

SUPPLEMENTAL MATERIAL

A genome-wide association study identifies *LIPA* as a susceptibility gene for coronary artery disease

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Part A. Supplementary Methods

a. Description of the CADomics and the GHSExpress study samples

CADomics (Coronary Artery Disease and Genomics) is a German case-control study for CAD. It is a pooled study from the hospital (catheter-lab)-based AtheroGene Registry and the population-based Gutenberg-Heart Study (GHS).

Atherogene Registry. Between June 1999 and February 2004, patients with documented CAD referred to the Department of Medicine II of the Johannes Gutenberg-University in Mainz, Germany and the Department of Medicine of the German Federal Armed Forces Central Hospital, Koblenz, were enrolled in the *AtheroGene registry*. Coronary angiography was performed in all patients. The study design has been described elsewhere.¹

The Gutenberg Heart Study (GHS) is designed as a population-based, prospective, observational single-center cohort study in the Rhein-Main-Region in western Mid-Germany to evaluate and improve cardiovascular risk stratification. The sample was drawn randomly from the governmental local registry offices in the city of Mainz and the district of Mainz-Bingen. The sample was stratified 1:1 for gender and for urban and rural residence with equal strata for decades of age. Individuals between 35 and 74 years of age were enrolled, and written informed consent was obtained from all participants. Exclusion criteria were insufficient knowledge of the German language, and physical or psychological inability to participate in the examinations at the study center. The study protocol and the sampling design were approved by the local ethics committee, and by the local and federal data safety commissioners.

Gutenberg Heart Express Study (GHSExpress). The GHSExpress study is a cohort study of a subsample of the Gutenberg Heart Study. The first 9 participants on each examination day of the baseline examination were included in the GHSExpress study. Monocytes were isolated from fresh blood samples and RNA was extracted within the same day. Data sets used in the present studies were from unrelated adults of European descent only.

b. Description of in-silico replication cohorts

In silico replication cohorts consisted of cases with CAD/MI and matched controls from 7 studies. All participants were European ancestry. The 7 cohorts were: Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium (CHARGE), German MI Family Study (GerMIFS) I and II, MedStar, PennCATH, Myocardial Infarction and Genetics Consortium (MIGen) and the Wellcome Trust Case Control Consortium CAD Study (WTCCC-CAD).

CHARGE. The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium was formed to facilitate genome-wide association studies meta-analyses and replication opportunities among multiple large population-based cohorts studies. It consists of the following five population-based cohorts: Age, Gene/Environment susceptibility (AGES)-Reykjavik Study, Atherosclerosis Risk in Communities (ARIC) Study, Cardiovascular Health Study (CHS), Framingham Heart Study (FHS) and Rotterdam study (RS). In short, the AGES – Reykjavik Study represents a sample from a population-based Reykjavik Study, originally comprising 31,795 individuals. Between 2002 and 2006, 5,764 survivors of the original cohorts were re-examined. The ARIC study is a population-based prospective cohort study including 15,792 individuals aged 45-64 years at baseline from 4 US communities. CHS is a population-based cohort study in adults over 65 years of age conducted at 4 field centers. The FHS started in 1948 with the recruitment of an original cohort of 5,209 men and women aged 28-62 years of age. In 1971, children and spouses of children of the original cohort were enrolled. The third generation cohort enrollment started in 2002 and comprises 4,095 children of offspring cohort participants. The RS is a prospective population-based cohort study comprising 7,983 subjects aged 55 years or older (RS-I). In 2000-2001, an additional 3,011 individuals aged 55 years or older were recruited (RS-II). Further details of the CHARGE consortium can be found elsewhere.²

GerMIFS I. The German MI Family Study I (GerMIFS I) comprises unrelated German MI patients (age of onset < 65 years) having at least one first-degree relative with premature CAD. The subjects used in this analysis are distinct from those used in the initial genome-wide association study. Patients were recruited between 1997 and 2002 from hospital clinics and were studied by physical examination, blood testing, echocardiography, as well as a standardized interview. All events were validated through inspection of hospital charts. Healthy German married-in spouses from the same recruitment centre served as controls. Further details of the GerMIFS I study can be found elsewhere ³.

GerMIFS II. The recruitment for German MI Family Study II (GerMIFS II) was similar to that for GMIFS I. All 1,222 patients had a validated MI with a strong genetic component as documented by an early age of onset (prior to the age of 60 years). Moreover, a positive family history for CAD was documented in 726 (59.4 %) of patients. Patients were identified following their admission for acute treatment of MI or in cardiac rehabilitation clinics. Population-based controls were derived from the MONICA/KORA Augsburg survey S4 1 (n=820). Further details of the GerMIFS II study can be found elsewhere ⁴.

MedStar. The MedStar study, conducted by the Cardiovascular Research Institute of the MedStar Health Research Institute, is a Washington Hospital Center based angiographic study of 1,500 subjects specifically designed for biomarker and genetic association studies of acute and chronic coronary atherosclerosis. Briefly, the MedStar study is a cross sectional study of coronary atherosclerosis in a consecutive cohort of selected patients undergoing cardiac catheterization at Washington Hospital Center between August 2004 and March 2007. All subjects were enrolled in a MedStar Health Research Institute Institutional Review Board approved protocol and all subjects gave written informed consent. Enrollment criteria included

any clinical indication for cardiac catheterization and ability to give informed consent. A case-control GWAS similar to PennCATH was performed in MedStar (n=1,322 Caucasians) composed of controls (n=447) who on coronary angiography showed no evidence of CAD and CAD (AngCAD) cases (n=875) with one or more coronary vessels with $\geq 50\%$ stenosis divided into AngCADMI+ cases (n=421) and AngCADMI- cases (n=454). Controls were aged over 45 in men and women. Cases were selected to be young with age at diagnosis of CAD < 55 for males and < 60 for females. Further details of the MedStar study can be found elsewhere ^{5,6}.

PennCATH. PennCATH is a University of Pennsylvania Medical Center based coronary angiographic study. Briefly, PennCATH, recruited between July 1998 and March 2003, provides an ongoing focus for analyzing the association of biochemical and genetic factors with coronary atherosclerosis in a consecutive cohort of patients undergoing cardiac catheterization and coronary angiography. A total of 3,850 subjects provided written informed consent in a Penn Institutional Review Board approved protocol. Enrollment criteria included any clinical indication for cardiac catheterization and ability to give informed consent.

A nested case-control GWAS was performed in PennCATH (n=1,401 Caucasians) composed of controls (n=468) who on coronary angiography showed no or minimal ($< 10\%$ stenosis of any vessel) evidence of CAD and angiographic CAD (AngCAD) cases (n=933) with one or more coronary vessels with $\geq 50\%$ stenosis. AngCAD cases were equally selected for cases with MI (AngCADMI+ cases; n=469) and cases without history or presentation with MI (AngCADMI- cases; n=464). Controls were aged over 40 in men and 45 in women. Cases were selected to be young < 60 for males and < 65 for females. Further details of the PennCATH study can be found elsewhere ^{5,6}.

The MIGen consortium. The Myocardial Infarction Genetics (MIGen) Consortium consists of 1,274 cases of early-onset MI (in men ≤ 50 years of age or women ≤ 60 years of age) and 1,407

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age- and sex- matched controls free of MI from five international sites: Boston and Seattle in the United States as well as Sweden, Finland. The five studies include Heart Attack Risk in Puget Sound (505 cases/ 559 controls), Registre Gironi del Cor (312/ 317), the Massachusetts General Hospital Premature Coronary Artery Disease Study (204/ 260), FINRISK (167/ 172), and Malmö Diet and Cancer (86/ 99). Each of the studies have been previously described 5-10. At each site, MI was diagnosed on the basis of autopsy evidence of fatal MI or a combination of chest pain, electrocardiographic evidence of MI, or elevation of one or more cardiac *biomarkers (creatinine kinase or cardiac troponin)*. Further details of the MIGen consortium can be found elsewhere ⁶.

WTCCC-CAD. For the Wellcome Trust Case Control Consortium for Coronary Artery Disease (WTCCC-CAD), cases were recruited from families of European descent with a strong familial basis of CAD, where cases (one per family) had a validated history of either MI or coronary revascularization (CABG or PCI) before the age of 66. Recruitment was carried out on a national basis in the UK. Controls were ascertained from two UK collections, namely the UKBS collection of Common Controls Panel 1 (UKBS-CC1 collection), and the 1985 Birth cohort. Further details of the WTCCC-CAD study can be found elsewhere.^{3, 7}

c. Description of wet lab replication cohorts

Wet lab replication studies consisted of cases with CAD/MI and matched controls from 6 studies. All participants were European ancestry. The 6 studies were: Etude Cas-Témoin sur l'Infarctus du Myocarde (ECTIM), Genetische Epidemiologie in der Kardiologie (GoKard) Study, popgen study , Monica Risk, Genetics, Archiving and Monograph (MORGAM) study, Angio-Lueb study and the Ludwigshafen Risk and Cardiovascular Health (LURIC) study.

AngioLueb. The Luebeck angiographic study includes 2,843 patients with angiographically proven CAD who underwent cardiac catheterization at the University Hospital Schleswig-

Holstein, Campus Lübeck between 2005 and 2007 (Lübeck angiographic registry of patients with structural heart disease). Patients were not selected for particular risk factors or phenotypes. Controls came from the KORA F3 populations based study. Further details of the AngioLueb can be found elsewhere ⁴.

ECTIM. The ECTIM (Etude Cas-Témoin sur l'Infarctus du Myocarde) Study is a case-control study of MI based on the MONICA (Multinational MONItoring of trends and determinants in Cardiovascular disease) project registers in the United-Kingdom, including Northern Ireland and France. 1,169 MI patients were recruited 3 to 9 months after the event and had to satisfy the WHO criteria for definite acute MI (category I). In each centre, controls (n=1,193) of similar age and sex were randomly selected in the areas covered by the MONICA registers. Further details of the ECTIM study can be found elsewhere ^{8,9}.

GoKard. The GoKard cohort included n=1,161 cases with angiographically proven CAD, who underwent coronary angiography because of chest pain or any other clinical reason requiring angiography at the cardiology department at the University of Regensburg. Controls (n=341) were free of CAD. The study was approved by the ethics committee of the University of Regensburg (Reg Nr. 06211).

LURIC. The LURIC (LUdwigshafen Risk and Cardiovascular Health) study included 2,279 consecutive white patients hospitalized for coronary angiography between June 1997 and May 2001. The 1,344 controls were from the GerBS (German Blood Service) control series that consists of healthy, unrelated blood donors. They were recruited from the Southwestern area of Germany which corresponds to the geographical origin of the LURIC patients. During May to July 2004 blood samples were taken by the Institute of Transfusion Medicine and Immunology

(Mannheim, Germany). According to the German guidelines for blood donation all blood donors were examined to rule out cardiovascular, malignant, and other diseases by a standard questionnaire, cardiac auscultation, blood pressure and pulse measurement. Blood donors with known disease were excluded from blood donation. Further details of the LURIC study can be found elsewhere ¹⁰.

MORGAM. MORGAM is a prospective follow-up of the respondents of representative population samples that were examined at baseline. The cohorts providing DNA samples for this study are Alpha-Tocopherol, Beta-Carotene Cancer Prevention (ATBC) Study, FINRISK, Prospective Epidemiological Study of Myocardial Infarction (PRIME), Northern Sweden MONICA Study and MONICA-KORA Augsburg. For its genetic component, MORGAM has a case-cohort design. Further details of the MORGAM study can be found elsewhere ¹¹. For the purposes of this study, cases are those who had a documented MI before the baseline examination. Controls were selected from the MORGAM case-cohort set in such a way that the sets of cases and controls from each cohort would be similar in size and comparable with respect to age and sex. A control was selected for each case in random from those who were at risk at the age of the case at baseline. The risk set, from which the controls were selected, constituted of those members of the random subcohort of the MORGAM case-cohort set who: (i) had not had documented or self-reported MI or stroke at baseline; and (ii) had not had definite or possible AMI, unstable angina or cardiac revascularization during follow-up before the age of the case; and (iii) were in the follow-up at the age of the case; and (iv) had not been selected as a control at an earlier stage. There is a slight overlap in the current study between the MORGAM wet lab replication cohort and MIGen in silico replication cohort 5 MI-cases and 1 control of FINRISK were included in both data sets.

popgen. The popgen sample comprised unrelated German CAD patients who were recruited in Schleswig-Holstein, the northernmost region in Germany, through the population-based popgen

biobank (www.popgen.de). In the recruitment area, all coronary angiograms of any of the five cardiac catheterization laboratories were screened. Study subjects were required to have coronary catheterization demonstrating significant CHD (at least a 70% stenosis in one major epicardial coronary vessel). 1,104 cases had a diagnosed disease onset <55 years, of whom a subset of 596 individuals had suffered a myocardial infarction. The majority had a history of severe CHD and had undergone a coronary revascularization procedure (percutaneous coronary intervention or coronary artery bypass grafting). Written informed consent was obtained from all participants and the recruitment and the experimental protocols were approved by the institutional ethics review board and data protection authorities.

The controls for the GWAS were recruited from the popgen biobank (popgen controls) and the Max Rubner-Institut, Bundesforschungsinstitut für Ernährung und Lebensmittel, Germany (MRI controls). In brief, they were randomly identified on the basis of the population registry of Schleswig-Holstein (n = 736) and by the Blood Service of the University Hospital Schleswig-Holstein (n = 621). All controls underwent a physical examination and a clinical checkup. Information on physical risk factors was obtained from a questionnaire. MRI controls were selected by age from the general population via the registration register of the region surrounding and encompassing the city of Kiel, Germany. Inclusion criteria were age 45-65 years and absence of self-reported diabetes. Exclusion criteria were intake of hormones or lipid-lowering medication, surgery of the intestinal tract in the last 3 months or other alterations of the gastrointestinal tract, malassimilation, active cancer, chronic renal or liver disease, anemia and alcohol abuse. All subjects gave written informed consent before participating. The study was approved by the Medical Ethical Committee of the University Clinic Kiel. Further details of the popgen study can be found elsewhere ¹².

d. Informed Consent

Participants from all studies gave written informed consent in accordance with the guidelines of the local ethics committees.

e. Definition of cardiovascular risk factors and assessment of phenotypes of subclinical atherosclerosis

For investigation of the association of eQTLs with prevalent classical cardiovascular risk factors and clinical variables, we used data from a computer-assisted personal interview, blood pressure, and anthropometric measurements and laboratory examinations from a venous blood sample. Cardiovascular risk factors were defined as follows: Hypertension was diagnosed, if antihypertensive drugs were taken, or a mean systolic blood pressure of ≥ 140 mmHg or a mean diastolic blood pressure of ≥ 90 mmHg was present in the 2nd and 3rd standardized measurement after 8 and 11 minutes of rest. Smoking was dichotomized into non-smokers (never and former smokers) and smokers. Obesity was defined as a body-mass index ≥ 30 m²/kg. Diabetes mellitus was defined in individuals with a blood glucose level of ≥ 126 mg/dl in the baseline examination after an overnight fast of at least 8 hours or a blood glucose level of ≥ 200 mg/dl in the baseline examination after a fasting period < 8 hours or definite diagnosis of diabetes by a physician. Dyslipidemia was defined as a LDL/HDL-ratio of > 3.5 or a definite diagnosis of dyslipidemia by a physician. A positive family history was defined as history of myocardial infarction in a female first-degree relative ≤ 65 years or a male first-degree relative ≤ 60 years.

The systemic atherosclerotic burden was evaluated by examination for present carotid macroangiopathy and measurement of endothelium-dependent, flow-mediated dilation. Carotid macroangiopathy was assessed in the common carotid artery, the internal and the external carotid artery by ultrasound with an ie33 ultrasound system (Philips, NL) using an 11 to 3 MHz linear array transducer. Plaques were defined as thickening of the IMT of at least 1.5 mm. The number of plaques from both sides was recorded. Subjects were classified as having macroangiopathy when at least one plaque was measured on either side.

Endothelium-dependent, flow-mediated dilation of the right brachial artery (FMD) was examined by two-dimensional ultrasound with a 7.5–12MHz linear array transducer and an HD11 XE ultrasound system (Philips, NL) as described previously.¹³ A 3.5" wide blood pressure cuff was inflated at the upper arm to 50mmHg above systolic blood pressure or at least 200mmHg for 5 min in order to induce a reactive hyperaemia after arterial occlusion. During occlusion, the transducer was carefully maintained in the identical position. Two-dimensional images and pulsed-Doppler flow velocity signals were obtained before and 60 s after arterial occlusion, approximately 5cm above the antecubital crease.

