A	+	8E-33	N	+	6E-1	+	3E-3	N	+	5E-7	N	+	1E-10	N
HPR	rs2000999	LDL	G	A	+	2E-22	N	+	6E-2	+	3E-6	N	+	1E-1	N	-	1	N
		TC	G	A	+	3E-24	N	+	1E-5	+	2E-4	N	+	6E-2	N	n.d.	n.d.	
CMIP	rs2925979	HDL	C	T	-	2E-11	N	-	1E-2	-	5E-2	N	-	1E-3	N	-	1E-1	N
STARD3	rs11869286	HDL	C	G	-	1E-13	N	-	5E-2	-	2E-2	N	-	4E-1	N	-	3E-2	N
OSBPL7	rs7206971	LDL	G	A	+	2E-8	N	+	4E-1	+	6E-1	N	-	7E-1	N	+	1E-1	N
		TC	G	A	+	1E-8	N	+	3E-1	+	2E-1	N	-	6E-1	N	n.d.	n.d.	
ABCA8	rs4148008	HDL	C	G	-	2E-10	N	-	1	-	6E-2	N	-	1E-1	N	-	9E-1	N
PGS1	rs4129767	HDL	A	G	-	8E-9	N	-	3E-1	-	8E-3	N	-	1E-1	N	-	7E-1	N
LIPG	rs7241918	HDL	T	G	-	3E-49	N	-	5E-4	-	3E-3	N	-	3E-5	N	-	8E-1	N
		TC	T	G	-	6E-19	N	-	3E-3	+	8E-1	Y	-	1E-2	N	n.d.	n.d.	
MC4R	rs12967135	HDL	G	A	-	7E-9	N	-	8E-2	-	7E-1	N	-	6E-4	N	-	6E-1	N
ANGPTL4	rs7255436	HDL	A	C	-	3E-8	N	-	4E-2	-	4E-1	N	-	6E-3	N	-	3E-1	N
LDLR	rs6511720	LDL	G	T	-	4E-117	Y	-	1E-14	-	7E-3	N	n.d.	n.d.		-	5E-8	N
		TC	G	T	-	7E-97	N	-	4E-11	-	7E-2	N	n.d.	n.d.		n.d.	n.d.	
LOC55908	rs737337	HDL	T	C	-	3E-9	N	-	2E-1	-	5E-4	N	-	6E-7	N	-	6E-6	N
CILP2	rs10401969	LDL	T	C	-	7E-22	Y	-	1E-1	-	2E-1	N	-	4E-1	N	+	2E-1	Y
		TC	T	C	-	3E-38	Y	-	3E-2	-	2E-2	N	-	8E-3	N	n.d.	n.d.	
		TG	T	C	-	2E-29	N	-	3E-4	-	9E-5	N	-	8E-10	N	+	5E-1	Y
APOE	rs439401	TG	C	T	-	1E-30	Y	-	5E-3	-	4E-5	N	-	1E-7	N	n.d.	n.d.	
	rs4420638	HDL	A	G	-	4E-21	N	-	2E-3	-	3E-10	N	-	5E-5	N	+	5E-2	Y
		LDL	A	G	+	9E-147	Y	+	5E-19	+	2E-5	Y	+	5E-2	Y	+	1	Y
		TC	A	G	+	5E-111	Y	+	5E-16	+	1E-5	Y	+	2E-2	N	n.d.	n.d.	
FLJ36070	rs492602	TC	A	G	+	2E-10	N	+	1E-1	-	9E-1	N	+	3E-7	N	n.d.	n.d.	
LILRA3	rs386000	HDL	G	C	+	4E-16	N	+	4E-1	-	5E-1	N	+	3E-4	N	-	6E-1	N
ERGIC3	rs2277862	TC	C	T	-	4E-10	N	-	6E-1	-	2E-1	N	-	4E-2	N	n.d.	n.d.	
MAFB	rs2902940	TC	A	G	-	6E-11	N	+	6E-1	+	2E-1	Y	-	2E-1	N	n.d.	n.d.	
		LDL	A	G	-	2E-8	N	-	5E-1	+	7E-1	Y	-	2E-1	N	-	9E-1	N
TOP1	rs6029526	TC	T	A	+	9E-17	N	+	4E-5	+	1E-3	N	+	1E-1	N	n.d.	n.d.	
		LDL	T	A	+	4E-19	N	+	7E-4	+	2E-3	N	+	1E-1	N	+	4E-1	N
HNF4A	rs1800961	HDL	C	T	-	1E-15	N	-	1E-5	-	5E-1	N	-	5E-3	N	+	9E-1	N
		TC	C	T	-	6E-13	N	+	2E-1	-	1E-1	N	-	2E-1	N	n.d.	n.d.	
PLTP	rs6065906	TG	T	C	+	3E-17	N	+	8E-4	+	9E-1	N	+	1E-1	N	+	4E-1	N
		HDL	T	C	-	2E-22	N	-	1E-2	+	1	N	-	4E-1	N	-	3E-2	N
UBE2L3	rs181362	HDL	C	T	-	1E-8	N	-	7E-2	-	1E-4	N	-	7E-3	N	-	7E-1	N
PLA2G6	rs5756931	TG	T	C	-	4E-8	N	-	3E-1	n.d.	n.d.		n.d.	n.d.		-	5E-2	N

n.d. = not determined.

* Alleles are designated with respect to the "+" strand.

† "Y" if inter-cohort heterogeneity $P < 0.0005$ (to account for multiple testing of 102 lead SNPs in 95 loci), "N" otherwise.

‡ "Y" if the heterogeneity *P*-value between effect size in the non-European group and effect size in the primary meta-analysis < 0.0005 (to account for multiple testing of 102 lead SNPs in 95 loci), "N" otherwise.

Supplementary Table 12. Multi-ethnic replication summary.

Cohort	Trait	# of SNPs tested	# of SNPs in same direction*	Binomial *P*-value	# of SNPs in same direction with $P < 0.05$†	Binomial *P*-value
European	HDL	47	44	1×10^{-10}	23	$< 2 \times 10^{-16}$
	LDL	36	35	5×10^{-10}	18	7×10^{-15}
	TC	51	46	1×10^{-9}	25	$< 2 \times 10^{-16}$
	TG	32	29	1×10^{-6}	15	4×10^{-12}
East Asian	HDL	44	38	5×10^{-7}	18	1×10^{-12}
	LDL	36	29	2×10^{-4}	16	4×10^{-12}
	TC	51	43	3×10^{-7}	24	4×10^{-18}
	TG	28	26	2×10^{-6}	16	3×10^{-14}
South Asian	HDL	39	35	2×10^{-7}	22	$< 2 \times 10^{-16}$
	LDL	32	29	1×10^{-6}	12	1×10^{-8}
	TC	46	43	2×10^{-10}	19	1×10^{-13}
	TG	27	24	3×10^{-5}	16	6×10^{-15}
African American‡	HDL	44	37	3×10^{-6}	14	8×10^{-9}
	LDL	36	33	1×10^{-7}	10	4×10^{-6}
	TC	n.d.	n.d.	n.d.	n.d.	n.d.
	TG	30	24	7×10^{-4}	10	6×10^{-7}

* The "Number of SNPs in same direction" column indicates the number of SNPs for which the direction of effect is concordant between GLGC and the European or non-European cohort for each trait. The *P*-value reported is one-tailed, based on a binomial draw with null expectation $P = 0.5$.

† The "Number of SNPs in same direction with $P < 0.05$" column indicates the number of SNPs for which the direction of effect is concordant between GLGC and the European or non-European cohort, and the p-value for SNP-trait association in the European or non-European cohort is < 0.05. The *P*-value reported is one-tailed, based on a binomial draw with null expectation $P = 0.05$.

‡ Analyses for total cholesterol were unavailable for the African American cohorts; n.d. = not determined.

Supplementary Table 13. Additional replication in Europeans.