Image acquisition and analysis were performed in a blinded manner to participants' clinical data. In general, all examinations were taken out according to standard operating procedures (SOPs) by certified medical technical assistants.

Levels of total cholesterol, high-density lipoprotein cholesterol, triglycerides and glycated haemoglobin (HbA_{1c}) were measured immediately after blood withdrawal by routine methods on an Architect c8000 System (Abbott Diagnostics, Wiesbaden, Germany). Low-density lipoprotein cholesterol was calculated by the Friedewald formula.

f. Genotyping Methods

CADomics: Discovery GWA

Genotyping was performed in individuals of European descent only and was conducted on the Affymetrix Genome-Wide Human SNP 6.0 Array between January 2008 and July 2008. Processing of DNA samples using the Affymetrix Genome-Wide Human SNP Nsp/Sty Assay 5.0 and hybridization was done in accordance with the manufactures' standard recommendations. Genotypes were determined using the Birdseed v2 calling algorithm. Only samples with a contrast QC \geq 0.4 were included in the final genotype calling. Quality control on sample level comprised exclusion of samples with a call rate \leq 97%, deviation from expected heterozygosity

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by more than three standard deviations and relatedness based on identity by state distance measures. On marker level we excluded polymorphisms with call rate $\leq 98\%$ in cases or controls, minor allele frequency ≤ 0.01 and deviation from Hardy-Weinberg equilibrium ($P \leq 0.0001$). Cluster plots were inspected for all markers with $P < 0.001$ in the GWA analysis. For statistical analysis an additive model without adjustments was used. The genomics control lambda was 1.06.

***In silico* Replication**

Studies were genotyped on the Affymetrix Mapping 500K Array Set, the Affymetrix Genome-Wide Human SNP 5.0 Array, or the Affymetrix Genome-Wide Human SNP 6.0 Array. Imputation of HapMap SNPs was performed using either IMPUTE or MACH. For detailed description refer to **Supplementary Table 3**.

Wet lab Replication

De novo genotyping was attempted for 20 SNPs in 6 studies (ECTIM, Angio-Lueb, popGen, GoKard, MORGAM, LURIC) by 5' Nuclease assay (TaqMan technology) or iPLEX Mass ARRAY technology.

In the ECTIM, popGen, GoKard genotyping of 19 SNPs was conducted using TaqMan probes (Applied Biosystems, Darmstadt, Germany). Genotyping was performed on 384-well plates (popgen and GoKard) or 96-well plates (ECTIM). The Genotyping Master Mix (Applied Biosystems, Darmstadt, Germany) was used in a 5- μ L (popGen and GoKard) or 7- μ L (ECTIM) total reaction volume including 10-20 ng DNA per reaction. After PCR, genotypes were automatically attributed by measuring the allele-specific fluorescence in the ABI 7900HT Real-Time PCR System (Applied Biosystems, Darmstadt, Germany), using the SDS 2.3 software for allele discrimination (auto caller confidence level, $\geq 95\%$). For technical reasons, no genotyping results were available in ECTIM, popGen and GoKard for SNP rs365302.

In LURIC all SNPs and in MORGAM 17 SNPs were genotyped using the iPLEX Mass ARRAY System and the iPLEX™ chemistry (Sequenom, San Diego, USA). One iPLEX multiplex reaction was designed by the Assay Design v.3.1.2. software. Primer extension products were loaded onto a 384-element chip using a nanoliter pipetting system (SpectroCHIP, SpectroPOINT Spotter Sequenom, San Diego, USA). The samples were analyzed in a MALDI TOF MS (matrix assisted laser desorption ionisation time of flight mass spectrometer, Bruker Daltonik GmbH, Leipzig, Germany). The resulting mass spectra were analyzed automatically for peak identification using the SpectroTYPER RT 3.4 software (Sequenom, San Diego, USA). For quality reasons 10% of the spectra were checked by two independent trained persons. In MORGAM, SNPs rs1348330, rs2782552 and rs17412370 were genotyped using the TaqMan technology as described above.

In AngioLueb, genotyping for 9 SNPs (rs1333049, rs7044859, rs7848524, rs4692845, rs1348330, rs16893523, rs13197670, rs2782552, and rs17412370) was performed with TaqMan technology as described above. Remaining 11 SNPs were genotyped using the iPLEX Mass ARRAY platform (Sequenom) as described above.

g. Gene Expression Methods

Isolation of total RNA from Monocytes

Isolation of total RNA and analysis of gene expression were performed as recently described.¹⁴. Separation of monocytes was conducted within 60 min after blood collection. Briefly, 8 mL blood was collected using the Vacutainer CPT Cell Preparation Tube System (BD, Heidelberg, Germany) and 400 µL Rosette Sep Monocyte Enrichment Cocktail (StemCell Technologies, Vancouver, Canada) was added immediately after blood collection. After separation, cells were washed twice in ice cold PBS buffer containing 2 mM EDTA. Success of monocyte separation was controlled using an ADVIA 2120 Analyzer (Siemens Healthcare Diagnostics, Eschborn,

Germany) for part of the samples. Total RNA from monocytes was isolated using Trizol extraction and purification by silica-based columns. Briefly, immediately after separation of monocytes, washed cells were resuspended in 1.5 mL Trizol Reagent (Invitrogen, Karlsruhe, Germany) and frozen at -20°C until isolation of RNA at the same day (maximal storage time 5 h). After thawing, samples were transferred into Phase Lock Gel Tubes (Eppendorf, Hamburg, Germany), 200 μ L chloroform was added and phases were separated by centrifugation at 4600 rpm for 15 min. Purification of total monocytes RNA was performed using the RNeasy Mini kit (Qiagen, Hilden, Germany) according to the manufacturer's Animal Cell Spin and RNA Cleanup protocol including an additional DNase digestion step. Total RNA was eluted in 20 μ L RNase-free water. Yield of RNA was checked spectrophotometrically by NanoDrop N-1000 measuring the OD260 as well as the ratio OD260 and OD280. The integrity of the total RNA was assessed through analysis on an Agilent Bioanalyzer 2100 (Agilent Technologies, Boeblingen, Germany).

Analysis of the monocyte transcriptome (Global Gene Expression Analysis)

For global gene expression analysis, only RNA with integrity (RIN) of ≥ 7 was used. Assessment of global gene expression was performed on 1,606 total RNA samples from monocytes using the Illumina HT-12 v3 BeadChip. RNA samples were processed in batches of 96 samples. Here, 200 ng of total RNA was reverse transcribed, amplified and biotinylated using the Illumina TotalPrep-96 RNA Amplification Kit (Ambion/Applied Biosystems, Darmstadt, Germany) according to the manufacturer's protocol. Steps of cDNA and cRNA purification were performed automatically using the MagMax Express96 magnetic particle processor (Applied Biosystems, Darmstadt, Germany). After amplification and purification cRNA was controlled on an Agilent Bioanalyzer 2100 (Agilent Technologies, Boeblingen, Germany). A Tecan InfiniTE M200 and a Tecan Freedom EVOlyzer (Tecan, Crailsheim, Germany) were used to determine concentration of cRNA and to perform dilution of each sample to 140 ng/ μ L automatically. 700 ng of each

biotinylated cRNA was hybridized to a single BeadChip at 58°C for 16-18 hours. After hybridization, BeadChips were washed and stained with 1 mg/mL Streptavidin-Cy3 conjugate (GE Healthcare/Amersham Bioscience; Germany), according to the manufacturer's Whole Genome Gene Expression with IntelliHyb Seal Protocol. BeadChips were scanned using the Illumina Bead Array Reader.

Raw data were pre-processed and quantile normalized using Beadstudio version 2.0. 1,494 arrays remained after removing technical replicates and arrays with hybridization problems. Transcripts were filtered based on detection p-values using negative controls present on the array. 21,305 transcripts with a detection $P < 0.1$ in at least 50% of the arrays were considered expressed. Furthermore, transcripts that could not be mapped uniquely to the RefSeq genome were removed. The resulting 14,027 transcripts were transformed using the arcsinh function to stabilize variances.

Semi-Quantitative RT-PCR

For "platform" validation of gene expression results, semi-quantitative real-time reverse transcriptase PCR (qRT-PCR) was performed on 119 monocytic total RNA samples of the GHSExpress Study that were not used for global gene expression analysis. For all subjects whose total RNA was used for qRT-PCR, GWA data were also available. Reverse transcription was performed in a total volume of 20 μ l including 20 ng total RNA with the High Capacity RNA-to-cDNA Master Mix (Applied Biosystems, Darmstadt, Germany) as recommended by the manufacturer. A sample without reverse transcriptase as negative control was included. Real-time PCR was performed in a total volume of 10 μ l on a 7900HT Real-Time PCR System (Applied Biosystems, Darmstadt, Germany) using TaqMan Gene Expression assays (Applied Biosystems, Darmstadt, Germany) as recommended by the manufacturer. Assays were selected according to the approximate location of Illumina probes within the gene sequence (LIPA:

SUPPLEMENTAL MATERIAL: A genome-wide association study identifies LIPA as a susceptibility gene for coronary artery disease

Hs01548819_m1, GAPDH: Hs99999905_m1) GAPDH was used as reference gene for normalization.

Part B – Supplementary Tables

Supplementary Table 1. Characteristics of the GHSExpress Study

	GHSExpress Total
No. of subjects	1,494
Study basis –	Population-based
Ethnicity	Caucasian
Country of origin	Germany
Age range, y	35 - 74
Age, y	55.2 ± 10.9
Female Gender, n (%)	732 (49.0)
Myocardial infarction n (%)	32 (2.1)
Cardiovascular risk factors	
Diabetes mellitus, n (%)	112 (7.5)
Dyslipidemia, n (%)	388 (26.0)
Family history of MI, n (%)	254 (17.0)
Hypertension , n (%)	740 (49.5)
Obesity, n (%)	331 (22.2)
Smoking	
Never, n (%)	670 (44.9)
Ex- smoker, n (%)	537 (36.0)
Smoker, n (%)	285 (19.1)
Body Mass Index, kg/m ²	26.9 ± 4.6
Total Cholesterol, mg/dl	225± 43
LDL-Cholesterol, mg/dl	142 ± 36
HDL-Cholesterol, mg/dl	57 ± 16
Trilycerides, mg/dl	129 ± 81
RR systolic, mmHg	132 ± 18
RR diastolic, mmHg	83 ± 10
HbA1c, %	5.49 ± 0.74
Phenotypes of subclinical atherosclerotic disease	
Flow-mediated vasodilation, %	8.40 ± 4.99
Carotid macroangiopathy (at least one plaque), n (%)	175 (11.7)

Supplementary Table 2A-M. Characteristics of the study samples for replication

A. GerMIFS I

	Cases	Controls
Number of subjects	875*	1,644*
Study characteristics		
Study basis – Ascertainment scheme	MI (<65 yrs) with > 1 first-degree sibling with severe CAD (PTCA; MI; CABG), controls: population sample	
Ethnicity	Caucasian	
Country of origin	Germany	
Age range (y) / Study criteria	24 – 64 (cases)	35-79 (controls)
Mean Age (y)	50.2 ± 7.9	62.5 ± 10.1
Gender (female, %)	32.5	50.8
Myocardial infarction (%)	100	0
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	12.3	11.0
Dyslipidemia (%)	76.1	78.0
Family history of MI (%)	100	100
Hypertension (%)	86.5	62.7
Obesity (%)	23.7	29.8
Smoking (%)	70.3**	49.3**
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	27.5 ± 3.7	28.1 ± 4.5
LDL-Cholesterol (mg/dL)	154.7 ± 42.5	na
HDL-Cholesterol (mg/dL)	50.3 ± 19.3	na
RR systolic (mmHg)	138.4 ± 20.0	na
RR diastolic (mmHg)	82.7 ± 10.3	na

* number of patients available varied for the different characteristics

**smoking ever

B. GerMIFS II

	Cases	Controls
Number of subjects	1,222*	1,298*
Study characteristics		
Study basis – Ascertainment scheme	cases: MI (<60 yrs); 59.4% with family history of CAD, cases: population sample	
Ethnicity	Caucasian	
Country of origin	Germany	
Age range (y) / Study criteria	25 – 59(cases) 19-70(controls)	
Mean Age (y)	51.3 ± 7.6	51.2 ± 11.9
Gender (female, %)	20.3	47.9
Myocardial infarction (%)	100	0
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	15.5	3.5
Dyslipidemia (%)	80.8	67.3
Family history of MI (%)	59.4	na
Hypertension (%)	88.1	41.7
Obesity (%)	22.6	na
Smoking (%)	64.7**	55.6**
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	27.9 ± 4.0	27.4 ± 4.6
LDL-Cholesterol (mg/dL)	143.1 ± 41.0	na
HDL-Cholesterol (mg/dL)	50.3 ± 15.46	na
RR systolic (mmHg)	135.0 ± 18.7	na
RR diastolic (mmHg)	83.0 ± 10.8	na

* number of patients available varied for the different characteristics

**smoking ever

C. Penn CATH

	Cases*	Controls*
Number of subjects	933	468
Study characteristics		
Study basis – Ascertainment scheme	hospital-based, cardiac catheterization lab	
Ethnicity	Caucasian	
Country of origin	U.S.	
Age range (y) / Study criteria	*	
Mean Age (y)	52.7 ± 7.6**	61.7 ± 9.6**
Gender (female, %)	23.7	51.9
Myocardial infarction (%)	50.3	0
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	24.4	11.2
Dyslipidemia (%)	80.2	62.3
Family history of MI (%)	48.7	29.2
Hypertension (%)	61.3	49.2
Obesity (%)	42.5	36.3
Smoking (%)	45.8	34.8
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	29.8 ± 5.6	28.9 ± 6.4
LDL-Cholesterol (mg/dL)	107.4 ± 36.2	108.2 ± 32.3
HDL-Cholesterol (mg/dL)	42.8 ± 11.9	48.5 ± 14.9
RR systolic (mmHg)	na	na
RR diastolic (mmHg)	na	na

*Cases: Age <66; Angiographic CAD >50% stenosis in at least 1 vessel

Controls: Age >45; Angiography normal or <10% stenosis in all vessels.

** Age at first CAD (cases) or recruitment (controls)

D. MedStar

	Cases*	Controls*
Number of subjects	875	447
Study characteristics		
Study basis – Ascertainment scheme	hospital-based, cardiac catheterization lab	
Ethnicity	Caucasian	
Country of origin	U.S.	
Age range (y) / Study criteria	*	
Mean Age (y)	48.9 ± 6.4**	59.7 ± 8.9**
Gender (female, %)	33.0	54.6
Myocardial infarction (%)	48.1	0
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	31.2	19.0
Dyslipidemia (%)	79.8	58.4
Family history of MI (%)	41.6	21.3
Hypertension (%)	76.3	60.6
Obesity (%)	52.3	50.0
Smoking (%)	53.1	49.9
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	31.7 ± 6.8	31.3 ± 7.9
LDL-Cholesterol (mg/dL)	101.2 ± 40.9	105.7 ± 32.8
HDL-Cholesterol (mg/dL)	42.7 ± 13.9	49.9 ± 15.7
RR systolic (mmHg)	na	na
RR diastolic (mmHg)	na	na

*Cases: Age <66; Angiographic CAD >50% stenosis in at least 1 vessel

Controls: Age >45; Angiography normal or <10% stenosis in all vessels.

** Age at first CAD (cases) or recruitment (controls)

E. MORGAM

	Cases	Controls
Number of subjects	512	512
Study characteristics		
Study basis – Ascertainment scheme		Population-based
Ethnicity		Caucasian
Country of origin		Finland, France, Sweden
Age range (y) / Study criteria		40 – 75
Mean Age (y)	63.3 ± 5.8*	63.3 ± 5.8*
Gender (female, %)	4.5	4.5
Myocardial infarction (%)	100	0
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	11.9	6.9
Dyslipidemia (%)	46.9	44.5
Family history of MI (%)	na	na
Hypertension (%)	66.5	64.1
Obesity (%)	26.4	19.3
Smoking (%)	45.1	59.2
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	28.0 ± 4.0	27.1 ± 4.3
LDL-Cholesterol (mg/dL)	139.2 ± 34.8	139.2 ± 38.7
HDL-Cholesterol (mg/dL)	42.5 ± 11.6	46.4 ± 11.6
RR systolic (mmHg)	140.8 ± 19.7 [#]	141.6 ± 19.9 [#]
RR diastolic (mmHg)	82.7 ± 10.1 [#]	85.1 ± 11.2 [#]

*Cases: age range and mean age refer to age at the baseline examination. The myocardial infarction took place before baseline examination.

Controls: age at baseline examination of the index case is used. This is the age which was used for matching the controls. Mean age of the controls at baseline examination, when the risk factors were measured, was 61.4 years.

[#]Mean of 1st and 2nd standardized measurements were used for blood pressure.

F. WTCCC-CAD

	Cases	Controls
Number of subjects	1,926	2,938
Study characteristics		
Study basis – Ascertainment scheme	CAD (<66 yrs) with ≥1 first-degree sibling validated for MI, PTCA, CABG or Angina, Controls: general population sample	
Ethnicity	Caucasian	
Country of origin	UK	
Age range (y) / Study criteria	26-66	11-70
Mean Age (y)	49.8 ± 7.7	na ^Ψ
Gender (female, %)	20.7	50.0
Myocardial infarction (%)	71.5	Na
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	11.6	na
Dyslipidemia (%)	80.0*	na
Family history of MI (%)	Na	na
Hypertension (%)	42.7†	na
Obesity (%)	23.3#	na
Smoking (%)	75.8§	na
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	27.6 ± 4.2	na
LDL-Cholesterol (mg/dL)	na	na
HDL-Cholesterol (mg/dL)	na	na
RR systolic (mmHg)	na	na
RR diastolic (mmHg)	na	na

^Ψ WTCCC-CAD controls comprised of an equal number of subjects from the 1958 Birth Cohort and from the National Blood Service (NBS) Donors. The latter were recruited in equal 10 years age bands from 11 to 70 yrs of age. Additional phenotypes are not available for these controls.

*Hyperlipidemia (total cholesterol ≥200 mg/dl or LDL cholesterol ≥130 mg/dl or receiving lipid lowering treatment).

†Hypertension (systolic blood pressure ≥140 or diastolic blood pressure ≥90 or receiving treatment for these conditions)

#Obesity (body mass index > 30 kg/m²)

§Smoking (ever)

G. MGen

	Cases	Controls
Number of subjects	1,274	1,407
Study characteristics		
Study basis – Ascertainment scheme	Hospital-based, community-based and population-based	
Ethnicity	European ancestry	
Country of origin	U.S., Spain, Finland, or Sweden	
Age range (y) / Study criteria	Cases were men with MI at ages ≤50 and women ≤60	
Mean Age (y)	42.4 ± 6.6	43.0 ± 7.8
Gender (female, %)	37.2	39.9
Myocardial infarction (%)	100	0
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	14.9*	3.0*
Dyslipidemia (%)	na*	na*
Family history of MI (%)	na*	na*
Hypertension (%)	50.5*	30.8*
Obesity (%)	na*	na*
Smoking (%)	73.9*	41.7*
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	27,6 ± 5.2*	25.8 ± 4.4*
LDL-Cholesterol (mg/dL)	na*	na*
HDL-Cholesterol (mg/dL)	na*	na*
RR systolic (mmHg)	na*	na*
RR diastolic (mmHg)	na*	na*

* The characteristics provided refer to the characteristics of the Heart Attack Risk in Puget Sound Study as part of the MGen consortium. Details on all cohorts included in the consortium are provided elsewhere.⁶

H. AngioLueb

	Cases	Controls
Number of subjects	2,843	1,563
Study characteristics		
Study basis – Ascertainment scheme	hospital-based, angiographic cases and population-based controls	
Ethnicity	Caucasian	
Country of origin	Germany	
Age range (y) / Study criteria	36 – 87	35 -84
Mean Age (y)	69 ± 12.5	52.2 ± 13.4
Gender (female, %)	21.0	52.1
Myocardial infarction (%)	65	0
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	23.2	5.3
Dyslipidemia (%)	62.1	67.8
Family history of MI (%)	28.3	24.1
Hypertension (%)	75.6	39.5
Obesity (%)	30.6	23.4
Smoking (%)	57.4	57.6
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	28.3 ± 4.9	27.1 ± 4.7
LDL-Cholesterol (mg/dL)	na	3.3 ± 0.8
HDL-Cholesterol (mg/dL)	na	1.5 ± 0.4
RR systolic (mmHg)	na	127.4 ± 19.6
RR diastolic (mmHg)	na	81.3 ± 10.7

I. CHARGE

	Cases	Controls
Number of subjects	2,287	22,024
Study characteristics	4 community-based cohorts CAD cases: definite or probable MI, PTCA or CABG, or ECG MI	
Ethnicity	Caucasian	
Country of origin	U.S. (ARIC, FHS), Iceland (AGES), Netherlands (RS)	
Age range (y) / Study criteria		
Mean Age (y)	60.0 ± 7.5	63.1 ± 7.6
Gender (female, %)	33.4	59.6
Myocardial infarction (%)	48.0	0
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	na	na
Dyslipidemia (%)	na	na
Family history of MI (%)	na	na
Hypertension (%)	na	na
Obesity (%)	na	na
Smoking (%)	na	na
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	28.1 ± 4.2	27.5 ± 7.0
LDL-Cholesterol (mg/dL)	na	na
HDL-Cholesterol (mg/dL)	na	na
RR systolic (mmHg)	na	na
RR diastolic (mmHg)	na	na

Details on all cohorts included in the consortium are provided elsewhere.²

AGES = Age, Gene/Environment Susceptibility Reykjavik Study; ARIC = Atherosclerosis Risk in Communities Study; FHS = Framingham Heart Study; RS = Rotterdam Study.

J. GoKard

	Cases	Controls
Number of subjects	1,111	391
Study characteristics		
Study basis – Ascertainment scheme		hospital-based
Ethnicity		Caucasian
Country of origin		Germany
Age range (y) / Study criteria		20 – 85
Mean Age (y)	66.8	59.6
Gender (female, %)	22.7	45.3
Myocardial infarction (%)	41.4	0
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	31.6	17.6
Dyslipidemia (%)	81.7	47.1
Family history of MI (%)	n. a.	n. a.
Hypertension (%)	88.9	69.8
Obesity (%)	29.5	32.1
Smoking (%)	14.7	12.0
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	28.1 ± 4.3	28.4 ± 5.6
LDL-Cholesterol (mg/dL)	na	na
HDL-Cholesterol (mg/dL)	na	na
RR systolic (mmHg)	na	na
RR diastolic (mmHg)	na	na

K. ECTIM

	Cases	Controls
Number of subjects	1,146	1,153
Study characteristics		
Study basis – Ascertainment scheme	MONICA registers and community	
Ethnicity	Caucasian	
Country of origin	France, Northern Ireland, Scotland (UK)	
Age range (y) / Study criteria	27 – 72	
Mean Age (y)	55.5 ± 8.3	55.8 ± 8.4
Gender (female, %)	22.4	21.9
Myocardial infarction (%)	100	0
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	11.2	4.7
Dyslipidemia (%)	24.8	4.7
Family history of MI (%)	38.5	28.0
Hypertension (%)	92.9	36.7
Obesity (%)	19.7	20.4
Smoking (%)	54.9	31.8
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	27.0 ± 4.2	26.8 ± 4.2
LDL-Cholesterol (mg/dL)	152.9 ± 39.5	150.1 ± 37.7
HDL-Cholesterol (mg/dL)	42.8 ± 11.3	50.9 ± 16.3
RR systolic (mmHg)	127.4 ± 21.6	135.5 ± 22.2
RR diastolic (mmHg)	77.2 ± 11.9	82.1 ± 12.7

L. LURIC

	Cases	Controls
Number of subjects	2,583	733
Study characteristics		
Study basis – Ascertainment scheme		hospital-based
Ethnicity		Caucasian
Country of origin		Germany
Age range (y) / Study criteria		17 – 92
Mean Age (y)	64	58
Gender (female, %)	25	48
Myocardial infarction (%)	63.1	0.3
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	35.8	19.1
Dyslipidemia (%)	71.5	57.3
Family history of MI (%)	10.8	10.0
Hypertension (%)	75.4	63.4
Obesity (%)	23.6	21.8
Smoking (%)	20.1	18.4
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	27.5 ± 4.0	27.4 ± 4.3
LDL-Cholesterol (mg/dL)	115.0 ± 35.0	120.0 ± 33.0
HDL-Cholesterol (mg/dL)	38.0 ± 10.0	43.0 ± 12.0
RR systolic (mmHg)	142.5 ± 23.8	136.2 ± 22.4
RR diastolic (mmHg)	81.2 ± 11.5	80.3 ± 11.3

M. popgen

	Cases*	Controls*
Number of subjects	2,200	3,166
Study characteristics		
Study basis – Ascertainment scheme	community based	community based
Ethnicity		Caucasian
Country of origin		Germany
Age range (y) / Study criteria	Cases with MI: 24 - 74	19 - 77
Mean Age (y)	51.0 ± 6.2	52.3 ± 10.5
Gender (female, %)	19.0	18.7
Myocardial infarction (%)	66.2	2.1
Cardiovascular risk factors – Frequencies		
Diabetes mellitus (%)	19.0	1.6
Dyslipidemia (%)	14.5	16.0
Family history of MI (%)	18.2	Na
Hypertension (%)	74.5	41.6
Obesity (%)	27.8	15.1
Smoking (%)	74.3	35.1
Cardiovascular risk factors – Continuous traits		
Body Mass Index (kg/m ²)	27.7 ± 3.3	26.3 ± 3.2
LDL-Cholesterol (mg/dL)	134.0 ± 36.4	133.6 ± 32.4
HDL-Cholesterol (mg/dL)	44.0 ± 11.7	59.3 ± 13.5
RR systolic (mmHg)	na	132.7 ± 13.8
RR diastolic (mmHg)	na	81.7 ± 7.9

Supplementary Table 3. Genotyping platforms and imputation methods of *in silico* replication studies

	GerMIFS I	GerMIFS II	Penn CATH	MedStar	WTCCC-CAD	MIGen	CHARGE
Genotyping							
GWA platform	Affymetrix Mapping 500k Array Set	Affymetrix Genome-Wide Human SNP Array 6.0	Affymetrix Genome-Wide Human SNP Array 6.0	Affymetrix Genome-Wide Human SNP Array 6.0	Affymetrix Mapping 500k Array Set	Affymetrix Genome-Wide Human SNP Array 6.0	several Affymetrix and Illumina*
Calling Algorithm	BRLMM	Birdseed v2	Birdseed	Birdseed v2	CHIAMO	Birdseed	Birdseed/BRLMM/BeaStudio
QC filters before imputation							
Sample call rate	MIND > 0.98	MIND > 0.98	MIND > 0.95	MIND > 0.95	MIND ≥ 0.98	>0.95	>0.95-0.98*
SNP call rate	GENO > 0.98	GENO > 0.98	GENO > 0.95	GENO > 0.95	GENO > 0.98	>0.95	>0.90-0.97*
HWE p-value	10 ⁻⁴ in controls	10 ⁻⁴ in controls	10 ⁻⁶ in controls	10 ⁻⁶ in controls	10 ⁻⁴ in controls	10 ⁻⁶ in controls	10 ⁻⁶ *
MAF	> 0.01	> 0.01	> 0.01	> 0.01	> 0.01	> 0.01	> 0.01*
Imputation							
No. SNPs for imputation [autosomal SNPs]	all matching QC filters	all matching QC filters	659,760	678,707	477,459	727,496	various (depending on GWA platform)*
NCBI build, HapMap CEU	36	36	36	36	36	36	35/36*
Software for imputation	MACH	MACH	MACH 1.0	MACH 1.0	IMPUTE	MACH / 35	MACH*
Statistical Analysis							
No. SNPs for analysis	2,543,887	2,543,887	2,659,852	2,433,405	2,614,446	2,557,744	~ 2,500,000
Model	Additive	Additive	Log-Additive PLINK	Log-Additive PLINK	Additive	Log-Additive PLINK	Additive*
Software	PLINK	PLINK	(genotyped); SNPTest (imputed)	(genotyped); SNPTest (imputed)	SNPTest	(genotyped); SNPTest (imputed)	2*
Adjustments	unadjusted	unadjusted	unadjusted	unadjusted	unadjusted	Age, gender, principal components of ancestry	adjusted for age and sex in all; for individual study as needed*
QC filters [imputed data]	--	--	IC ≥ 0.50; R2>0.3	IC ≥ 0.50; R2>0.3	--	--	2*
genomics control lambda	1.02 (genotyped)	1.04 (genotyped)	0.993 (genotyped)	0.991 (genotyped)	1.05 (genotyped)	1.01 (genotyped)	2*

*Further genotyping details in the individual cohorts in the CHARGE Consortium are described elsewhere.²

Supplementary Table 4. Genome-Wide Association Analysis of Coronary Artery Disease: SNPs associated with CAD at a level of significance of $P < 10^{-3}$ in the discovery GWAS and respective P-value of the pooled analysis of GWAS and *in silico* replication stage.