Locus	Lead SNP	Trait	Major Allele*	Minor Allele*	Primary meta-analysis (n = 100,184)		MDC-CC & FINRISK97 meta-analysis (n =12,017)†	
					Dir.	*P*-value	Dir.	*P*-value
PABPC4	rs4660293	HDL	A	G	-	4E-10	-	3E-1
ZNF648	rs1689800	HDL	A	G	-	3E-10	-	3E-3
IRF2BP2	rs514230	LDL	T	A	-	9E-12	+	8E-1
MSL2L1	rs645040	TG	T	G	-	3E-8	-	4E-2
KLHL8	rs442177	TG	T	G	-	9E-12	-	6E-2
SLC39A8	rs13107325	HDL	C	T	-	7E-11	-	6E-3
MAP3K1	rs9686661	TG	C	T	+	1E-10	+	4E-3
MYLIP	rs3757354	LDL	C	T	-	1E-11	-	2E-3
HFE	rs1800562	LDL	G	A	-	6E-10	+	9E-1
HLA	rs3177928	LDL	G	A	+	2E-15	+	9E-3
NPC1L1	rs2072183	LDL	G	C	+	7E-11	+	1E-2
KLF14	rs4731702	HDL	C	T	+	1E-15	+	1E-2
PPP1R3B	rs9987289	HDL	G	A	-	6E-25	-	7E-6
JMJD1C	rs10761731	TG	A	T	-	4E-12	-	6E-1
UBASH3B	rs7941030	HDL	T	C	+	3E-8	+	3E-2
PDE3A	rs7134375	HDL	C	A	+	4E-8	+	5E-2
SCARB1	rs838880	HDL	T	C	+	3E-14	+	8E-5
KIAA1305	rs8017377	LDL	G	A	+	5E-11	+	1E-1
CAPN3	rs2412710	TG	G	A	+	2E-8	+	2E-2
HPR	rs2000999	LDL	G	A	+	2E-22	+	7E-1
CMIP	rs2925979	HDL	C	T	-	2E-11	-	1E-2
STARD3	rs11869286	HDL	C	G	-	1E-13	-	1E-1
PGS1	rs4129767	HDL	A	G	-	8E-9	-	9E-1
LOC55908	rs737337	HDL	T	C	-	3E-9	-	6E-5
LILRA3	rs386000	HDL	G	C	+	4E-16	+	1E-4
TOP1	rs6029526	LDL	T	A	+	4E-19	+	4E-1

* Alleles are designated with respect to the "+" strand.

† Includes 7,026 individuals from the National FINRISK 1997 Study (FINRISK97) and 4,991 individuals from Malmö Diet and Cancer Study – Cardiovascular Cohort (MDC-CC).

Supplementary Table 14. HapMap SNPs in high linkage disequilibrium with lead SNPs.

Locus	Trait(s)	Lead SNP	# SNPs with $r^2 \geq$ 0.8 in CEU*	# SNPs with $r^2 \geq$ 0.8 in CEU & JPT+CHB*	# SNPs with $r^2 \geq$ 0.8 in CEU & YRI*
SPTY2D1	TC	rs10128711	7	7 (7)	5 (7)
COBLL1	TG	rs10195252	6	6 (6)	5 (6)
CILP2	TC, TG, LDL	rs10401969	5	0 (4)	0 (5)
APOB	TG, HDL	rs1042034	10	9 (10)	4 (10)
JMJD1C	TG	rs10761731	56	37 (56)	48 (53)
LPA	HDL	rs1084651	3	0 (3)	0 (3)
BRAP	TC, LDL	rs11065987	5	0 (5)	0 (5)
PLEC1	LDL, TC	rs11136341	0	0 (0)	0 (0)
ST3GAL4	LDL, TC	rs11220462	8	8 (8)	1 (7)
LRP1	TG, HDL	rs11613352	9	0 (9)	0 (9)
CTF1	TG	rs11649653	0	0 (0)	0 (0)
HNF1A	TC, LDL	rs1169288	5	0 (5)	0 (5)
PINX1	TG	rs11776767	17	16 (17)	15 (17)
STARD3	HDL	rs11869286	3	3 (3)	3 (3)
LDLRAP1	TC, LDL	rs12027135	10	9 (9)	0 (9)
COBLL1	HDL	rs12328675	2	0 (2)	2 (2)
GCKR	TG, TC	rs1260326	4	4 (4)	0 (4)
DNAH11	TC, LDL	rs12670798	9	4 (9)	3 (9)
LPL	TG, HDL	rs12678919	34	18 (34)	0 (32)
HMGCR	TC, LDL	rs12916	17	15 (16)	2 (16)
MC4R	HDL	rs12967135	14	10 (14)	3 (14)
SLC39A8	HDL	rs13107325	1	0 (1)	0 (1)
TYW1B	TG	rs13238203	0	0 (0)	0 (0)
APOB	LDL, TC	rs1367117	6	0 (6)	0 (6)
NAT2	TG, TC	rs1495741	5	4 (5)	4 (5)
LIPC	HDL, TC, TG	rs1532085	1	1 (1)	0 (1)
LPA	LDL, TC	rs1564348	2	0 (2)	0 (2)
ZNF648	HDL	rs1689800	11	11 (11)	2 (10)
LCAT	HDL	rs16942887	8	5 (8)	6 (8)
MLXIPL	TG, HDL	rs17145738	9	8 (9)	1 (9)
FADS1-2-3	TG, HDL, TC, LDL	rs174546	22	21 (21)	10 (22)
HFE	LDL, TC	rs1800562	1	0 (1)	0 (1)
HNF4A	HDL, TC	rs1800961	0	0 (0)	0 (0)
UBE2L3	HDL	rs181362	36	23 (35)	4 (35)
ABCA1	HDL, TC	rs1883025	1	1 (1)	0 (1)
HPR	TC, LDL	rs2000999	0	0 (0)	0 (0)
CYP26A1	TG	rs2068888	1	1 (1)	1 (1)
NPC1L1	TC, LDL	rs2072183	0	0 (0)	0 (0)
CYP7A1	TC, LDL	rs2081687	20	7 (18)	2 (17)
ANGPTL3	TG, TC, LDL	rs2131925	103	66 (102)	61 (101)
HLA	TG	rs2247056	20	18 (20)	1 (19)
GPAM	TC, LDL	rs2255141	18	15 (16)	0 (18)
ERGIC3	TC	rs2277862	8	5 (8)	3 (8)
RAF1	TC	rs2290159	16	14 (14)	6 (15)
TRPS1	HDL	rs2293889	105	104 (105)	55 (105)
CAPN3	TG	rs2412710	0	0 (0)	0 (0)
PCSK9	LDL, TC	rs2479409	0	0 (0)	0 (0)
MOSC1	TC, LDL	rs2642442	4	3 (4)	0 (4)
LACTB	HDL	rs2652834	2	0 (2)	0 (1)
TRPS1	TC	rs2737229	13	0 (13)	3 (13)
C6orf106	HDL	rs2814944	23	17 (23)	0 (23)

C6orf106	TC	rs2814982	0	0 (0)	0 (0)
MAFB	TC, LDL	rs2902940	4	3 (4)	1 (4)
AMPD3	HDL	rs2923084	1	0 (1)	0 (1)
CMIP	HDL	rs2925979	1	0 (1)	0 (1)
FRMD5	TG	rs2929282	15	2 (15)	1 (14)
TRIB1	TG, TC, LDL, HDL	rs2954029	16	10 (16)	0 (16)
IRS1	HDL, TG	rs2972146	40	13 (40)	0 (39)
LRP4	HDL	rs3136441	21	18 (19)	0 (20)
HLA	TC, LDL	rs3177928	4	3 (4)	3 (4)
MYLIP	LDL, TC	rs3757354	3	3 (3)	2 (3)
CETP	HDL, TC, LDL, TG	rs3764261	4	3 (3)	0 (2)
LILRA3	HDL	rs386000	6	1 (4)	2 (6)
PGS1	HDL	rs4129767	8	7 (8)	4 (6)
ABCA8	HDL	rs4148008	3	3 (3)	1 (3)
ABCG5/8	LDL, TC	rs4299376	2	0 (2)	0 (2)
APOE	TG	rs439401	0	0 (0)	0 (0)
APOE	LDL, TC, HDL	rs4420638	0	0 (0)	0 (0)
KLHL8	TG	rs442177	26	25 (25)	6 (23)
PABPC4	HDL	rs4660293	5	4 (5)	0 (5)
KLF14	HDL	rs4731702	12	8 (10)	9 (12)
SBNO1	HDL	rs4759375	0	0 (0)	0 (0)
ZNF664	HDL, TG	rs4765127	51	31 (48)	26 (47)
GALNT2	HDL, TG	rs4846914	10	4 (10)	7 (10)
FLJ36070	TC	rs492602	10	10 (10)	6 (9)
IRF2BP2	TC, LDL	rs514230	10	9 (10)	0 (10)
PLA2G6	TG	rs5756931	9	1 (9)	0 (9)
TTC39B	HDL, TC	rs581080	0	0 (0)	0 (0)
TOP1	LDL, TC	rs6029526	33	33 (33)	4 (33)
CITED2	HDL	rs605066	9	6 (9)	1 (9)
PLTP	HDL, TG	rs6065906	5	3 (5)	0 (5)
SORT1	LDL, TC	rs629301	7	1 (7)	2 (7)
ABO	LDL, TC	rs9411489	4	4 (4)	0 (4)
ARL15	HDL	rs6450176	20	20 (20)	18 (20)
MSL2L1	TG	rs645040	22	15 (22)	1 (22)
LDLR	LDL, TC	rs6511720	0	0 (0)	0 (0)
TIMD4	TC, LDL, TG	rs6882076	6	1 (6)	1 (6)
PDE3A	HDL	rs7134375	1	1 (1)	0 (1)
MVK	HDL	rs7134594	33	23 (29)	26 (31)
OSBPL7	LDL, TC	rs7206971	39	12 (36)	4 (35)
LIPG	HDL, TC	rs7241918	10	4 (10)	0 (9)
ANGPTL4	HDL	rs7255436	3	2 (2)	1 (3)
LOC55908	HDL	rs737337	1	1 (1)	0 (1)
EVI5	TC	rs7515577	57	36 (57)	30 (56)
RAB3GAP1	TC	rs7570971	3	0 (3)	0 (3)
UBASH3B	TC, HDL	rs7941030	16	11 (16)	0 (14)
NYNRIN	LDL	rs8017377	1	1 (1)	1 (1)
SCARB1	HDL	rs838880	5	0 (5)	0 (5)
FRK	TC, LDL	rs9488822	3	1 (3)	0 (3)
APOA1	TG, TC, HDL, LDL	rs964184	0	0 (0)	0 (0)
MAP3K1	TG	rs9686661	6	4 (6)	4 (6)
PPP1R3B	HDL, TC, LDL	rs9987289	6	6 (6)	3 (6)