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs17390062	1	3079709	PRDM16	T/C	0.9116	5.26×10^{-05}	1.28 (1.10 - 1.48)	2.01×10^{-04}	1.15 (1.07 - 1.24)
rs12135834	1	5209527	intergenic	C/T	0.4970	7.50×10^{-04}	1.15 (1.06 - 1.24)	2.00×10^{-02}	1.05 (1.01 - 1.10)
rs6686714	1	5210469	intergenic	G/T	0.4993	8.90×10^{-04}	1.14 (1.06 - 1.24)	6.57×10^{-02}	1.04 (1.00 - 1.08)
rs7535812	1	18659366	intergenic	G/C	0.2657	1.12×10^{-04}	1.16 (1.06 - 1.27)	9.23×10^{-01}	1.00 (0.96 - 1.05)
rs829406	1	21822049	RAP1GAP	G/A	0.1179	9.04×10^{-04}	1.23 (1.09 - 1.39)	4.81×10^{-01}	1.02 (0.96 - 1.09)
rs6679565	1	21835138	RAP1GAP	A/G	0.1187	2.13×10^{-04}	1.26 (1.11 - 1.42)	1.90×10^{-02}	1.11 (1.02 - 1.21)
rs9793263	1	46494976	RAD54L, C1orf190	A/G	0.3973	5.33×10^{-04}	1.15 (1.06 - 1.25)	2.40×10^{-01}	1.03 (0.98 - 1.08)
rs12410307	1	46502985	RAD54L, C1orf190	A/G	0.0900	1.94×10^{-04}	1.30 (1.13 - 1.49)	1.39×10^{-02}	1.09 (1.02 - 1.17)
rs581554	1	54386997	CDCP2	C/T	0.7299	7.91×10^{-04}	1.17 (1.06 - 1.28)	1.06×10^{-01}	1.03 (0.99 - 1.08)
rs625643	1	54409755	CDCP2, AL357673.12-202	C/T	0.7464	3.23×10^{-04}	1.17 (1.07 - 1.29)	1.32×10^{-01}	1.03 (0.99 - 1.08)
rs17302852	1	61047387	intergenic	C/T	0.0272	9.87×10^{-04}	1.50 (1.18 - 1.91)	1.42×10^{-01}	1.13 (0.96 - 1.34)
rs6659197	1	66012485	intergenic	C/A	0.4021	8.25×10^{-05}	1.14 (1.05 - 1.24)	2.10×10^{-02}	1.05 (1.01 - 1.09)
rs12060353	1	78774508	PTGFR	T/G	0.8068	7.28×10^{-04}	1.20 (1.08 - 1.33)	6.32×10^{-02}	1.06 (1.00 - 1.13)
rs12074883	1	78775132	PTGFR	C/T	0.8070	2.94×10^{-04}	1.21 (1.09 - 1.34)	1.67×10^{-01}	1.04 (0.98 - 1.10)
rs12133510	1	78994263	intergenic	G/A	0.6810	2.31×10^{-04}	1.17 (1.07 - 1.28)	2.97×10^{-02}	1.04 (1.00 - 1.09)
rs6694893	1	79071703	intergenic	T/A	0.7627	6.30×10^{-04}	1.18 (1.07 - 1.30)	2.47×10^{-01}	1.03 (0.98 - 1.08)
rs6680564	1	79073527	intergenic	A/C	0.7624	5.40×10^{-04}	1.18 (1.08 - 1.30)	2.52×10^{-01}	1.03 (0.98 - 1.08)
rs12026347	1	79076338	intergenic	C/T	0.6880	8.83×10^{-04}	1.16 (1.06 - 1.27)	2.32×10^{-01}	1.03 (0.98 - 1.07)
rs17411879	1	79130799	ELTD1	A/C	0.7707	3.52×10^{-04}	1.20 (1.08 - 1.32)	1.02×10^{-01}	1.04 (0.99 - 1.08)
rs1352556	1	79233222	ELTD1	C/G	0.5747	9.26×10^{-04}	1.15 (1.06 - 1.25)	1.45×10^{-02}	1.05 (1.01 - 1.10)
rs12117862	1	81882643	LPHN2	T/C	0.8584	1.11×10^{-04}	1.22 (1.09 - 1.37)	3.41×10^{-02}	1.07 (1.01 - 1.14)
rs1413536	1	88195985	intergenic	T/C	0.4997	1.64×10^{-04}	1.16 (1.07 - 1.26)	6.01×10^{-02}	1.04 (1.00 - 1.08)
rs1334331	1	88213654	intergenic	A/C	0.3488	1.18×10^{-04}	1.17 (1.07 - 1.27)	2.89×10^{-01}	1.02 (0.98 - 1.06)
rs1932757	1	88437917	intergenic	C/T	0.1819	7.08×10^{-05}	1.23 (1.11 - 1.37)	1.06×10^{-01}	1.04 (0.99 - 1.09)
rs10493803	1	88446264	intergenic	T/G	0.1692	1.85×10^{-04}	1.20 (1.08 - 1.34)	1.88×10^{-01}	1.03 (0.98 - 1.08)
rs12403601	1	88447133	intergenic	T/G	0.1691	2.14×10^{-04}	1.20 (1.08 - 1.34)	1.96×10^{-01}	1.03 (0.98 - 1.08)
rs10923044	1	88454168	intergenic	C/T	0.1768	7.72×10^{-05}	1.22 (1.10 - 1.36)	7.22×10^{-02}	1.05 (1.00 - 1.10)
rs4300194	1	88472538	intergenic	C/T	0.1695	1.16×10^{-04}	1.21 (1.09 - 1.35)	8.74×10^{-02}	1.05 (0.99 - 1.11)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs12730130	1	88474179	intergenic	A/T	0.1702	1.21*10 ⁻⁰⁴	1.21 (1.09 - 1.35)	7.35*10 ⁻⁰²	1.05 (1.00 - 1.11)
rs569619	1	88514598	intergenic	T/G	0.1644	1.36*10 ⁻⁰⁴	1.22 (1.09 - 1.36)	4.86*10 ⁻⁰²	1.06 (1.00 - 1.12)
rs608410	1	88543251	intergenic	T/C	0.2688	7.44*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	9.55*10 ⁻⁰²	1.04 (0.99 - 1.08)
rs591604	1	88551814	intergenic	A/G	0.3192	1.90*10 ⁻⁰⁴	1.18 (1.08 - 1.28)	3.49*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs589824	1	88552213	intergenic	C/T	0.3354	6.17*10 ⁻⁰⁵	1.18 (1.09 - 1.29)	3.60*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs555994	1	88553150	intergenic	C/T	0.2446	1.11*10 ⁻⁰⁵	1.21 (1.10 - 1.32)	2.12*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs473821	1	88553930	intergenic	C/T	0.2624	3.09*10 ⁻⁰⁶	1.21 (1.11 - 1.33)	1.95*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs127382	1	88561536	intergenic	T/C	0.2511	4.21*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	8.93*10 ⁻⁰²	1.04 (0.99 - 1.08)
rs127384	1	88563548	intergenic	T/C	0.3199	1.43*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	5.25*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs480054	1	88564020	intergenic	G/A	0.3003	1.97*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	5.90*10 ⁻⁰⁴	1.11 (1.05 - 1.18)
rs766353	1	88594104	intergenic	A/G	0.3306	2.18*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	5.34*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs6682490	1	88597878	intergenic	A/T	0.1630	6.25*10 ⁻⁰⁴	1.21 (1.09 - 1.35)	7.20*10 ⁻⁰⁵	1.17 (1.08 - 1.26)
rs10494161	1	113720977	intergenic	C/G	0.9292	4.07*10 ⁻⁰⁴	1.34 (1.14 - 1.57)	3.76*10 ⁻⁰¹	1.03 (0.96 - 1.11)
rs4839321	1	113848987	MAGI3	A/G	0.9274	9.07*10 ⁻⁰⁴	1.31 (1.11 - 1.53)	4.61*10 ⁻⁰¹	1.03 (0.95 - 1.12)
rs9661113	1	118600962	intergenic	T/C	0.5177	2.94*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	8.79*10 ⁻⁰³	1.05 (1.01 - 1.09)
rs7551954	1	118601450	intergenic	C/T	0.5179	3.21*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	3.40*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs10802017	1	118612357	AL391557.11, 5S_rRNA	C/T	0.5149	2.41*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	3.58*10 ⁻⁰³	1.06 (1.02 - 1.09)
rs7515420	1	118624670	intergenic	A/G	0.5189	3.25*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	3.84*10 ⁻⁰³	1.06 (1.02 - 1.09)
rs1938283	1	118633460	intergenic	A/C	0.5163	3.31*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	5.84*10 ⁻⁰³	1.05 (1.01 - 1.09)
rs942835	1	120064541	PHGDH	T/C	0.8657	4.50*10 ⁻⁰⁴	1.24 (1.10 - 1.40)	6.98*10 ⁻⁰²	1.05 (1.00 - 1.11)
rs894079	1	120065180	PHGDH	A/G	0.8680	7.55*10 ⁻⁰⁵	1.29 (1.14 - 1.45)	8.75*10 ⁻⁰²	1.05 (0.99 - 1.10)
rs6658925	1	150749425	CRCT1, LCE5A	A/G	0.3667	3.59*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	4.19*10 ⁻⁰²	1.04 (1.00 - 1.09)
rs548252	1	150756366	CRCT1	C/T	0.3666	7.96*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	9.66*10 ⁻⁰²	1.03 (0.99 - 1.07)
rs4845443	1	150773780	intergenic	G/A	0.3659	9.82*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.16*10 ⁻⁰¹	1.04 (0.99 - 1.08)
rs16838818	1	155801783	intergenic	A/C	0.0706	9.31*10 ⁻⁰⁴	1.30 (1.11 - 1.51)	4.07*10 ⁻⁰³	1.18 (1.05 - 1.32)
rs16832790	1	159542567	MPZ	T/C	0.0243	2.13*10 ⁻⁰⁴	1.47 (1.14 - 1.89)	7.68*10 ⁻⁰¹	1.02 (0.89 - 1.17)
rs16832872	1	159602526	SDHC, C1orf192	A/G	0.0240	9.20*10 ⁻⁰⁴	1.38 (1.07 - 1.78)	8.95*10 ⁻⁰¹	1.01 (0.89 - 1.15)
rs723821	1	163283336	intergenic	C/A	0.8972	7.80*10 ⁻⁰⁴	1.26 (1.10 - 1.44)	2.19*10 ⁻⁰¹	1.04 (0.98 - 1.11)
rs723822	1	163283356	intergenic	A/T	0.8867	7.44*10 ⁻⁰⁴	1.23 (1.08 - 1.4)	4.64*10 ⁻⁰¹	1.03 (0.95 - 1.13)
rs12122751	1	169660773	intergenic	A/G	0.7624	3.54*10 ⁻⁰⁴	1.18 (1.08 - 1.30)	2.12*10 ⁻⁰⁴	1.09 (1.04 - 1.14)
rs873525	1	173685824	TNR	A/G	0.0390	7.35*10 ⁻⁰⁴	1.42 (1.16 - 1.73)	1.58*10 ⁻⁰¹	1.07 (0.97 - 1.18)
rs12043681	1	197042097	intergenic	T/C	0.6092	6.17*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	1.90*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs9427431	1	197044095	intergenic	T/C	0.6075	5.52*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	4.76*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs1407684	1	197044377	intergenic	T/C	0.6094	5.35*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	5.05*10 ⁻⁰²	1.04 (1.00 - 1.08)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs10494874	1	204021311	SLC41A1	G/C	0.7403	3.03*10 ⁻⁰⁴	1.18 (1.08 - 1.30)	1.58*10 ⁻⁰²	1.08 (1.01 - 1.15)
rs6679073	1	204023107	SLC41A1	C/A	0.7394	1.13*10 ⁻⁰⁴	1.20 (1.09 - 1.32)	9.45*10 ⁻⁰²	1.04 (0.99 - 1.08)
rs4347270	1	215955595	SPATA17	G/A	0.0624	4.40*10 ⁻⁰⁵	1.40 (1.19 - 1.64)	4.88*10 ⁻⁰²	1.08 (1.00 - 1.16)
rs10429870	1	222907422	CNIH3	C/T	0.8822	4.83*10 ⁻⁰⁴	1.25 (1.10 - 1.42)	1.74*10 ⁻⁰³	1.09 (1.03 - 1.16)
rs12025142	1	222942724	CNIH3	C/A	0.8814	8.45*10 ⁻⁰⁴	1.24 (1.09 - 1.40)	1.35*10 ⁻⁰³	1.10 (1.04 - 1.16)
rs12410483	1	228212800	intergenic	A/G	0.9030	5.37*10 ⁻⁰⁴	1.28 (1.11 - 1.47)	7.46*10 ⁻⁰¹	1.01 (0.95 - 1.08)
rs4411137	1	228213090	intergenic	C/A	0.8761	2.81*10 ⁻⁰⁴	1.26 (1.11 - 1.42)	1.14*10 ⁻⁰¹	1.05 (0.99 - 1.12)
rs16857696	1	230771342	intergenic	G/T	0.0234	2.83*10 ⁻⁰⁴	1.60 (1.24 - 2.07)	2.62*10 ⁻⁰¹	1.08 (0.95 - 1.23)
rs12474647	2	9471731	ITGB1BP1	T/A	0.3909	2.49*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	1.17*10 ⁻⁰³	1.07 (1.03 - 1.11)
rs4669402	2	9696864	intergenic	G/C	0.9381	5.45*10 ⁻⁰⁴	1.35 (1.14 - 1.61)	1.78*10 ⁻⁰⁴	1.16 (1.07 - 1.25)
rs6721977	2	11740888	intergenic	C/A	0.0255	1.41*10 ⁻⁰⁴	1.62 (1.26 - 2.09)	8.69*10 ⁻⁰²	1.11 (0.98 - 1.25)
rs916524	2	12197847	intergenic	T/C	0.2108	8.18*10 ⁻⁰⁴	1.18 (1.07 - 1.30)	2.69*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs6739656	2	15749709	intergenic	C/G	0.0999	4.31*10 ⁻⁰⁴	1.27 (1.11 - 1.45)	3.08*10 ⁻⁰¹	1.04 (0.97 - 1.11)
rs6754458	2	15751503	intergenic	G/A	0.1007	4.72*10 ⁻⁰⁴	1.26 (1.11 - 1.44)	2.52*10 ⁻⁰¹	1.04 (0.97 - 1.11)
rs16985872	2	19120878	intergenic	C/T	0.0288	7.12*10 ⁻⁰⁴	1.50 (1.18 - 1.89)	4.27*10 ⁻⁰³	1.19 (1.06 - 1.34)
rs11124408	2	35051809	intergenic	T/C	0.1173	5.40*10 ⁻⁰⁴	1.25 (1.10 - 1.41)	1.30*10 ⁻⁰²	1.08 (1.02 - 1.15)
rs1579491	2	37872165	intergenic	G/A	0.9426	6.77*10 ⁻⁰⁴	1.36 (1.14 - 1.62)	9.71*10 ⁻⁰¹	1.00 (0.92 - 1.09)
rs17021567	2	37961598	intergenic	C/A	0.1129	5.63*10 ⁻⁰⁴	1.25 (1.10 - 1.41)	4.09*10 ⁻⁰²	1.08 (1.00 - 1.16)
rs17022010	2	38185435	intergenic	T/A	0.0835	5.30*10 ⁻⁰⁴	1.29 (1.12 - 1.48)	1.50*10 ⁻⁰²	1.09 (1.02 - 1.17)
rs232535	2	38185807	intergenic	C/T	0.6785	1.61*10 ⁻⁰⁴	1.18 (1.08 - 1.28)	6.78*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs2432662	2	38205678	intergenic	C/T	0.8193	8.57*10 ⁻⁰⁴	1.20 (1.08 - 1.33)	3.05*10 ⁻⁰¹	1.03 (0.97 - 1.09)
rs232620	2	38212168	intergenic	A/G	0.6494	4.03*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	8.27*10 ⁻⁰¹	1.00 (0.97 - 1.04)
rs170818	2	38228071	U6	C/T	0.8046	2.50*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	5.46*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs232576	2	38239724	intergenic	A/G	0.6577	4.18*10 ⁻⁰⁶	1.22 (1.12 - 1.33)	2.34*10 ⁻⁰³	1.07 (1.02 - 1.12)
rs232569	2	38247867	intergenic	C/T	0.6605	4.89*10 ⁻⁰⁵	1.19 (1.09 - 1.3)	4.48*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs2447738	2	38264671	intergenic	C/T	0.7147	3.66*10 ⁻⁰⁵	1.21 (1.1 - 1.32)	1.30*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs232587	2	38274357	intergenic	T/A	0.6985	6.36*10 ⁻⁰⁵	1.20 (1.09 - 1.31)	2.19*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs1965752	2	38797113	GALM	G/A	0.0229	3.33*10 ⁻⁰⁴	1.61 (1.24 - 2.08)	2.78*10 ⁻⁰¹	1.06 (0.95 - 1.19)
rs17030342	2	43152887	intergenic	A/G	0.1046	4.23*10 ⁻⁰⁴	1.26 (1.10 - 1.43)	5.10*10 ⁻⁰¹	1.02 (0.96 - 1.08)
rs17326067	2	48700601	STON1	C/T	0.9672	4.89*10 ⁻⁰⁴	1.52 (1.20 - 1.93)	1.54*10 ⁻⁰¹	1.08 (0.97 - 1.2)
rs1589749	2	48716002	STON1, AC073082.3	G/A	0.2127	7.03*10 ⁻⁰⁴	1.18 (1.07 - 1.30)	4.72*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs2349099	2	48716406	STON1, AC073082.3	T/C	0.2072	9.88*10 ⁻⁰⁴	1.18 (1.07 - 1.30)	5.76*10 ⁻⁰²	1.04 (1.00 - 1.09)
rs6738590	2	64913107	Y_RNA	A/G	0.2196	1.40*10 ⁻⁰⁴	1.18 (1.07 - 1.30)	5.89*10 ⁻⁰⁴	1.09 (1.04 - 1.14)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs17033861	2	67681582	intergenic	G/A	0.8168	1.53*10 ⁻⁰⁴	1.22 (1.10 - 1.36)	3.26*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs13398112	2	67682118	intergenic	T/C	0.8141	2.09*10 ⁻⁰⁴	1.22 (1.10 - 1.35)	2.73*10 ⁻⁰¹	1.03 (0.98 - 1.07)
rs10210930	2	70283309	intergenic	T/C	0.0652	4.47*10 ⁻⁰⁴	1.30 (1.11 - 1.53)	8.86*10 ⁻⁰¹	1.01 (0.93 - 1.09)
rs6751173	2	70359412	PCYOX1, SNRPG	A/G	0.0652	3.53*10 ⁻⁰⁴	1.31 (1.12 - 1.54)	8.35*10 ⁻⁰¹	1.01 (0.93 - 1.09)
rs13399467	2	70399046	intergenic	G/C	0.1006	4.57*10 ⁻⁰⁴	1.25 (1.1 - 1.43)	1.58*10 ⁻⁰¹	1.05 (0.98 - 1.13)
rs10221875	2	88481280	intergenic	A/G	0.9272	5.54*10 ⁻⁰⁴	1.33 (1.13 - 1.56)	4.43*10 ⁻⁰²	1.09 (1.00 - 1.18)
rs1530128	2	104530881	intergenic	A/G	0.5036	2.78*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	1.75*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs13005764	2	104550787	AC013402.9	A/G	0.8984	2.15*10 ⁻⁰⁴	1.29 (1.13 - 1.48)	3.79*10 ⁻⁰¹	1.03 (0.97 - 1.09)
rs4849561	2	117990472	intergenic	C/T	0.8517	4.35*10 ⁻⁰⁴	1.22 (1.09 - 1.37)	8.27*10 ⁻⁰⁵	1.13 (1.06 - 1.20)
rs6753213	2	118208283	intergenic	A/G	0.8945	2.05*10 ⁻⁰⁴	1.29 (1.12 - 1.47)	1.40*10 ⁻⁰³	1.10 (1.04 - 1.17)
rs10170205	2	125272583	CNTNAP5	C/T	0.0376	8.73*10 ⁻⁰⁴	1.41 (1.15 - 1.73)	8.23*10 ⁻⁰⁴	1.28 (1.11 - 1.48)
rs7575461	2	130250800	intergenic	G/A	0.3781	6.05*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	5.03*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs9646794	2	152418677	CACNB4	A/T	0.0843	9.49*10 ⁻⁰⁴	1.27 (1.1 - 1.47)	7.29*10 ⁻⁰¹	1.01 (0.94 - 1.09)
rs2007857	2	153696168	intergenic	A/G	0.7704	5.38*10 ⁻⁰⁴	1.18 (1.08 - 1.3)	3.13*10 ⁻⁰³	1.11 (1.03 - 1.18)
rs13025412	2	153697833	intergenic	C/T	0.7892	9.53*10 ⁻⁰⁴	1.18 (1.07 - 1.3)	3.41*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs1806328	2	169215125	LASS6	G/A	0.4728	5.47*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.74*10 ⁻⁰³	1.07 (1.03 - 1.12)
rs2193193	2	169784327	LRP2	A/G	0.4878	8.71*10 ⁻⁰⁵	1.17 (1.08 - 1.27)	3.11*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs2268370	2	169785809	LRP2	C/A	0.4237	3.20*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	3.52*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs2239594	2	169798577	LRP2	T/C	0.4727	3.18*10 ⁻⁰⁵	1.19 (1.09 - 1.28)	2.79*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs830957	2	169820344	LRP2	T/C	0.4592	6.35*10 ⁻⁰⁵	1.18 (1.09 - 1.28)	2.37*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs830959	2	169821344	LRP2	T/C	0.4655	7.76*10 ⁻⁰⁵	1.17 (1.08 - 1.27)	3.40*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs830960	2	169821642	LRP2	T/C	0.4659	8.28*10 ⁻⁰⁵	1.17 (1.08 - 1.27)	4.38*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs831002	2	169841998	LRP2	T/C	0.2104	3.01*10 ⁻⁰⁴	1.2 (1.08 - 1.32)	4.06*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs831004	2	169843988	LRP2	C/T	0.4076	3.21*10 ⁻⁰⁶	1.21 (1.12 - 1.32)	2.41*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs831007	2	169846752	LRP2	T/C	0.2394	4.58*10 ⁻⁰⁵	1.21 (1.11 - 1.33)	1.44*10 ⁻⁰²	1.07 (1.01 - 1.12)
rs831008	2	169847142	LRP2	C/T	0.1618	3.56*10 ⁻⁰⁴	1.22 (1.09 - 1.36)	6.72*10 ⁻⁰²	1.06 (1.00 - 1.12)
rs6721083	2	170789898	MYO3B	G/C	0.0637	7.43*10 ⁻⁰⁴	1.32 (1.12 - 1.54)	5.47*10 ⁻⁰¹	1.03 (0.94 - 1.12)
rs1816811	2	173871566	intergenic	G/C	0.7535	6.18*10 ⁻⁰⁴	1.18 (1.07 - 1.29)	2.74*10 ⁻⁰⁴	1.08 (1.04 - 1.13)
rs6712331	2	173873289	intergenic	A/C	0.7529	5.54*10 ⁻⁰⁴	1.18 (1.07 - 1.29)	6.15*10 ⁻⁰⁴	1.08 (1.03 - 1.13)
rs2303536	2	179066911	PLEKHA3	G/A	0.1441	3.72*10 ⁻⁰⁴	1.23 (1.1 - 1.37)	2.93*10 ⁻⁰²	1.07 (1.01 - 1.13)
rs1377767	2	184294872	intergenic	G/A	0.6738	7.08*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	3.57*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs6712217	2	188209175	intergenic	G/A	0.1748	2.29*10 ⁻⁰⁴	1.22 (1.1 - 1.35)	2.29*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs13034939	2	188219341	intergenic	A/G	0.1779	3.01*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	1.56*10 ⁻⁰¹	1.04 (0.99 - 1.09)
rs6728009	2	188408860	intergenic	G/T	0.0120	2.64*10 ⁻⁰⁵	2.14 (1.49 - 3.08)	9.39*10 ⁻⁰¹	1.01 (0.87 - 1.17)
rs6727168	2	207697715	KLF7	T/C	0.6777	4.73*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	2.28*10 ⁻⁰¹	1.03 (0.98 - 1.07)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs7582312	2	207813763	intergenic	T/C	0.0856	3.45*10 ⁻⁰⁴	1.3 (1.12 - 1.49)	3.02*10 ⁻⁰²	1.08 (1.01 - 1.16)
rs11676172	2	218355367	intergenic	C/T	0.0488	1.18*10 ⁻⁰⁴	1.42 (1.18 - 1.7)	3.42*10 ⁻⁰²	1.11 (1.01 - 1.23)
rs7581631	2	228167188	intergenic	T/A	0.0425	5.15*10 ⁻⁰⁴	1.41 (1.16 - 1.71)	4.13*10 ⁻⁰²	1.10 (1.00 - 1.21)
rs6728087	2	229919505	intergenic	A/C	0.5615	4.29*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	9.63*10 ⁻⁰¹	1.00 (0.96 - 1.04)
rs7584396	2	235048006	intergenic	C/T	0.0689	2.38*10 ⁻⁰⁴	1.33 (1.14 - 1.55)	4.53*10 ⁻⁰²	1.12 (1.00 - 1.25)
rs3792085	2	240597462	NDUFA10	G/A	0.2813	5.02*10 ⁻⁰⁴	1.18 (1.07 - 1.29)	4.72*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs3792083	2	240603577	NDUFA10	G/A	0.3101	8.65*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	4.13*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs7630409	3	76192	intergenic	A/T	0.2236	4.23*10 ⁻⁰⁵	1.22 (1.11 - 1.34)	9.35*10 ⁻⁰¹	1.00 (0.96 - 1.05)
rs990284	3	79972	intergenic	G/A	0.3706	8.20*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.69*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs17047384	3	102933	intergenic	A/C	0.1896	8.88*10 ⁻⁰⁵	1.22 (1.1 - 1.35)	8.01*10 ⁻⁰¹	1.01 (0.96 - 1.05)
rs7629216	3	127005	intergenic	T/G	0.1829	2.48*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	7.07*10 ⁻⁰¹	1.01 (0.96 - 1.07)
rs9857814	3	127047	intergenic	G/A	0.1841	7.24*10 ⁻⁰⁵	1.23 (1.11 - 1.36)	5.83*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs6786696	3	127592	intergenic	A/G	0.1602	1.52*10 ⁻⁰⁴	1.23 (1.1 - 1.37)	6.47*10 ⁻⁰¹	1.01 (0.96 - 1.07)
rs4685564	3	2826955	CNTN4	T/G	0.2763	6.98*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	4.91*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs771000	3	3317533	intergenic	A/G	0.4527	7.52*10 ⁻⁰⁵	1.18 (1.09 - 1.28)	1.50*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs2730313	3	5879553	intergenic	G/T	0.0804	2.64*10 ⁻⁰⁴	1.3 (1.13 - 1.5)	5.43*10 ⁻⁰¹	1.02 (0.96 - 1.09)
rs1568170	3	5940594	intergenic	G/C	0.0700	1.00*10 ⁻⁰⁴	1.36 (1.16 - 1.58)	1.32*10 ⁻⁰¹	1.06 (0.98 - 1.15)
rs157462	3	6339784	intergenic	G/C	0.1202	4.65*10 ⁻⁰⁵	1.24 (1.1 - 1.41)	2.44*10 ⁻⁰¹	1.03 (0.98 - 1.09)
rs164336	3	6737242	intergenic	C/T	0.8467	9.40*10 ⁻⁰⁴	1.21 (1.08 - 1.35)	2.15*10 ⁻⁰¹	1.04 (0.98 - 1.10)
rs345244	3	6742906	intergenic	C/G	0.8450	4.09*10 ⁻⁰⁴	1.22 (1.09 - 1.37)	1.05*10 ⁻⁰²	1.11 (1.02 - 1.20)
rs17288435	3	6838813	intergenic	C/A	0.1398	8.13*10 ⁻⁰⁵	1.26 (1.12 - 1.41)	3.77*10 ⁻⁰³	1.09 (1.03 - 1.16)
rs7611030	3	8486921	intergenic	A/G	0.5089	9.00*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	4.93*10 ⁻⁰⁴	1.07 (1.03 - 1.12)
rs11720160	3	8492932	intergenic	T/A	0.5259	4.27*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.41*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs345069	3	8831126	intergenic	C/T	0.9715	4.96*10 ⁻⁰⁴	1.57 (1.22 - 2.03)	3.91*10 ⁻⁰²	1.12 (1.01 - 1.25)
rs666743	3	9016346	SRGAP3	T/C	0.2084	8.20*10 ⁻⁰⁴	1.18 (1.07 - 1.3)	3.53*10 ⁻⁰²	1.06 (1.00 - 1.11)
rs1161765	3	9023152	SRGAP3	A/G	0.2037	7.31*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	1.19*10 ⁻⁰¹	1.04 (0.99 - 1.10)
rs341788	3	9025659	SRGAP3	C/T	0.2052	9.31*10 ⁻⁰⁴	1.18 (1.07 - 1.3)	2.89*10 ⁻⁰²	1.06 (1.01 - 1.12)
rs1719571	3	10344180	ATP2B2	A/G	0.8562	5.05*10 ⁻⁰⁴	1.21 (1.08 - 1.36)	4.51*10 ⁻⁰¹	1.02 (0.97 - 1.08)
rs1710887	3	11014960	SLC6A1	G/T	0.6100	6.70*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	4.70*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs2731334	3	14082388	TPRXL	C/T	0.8633	9.70*10 ⁻⁰⁴	1.22 (1.08 - 1.37)	2.87*10 ⁻⁰²	1.08 (1.01 - 1.15)
rs2929343	3	19956418	EFHB, AC097635.2	A/T	0.2458	7.52*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	4.50*10 ⁻⁰¹	1.02 (0.97 - 1.07)
rs2364515	3	19956559	EFHB, AC097635.2	G/C	0.2451	6.38*10 ⁻⁰⁴	1.17 (1.07 - 1.29)	4.78*10 ⁻⁰¹	1.02 (0.97 - 1.07)
rs2577120	3	29773438	RBMS3	C/G	0.9113	5.87*10 ⁻⁰⁴	1.29 (1.11 - 1.49)	9.16*10 ⁻⁰²	1.07 (0.99 - 1.15)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs11714423	3	31768861	OSBPL10	A/G	0.5787	2.56*10 ⁻⁰⁵	1.19 (1.09 - 1.29)	1.03*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs11710822	3	31768875	OSBPL10	T/C	0.5721	6.26*10 ⁻⁰⁵	1.18 (1.09 - 1.27)	4.65*10 ⁻⁰¹	1.01 (0.98 - 1.05)
rs936160	3	31787589	OSBPL10	C/T	0.2618	2.16*10 ⁻⁰⁴	1.18 (1.08 - 1.3)	4.90*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs2219250	3	31792548	OSBPL10	T/C	0.2341	4.65*10 ⁻⁰⁴	1.18 (1.07 - 1.3)	3.18*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs2068100	3	31812208	OSBPL10	A/T	0.2794	4.65*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	5.63*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs7628972	3	31814101	OSBPL10	C/T	0.2781	3.70*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	4.75*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs7643025	3	31814246	OSBPL10	T/C	0.2629	5.32*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	2.29*10 ⁻⁰¹	1.03 (0.98 - 1.07)
rs6550070	3	31817639	OSBPL10	C/A	0.2738	8.84*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	4.61*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs6808708	3	31822981	OSBPL10	T/A	0.2433	7.71*10 ⁻⁰⁵	1.2 (1.1 - 1.32)	2.16*10 ⁻⁰¹	1.03 (0.98 - 1.07)
rs11915888	3	41428940	ULK4	G/A	0.2965	9.50*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	3.66*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs9872216	3	41433642	ULK4	C/T	0.3362	4.39*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	3.23*10 ⁻⁰²	1.04 (1.00 - 1.09)
rs1504915	3	59541524	intergenic	G/A	0.1344	6.56*10 ⁻⁰⁴	1.22 (1.08 - 1.37)	6.96*10 ⁻⁰²	1.06 (1.00 - 1.12)
rs11130879	3	62132537	PTPRG	A/G	0.7745	5.93*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	1.58*10 ⁻⁰²	1.06 (1.01 - 1.11)
rs1508401	3	62133412	PTPRG	T/C	0.7743	6.12*10 ⁻⁰⁴	1.18 (1.08 - 1.3)	2.25*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs17066234	3	62134785	PTPRG	C/T	0.9111	2.89*10 ⁻⁰⁴	1.3 (1.13 - 1.5)	1.32*10 ⁻⁰²	1.09 (1.02 - 1.17)
rs6765895	3	63439410	SYNPR	G/A	0.5610	9.01*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	4.21*10 ⁻⁰¹	1.02 (0.97 - 1.08)
rs6772726	3	63441422	SYNPR	G/T	0.5627	4.85*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	7.19*10 ⁻⁰¹	1.01 (0.97 - 1.04)
rs13082646	3	65707153	AC121493.1	T/C	0.4947	2.01*10 ⁻⁰⁵	1.19 (1.1 - 1.29)	1.18*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs814756	3	65728454	AC121493.1	T/C	0.2091	9.37*10 ⁻⁰⁴	1.18 (1.07 - 1.3)	5.78*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs984038	3	65737292	AC121493.1	C/T	0.4010	4.95*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	3.71*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs1495453	3	65737587	AC121493.1	G/A	0.4763	1.15*10 ⁻⁰⁵	1.2 (1.1 - 1.29)	4.82*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs3853157	3	69209318	UBA3	T/C	0.2122	6.01*10 ⁻⁰⁴	1.18 (1.07 - 1.3)	1.81*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs3772979	3	69209823	UBA3	C/T	0.2133	9.38*10 ⁻⁰⁴	1.17 (1.06 - 1.29)	1.62*10 ⁻⁰²	1.07 (1.01 - 1.12)
rs13089190	3	73041567	GLT8D4	T/C	0.0868	6.10*10 ⁻⁰⁵	1.33 (1.16 - 1.53)	1.38*10 ⁻⁰²	1.08 (1.02 - 1.16)