* SNP counts and linkage disequilibrium based on HapMap Phase II data. Numbers in parentheses indicate the number of CEU SNPs that were genotyed in JPT+CHB or in YRI in HapMap Phase II and for which LD could be estimated.

Supplementary Table 15. Associations with coronary artery disease.

Locus	Lead SNP*	Chr	Position†	Lead trait	Other traits	Major allele, minor allele‡	Lipid effect§	CAD effect§	CAD *P*-value‖
SORT1	rs629301	1	109,619,829	LDL	TC	T, G	–	–	4E-9
LDLR	rs6511720	19	11,063,306	LDL	TC	G, T	–	–	5E-9
APOA1–C3–A4–A5	rs964184	11	116,154,127	TG	TC, HDL, LDL	C, G	+	+	2E-8
BRAP	rs11065987	12	110,556,807	TC	LDL	A, G	–	+	1E-6
NAT2	rs1495741	8	18,317,161	TG	TC	A, G	+	+	2E-5
TCF1	rs1169288	12	119,901,033	LDL	TC	A, C	+	+	4E-5
TRIB1	rs2954029	8	126,560,154	TG	TC, LDL, HDL	A, T	–	–	5E-5
APOE–C1–C2	rs4420638	19	50,114,786	LDL	TC, HDL	A, G	+	+	7E-5
IRS1	rs2972146	2	226,808,942	HDL	TG	T, G	+	–	4E-4
CILP2	rs10401969	19	19,268,718	TC	TG, LDL	T, C	–	–	5E-4
C6orf106	rs2814982	6	34,654,538	TC		C, T	–	+	5E-4
LPA	rs1564348	6	160,498,850	LDL	TC	T, C	+	+	6E-4
LPL	rs12678919	8	19,888,502	TG	HDL	A, G	–	–	7E-4
KLF14	rs4731702	7	130,083,924	HDL		C, T	+	–	9E-4
CYP26A1	rs2068888	10	94,829,632	TG		G, A	–	–	0.001
C6orf106	rs2814944	6	34,660,775	HDL		G, A	–	+	0.002
ABCG5/8	rs4299376	2	43,926,080	LDL	TC	T, G	+	+	0.002
MAP3K1	rs9686661	5	55,897,543	TG		C, T	+	+	0.003
ZNF664	rs4765127	12	123,026,120	HDL	TG	G, T	+	–	0.004
HMGCR	rs12916	5	74,692,295	TC	LDL	T, C	+	+	0.004
ABCA8	rs4148008	17	64,386,889	HDL		C, G	–	+	0.008
SPTY2D1	rs10128711	11	18,589,560	TC		C, T	–	–	0.01
FRMD5	rs2929282	15	42,033,223	TG		A, T	+	+	0.01
PINX1	rs11776767	8	10,721,339	TG		G, C	+	–	0.02
PCSK9	rs2479409	1	55,277,238	LDL	TC	A, G	+	+	0.03
APOB	rs1367117	2	21,117,405	LDL	TC	G, A	+	+	0.03
CAPN3	rs2412710	15	40,471,079	TG		G, A	+	+	0.04
CETP	rs3764261	16	55,550,825	HDL	TC, LDL, TG	C, A	+	–	0.05
CITED2	rs605066	6	139,871,359	HDL		T, C	–	+	0.05
ST3GAL4	rs11220462	11	125,749,162	LDL	TC	G, A	+	+	0.06
GALNT2	rs4846914	1	228,362,314	HDL	TG	A, G	–	+	0.06
HPR	rs2000999	16	70,665,594	TC	LDL	G, A	+	+	0.06
KLHL8	rs442177	4	88,249,285	TG		T, G	–	–	0.06
MLXIPL	rs17145738	7	72,620,810	TG	HDL	C, T	–	+	0.06
ARL15	rs6450176	5	53,333,782	HDL		G, A	–	+	0.07
ANGPTL4	rs7255436	19	8,339,196	HDL		A, C	–	+	0.07
PLA2G6	rs5756931	22	36,875,979	TG		T, C	–	+	0.08
APOB	rs1042034	2	21,078,786	TG	HDL	T, C	–	–	0.08
MOSC1	rs2642442	1	219,040,186	TC	LDL	T, C	–	–	0.09
CMIP	rs2925979	16	80,092,291	HDL		C, T	–	+	0.09
LPA	rs1084651	6	161,009,807	HDL		G, A	+	–	0.10
HLA	rs2247056	6	31,373,469	TG		C, T	–	–	0.11
ABCA1	rs1883025	9	106,704,122	HDL	TC	C, T	–	–	0.14
GCKR	rs1260326	2	27,584,444	TG	TC	C, T	+	+	0.14
ANGPTL3	rs2131925	1	62,798,530	TG	LDL, TC	T, G	–	+	0.14
MAFB	rs2902940	20	38,524,901	TC	LDL	A, G	–	–	0.15
MSL2L1	rs645040	3	137,409,312	TG		T, G	–	–	0.15
PLTP	rs6065906	20	43,987,422	HDL	TG	T, C	–	–	0.16
JMJD1C	rs10761731	10	64,697,616	TG		A, T	–	+	0.17
ERGIC3	rs2277862	20	33,616,196	TC		C, T	–	+	0.19
TTC39B	rs581080	9	15,295,378	HDL	TC	C, G	–	–	0.19
EVI5	rs7515577	1	92,782,026	TC		A, C	–	–	0.20
MC4R	rs12967135	18	56,000,003	HDL		G, A	–	+	0.21
TYW1B	rs13238203	7	71,767,603	TG		C, T	–	+	0.22
LCAT	rs16942887	16	66,485,543	HDL		G, A	+	–	0.23
UBASH3B	rs7941030	11	122,027,585	TC	HDL	T, C	+	+	0.25
RAB3GAP1	rs7570971	2	135,554,376	TC		C, A	+	–	0.25
PLEC1	rs11136341	8	145,115,531	LDL	TC	A, G	+	–	0.25
FRK	rs9488822	6	116,419,586	TC	LDL	A, T	–	–	0.27
ZNF648	rs1689800	1	180,435,508	HDL		A, G	–	+	0.27
COBLL1	rs12328675	2	165,249,046	HDL		T, C	+	–	0.34
CYP7A1	rs2081687	8	59,551,119	TC	LDL	C, T	+	–	0.35
TOP1	rs6029526	20	39,106,032	LDL	TC	T, A	+	+	0.36
HFE	rs1800562	6	26,201,120	LDL	TC	G, A	–	–	0.37
TRPS1	rs2737229	8	116,717,740	TC		A, C	–	+	0.39

LRP4	rs3136441	11	46,699,823	HDL		T, C	+	–	0.39
NYNRIN	rs8017377	14	23,953,727	LDL		G, A	+	–	0.41
LDLRAP1	rs12027135	1	25,648,320	TC	LDL	T, A	–	–	0.41
MYLIP	rs3757354	6	16,235,386	LDL	TC	C, T	–	–	0.45
LIPC	rs1532085	15	56,470,658	HDL	TC, TG	G, A	+	+	0.46
PPP1R3B	rs9987289	8	9,220,768	HDL	TC, LDL	G, A	–	–	0.46
CTF1	rs11649653	16	30,825,988	TG		C, G	–	–	0.49
AMPD3	rs2923084	11	10,345,358	HDL		A, G	–	–	0.51
LACTB	rs2652834	15	61,183,920	HDL		G, A	–	+	0.53
FADS1–2–3	rs174546	11	61,326,406	TG	HDL, TC, LDL	C, T	+	–	0.54
GPAM	rs2255141	10	113,923,876	TC	LDL	G, A	+	–	0.55
PABPC4	rs4660293	1	39,800,767	HDL		A, G	–	+	0.56
DNAH11	rs12670798	7	21,573,877	LDL	TC	T, C	+	–	0.58
HLA	rs3177928	6	32,520,413	TC	LDL	G, A	+	+	0.58
TIMD4	rs6882076	5	156,322,875	TC	LDL, TG	C, T	–	–	0.58
PDE3A	rs7134375	12	20,365,025	HDL		C, A	+	–	0.58
APOE–C1–C2	rs439401	19	50,106,291	TG		C, T	–	–	0.59
SBNO1	rs4759375	12	122,362,191	HDL		C, T	+	–	0.60
NPC1L1	rs2072183	7	44,545,705	TC	LDL	G, C	+	+	0.61
LOC55908	rs737337	19	11,208,493	HDL		T, C	–	+	0.65
TRPS1	rs2293889	8	116,668,374	HDL		G, T	–	–	0.66
SLC39A8	rs13107325	4	103,407,732	HDL		C, T	–	–	0.66
FLJ36070	rs492602	19	53,898,229	TC		A, G	+	–	0.73
LILRA3	rs386000	19	59,484,573	HDL		G, C	+	+	0.74
COBLL1	rs10195252	2	165,221,337	TG		T, C	–	–	0.75
IRF2BP2	rs514230	1	232,925,220	TC	LDL	T, A	–	+	0.78
HNF4A	rs1800961	20	42,475,778	HDL	TC	C, T	–	+	0.81
MVK	rs7134594	12	108,484,576	HDL		T, C	–	+	0.82
STARD3	rs11869286	17	35,067,382	HDL		C, G	–	+	0.82
PGS1	rs4129767	17	73,915,579	HDL		A, G	–	–	0.83
SCARB1	rs838880	12	123,827,546	HDL		T, C	+	+	0.87
UBE2L3	rs181362	22	20,262,068	HDL		C, T	–	–	0.88
LRP1	rs11613352	12	56,078,847	TG	HDL	C, T	–	+	0.91
OSBPL7	rs7206971	17	42,780,114	LDL	TC	G, A	+	–	0.96
LIPG	rs7241918	18	45,414,951	HDL	TC	T, G	–	+	0.97
RAF1	rs2290159	3	12,603,920	TC		G, C	–	–	1.0

***** Except for the *ABO* locus, for which the lead SNP was unavailable in the CAD cohorts.

† Positions are relative to Human Genome NCBI Build 36.

‡ Alleles are designated with respect to the "+" strand.

§ The lipid effect and CAD effect are both modeled on the minor allele.

|| Shaded are loci having concordance between the direction of lipid effect and the change in CAD risk (increased TC = increased CAD risk; increased LDL-C = increased CAD risk; decreased HDL = increased CAD risk; increased TG = increased CAD risk). SNPs meeting the pre-specified statistical significance threshold of $P < 0.001$ for CAD are above the demarcated horizontal line.

Supplementary Table 16. Associations of genotype scores with hyperlipidemia status.

	Genotype score quartile	# of cases	# of controls	Odds ratio estimates*			Pr > Z
				Point estimate	2.5%	97.5%	
LDL-C	Q1	50	216	-	-	-	-
	Q2	111	155	3.5	2.6	4.7	5×10^{-5}
	Q3	162	104	7.9	5.9	10.8	1×10^{-11}
	Q4	209	57	12.6	9.1	17.5	1×10^{-14}
	Total	532	532				
HDL-C	Q1	98	263	-	-	-	-
	Q2	156	203	2.0	1.5	2.8	1×10^{-5}
	Q3	180	177	2.7	2.3	3.2	6×10^{-10}
	Q4	219	141	4.2	3.6	5.0	2×10^{-16}
	Total	653	784				
TG	Q1	36	84	-	-	-	-
	Q2	85	35	5.7	3.3	9.9	2×10^{-10}
	Q3	102	18	13.2	7.0	25.0	1×10^{-18}
	Q4	114	6	44.3	17.8	110.0	4×10^{-28}
	Total	337	143				

* For each trait, odds ratios are relative to the reference group (Q1). Note that the genetic risk score itself is created from the sum of the allele counts weighted by effect size, adjusted for the number of SNPs genotyped, age, and sex. These genetic risk scores were ranked in ascending order and divided into quantiles, with the maximum possible genetic risk score set at one. For LDL-C, the ranges of scores for the quartiles were: Q1 = 0.43-0.66, Q2 = 0.66-0.72, Q3 = 0.72-0.78, Q4 = 0.78-1.00. For HDL-C, the ranges of scores for the quartiles were: Q1 = 0.56-0.73, Q2 = 0.73-0.77, Q3 = 0.77-0.83, Q4 = 0.83-1.00. For TG, the ranges of scores for the quartiles were: Q1 = 0.28-0.72, Q2 = 0.72-0.78, Q3 = 0.78-0.84, Q4 = 0.84-1.00.

Supplementary Table 17. Hyperlipidemia cohort characteristics.

	Low LDL-C	High LDL-C	Low HDL-C	High HDL-C	Low TG	High TG
# of individuals	532	532	784	652	144	344
Sex (% female)	49.8%	52.8%	47.1%	47.6%	52.1%	33.7%
Age mean (SD)	65.7 (9)	42.2 (17)	61.8 (13)	58.4 (12)	45.3 (20)	50.2 (13)
HDL-C, mean (SD)	54.4 (16)	n.a.	36.2 (7)	89.8 (20)	50.2 (16)	34.7 (12)
LDL-C, mean (SD)	110 (17)	219 (47)	104.7 (36)	122.2 (36)	166.0 (73)	n.c.
TG, mean (SD)	123 (64)	n.a.	n.a.	n.a.	106.2 (44)	1070.9 (1460)
TC, mean (SD)	188.8 (21)	308 (57)	169.0 (40)	228.8 (42)	239.3 (89)	324.2 (154)

n.a. = not available; n.c. = not calculated (Friedewald equation not valid for TG levels above 400 mg/dL).

Supplementary Table 18. Monogenic lipid disorders.

Gene	Locus	Lead SNP*	Associated traits	Lipid disorder
ABCA1	9q31.1	rs1883025	Low HDL-C	Tangier disease
ABCG5	2p21	rs4299376	High LDL-C	Sitosterolemia
ABCG8	2p21	rs4299376	High LDL-C	Sitosterolemia
APOA1	11q23	rs964184	Low HDL-C	ApoA-I deficiency
APOA5	11q23	rs964184	High VLDL, high chylomicrons	ApoA-V deficiency
APOB	2p24	rs1367117	Low LDL-C High LDL-C	Familial hypobetalipoproteinemia Familial defective ApoB-100
APOC2	19q13	rs4420638	High chylomicrons	Familial ApoC-II deficiency
APOE	19q13	rs4420638	High VLDL, high chylomicrons	Familial dysbetalipoproteinemia
CETP	16q13	rs3764261	High HDL-C	Cholesteryl ester transfer protein deficiency
LCAT	16q22	rs16942887	Low HDL-C	Lecithin-cholesterol acyltransferase deficiency (fish-eye disease)
LDLR	19p13	rs6511720	High LDL-C	Familial hypercholesterolemia
LDLRAP1	1p36	rs12027135	High LDL-C	Autosomal recessive hypercholesterolemia
LIPC	15q22	rs1532085	High VLDL remnants	Familial hepatic lipase deficiency
LMF1	16p13	–	High triglycerides	Combined lipase deficiency
LPL	8p21	rs12678919	High chylomicrons	Lipoprotein lipase deficiency
MTTP	4q24	–	Low LDL-C	Abetalipoproteinemia
PCSK9	1p32	rs2479409	Low LDL-C High LDL-C	PCSK9 deficiency Autosomal-dominant hypercholesterolemia
SAR1B	5q31.1	–	Low chylomicrons	Chylomicron retention disease

*Where available, the lead SNP (from the primary meta-analysis) in the vicinity of the causal gene is listed.

Supplementary Table 19. Comparison of studies that used principal component analysis to adjust for population structure to those that did not.