rs17010249	3	73041922	GLT8D4	A/G	0.1073	7.78*10 ⁻⁰⁵	1.29 (1.14 - 1.47)	1.81*10 ⁻⁰¹	1.04 (0.98 - 1.10)
rs17010250	3	73042162	GLT8D4	G/C	0.1068	8.90*10 ⁻⁰⁵	1.29 (1.14 - 1.47)	1.50*10 ⁻⁰¹	1.07 (0.98 - 1.17)
rs7649077	3	73046747	GLT8D4	T/C	0.1044	2.00*10 ⁻⁰⁵	1.33 (1.16 - 1.51)	1.75*10 ⁻⁰¹	1.04 (0.98 - 1.11)
rs9876619	3	73054439	GLT8D4	T/C	0.1042	2.75*10 ⁻⁰⁵	1.32 (1.16 - 1.5)	9.20*10 ⁻⁰²	1.05 (0.99 - 1.12)
rs7640661	3	73056422	GLT8D4	A/G	0.1308	3.83*10 ⁻⁰⁴	1.24 (1.1 - 1.4)	2.93*10 ⁻⁰¹	1.03 (0.98 - 1.09)
rs17742733	3	73087270	GLT8D4	A/T	0.0774	3.10*10 ⁻⁰⁴	1.29 (1.11 - 1.49)	4.78*10 ⁻⁰²	1.07 (1.00 - 1.15)
rs17691949	3	73093053	GLT8D4	G/A	0.0773	1.77*10 ⁻⁰⁴	1.3 (1.12 - 1.51)	4.51*10 ⁻⁰²	1.08 (1.00 - 1.15)
rs13320194	3	81802766	GBE1	A/G	0.0142	8.63*10 ⁻⁰⁵	1.87 (1.34 - 2.61)	1.50*10 ⁻⁰¹	1.11 (0.96 - 1.28)
rs9289587	3	99591060	OR5K3	A/G	0.8035	4.93*10 ⁻⁰⁴	1.19 (1.07 - 1.32)	2.46*10 ⁻⁰¹	1.03 (0.98 - 1.07)
rs709465	3	109191567	intergenic	T/G	0.4600	7.77*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	9.45*10 ⁻⁰¹	1.00 (0.97 - 1.04)
rs7638293	3	109192547	intergenic	A/T	0.3073	1.65*10 ⁻⁰⁴	1.18 (1.08 - 1.29)	6.65*10 ⁻⁰¹	1.01 (0.97 - 1.05)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs877859	3	109196765	intergenic	G/A	0.3159	9.14*10 ⁻⁰⁵	1.19 (1.09 - 1.29)	6.40*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs722927	3	115163865	KIAA1407, ZDHHC23	G/C	0.0691	2.40*10 ⁻⁰⁴	1.34 (1.15 - 1.56)	6.29*10 ⁻⁰²	1.11 (0.99 - 1.23)
rs9875005	3	118102817	intergenic	G/A	0.3627	8.72*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.84*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs6777242	3	118113033	intergenic	G/A	0.3639	6.31*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	5.85*10 ⁻⁰²	1.04 (1.00 - 1.09)
rs1523517	3	123209681	ILDR1	C/G	0.5881	5.53*10 ⁻⁰⁴	1.13 (1.05 - 1.23)	8.14*10 ⁻⁰¹	1.00 (0.97 - 1.04)
rs7624556	3	148166362	intergenic	A/G	0.0641	9.19*10 ⁻⁰⁴	1.31 (1.12 - 1.55)	2.01*10 ⁻⁰¹	1.06 (0.97 - 1.15)
rs6440602	3	150558049	AC073522.19	C/G	0.9267	4.86*10 ⁻⁰⁴	1.34 (1.14 - 1.58)	3.14*10 ⁻⁰¹	1.04 (0.97 - 1.12)
rs6772563	3	161933942	intergenic	G/A	0.8943	1.20*10 ⁻⁰⁴	1.3 (1.14 - 1.49)	1.13*10 ⁻⁰³	1.16 (1.06 - 1.27)
rs9849216	3	161940045	intergenic	C/T	0.8931	4.10*10 ⁻⁰⁴	1.27 (1.11 - 1.46)	3.58*10 ⁻⁰²	1.07 (1.00 - 1.14)
rs13072299	3	163477333	intergenic	C/T	0.9278	1.84*10 ⁻⁰⁴	1.33 (1.13 - 1.56)	2.24*10 ⁻⁰²	1.1 (1.01 - 1.19)
rs1605389	3	169456755	intergenic	T/C	0.3716	5.67*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	6.26*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs4425233	3	190751492	intergenic	C/T	0.8719	1.73*10 ⁻⁰⁴	1.26 (1.12 - 1.43)	1.06*10 ⁻⁰¹	1.05 (0.99 - 1.10)
rs1719615	3	191236401	LEPREL1	A/C	0.2114	4.50*10 ⁻⁰⁴	1.19 (1.08 - 1.32)	6.23*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs6444501	3	192302936	intergenic	T/G	0.3716	1.96*10 ⁻⁰⁴	1.17 (1.08 - 1.27)	1.99*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs4834896	4	12402859	AC096750.3	T/A	0.6574	1.69*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	1.04*10 ⁻⁰⁴	1.09 (1.04 - 1.14)
rs807423	4	12411153	AC096750.3	C/T	0.6442	1.84*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	9.40*10 ⁻⁰⁴	1.07 (1.03 - 1.11)
rs807424	4	12411472	AC096750.3	T/C	0.6075	2.22*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	3.48*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs17829676	4	16743156	intergenic	G/A	0.1242	6.64*10 ⁻⁰⁴	1.23 (1.09 - 1.39)	7.95*10 ⁻⁰¹	1.01 (0.95 - 1.07)
rs17771233	4	16817698	intergenic	A/G	0.0892	3.75*10 ⁻⁰⁴	1.28 (1.12 - 1.47)	1.45*10 ⁻⁰¹	1.06 (0.98 - 1.14)
rs429783	4	21181666	KCNIP4	C/A	0.1651	2.95*10 ⁻⁰⁴	1.2 (1.08 - 1.34)	2.81*10 ⁻⁰⁴	1.15 (1.07 - 1.24)
rs10517008	4	22881295	intergenic	C/G	0.1118	6.49*10 ⁻⁰⁴	1.24 (1.1 - 1.41)	8.01*10 ⁻⁰³	1.11 (1.03 - 1.19)
rs2968711	4	22958419	intergenic	A/G	0.2176	1.24*10 ⁻⁰⁴	1.21 (1.1 - 1.33)	3.55*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs2940774	4	22958441	intergenic	T/C	0.2169	4.26*10 ⁻⁰⁵	1.22 (1.11 - 1.35)	3.22*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs7666498	4	22965822	intergenic	C/T	0.2334	2.73*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	9.32*10 ⁻⁰³	1.06 (1.01 - 1.11)
rs1467030	4	22972687	intergenic	C/T	0.2529	1.40*10 ⁻⁰⁴	1.19 (1.09 - 1.31)	6.87*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs1509241	4	22973591	intergenic	T/C	0.5719	7.89*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.37*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs7672988	4	22975875	intergenic	A/C	0.2307	2.54*10 ⁻⁰⁵	1.23 (1.11 - 1.35)	3.88*10 ⁻⁰³	1.07 (1.02 - 1.13)
rs215475	4	22997497	intergenic	A/G	0.2443	3.51*10 ⁻⁰⁴	1.18 (1.08 - 1.3)	2.64*10 ⁻⁰³	1.12 (1.04 - 1.21)
rs1605813	4	23039866	intergenic	A/G	0.5626	8.17*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	8.20*10 ⁻⁰²	1.04 (0.99 - 1.09)
rs177357	4	23053543	intergenic	T/C	0.3015	3.07*10 ⁻⁰⁵	1.2 (1.1 - 1.31)	6.50*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs123495	4	23054277	intergenic	T/C	0.3041	1.09*10 ⁻⁰⁵	1.22 (1.11 - 1.33)	4.93*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs123494	4	23054310	intergenic	G/C	0.3036	2.66*10 ⁻⁰⁵	1.2 (1.1 - 1.31)	5.24*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs215437	4	23056004	intergenic	C/G	0.3001	3.92*10 ⁻⁰⁵	1.2 (1.1 - 1.31)	5.37*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs4692290	4	27791972	intergenic	G/A	0.5136	1.98*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	1.45*10 ⁻⁰²	1.07 (1.01 - 1.13)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs1907472	4	31838960	intergenic	A/G	0.4573	8.40*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	2.59*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs17365051	4	31845185	intergenic	T/C	0.4167	2.83*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	6.99*10 ⁻⁰¹	1.01 (0.97 - 1.04)
rs17299248	4	31845304	intergenic	G/A	0.4150	5.42*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	6.77*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs7673436	4	31863047	intergenic	T/G	0.4058	3.86*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	1.24*10 ⁻⁰²	1.07 (1.02 - 1.14)
rs902658	4	31864983	intergenic	T/C	0.4052	5.95*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.94*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs902660	4	31865092	intergenic	C/A	0.4588	7.51*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	4.66*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs2404759	4	31865170	intergenic	A/C	0.4047	6.91*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	3.06*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs874498	4	31865900	intergenic	T/C	0.4043	6.31*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.88*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs10001109	4	44599410	intergenic	T/C	0.9039	5.23*10 ⁻⁰⁴	1.28 (1.11 - 1.48)	1.73*10 ⁻⁰²	1.08 (1.01 - 1.14)
rs13106834	4	55196485	intergenic	A/G	0.5343	4.82*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	9.00*10 ⁻⁰¹	1.00 (0.96 - 1.04)
rs17086853	4	57047076	SRP72	A/G	0.8234	9.49*10 ⁻⁰⁴	1.19 (1.07 - 1.33)	1.83*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs869894	4	71086741	intergenic	C/A	0.5648	9.04*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	7.05*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs1825032	4	71241407	C4orf35	C/T	0.6124	3.85*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	6.12*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs17146505	4	71326067	intergenic	T/C	0.8873	1.12*10 ⁻⁰⁴	1.29 (1.13 - 1.47)	2.31*10 ⁻⁰²	1.08 (1.01 - 1.16)
rs16996713	4	75989935	intergenic	G/T	0.9174	2.37*10 ⁻⁰⁴	1.32 (1.14 - 1.54)	7.00*10 ⁻⁰²	1.08 (0.99 - 1.17)
rs1580043	4	75992411	intergenic	A/C	0.9162	3.40*10 ⁻⁰⁴	1.31 (1.13 - 1.52)	1.26*10 ⁻⁰¹	1.06 (0.98 - 1.14)
rs16999967	4	76016027	intergenic	A/C	0.9160	8.35*10 ⁻⁰⁴	1.28 (1.11 - 1.49)	1.59*10 ⁻⁰¹	1.06 (0.98 - 1.14)
rs10518131	4	76018616	intergenic	C/T	0.9168	5.00*10 ⁻⁰⁴	1.3 (1.12 - 1.51)	1.78*10 ⁻⁰¹	1.05 (0.98 - 1.12)
rs17248248	4	76031071	intergenic	G/A	0.9163	3.77*10 ⁻⁰⁴	1.31 (1.13 - 1.51)	1.26*10 ⁻⁰¹	1.05 (0.99 - 1.13)
rs7660335	4	76034905	intergenic	C/G	0.9163	3.77*10 ⁻⁰⁴	1.31 (1.13 - 1.51)	1.19*10 ⁻⁰¹	1.06 (0.99 - 1.13)
rs7668508	4	76038964	intergenic	G/C	0.9170	2.99*10 ⁻⁰⁴	1.31 (1.13 - 1.52)	1.43*10 ⁻⁰¹	1.06 (0.98 - 1.14)
rs6533486	4	76078596	AC110760.3	C/T	0.9087	2.99*10 ⁻⁰⁴	1.3 (1.13 - 1.5)	3.62*10 ⁻⁰¹	1.03 (0.97 - 1.10)
rs17248887	4	76080991	AC110760.3	G/A	0.9073	7.20*10 ⁻⁰⁴	1.27 (1.11 - 1.47)	4.56*10 ⁻⁰¹	1.03 (0.96 - 1.10)
rs7666000	4	77643030	SHROOM3	G/A	0.8561	2.71*10 ⁻⁰⁴	1.24 (1.1 - 1.39)	7.93*10 ⁻⁰⁴	1.10 (1.04 - 1.16)
rs7696372	4	77643191	SHROOM3	T/C	0.8564	3.43*10 ⁻⁰⁴	1.23 (1.1 - 1.39)	4.55*10 ⁻⁰⁴	1.10 (1.04 - 1.16)
rs6532433	4	77643282	SHROOM3	T/C	0.8565	3.69*10 ⁻⁰⁴	1.23 (1.1 - 1.38)	1.09*10 ⁻⁰³	1.09 (1.04 - 1.16)
rs17012341	4	88202140	AFF1	A/T	0.0239	1.41*10 ⁻⁰⁴	1.62 (1.25 - 2.08)	9.15*10 ⁻⁰¹	1.01 (0.89 - 1.14)
rs236990	4	88234410	AFF1	G/A	0.0250	4.68*10 ⁻⁰⁴	1.54 (1.2 - 1.97)	6.48*10 ⁻⁰¹	1.03 (0.9 - 1.18)
rs17012552	4	88345242	KLHL8, AC092658.2	T/C	0.0345	1.21*10 ⁻⁰⁴	1.44 (1.17 - 1.79)	3.81*10 ⁻⁰¹	1.07 (0.92 - 1.24)
rs10012150	4	89124819	SPP1	C/T	0.2201	1.92*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	1.58*10 ⁻⁰¹	1.04 (0.99 - 1.09)
rs2658535	4	103190039	BANK1	A/G	0.5619	9.01*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	4.14*10 ⁻⁰³	1.09 (1.03 - 1.15)
rs1395306	4	103204873	BANK1	T/C	0.5585	7.38*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	9.93*10 ⁻⁰²	1.04 (0.99 - 1.08)
rs2129292	4	103210162	BANK1	G/C	0.5596	8.30*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	7.69*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs7675363	4	103217890	BANK1	T/C	0.5613	2.15*10 ⁻⁰⁴	1.16 (1.08 - 1.26)	3.64*10 ⁻⁰³	1.06 (1.02 - 1.10)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs1506504	4	103266786	intergenic	C/T	0.5629	8.50*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	5.36*10 ⁻⁰²	1.04 (1.00 - 1.09)
rs1216413	4	129749566	intergenic	A/G	0.6617	8.55*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	8.70*10 ⁻⁰²	1.04 (0.99 - 1.08)
rs17401445	4	129751887	intergenic	T/C	0.6653	1.86*10 ⁻⁰⁴	1.18 (1.08 - 1.28)	8.74*10 ⁻⁰²	1.03 (1.00 - 1.08)
rs4975242	4	129752818	intergenic	T/A	0.6629	8.57*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	8.95*10 ⁻⁰²	1.04 (0.99 - 1.08)
rs6822222	4	136981443	intergenic	G/T	0.8962	7.82*10 ⁻⁰⁴	1.23 (1.08 - 1.41)	4.14*10 ⁻⁰¹	1.03 (0.96 - 1.09)
rs12646936	4	136982089	intergenic	G/T	0.7513	2.19*10 ⁻⁰⁷	1.25 (1.14 - 1.38)	1.98*10 ⁻⁰⁴	1.08 (1.04 - 1.13)
rs1115338	4	137402957	intergenic	C/A	0.9489	1.02*10 ⁻⁰⁴	1.38 (1.15 - 1.67)	5.06*10 ⁻⁰²	1.14 (1.00 - 1.30)
rs17644158	4	138347295	intergenic	G/T	0.1756	2.44*10 ⁻⁰⁴	1.22 (1.1 - 1.35)	7.19*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs2138071	4	138373178	AC060835.7	A/G	0.4905	2.50*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	6.80*10 ⁻⁰³	1.05 (1.01 - 1.09)
rs1822841	4	145062088	intergenic	G/T	0.3226	2.77*10 ⁻⁰⁴	1.15 (1.06 - 1.26)	4.21*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs7686794	4	145068523	intergenic	G/A	0.3229	2.75*10 ⁻⁰⁴	1.15 (1.06 - 1.26)	1.64*10 ⁻⁰¹	1.04 (0.98 - 1.11)
rs4407483	4	150076291	intergenic	C/T	0.1166	2.50*10 ⁻⁰⁴	1.23 (1.09 - 1.4)	1.11*10 ⁻⁰²	1.12 (1.03 - 1.22)
rs1124359	4	151338803	DCLK2	A/G	0.0656	9.13*10 ⁻⁰⁴	1.31 (1.12 - 1.54)	1.78*10 ⁻⁰¹	1.06 (0.97 - 1.15)
rs17504359	4	151526571	LRBA	G/C	0.1765	9.77*10 ⁻⁰⁴	1.19 (1.07 - 1.32)	2.68*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs12499470	4	151540691	LRBA	C/A	0.1766	7.96*10 ⁻⁰⁴	1.19 (1.07 - 1.32)	2.63*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs2036552	4	151617209	LRBA	G/A	0.1757	4.80*10 ⁻⁰⁴	1.2 (1.08 - 1.33)	3.08*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs35198214	4	152406827	intergenic	A/G	0.0610	3.90*10 ⁻⁰⁴	1.32 (1.12 - 1.56)	2.21*10 ⁻⁰³	1.19 (1.07 - 1.33)
rs7676376	4	158061609	PDGFC	C/T	0.7157	6.08*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	1.25*10 ⁻⁰¹	1.04 (0.99 - 1.09)
rs1505387	4	165583359	intergenic	A/C	0.1995	6.00*10 ⁻⁰⁵	1.2 (1.09 - 1.32)	1.96*10 ⁻⁰²	1.09 (1.01 - 1.16)
rs325597	4	165602971	intergenic	T/C	0.1817	1.11*10 ⁻⁰⁴	1.19 (1.08 - 1.32)	1.04*10 ⁻⁰²	1.06 (1.01 - 1.11)
rs1587920	4	165608336	intergenic	A/G	0.1785	9.59*10 ⁻⁰⁵	1.2 (1.08 - 1.33)	6.81*10 ⁻⁰³	1.07 (1.02 - 1.12)
rs1463926	4	165628896	intergenic	C/A	0.1842	6.96*10 ⁻⁰⁵	1.19 (1.08 - 1.32)	2.46*10 ⁻⁰²	1.06 (1.01 - 1.12)
rs12511498	4	168890172	intergenic	C/G	0.2087	2.08*10 ⁻⁰⁴	1.18 (1.07 - 1.31)	8.08*10 ⁻⁰³	1.08 (1.02 - 1.14)
rs4331802	4	168892949	intergenic	G/T	0.2325	1.18*10 ⁻⁰⁵	1.2 (1.09 - 1.32)	1.90*10 ⁻⁰³	1.11 (1.04 - 1.19)
rs7686609	4	168895506	intergenic	G/A	0.2580	8.17*10 ⁻⁰⁵	1.17 (1.07 - 1.28)	1.12*10 ⁻⁰⁴	1.10 (1.05 - 1.16)
rs11131794	4	168896676	intergenic	G/A	0.2317	3.43*10 ⁻⁰⁶	1.21 (1.11 - 1.33)	1.13*10 ⁻⁰⁴	1.09 (1.04 - 1.14)
rs1507696	4	171684809	intergenic	T/C	0.3369	9.29*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	2.86*10 ⁻⁰⁶	1.12 (1.07 - 1.17)
rs2612412	4	171695929	intergenic	A/G	0.3380	4.03*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	2.03*10 ⁻⁰⁵	1.09 (1.05 - 1.13)
rs368771	4	171750312	HSP90AA6P	C/A	0.3343	5.07*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	9.11*10 ⁻⁰⁶	1.09 (1.05 - 1.13)
rs4692845	4	171771856	intergenic	A/G	0.3363	5.15*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	6.57*10 ⁻⁰⁶	1.09 (1.05 - 1.13)
rs1348330	4	171789432	intergenic	C/T	0.3376	2.79*10 ⁻⁰⁴	1.17 (1.08 - 1.27)	6.44*10 ⁻⁰⁶	1.09 (1.05 - 1.13)
rs1533835	4	171881782	intergenic	T/G	0.0323	3.61*10 ⁻⁰⁴	1.49 (1.2 - 1.86)	7.10*10 ⁻⁰³	1.16 (1.04 - 1.29)
rs17059546	4	174689637	HAND2	C/T	0.2524	1.19*10 ⁻⁰⁴	1.2 (1.09 - 1.31)	1.57*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs2010595	4	182852097	intergenic	T/G	0.8444	7.28*10 ⁻⁰⁵	1.26 (1.12 - 1.42)	4.16*10 ⁻⁰¹	1.02 (0.97 - 1.07)
rs715654	4	182852487	intergenic	G/A	0.8384	2.42*10 ⁻⁰⁵	1.27 (1.14 - 1.42)	3.83*10 ⁻⁰¹	1.02 (0.97 - 1.07)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs7696504	4	182853489	intergenic	G/C	0.8385	4.71*10 ⁻⁰⁵	1.26 (1.13 - 1.41)	4.60*10 ⁻⁰¹	1.02 (0.97 - 1.07)
rs7697691	4	182853951	intergenic	A/G	0.8381	6.88*10 ⁻⁰⁵	1.25 (1.12 - 1.4)	3.93*10 ⁻⁰¹	1.02 (0.97 - 1.07)
rs35306465	4	183306697	AC108142.1	C/G	0.1008	5.48*10 ⁻⁰⁴	1.25 (1.1 - 1.43)	2.37*10 ⁻⁰³	1.15 (1.05 - 1.27)
rs12504307	4	186980251	SORBS2	G/C	0.5285	4.35*10 ⁻⁰⁵	1.19 (1.09 - 1.29)	8.63*10 ⁻⁰¹	1.00 (0.97 - 1.04)
rs1499012	4	186996149	SORBS2	G/A	0.2509	9.12*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	2.76*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs4241895	4	189765825	intergenic	C/T	0.2201	9.01*10 ⁻⁰⁴	1.17 (1.07 - 1.29)	5.10*10 ⁻⁰³	1.08 (1.02 - 1.14)
rs2099821	5	3276744	intergenic	A/G	0.1715	1.33*10 ⁻⁰⁴	1.19 (1.07 - 1.32)	6.07*10 ⁻⁰¹	1.01 (0.96 - 1.07)
rs12658153	5	3277850	intergenic	G/A	0.1709	9.45*10 ⁻⁰⁵	1.2 (1.08 - 1.33)	9.49*10 ⁻⁰¹	1.00 (0.95 - 1.05)
rs6892726	5	3288797	intergenic	T/C	0.1680	4.20*10 ⁻⁰⁵	1.2 (1.08 - 1.34)	9.31*10 ⁻⁰¹	1.00 (0.95 - 1.05)
rs13165026	5	3302967	intergenic	T/C	0.1597	5.33*10 ⁻⁰⁶	1.24 (1.11 - 1.38)	9.80*10 ⁻⁰¹	1.00 (0.95 - 1.06)
rs10462777	5	3847274	intergenic	C/T	0.1967	4.19*10 ⁻⁰⁴	1.2 (1.08 - 1.32)	4.02*10 ⁻⁰¹	1.02 (0.97 - 1.07)
rs4407602	5	4721289	intergenic	A/G	0.7377	2.23*10 ⁻⁰⁴	1.19 (1.08 - 1.3)	1.31*10 ⁻⁰³	1.07 (1.03 - 1.12)
rs835129	5	14964568	AC016575.7	G/A	0.4956	5.57*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.35*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs10077552	5	14964899	AC016575.7	T/C	0.4436	5.15*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	3.52*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs17579256	5	29918764	intergenic	T/G	0.8413	9.84*10 ⁻⁰⁴	1.2 (1.08 - 1.34)	8.39*10 ⁻⁰⁴	1.10 (1.04 - 1.17)
rs27573	5	55603506	intergenic	C/A	0.9452	7.71*10 ⁻⁰⁶	1.52 (1.26 - 1.84)	1.45*10 ⁻⁰²	1.12 (1.02 - 1.23)
rs4613646	5	65949148	MAST4	C/T	0.6552	7.43*10 ⁻⁰⁴	1.15 (1.06 - 1.26)	2.00*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs12521662	5	88117252	MEF2C	A/G	0.1495	1.88*10 ⁻⁰⁴	1.23 (1.1 - 1.37)	9.97*10 ⁻⁰⁴	1.10 (1.04 - 1.16)
rs10070532	5	88799971	intergenic	G/A	0.7199	5.65*10 ⁻⁰⁵	1.2 (1.1 - 1.32)	5.98*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs27515	5	111424577	intergenic	G/T	0.0464	5.13*10 ⁻⁰⁴	1.39 (1.15 - 1.68)	1.58*10 ⁻⁰¹	1.06 (0.98 - 1.16)
rs163622	5	111821853	intergenic	T/C	0.0587	3.77*10 ⁻⁰⁴	1.35 (1.14 - 1.6)	3.32*10 ⁻⁰¹	1.06 (0.94 - 1.19)
rs13181732	5	112752677	MCC	T/C	0.8137	3.09*10 ⁻⁰⁴	1.21 (1.09 - 1.35)	7.59*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs269498	5	114685142	intergenic	A/G	0.8999	6.16*10 ⁻⁰⁴	1.27 (1.11 - 1.45)	1.51*10 ⁻⁰¹	1.05 (0.98 - 1.12)
rs13357651	5	115286854	intergenic	G/A	0.9576	1.58*10 ⁻⁰⁴	1.5 (1.21 - 1.85)	1.07*10 ⁻⁰⁴	1.32 (1.15 - 1.53)
rs3861862	5	141822876	intergenic	C/G	0.8926	4.95*10 ⁻⁰⁴	1.27 (1.11 - 1.45)	4.16*10 ⁻⁰¹	1.03 (0.96 - 1.09)
rs13184016	5	145140536	PRELID2	C/T	0.9620	5.93*10 ⁻⁰⁴	1.47 (1.18 - 1.83)	8.80*10 ⁻⁰¹	1.02 (0.81 - 1.28)
rs304842	5	152763791	intergenic	T/C	0.3454	8.81*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	2.94*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs1874161	5	157548288	intergenic	C/A	0.9276	7.51*10 ⁻⁰⁵	1.34 (1.14 - 1.57)	4.47*10 ⁻⁰¹	1.03 (0.95 - 1.11)
rs1874160	5	157548726	intergenic	C/T	0.9266	8.70*10 ⁻⁰⁵	1.34 (1.14 - 1.57)	5.91*10 ⁻⁰¹	1.02 (0.95 - 1.10)
rs11746023	5	157579894	intergenic	C/T	0.8424	4.47*10 ⁻⁰⁴	1.21 (1.08 - 1.35)	3.38*10 ⁻⁰¹	1.03 (0.97 - 1.09)
rs4704967	5	158192277	EBF1	G/T	0.7720	9.94*10 ⁻⁰⁴	1.17 (1.07 - 1.29)	6.01*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs6868079	5	164043770	intergenic	A/G	0.1318	3.10*10 ⁻⁰⁴	1.24 (1.1 - 1.39)	9.03*10 ⁻⁰¹	1.00 (0.95 - 1.06)
rs11739137	5	164115462	intergenic	G/C	0.1333	8.62*10 ⁻⁰⁴	1.22 (1.08 - 1.36)	7.92*10 ⁻⁰¹	1.01 (0.95 - 1.06)
rs10462960	5	166058138	intergenic	T/G	0.0355	5.13*10 ⁻⁰⁴	1.45 (1.17 - 1.79)	2.13*10 ⁻⁰²	1.14 (1.02 - 1.26)
rs10067964	5	168458268	SLIT3	T/C	0.6715	2.45*10 ⁻⁰⁴	1.17 (1.08 - 1.28)	1.34*10 ⁻⁰¹	1.04 (0.99 - 1.09)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs703745	5	174726970	intergenic	A/G	0.7150	2.59*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	8.58*10 ⁻⁰¹	1.00 (0.96 - 1.05)
rs2303010	5	179684637	GFPT2	T/C	0.0108	9.48*10 ⁻⁰⁴	1.85 (1.26 - 2.71)	2.74*10 ⁻⁰²	1.40 (1.04 - 1.89)
rs2505675	6	2300674	intergenic	C/T	0.6913	9.57*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	1.36*10 ⁻⁰²	1.06 (1.01 - 1.10)
rs9328347	6	6219946	F13A1	A/G	0.1563	4.87*10 ⁻⁰⁴	1.22 (1.09 - 1.36)	2.86*10 ⁻⁰¹	1.03 (0.98 - 1.09)
rs9396814	6	10126510	intergenic	T/C	0.2785	8.06*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	1.72*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs9383331	6	10126740	intergenic	G/A	0.2785	8.74*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	8.12*10 ⁻⁰²	1.04 (0.99 - 1.09)
rs1267505	6	14822174	intergenic	T/C	0.8099	5.83*10 ⁻⁰⁴	1.2 (1.08 - 1.33)	8.49*10 ⁻⁰¹	1.00 (0.96 - 1.05)
rs1267500	6	14823804	intergenic	T/C	0.8118	7.99*10 ⁻⁰⁴	1.19 (1.08 - 1.32)	7.77*10 ⁻⁰¹	1.01 (0.96 - 1.05)
rs1267496	6	14823996	intergenic	C/G	0.8098	3.10*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	5.91*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs1267495	6	14824016	intergenic	T/C	0.8099	3.55*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	6.43*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs1267494	6	14824189	intergenic	C/G	0.8200	7.17*10 ⁻⁰⁴	1.2 (1.08 - 1.33)	6.94*10 ⁻⁰¹	1.01 (0.96 - 1.06)
rs17119	6	14827475	intergenic	A/G	0.8058	2.98*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	6.81*10 ⁻⁰¹	1.01 (0.96 - 1.06)
rs1267488	6	14827973	intergenic	A/G	0.8325	9.71*10 ⁻⁰⁴	1.2 (1.08 - 1.34)	7.58*10 ⁻⁰¹	1.01 (0.96 - 1.06)
rs4712625	6	21807321	intergenic	A/G	0.1360	8.03*10 ⁻⁰⁴	1.22 (1.09 - 1.37)	5.89*10 ⁻⁰³	1.12 (1.03 - 1.22)
rs1610585	6	29783655	AL844851.4-205, ZDHHHC20P1, AL669813.6-206	C/G	0.2876	4.50*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	7.71*10 ⁻⁰³	1.06 (1.01 - 1.10)
rs1610586	6	29784295	AL844851.4-205, ZDHHHC20P1, AL669813.6-206	T/C	0.2871	5.45*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	7.86*10 ⁻⁰³	1.06 (1.01 - 1.10)
rs1611356	6	29786995	AL844851.4-205, ZDHHHC20P1, AL669813.6-206	C/G	0.2873	7.27*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	1.42*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs1611381	6	29788471	AL844851.4-205, ZDHHHC20P1, AL669813.6-206	T/C	0.2873	7.08*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	1.28*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs2272874	6	29804224	AL669813.6-201, HLA-F, AL669813.6-202, AL844851.4-202, AL844851.4-203, AL645939.6-204, HCG4P11, AL844851.4-207, AL669813.6-207	C/T	0.1144	8.07*10 ⁻⁰⁴	1.23 (1.09 - 1.39)	1.17*10 ⁻⁰¹	1.05 (0.99 - 1.12)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs521977	6	31944806	SLC44A4, AL662834.8-207, AL844853.23-210 AL662834.8-205,	G/T	0.7466	6.97*10 ⁻⁰⁴	1.17 (1.06 - 1.28)	1.65*10 ⁻⁰²	1.08 (1.01 - 1.15)
rs486416	6	31964049	HLA-DRB5, EHMT2, AL844853.23-209	A/G	0.7078	2.73*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	1.21*10 ⁻⁰³	1.08 (1.03 - 1.12)
rs3115572	6	32328462	HLA-DRB5	G/C	0.6442	9.46*10 ⁻⁰⁴	1.13 (1.03 - 1.22)	3.08*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs9366917	6	36898644	CPNE5	G/A	0.7541	1.53*10 ⁻⁰⁴	1.2 (1.09 - 1.32)	7.74*10 ⁻⁰¹	1.01 (0.96 - 1.05)
rs4302661	6	39672207	KIF6	C/T	0.8226	6.57*10 ⁻⁰⁴	1.2 (1.08 - 1.33)	1.22*10 ⁻⁰²	1.07 (1.01 - 1.12)
rs10948714	6	52637625	RP1-152L7.5	A/C	0.7974	6.23*10 ⁻⁰⁴	1.2 (1.08 - 1.32)	2.64*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs16879841	6	64677764	intergenic	A/G	0.2647	2.81*10 ⁻⁰⁴	1.18 (1.08 - 1.29)	3.28*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs4535528	6	64681158	intergenic	T/C	0.2625	3.01*10 ⁻⁰⁴	1.18 (1.08 - 1.29)	3.84*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs397228	6	64684551	intergenic	C/T	0.2629	3.64*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	3.96*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs7757616	6	64712492	intergenic	A/C	0.2965	1.52*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	1.08*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs7753314	6	64716611	intergenic	T/G	0.3092	1.89*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	1.48*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs3806095	6	71044697	COL9A1	A/G	0.3112	8.70*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	4.89*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs12207159	6	76609496	MYO6	T/C	0.0359	7.98*10 ⁻⁰⁵	1.52 (1.23 - 1.87)	2.27*10 ⁻⁰¹	1.06 (0.96 - 1.17)