				All studies*		Studies with PCA†		Studies without PCA‡		Combined§	Heterogeneity
Nearby genes	Lead_SNP	Best_SNP	Trait	N	P-value	N	P-value	N	P-value	P-value	P-value
LDLRAP1	rs12027135	rs12027135	LDL	86,707	1.2×10^{-10}	47,367	3.1×10^{-5}	38,925	3.1×10^{-7}	5.2×10^{-11}	0.52
LDLRAP1	rs12027135	rs12027135	TC	95,070	4.1×10^{-11}	47,776	1.3×10^{-4}	47,288	1.3×10^{-8}	1.4×10^{-11}	0.25
PABPC4	rs4660293	rs4660293	HDL	98,409	4.0×10^{-10}	47,772	6.4×10^{-6}	50,637	3.6×10^{-6}	1.0×10^{-10}	0.96
PCSK9	rs2479409	rs2479409	LDL	98,656	1.9×10^{-28}	47,366	8.7×10^{-13}	50,880	1.3×10^{-18}	1.6×10^{-29}	0.26
PCSK9	rs2479409	rs2479409	TC	95,070	3.8×10^{-24}	47,775	1.3×10^{-10}	47,288	2.2×10^{-16}	3.1×10^{-25}	0.31
ANGPTL3	rs2131925	rs3850634	LDL	98,409	2.6×10^{-18}	47,367	7.8×10^{-11}	50,637	1.2×10^{-9}	5.4×10^{-19}	0.85
ANGPTL3	rs2131925	rs3850634	TC	95,034	4.9×10^{-41}	47,776	5.9×10^{-19}	47,264	7.0×10^{-26}	6.1×10^{-43}	0.30
ANGPTL3	rs2131925	rs2131925	TG	94,225	8.8×10^{-43}	47,782	4.4×10^{-17}	46,453	1.8×10^{-30}	6.2×10^{-45}	0.036
EVI5	rs7515577	rs7515577	TC	89,838	2.8×10^{-8}	47,757	2.0×10^{-3}	42,471	8.9×10^{-7}	1.3×10^{-8}	0.25
SORT1	rs629301	rs629301	LDL	94,472	9.7×10^{-171}	47,367	9.0×10^{-100}	46,696	1.9×10^{-80}	1.2×10^{-177}	0.095
SORT1	rs629301	rs629301	TC	95,070	5.8×10^{-131}	47,776	5.9×10^{-75}	47,288	1.1×10^{-64}	3.2×10^{-137}	0.13
ZNF648	rs1689800	rs1689800	HDL	98,409	3.2×10^{-10}	47,772	5.8×10^{-4}	50,637	1.1×10^{-8}	7.5×10^{-11}	0.14
MOSC1	rs2642442	rs2807834	LDL	93,999	5.6×10^{-11}	47,355	5.3×10^{-6}	46,632	9.6×10^{-7}	2.3×10^{-11}	0.83
MOSC1	rs2642442	rs2807834	TC	98,656	4.9×10^{-13}	47,764	1.9×10^{-6}	50,880	1.3×10^{-8}	1.4×10^{-13}	0.63
GALNT2	rs4846914	rs4846914	HDL	98,409	3.7×10^{-21}	47,772	2.0×10^{-10}	50,637	1.1×10^{-13}	1.6×10^{-22}	0.59
GALNT2	rs4846914	rs1321257	TG	98,409	2.1×10^{-14}	47,782	1.3×10^{-6}	50,637	3.5×10^{-10}	4.4×10^{-15}	0.25
IRF2BP2	rs514230	rs514230	LDL	93,999	9.4×10^{-12}	47,367	5.6×10^{-7}	46,632	1.4×10^{-6}	3.6×10^{-12}	0.88
IRF2BP2	rs514230	rs514230	TC	90,614	5.4×10^{-14}	47,776	1.6×10^{-6}	50,677	1.3×10^{-9}	1.3×10^{-14}	0.47
APOB	rs1042034	rs1042034	HDL	98,409	1.2×10^{-30}	47,772	6.8×10^{-15}	50,637	2.0×10^{-19}	1.2×10^{-32}	0.54
APOB	rs1367117	rs1367117	LDL	98,409	4.5×10^{-114}	47,367	2.8×10^{-62}	50,637	2.6×10^{-58}	1.2×10^{-118}	0.63
APOB	rs1367117	rs1367117	TC	98,409	4.1×10^{-96}	47,776	1.5×10^{-49}	50,637	5.6×10^{-53}	1.1×10^{-100}	0.90
APOB	rs1042034	rs1042034	TG	98,656	1.4×10^{-45}	47,782	3.5×10^{-26}	50,880	2.1×10^{-23}	7.9×10^{-48}	0.61
GCKR	rs1260326	rs1260326	TC	98,409	7.3×10^{-27}	47,776	6.6×10^{-24}	50,637	2.6×10^{-8}	4.4×10^{-28}	0.00056
GCKR	rs1260326	rs1260326	TG	98,409	5.7×10^{-133}	47,782	1.6×10^{-77}	50,637	2.1×10^{-64}	1.3×10^{-139}	0.18
ABCG5/8	rs4299376	rs4299376	LDL	93,131	1.7×10^{-47}	47,367	8.1×10^{-26}	46,632	3.0×10^{-25}	2.3×10^{-49}	0.85
ABCG5/8	rs4299376	rs4299376	TC	97,764	4.0×10^{-45}	47,776	1.0×10^{-23}	50,880	3.4×10^{-25}	3.2×10^{-47}	0.84
RAB3GAP1	rs7570971	rs6759321	TC	98,409	1.4×10^{-8}	47,026	1.0×10^{-3}	50,637	8.2×10^{-7}	6.2×10^{-9}	0.26
COBLL1	rs12328675	rs12328675	HDL	93,983	2.7×10^{-10}	47,772	3.8×10^{-8}	46,632	1.7×10^{-4}	7.0×10^{-11}	0.17
COBLL1	rs10195252	rs10195252	TG	98,640	1.6×10^{-10}	47,782	1.9×10^{-8}	50,880	2.6×10^{-4}	5.8×10^{-11}	0.15
IRS1	rs2972146	rs1515100	HDL	95,054	2.0×10^{-9}	47,747	4.4×10^{-4}	47,288	1.6×10^{-7}	5.5×10^{-10}	0.24
IRS1	rs2972146	rs2943645	TG	87,520	2.4×10^{-8}	47,782	4.2×10^{-6}	47,608	5.1×10^{-4}	1.1×10^{-8}	0.46
RAF1	rs2290159	rs2290159	TC	83,209	4.2×10^{-9}	47,026	5.3×10^{-6}	43,613	7.1×10^{-5}	1.8×10^{-9}	0.57
MSL2L1	rs645040	rs645040	TG	87,766	2.5×10^{-8}	47,781	4.4×10^{-5}	47,852	6.5×10^{-5}	1.1×10^{-8}	0.92
KLHL8	rs442177	rs442177	TG	65,871	8.7×10^{-12}	47,782	2.9×10^{-5}	33,806	1.1×10^{-8}	2.5×10^{-12}	0.30
SLC39A8	rs13107325	rs13107325	HDL	97,148	7.2×10^{-11}	39,931	3.6×10^{-9}	49,372	1.6×10^{-4}	1.7×10^{-11}	0.051

ARL15	rs6450176	rs6450176	HDL	86,430	5.0×10^{-8}	47,772	2.2×10^{-7}	38,658	4.7×10^{-3}	1.8×10^{-8}	0.074
MAP3K1	rs9686661	rs9686661	TG	98,656	1.3×10^{-10}	47,032	9.4×10^{-7}	50,880	1.0×10^{-5}	4.5×10^{-11}	0.68
HMGCR	rs12916	rs12916	LDL	93,999	5.1×10^{-45}	47,367	2.2×10^{-22}	46,632	3.9×10^{-26}	8.8×10^{-47}	0.59
HMGCR	rs12916	rs12916	TC	98,656	8.8×10^{-47}	47,776	8.4×10^{-20}	50,880	2.6×10^{-31}	5.8×10^{-49}	0.15
TIMD4	rs6882076	rs6882076	LDL	93,999	1.9×10^{-22}	47,367	5.8×10^{-17}	46,632	1.2×10^{-8}	2.6×10^{-23}	0.055
TIMD4	rs6882076	rs6882076	TC	98,588	7.5×10^{-28}	47,776	1.1×10^{-18}	50,814	1.6×10^{-12}	4.0×10^{-29}	0.13
TIMD4	rs6882076	rs1553318	TG	71,749	3.7×10^{-12}	47,782	3.5×10^{-5}	37,253	2.9×10^{-9}	1.0×10^{-12}	0.22
MYLIP	rs3757354	rs3757354	LDL	70,383	1.2×10^{-11}	47,367	5.4×10^{-10}	35,885	4.1×10^{-4}	4.4×10^{-12}	0.079
MYLIP	rs3757354	rs3757354	TC	98,409	2.8×10^{-9}	47,776	2.9×10^{-7}	50,637	5.0×10^{-4}	1.2×10^{-9}	0.24
HFE	rs1800562	rs1800562	LDL	95,070	6.1×10^{-10}	47,365	1.3×10^{-4}	47,288	3.2×10^{-7}	2.7×10^{-10}	0.35
HFE	rs1800562	rs1800562	TC	96,905	2.5×10^{-8}	47,774	3.6×10^{-4}	49,133	7.0×10^{-6}	1.1×10^{-8}	0.57
HLA	rs3177928	rs3177928	LDL	95,067	2.4×10^{-15}	47,338	3.1×10^{-11}	47,285	1.7×10^{-6}	6.5×10^{-16}	0.18
HLA	rs3177928	rs3177928	TC	86,707	4.0×10^{-19}	47,743	1.8×10^{-12}	38,925	3.1×10^{-9}	5.6×10^{-20}	0.31
HLA	rs2247056	rs2247056	TG	95,070	1.6×10^{-15}	47,782	3.3×10^{-10}	47,288	1.3×10^{-7}	3.1×10^{-16}	0.45
C6orf106	rs2814944	rs2814944	HDL	98,409	3.8×10^{-9}	47,764	5.2×10^{-4}	50,637	3.1×10^{-7}	1.1×10^{-9}	0.30
C6orf106	rs2814982	rs2814982	TC	98,656	4.7×10^{-11}	47,776	5.3×10^{-7}	50,880	6.0×10^{-6}	1.6×10^{-11}	0.62
FRK	rs9488822	rs11153594	LDL	95,070	3.0×10^{-9}	47,363	4.2×10^{-4}	47,288	4.9×10^{-7}	1.4×10^{-9}	0.30
FRK	rs9488822	rs9488822	TC	98,409	1.7×10^{-10}	47,776	1.7×10^{-5}	50,637	8.2×10^{-7}	6.2×10^{-11}	0.77
CITED2	rs605066	rs605066	HDL	95,034	2.6×10^{-8}	47,772	3.6×10^{-5}	47,264	6.0×10^{-5}	8.6×10^{-9}	0.83
LPA	rs1084651	rs1084651	HDL	94,225	3.0×10^{-8}	47,772	3.1×10^{-6}	46,453	5.3×10^{-4}	1.0×10^{-8}	0.33
LPA	rs1564348	rs1564348	LDL	89,838	1.7×10^{-17}	47,352	3.5×10^{-11}	42,471	$1.5 \times 10^{-}8$	3.8×10^{-18}	0.48
LPA	rs1564348	rs1564348	TC	94,472	9.7×10^{-17}	47,760	3.5×10^{-9}	46,696	9.3×10^{-10}	1.8×10^{-17}	0.96
DNAH11	rs12670798	rs12670798	LDL	95,070	6.9×10^{-10}	47,367	5.0×10^{-4}	47,288	6.2×10^{-8}	3.1×10^{-10}	0.18
DNAH11	rs12670798	rs2285942	TC	98,409	6.6×10^{-10}	47,776	5.2×10^{-3}	50,637	1.3×10^{-9}	2.5×10^{-10}	0.03
NPC1L1	rs2072183	rs217386	LDL	93,999	4.3×10^{-11}	47,367	9.9×10^{-6}	46,632	3.5×10^{-7}	1.7×10^{-11}	0.65
NPC1L1	rs2072183	rs2072183	TC	98,656	3.2×10^{-11}	47,776	1.2×10^{-5}	50,880	1.8×10^{-7}	1.1×10^{-11}	0.59
TYW1B	rs13238203	rs13238203	TG	98,409	1.1×10^{-9}	47,782	2.2×10^{-7}	50,637	4.5×10^{-4}	4.5×10^{-10}	0.60
MLXIPL	rs17145738	rs17145738	HDL	98,409	1.2×10^{-9}	47,772	1.5×10^{-4}	50,637	3.8×10^{-7}	3.2×10^{-10}	0.44
MLXIPL	rs17145738	rs7811265	TG	93,999	9.1×10^{-59}	47,782	6.6×10^{-36}	46,632	8.3×10^{-28}	1.2×10^{-61}	0.23
KLF14	rs4731702	rs4731702	HDL	90,614	1.2×10^{-15}	47,772	1.2×10^{-10}	50,677	1.3×10^{-7}	1.4×10^{-16}	0.32
PPP1R3B	rs9987289	rs9987289	HDL	98,409	6.4×10^{-25}	47,772	4.5×10^{-16}	50,637	3.2×10^{-12}	1.7×10^{-26}	0.29
PPP1R3B	rs9987289	rs2126259	LDL	98,409	7.4×10^{-15}	47,367	8.0×10^{-7}	50,637	3.4×10^{-10}	2.1×10^{-15}	0.36
PPP1R3B	rs9987289	rs2126259	TC	98,409	9.0×10^{-24}	47,776	6.4×10^{-10}	50,637	8.1×10^{-17}	7.6×10^{-25}	0.20
PINX1	rs11776767	rs11776767	TG	98,656	1.3×10^{-8}	47,782	5.0×10^{-5}	50,880	2.8×10^{-5}	5.5×10^{-9}	0.95
NAT2	rs1495741	rs1961456	TC	98,409	1.7×10^{-9}	47,776	1.0×10^{-4}	50,637	1.4×10^{-6}	6.8×10^{-10}	0.60
NAT2	rs1495741	rs1495743	TG	98,409	4.1×10^{-14}	47,778	5.9×10^{-8}	50,637	3.1×10^{-8}	9.3×10^{-15}	0.97
LPL	rs12678919	rs12678919	HDL	93,131	9.7×10^{-98}	47,772	2.4×10^{-49}	46,632	7.4×10^{-57}	2.5×10^{-104}	0.75
LPL	rs12678919	rs12678919	TG	97,764	1.5×10^{-115}	47,782	3.1×10^{-59}	50,880	4.5×10^{-64}	2.2×10^{-121}	0.73
CYP7A1	rs2081687	rs1030431	LDL	98,409	3.9×10^{-9}	47,367	4.0×10^{-5}	50,637	1.1×10^{-5}	1.9×10^{-9}	0.86

CYP7A1	rs2081687	rs1030431	TC	93,983	8.8×10^{-13}	47,776	2.3×10^{-8}	46,632	1.7×10^{-6}	2.5×10^{-13}	0.46
TRPS1	rs2293889	rs2293889	HDL	98,640	5.8×10^{-11}	47,772	2.5 x 10-7	50,880	9.5×10^{-6}	1.3×10^{-11}	0.51
TRPS1	rs2737229	rs2737229	TC	95,054	2.5×10^{-8}	47,776	5.6×10^{-4}	47,288	4.2×10^{-6}	1.1×10^{-8}	0.49
TRIB1	rs2954029	rs10808546	HDL	87,520	6.4×10^{-19}	47,772	1.9×10^{-10}	47,608	3.6×10^{-11}	4.1×10^{-20}	0.98
TRIB1	rs2954029	rs2954022	LDL	83,209	2.6×10^{-29}	47,367	3.0×10^{-13}	43,613	4.9×10^{-19}	1.9×10^{-30}	0.27
TRIB1	rs2954029	rs2954022	TC	87,766	5.0×10^{-36}	47,776	4.7×10^{-15}	47,852	1.1×10^{-24}	1.1×10^{-37}	0.16
TRIB1	rs2954029	rs2954029	TG	65,871	3.3×10^{-55}	47,782	8.5×10^{-23}	33,806	7.4×10^{-38}	5.3×10^{-58}	0.04
PLEC1	rs11136341	rs11136341	LDL	97,148	4.4×10^{-13}	40,289	5.2×10^{-6}	49,372	5.1×10^{-9}	1.5×10^{-13}	0.56
PLEC1	rs11136341	rs11136341	TC	86,430	9.0×10^{-10}	40,644	2.9×10^{-4}	38,658	2.4×10^{-7}	3.5×10^{-10}	0.49
TTC39B	rs581080	rs643531	HDL	98,656	1.3×10^{-13}	47,767	3.8×10^{-9}	50,880	7.3×10^{-7}	2.0×10^{-14}	0.41
TTC39B	rs581080	rs581080	TC	93,999	3.1×10^{-9}	47,776	7.9×10^{-9}	46,632	4.0×10^{-3}	1.3×10^{-9}	0.029
ABCA1	rs1883025	rs1883025	HDL	98,656	1.8×10^{-33}	47,051	4.9×10^{-17}	50,880	2.8×10^{-20}	1.1×10^{-35}	0.78
ABCA1	rs1883025	rs1883025	TC	93,999	3.4×10^{-27}	47,055	4.7×10^{-17}	46,632	3.3×10^{-13}	2.0×10^{-28}	0.28
ABO	rs9411489	rs649129	LDL	98,588	7.9×10^{-22}	47,367	1.4×10^{-15}	50,814	4.3×10^{-9}	1.2×10^{-22}	0.13
ABO	rs9411489	rs651007	TC	71,749	8.7×10^{-21}	47,765	6.3×10^{-15}	37,253	7.6×10^{-9}	1.0×10^{-21}	0.12
JMJD1C	rs10761731	rs10761731	TG	70,383	3.5×10^{-12}	47,782	6.1×10^{-11}	35,885	3.9×10^{-4}	1.0×10^{-12}	0.031
CYP26A1	rs2068888	rs2068888	TG	98,409	2.4×10^{-8}	47,782	2.4×10^{-3}	50,637	4.4×10^{-7}	1.0×10^{-8}	0.16
GPAM	rs2255141	rs1129555	LDL	95,070	2.1×10^{-9}	47,366	9.1×10^{-5}	47,288	2.3×10^{-6}	1.0×10^{-9}	0.58
GPAM	rs2255141	rs2255141	TC	96,905	2.0×10^{-10}	47,776	6.9×10^{-5}	49,133	2.0×10^{-7}	7.5×10^{-11}	0.48
AMPD3	rs2923084	rs2923084	HDL	95,067	4.6×10^{-8}	47,770	6.5×10^{-5}	47,285	6.4×10^{-5}	1.6×10^{-8}	0.90
SPTY2D1	rs10128711	rs10832963	TC	86,707	2.5×10^{-8}	47,776	1.7×10^{-2}	38,925	2.1×10^{-8}	1.2×10^{-8}	0.032
LRP4	rs3136441	rs3136441	HDL	95,070	3.5×10^{-18}	47,772	4.8×10^{-6}	47,288	6.4×10^{-16}	2.3×10^{-19}	0.022
FADS1–2–3	rs174546	rs174601	HDL	98,409	1.5×10^{-22}	47,772	7.0×10^{-15}	50,637	6.9×10^{-11}	5.8×10^{-24}	0.27
FADS1–2–3	rs174546	rs174583	LDL	98,656	1.2×10^{-21}	47,356	4.9×10^{-10}	50,880	3.9×10^{-14}	1.8×10^{-22}	0.36
FADS1–2–3	rs174546	rs174550	TC	95,070	2.1×10^{-22}	47,776	1.4×10^{-11}	47,288	2.2×10^{-13}	2.0×10^{-23}	0.86
FADS1–2–3	rs174546	rs174546	TG	98,409	5.4×10^{-24}	47,782	1.9×10^{-16}	50,637	1.4×10^{-10}	4.1×10^{-25}	0.18
APOA1–C3–A4–A5	rs964184	rs964184	HDL	95,034	5.2×10^{-47}	47,750	4.5×10^{-37}	47,264	4.3×10^{-17}	5.3×10^{-50}	0.00073
APOA1–C3–A4–A5	rs964184	rs964184	LDL	94,225	1.5×10^{-26}	47,345	1.7×10^{-14}	46,453	1.2×10^{-14}	1.4×10^{-27}	0.99
APOA1–C3–A4–A5	rs964184	rs964184	TC	89,838	6.2×10^{-57}	47,754	9.1×10^{-29}	42,471	1.4×10^{-32}	1.3×10^{-59}	0.87
APOA1–C3–A4–A5	rs964184	rs964184	TG	94,472	6.7×10^{-240}	47,760	3.8×10^{-158}	46,696	1.7×10^{-99}	7.6×10^{-252}	3.2×10^{-5}
UBASH3B	rs7941030	rs7115089	HDL	95,070	2.7×10^{-8}	47,772	1.7×10^{-2}	47,288	1.3×10^{-8}	8.4×10^{-9}	0.027
UBASH3B	rs7941030	rs7941030	TC	98,409	1.5×10^{-10}	47,776	1.1×10^{-5}	50,637	1.1×10^{-6}	5.5×10^{-11}	0.85
ST3GAL4	rs11220462	rs11220462	LDL	93,999	1.2×10^{-15}	47,367	5.9×10^{-8}	46,632	9.2×10^{-10}	3.2×10^{-16}	0.64
ST3GAL4	rs11220462	rs11220463	TC	98,656	2.1×10^{-11}	47,776	3.1×10^{-6}	50,880	5.0×10^{-7}	7.0×10^{-12}	0.92
PDE3A	rs7134375	rs7134375	HDL	98,409	3.8×10^{-8}	47,772	7.7×10^{-8}	50,637	6.7×10^{-3}	1.4×10^{-8}	0.045
LRP1	rs11613352	rs3741414	HDL	98,409	1.6×10^{-8}	47,772	9.9×10^{-7}	50,637	7.0×10^{-4}	5.5×10^{-9}	0.23
LRP1	rs11613352	rs11613352	TG	93,999	4.4×10^{-10}	47,782	2.8×10^{-9}	46,632	1.9×10^{-3}	1.7×10^{-10}	0.041
MVK	rs7134594	rs7134594	HDL	90,614	6.9×10^{-15}	47,772	1.8×10^{-7}	50,677	7.7×10^{-10}	8.2×10^{-16}	0.63
BRAP	rs11065987	rs11065987	LDL	98,409	1.5×10^{-9}	47,367	1.5×10^{-4}	50,637	8.7×10^{-7}	7.0×10^{-10}	0.44

BRAP	rs11065987	rs11065987	TC	98,409	6.8×10^{-12}	47,776	2.2×10^{-5}	50,637	1.5×10^{-8}	2.1×10^{-12}	0.40
HNF1A	rs1169288	rs1169288	LDL	98,409	1.1×10^{-15}	47,367	2.9×10^{-10}	50,637	1.5×10^{-7}	3.0×10^{-16}	0.44
HNF1A	rs1169288	rs1169288	TC	98,656	1.5×10^{-14}	47,776	5.7×10^{-9}	50,880	1.0×10^{-7}	3.5×10^{-15}	0.59
SBNO1	rs4759375	rs4759375	HDL	98,409	7.5×10^{-9}	47,772	1.1×10^{-7}	50,637	1.5×10^{-3}	2.4×10^{-9}	0.10
ZNF664	rs4765127	rs4765127	HDL	98,409	2.9×10^{-10}	47,754	2.4×10^{-7}	50,637	4.7×10^{-5}	7.4×10^{-11}	0.36
ZNF664	rs4765127	rs12310367	TG	93,131	1.2×10^{-8}	47,782	2.0×10^{-7}	46,632	2.2×10^{-3}	5.4×10^{-9}	0.12
SCARB1	rs838880	rs838880	HDL	97,764	2.6×10^{-14}	41,639	5.2×10^{-7}	50,880	8.2×10^{-10}	3.4×10^{-15}	0.35
NYNRIN	rs8017377	rs2332328	LDL	98,409	4.4×10^{-11}	47,367	1.2×10^{-6}	50,637	3.3×10^{-6}	1.8×10^{-11}	0.87
CAPN3	rs2412710	rs2412710	TG	93,983	1.9×10^{-8}	47,782	6.9×10^{-5}	46,632	2.7×10^{-5}	8.1×10^{-9}	0.65
FRMD5	rs2929282	rs2929282	TG	98,640	1.6×10^{-11}	47,782	5.4×10^{-9}	50,880	8.8×10^{-5}	5.2×10^{-12}	0.18
LIPC	rs1532085	rs1532085	HDL	95,054	2.9×10^{-96}	47,772	2.3×10^{-37}	47,288	1.9×10^{-69}	7.3×10^{-103}	0.0019
LIPC	rs1532085	rs1532085	TC	87,520	8.8×10^{-20}	47,776	1.3×10^{-9}	47,608	1.3×10^{-12}	1.2×10^{-20}	0.56
LIPC	rs1532085	rs261342	TG	83,209	2.4×10^{-13}	47,782	1.1×10^{-6}	43,613	8.7×10^{-9}	5.9×10^{-14}	0.52
LACTB	rs2652834	rs2652834	HDL	87,766	8.8×10^{-9}	47,772	2.9×10^{-5}	47,852	2.3×10^{-5}	2.7×10^{-9}	0.96
CTF1	rs11649653	rs11649653	TG	65,871	3.4×10^{-8}	47,770	1.0×10^{-5}	33,806	3.3×10^{-4}	1.5×10^{-8}	0.58
CETP	rs3764261	rs3764261	HDL	97,148	7.10×10^{-380}	47,772	2.7×10^{-191}	49,372	3.5×10^{-217}	1.03×10^{-405}	0.092
CETP	rs3764261	rs247616	LDL	86,430	9.3×10^{-13}	47,367	6.7×10^{-7}	38,658	8.9×10^{-8}	3.2×10^{-13}	0.64
CETP	rs3764261	rs3764261	TC	98,656	6.7×10^{-14}	47,776	7.7×10^{-9}	50,880	3.9×10^{-7}	1.7×10^{-14}	0.65
CETP	rs3764261	rs7205804	TG	93,999	1.2×10^{-12}	47,782	5.5×10^{-9}	46,632	7.8×10^{-6}	3.2×10^{-13}	0.35
LCAT	rs16942887	rs16942887	HDL	98,656	8.4×10^{-33}	47,772	3.4×10^{-13}	50,880	3.9×10^{-24}	5.5×10^{-35}	0.065
HPR	rs2000999	rs2000999	LDL	93,999	1.8×10^{-22}	47,367	6.6×10^{-11}	46,632	4.4×10^{-14}	2.5×10^{-23}	0.45
HPR	rs2000999	rs2000999	TC	98,588	3.2×10^{-24}	47,776	4.9×10^{-12}	50,814	7.2×10^{-15}	2.6×10^{-25}	0.65
CMIP	rs2925979	rs2925979	HDL	71,749	2.1×10^{-11}	47,772	2.4×10^{-6}	37,253	3.9×10^{-7}	4.3×10^{-12}	0.88
STARD3	rs11869286	rs881844	HDL	70,383	2.8×10^{-14}	47,772	1.9×10^{-6}	35,885	2.3×10^{-10}	3.7×10^{-15}	0.32
OSBPL7	rs7206971	rs7225700	LDL	98,409	3.9×10^{-9}	47,367	2.0×10^{-6}	50,637	1.9×10^{-4}	1.9×10^{-9}	0.49
OSBPL7	rs7206971	rs7206971	TC	95,070	1.1×10^{-8}	39,937	1.6×10^{-3}	47,288	4.8×10^{-7}	4.6×10^{-9}	0.33
ABCA8	rs4148008	rs4148008	HDL	96,905	1.8×10^{-10}	47,772	3.5×10^{-8}	49,133	1.3×10^{-4}	4.5×10^{-11}	0.20
PGS1	rs4129767	rs4082919	HDL	95,067	5.0×10^{-9}	47,772	7.9×10^{-8}	47,285	1.4×10^{-3}	1.6×10^{-9}	0.10
LIPG	rs7241918	rs7241918	HDL	86,707	2.7×10^{-49}	47,772	8.6×10^{-25}	38,925	1.6×10^{-29}	1.5×10^{-52}	0.63
LIPG	rs7241918	rs7239867	TC	95,070	2.0×10^{-19}	47,776	1.3×10^{-9}	47,288	3.1×10^{-12}	2.8×10^{-20}	0.62
MC4R	rs12967135	rs12967135	HDL	98,409	6.6×10^{-9}	47,772	1.3×10^{-5}	50,637	3.8×10^{-5}	2.0×10^{-9}	0.80
ANGPTL4	rs7255436	rs7255436	HDL	98,656	3.3×10^{-8}	47,772	6.7×10^{-5}	50,880	4.3×10^{-5}	1.1×10^{-8}	0.99
LDLR	rs6511720	rs6511720	LDL	95,070	4.3×10^{-117}	46,499	1.6×10^{-56}	47,288	2.1×10^{-67}	8.6×10^{-122}	0.29
LDLR	rs6511720	rs6511720	TC	98,409	6.7×10^{-97}	46,884	2.4×10^{-42}	50,637	1.4×10^{-61}	1.7×10^{-101}	0.10
LOC55908	rs737337	rs737337	HDL	95,034	3.1×10^{-9}	47,772	1.3×10^{-5}	47,264	1.7×10^{-5}	9.1×10^{-10}	0.89
CILP2	rs10401969	rs10401969	LDL	94,225	6.7×10^{-22}	47,351	2.0×10^{-9}	46,453	3.1×10^{-15}	1.0×10^{-22}	0.17
CILP2	rs10401969	rs10401969	TC	89,838	2.9×10^{-38}	47,760	3.2×10^{-13}	42,471	5.2×10^{-30}	4.9×10^{-40}	0.0072
CILP2	rs10401969	rs10401969	TG	94,472	1.6×10^{-29}	47,766	9.8×10^{-16}	46,696	8.0×10^{-17}	6.0×10^{-31}	0.81
APOE–C1–C2	rs4420638	rs4420638	HDL	95,070	4.4×10^{-21}	39,912	2.2×10^{-18}	47,288	2.2×10^{-7}	2.3×10^{-22}	0.0031

APOE–C1–C2	rs4420638	rs4420638	LDL	98,409	8.7×10^{-147}	39,596	1.1×10^{-74}	50,637	5.7×10^{-80}	1.1×10^{-152}	0.86
APOE–C1–C2	rs4420638	rs4420638	TC	93,999	5.2×10^{-111}	39,914	1.1×10^{-47}	46,632	7.8×10^{-71}	2.7×10^{-116}	0.20
APOE–C1–C2	rs439401	rs439401	TG	98,656	1.1×10^{-30}	32,065	1.8×10^{-21}	50,880	5.9×10^{-13}	4.0×10^{-32}	0.073
FLJ36070	rs492602	rs492602	TC	98,409	2.0×10^{-10}	47,776	3.0×10^{-4}	50,637	2.4×10^{-8}	7.4×10^{-11}	0.18
LILRA3	rs386000	rs386000	HDL	98,409	4.3×10^{-16}	47,772	1.5×10^{-6}	50,637	5.0×10^{-13}	4.1×10^{-17}	0.031
ERGIC3	rs2277862	rs2277862	TC	93,999	3.8×10^{-10}	47,776	1.5×10^{-3}	46,632	5.1×10^{-9}	1.4×10^{-10}	0.074
MAFB	rs2902940	rs2902941	LDL	90,614	1.1×10^{-8}	47,367	5.7×10^{-5}	50,677	2.5×10^{-5}	5.6×10^{-9}	0.87
MAFB	rs2902940	rs2902940	TC	98,409	6.1×10^{-11}	47,776	1.9×10^{-6}	50,637	2.4×10^{-6}	2.1×10^{-11}	0.89
TOP1	rs6029526	rs909802	LDL	98,409	3.2×10^{-19}	47,367	3.4×10^{-14}	50,637	9.2×10^{-8}	6.0×10^{-20}	0.12
TOP1	rs6029526	rs4297946	TC	98,409	2.8×10^{-17}	47,774	7.1×10^{-14}	50,637	1.6×10^{-6}	4.8×10^{-18}	0.042
HNF4A	rs1800961	rs1800961	HDL	98,656	1.1×10^{-15}	34,496	1.2×10^{-6}	50,880	8.2×10^{-12}	1.1×10^{-16}	0.22
HNF4A	rs1800961	rs1800961	TC	98,409	5.7×10^{-13}	34,498	2.6×10^{-8}	50,637	1.1×10^{-6}	1.6×10^{-13}	0.57
PLTP	rs6065906	rs6065906	HDL	98,409	1.9×10^{-22}	47,772	5.4×10^{-14}	50,637	1.6×10^{-11}	7.4×10^{-24}	0.48
PLTP	rs6065906	rs4810479	TG	93,131	4.7×10^{-18}	47,782	7.7×10^{-10}	46,632	1.5×10^{-10}	6.7×10^{-19}	0.84
UBE2L3	rs181362	rs181362	HDL	97,764	1.1×10^{-8}	47,772	4.0×10^{-4}	50,880	1.5×10^{-6}	3.5×10^{-9}	0.39
PLA2G6	rs5756931	rs5756931	TG	98,409	3.8×10^{-8}	47,782	1.3×10^{-4}	50,637	3.4×10^{-5}	1.7×10^{-8}	0.81

* Sample sizes and *P*-values for "All Studies" correspond to the primary meta-analysis and are identical to those shown in Supplementary Table 2.

† Meta-analysis of studies that used Principal Component Analysis (PCA) to account for population structure, as per Supplementary Table 3.

‡ Meta-analysis of studies that did not use PCA to account for population structure, as per Supplementary Table 3.

§ Meta-analysis of "Studies with PCA" and "Studies without PCA" *P*-values. Pearson's correlation between "All Studies" *P*-values and "Combined" *P*-values = 0.98.

|| Heterogeneity *P*-values comparing *Z*-statistics for "Studies with PCA" and "Studies without PCA" calculated using METAL.

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