rs10943829	6	82456630	intergenic	A/G	0.4882	1.06*10 ⁻⁰⁴	1.17 (1.08 - 1.27)	6.78*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs194877	6	82463596	intergenic	C/T	0.5042	6.43*10 ⁻⁰⁵	1.18 (1.09 - 1.28)	1.33*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs915125	6	82520095	FAM46A	T/C	0.2944	6.39*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	3.28*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs9361858	6	82520935	FAM46A	G/T	0.4310	1.07*10 ⁻⁰⁵	1.2 (1.1 - 1.3)	1.33*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs1034241	6	82530672	SNORA70, RP5-991C6.2	T/A	0.9120	8.43*10 ⁻⁰⁴	1.26 (1.09 - 1.46)	1.68*10 ⁻⁰⁴	1.14 (1.06 - 1.21)
rs16893523	6	82560898	intergenic	G/A	0.9113	2.99*10 ⁻⁰⁴	1.31 (1.13 - 1.51)	1.54*10 ⁻⁰⁵	1.15 (1.08 - 1.23)
rs16893526	6	82572034	intergenic	G/A	0.9123	8.71*10 ⁻⁰⁴	1.26 (1.09 - 1.46)	9.21*10 ⁻⁰⁵	1.14 (1.07 - 1.22)
rs9344225	6	82581262	intergenic	G/C	0.8567	3.55*10 ⁻⁰⁴	1.21 (1.08 - 1.36)	1.36*10 ⁻⁰¹	1.04 (0.99 - 1.10)
rs13197670	6	82626603	intergenic	G/C	0.9223	1.98*10 ⁻⁰⁴	1.31 (1.12 - 1.52)	1.54*10 ⁻⁰⁶	1.19 (1.11 - 1.27)
rs592728	6	87477371	intergenic	T/C	0.9031	7.30*10 ⁻⁰⁴	1.27 (1.1 - 1.46)	4.15*10 ⁻⁰³	1.10 (1.03 - 1.17)
rs13194247	6	92743791	intergenic	G/A	0.2228	1.46*10 ⁻⁰⁴	1.2 (1.09 - 1.33)	1.89*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs9377366	6	102998331	intergenic	G/A	0.4009	2.77*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	2.67*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs9404214	6	103080821	intergenic	G/A	0.3931	7.07*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	5.53*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs571060	6	112403213	intergenic	T/C	0.9688	7.44*10 ⁻⁰⁴	1.52 (1.19 - 1.95)	2.13*10 ⁻⁰³	1.19 (1.07 - 1.33)
rs9385199	6	121879013	intergenic	A/G	0.4272	3.65*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	9.21*10 ⁻⁰²	1.03 (0.99 - 1.08)
rs2040424	6	122166793	intergenic	T/C	0.2296	2.79*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	1.74*10 ⁻⁰²	1.06 (1.01 - 1.10)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs10457626	6	134814920	intergenic	T/C	0.4928	8.12*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	7.00*10 ⁻⁰³	1.05 (1.01 - 1.09)
rs12526230	6	137752459	intergenic	G/A	0.8161	4.82*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	1.10*10 ⁻⁰¹	1.04 (0.99 - 1.09)
rs17077870	6	148369321	intergenic	G/C	0.2166	3.84*10 ⁻⁰⁴	1.19 (1.08 - 1.32)	5.27*10 ⁻⁰³	1.07 (1.02 - 1.12)
rs6938902	6	148369869	intergenic	T/C	0.2162	3.30*10 ⁻⁰⁴	1.2 (1.09 - 1.32)	6.04*10 ⁻⁰³	1.07 (1.02 - 1.12)
rs1404485	6	148370023	intergenic	T/G	0.2153	1.93*10 ⁻⁰⁴	1.2 (1.09 - 1.33)	9.21*10 ⁻⁰³	1.07 (1.02 - 1.12)
rs1404484	6	148370060	intergenic	T/C	0.2164	2.77*10 ⁻⁰⁴	1.2 (1.09 - 1.32)	5.09*10 ⁻⁰³	1.07 (1.02 - 1.13)
rs9399630	6	148379354	intergenic	C/G	0.2141	2.13*10 ⁻⁰⁴	1.2 (1.09 - 1.33)	3.37*10 ⁻⁰³	1.08 (1.02 - 1.13)
rs7765812	6	148380733	intergenic	A/G	0.3378	6.22*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	1.20*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs9383934	6	151963030	C6orf97	T/A	0.1884	9.81*10 ⁻⁰⁴	1.18 (1.07 - 1.31)	4.76*10 ⁻⁰¹	1.02 (0.97 - 1.07)
rs9383935	6	151981541	C6orf97, U6	T/C	0.0799	3.40*10 ⁻⁰⁴	1.31 (1.13 - 1.51)	3.36*10 ⁻⁰¹	1.03 (0.97 - 1.11)
rs12665607	6	151988322	C6orf97	A/T	0.0817	2.05*10 ⁻⁰⁴	1.31 (1.14 - 1.52)	2.56*10 ⁻⁰¹	1.04 (0.97 - 1.11)
rs9397436	6	151993695	intergenic	G/A	0.0725	3.46*10 ⁻⁰⁴	1.32 (1.13 - 1.53)	2.11*10 ⁻⁰¹	1.05 (0.97 - 1.14)
rs294917	6	159547065	FNDC1	T/C	0.2359	7.56*10 ⁻⁰⁴	1.17 (1.07 - 1.29)	4.58*10 ⁻⁰⁵	1.11 (1.05 - 1.16)
rs444245	6	159562951	FNDC1	T/C	0.2357	4.40*10 ⁻⁰⁴	1.18 (1.07 - 1.29)	6.97*10 ⁻⁰⁵	1.14 (1.07 - 1.22)
rs2782552	6	159563684	FNDC1	A/C	0.2393	2.25*10 ⁻⁰⁴	1.18 (1.07 - 1.29)	3.25*10 ⁻⁰⁵	1.11 (1.06 - 1.16)
rs365302	6	159566321	FNDC1	C/T	0.2393	3.72*10 ⁻⁰⁴	1.17 (1.07 - 1.29)	3.24*10 ⁻⁰⁵	1.11 (1.06 - 1.16)
rs12193425	6	170614147	intergenic	G/A	0.8436	4.33*10 ⁻⁰⁴	1.22 (1.09 - 1.37)	8.32*10 ⁻⁰³	1.07 (1.02 - 1.13)
rs7792601	7	4350550	intergenic	T/C	0.7623	3.90*10 ⁻⁰⁴	1.19 (1.08 - 1.3)	2.97*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs12668791	7	4352868	intergenic	T/C	0.1060	4.60*10 ⁻⁰⁴	1.24 (1.09 - 1.41)	8.15*10 ⁻⁰¹	1.01 (0.94 - 1.09)
rs2097903	7	10648934	intergenic	T/A	0.5048	2.69*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	2.89*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs2079389	7	10649158	intergenic	T/C	0.5048	2.68*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	3.04*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs17526402	7	10649450	intergenic	A/C	0.5046	3.07*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	3.10*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs2059448	7	23921770	intergenic	T/C	0.7529	6.62*10 ⁻⁰⁴	1.18 (1.07 - 1.29)	1.40*10 ⁻⁰¹	1.04 (0.99 - 1.09)
rs10252043	7	23927625	intergenic	G/A	0.6189	1.12*10 ⁻⁰⁴	1.18 (1.08 - 1.28)	9.73*10 ⁻⁰¹	1.00 (0.96 - 1.04)
rs774257	7	26943717	intergenic	G/A	0.8755	5.66*10 ⁻⁰⁵	1.26 (1.11 - 1.43)	1.74*10 ⁻⁰¹	1.04 (0.98 - 1.10)
rs13243958	7	33979703	BMPER	T/G	0.6432	3.25*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	1.21*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs7791331	7	37521323	intergenic	G/A	0.3552	4.92*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	5.78*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs2598098	7	37946977	EPDR1	A/T	0.6642	8.16*10 ⁻⁰⁵	1.19 (1.09 - 1.29)	3.45*10 ⁻⁰²	1.07 (1.00 - 1.13)
rs6974655	7	42141121	GLI3	T/G	0.2625	1.85*10 ⁻⁰⁴	1.19 (1.09 - 1.3)	3.11*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs13231378	7	47049803	intergenic	C/T	0.1152	4.48*10 ⁻⁰⁴	1.24 (1.1 - 1.41)	6.68*10 ⁻⁰¹	1.01 (0.96 - 1.07)
rs10240369	7	51675610	intergenic	T/C	0.0438	1.76*10 ⁻⁰⁴	1.41 (1.17 - 1.7)	1.03*10 ⁻⁰¹	1.08 (0.98 - 1.19)
rs10234700	7	51684178	intergenic	A/C	0.0441	6.96*10 ⁻⁰⁵	1.42 (1.18 - 1.72)	2.07*10 ⁻⁰¹	1.06 (0.97 - 1.16)
rs4718795	7	67739216	intergenic	C/A	0.9272	3.97*10 ⁻⁰⁴	1.32 (1.12 - 1.55)	2.66*10 ⁻⁰³	1.12 (1.04 - 1.21)
rs798334	7	77749883	MAGI2	A/G	0.8533	1.00*10 ⁻⁰⁴	1.26 (1.12 - 1.41)	2.76*10 ⁻⁰¹	1.03 (0.97 - 1.09)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs11974883	7	77906460	MAGI2	G/A	0.0244	7.17*10 ⁻⁰⁴	1.54 (1.2 - 1.98)	1.79*10 ⁻⁰¹	1.08 (0.96 - 1.22)
rs12532467	7	78722789	MAGI2	A/G	0.3381	7.29*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	3.20*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs10225262	7	78725861	MAGI2	A/C	0.3313	7.08*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	3.16*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs6952164	7	78728534	MAGI2	G/A	0.3386	6.53*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	2.24*10 ⁻⁰¹	1.03 (0.98 - 1.07)
rs1528269	7	78749568	MAGI2	A/G	0.3355	3.86*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	2.69*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs8180764	7	82172260	intergenic	A/G	0.9621	1.39*10 ⁻⁰⁴	1.5 (1.2 - 1.87)	9.02*10 ⁻⁰¹	1.01 (0.91 - 1.11)
rs17156589	7	82176234	intergenic	C/A	0.9639	3.64*10 ⁻⁰⁴	1.51 (1.2 - 1.89)	9.53*10 ⁻⁰¹	1.00 (0.91 - 1.10)
rs10238984	7	82178197	intergenic	C/T	0.9637	6.32*10 ⁻⁰⁴	1.48 (1.18 - 1.86)	8.90*10 ⁻⁰³	1.21 (1.05 - 1.41)
rs10250565	7	82208757	intergenic	G/A	0.9782	5.12*10 ⁻⁰⁴	1.64 (1.22 - 2.2)	2.83*10 ⁻⁰¹	1.07 (0.94 - 1.23)
rs17647248	7	84582758	SEMA3D	T/A	0.4930	2.76*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	3.71*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs764077	7	84602330	intergenic	A/G	0.5009	1.23*10 ⁻⁰⁴	1.17 (1.08 - 1.27)	4.18*10 ⁻⁰¹	1.02 (0.98 - 1.05)
rs7779590	7	85937617	intergenic	A/G	0.6707	6.40*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	3.98*10 ⁻⁰²	1.06 (1.00 - 1.13)
rs12537221	7	85938945	intergenic	C/T	0.3160	2.14*10 ⁻⁰⁴	1.18 (1.08 - 1.29)	1.23*10 ⁻⁰¹	1.05 (0.99 - 1.11)
rs10952882	7	85942672	intergenic	G/A	0.5396	5.33*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	3.84*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs17161604	7	98620286	AC073468.9	T/G	0.0686	2.57*10 ⁻⁰⁴	1.34 (1.15 - 1.57)	6.02*10 ⁻⁰¹	1.02 (0.95 - 1.10)
rs12706029	7	114776192	intergenic	G/A	0.9388	8.23*10 ⁻⁰⁴	1.34 (1.13 - 1.59)	2.51*10 ⁻⁰¹	1.05 (0.97 - 1.13)
rs17228457	7	114819130	intergenic	C/T	0.9402	6.75*10 ⁻⁰⁴	1.35 (1.14 - 1.61)	2.59*10 ⁻⁰¹	1.04 (0.97 - 1.13)
rs1527741	7	114837951	intergenic	T/C	0.9386	8.93*10 ⁻⁰⁴	1.34 (1.13 - 1.59)	2.17*10 ⁻⁰¹	1.05 (0.97 - 1.13)
rs4645504	7	114874869	intergenic	C/T	0.9403	3.76*10 ⁻⁰⁴	1.37 (1.15 - 1.64)	5.89*10 ⁻⁰¹	1.02 (0.94 - 1.11)
rs17138675	7	115842764	intergenic	C/T	0.8938	3.04*10 ⁻⁰⁴	1.28 (1.12 - 1.46)	2.08*10 ⁻⁰²	1.12 (1.02 - 1.23)
rs11980527	7	130364161	intergenic	T/C	0.0392	2.29*10 ⁻⁰⁴	1.46 (1.19 - 1.78)	6.68*10 ⁻⁰¹	1.02 (0.92 - 1.14)
rs6951855	7	130375036	intergenic	A/T	0.0397	1.17*10 ⁻⁰⁴	1.48 (1.21 - 1.81)	2.93*10 ⁻⁰¹	1.07 (0.95 - 1.20)
rs6973492	7	130375154	intergenic	G/C	0.0396	1.99*10 ⁻⁰⁴	1.46 (1.2 - 1.78)	3.49*10 ⁻⁰¹	1.06 (0.94 - 1.19)
rs1514055	7	131329830	intergenic	C/A	0.0622	3.39*10 ⁻⁰⁴	1.32 (1.12 - 1.55)	1.58*10 ⁻⁰¹	1.07 (0.97 - 1.17)
rs17161447	7	139590942	U1	C/A	0.8918	3.23*10 ⁻⁰⁶	1.33 (1.16 - 1.52)	6.12*10 ⁻⁰⁴	1.12 (1.05 - 1.19)
rs6464620	7	139592008	U1	G/A	0.9072	9.17*10 ⁻⁰⁵	1.27 (1.1 - 1.47)	2.31*10 ⁻⁰¹	1.04 (0.97 - 1.11)
rs6950043	7	142270823	EPHB6	C/G	0.0279	9.91*10 ⁻⁰⁴	1.38 (1.09 - 1.74)	1.88*10 ⁻⁰²	1.14 (1.02 - 1.28)
rs4987612	7	142291790	TRPV6	C/T	0.0281	9.37*10 ⁻⁰⁴	1.38 (1.09 - 1.74)	1.99*10 ⁻⁰²	1.14 (1.02 - 1.28)
rs1676904	7	148287213	Y_RNA	G/A	0.1553	9.56*10 ⁻⁰⁴	1.2 (1.08 - 1.33)	5.24*10 ⁻⁰²	1.07 (1.00 - 1.15)
rs7801616	7	151083561	PRKAG2	T/C	0.4649	8.70*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	1.43*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs749120	7	154038740	DPP6	T/G	0.4216	1.20*10 ⁻⁰⁴	1.17 (1.08 - 1.27)	2.51*10 ⁻⁰²	1.04 (1.01 - 1.08)
rs10246702	7	154597467	intergenic	G/A	0.0849	7.38*10 ⁻⁰⁴	1.28 (1.11 - 1.48)	8.66*10 ⁻⁰³	1.10 (1.02 - 1.18)
rs10263087	7	154601402	7SK	G/C	0.0839	5.96*10 ⁻⁰⁴	1.29 (1.12 - 1.49)	9.15*10 ⁻⁰³	1.10 (1.02 - 1.18)
rs7798373	7	156951420	intergenic	C/T	0.8594	1.26*10 ⁻⁰⁴	1.26 (1.12 - 1.41)	6.07*10 ⁻⁰³	1.08 (1.02 - 1.14)
rs4716745	7	156954036	intergenic	T/C	0.8700	6.06*10 ⁻⁰⁴	1.23 (1.09 - 1.39)	2.46*10 ⁻⁰²	1.10 (1.01 - 1.19)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs7785035	7	156956293	intergenic	T/C	0.8427	5.62*10 ⁻⁰⁴	1.21 (1.09 - 1.36)	1.65*10 ⁻⁰¹	1.05 (0.98 - 1.14)
rs1806612	7	157679219	PTPRN2	C/T	0.3845	8.25*10 ⁻⁰⁵	1.18 (1.08 - 1.28)	5.25*10 ⁻⁰²	1.06 (1.00 - 1.12)
rs12546771	8	287118	intergenic	T/C	0.0631	7.21*10 ⁻⁰⁴	1.31 (1.12 - 1.53)	1.42*10 ⁻⁰¹	1.06 (0.98 - 1.15)
rs6980727	8	4961603	intergenic	C/T	0.5503	4.00*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	3.35*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs7841137	8	15589523	TUSC3	T/C	0.5173	1.28*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	4.91*10 ⁻⁰¹	1.01 (0.98 - 1.05)
rs1362865	8	15591821	TUSC3	T/C	0.5264	2.99*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.55*10 ⁻⁰²	1.07 (1.01 - 1.13)
rs7834392	8	26951349	intergenic	T/C	0.1279	6.94*10 ⁻⁰⁴	1.23 (1.09 - 1.38)	2.21*10 ⁻⁰¹	1.04 (0.98 - 1.11)
rs3943670	8	33599038	intergenic	T/C	0.5434	6.86*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	1.30*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs4733161	8	33617193	AC013603.17	C/T	0.5836	8.91*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	4.14*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs1838041	8	33644324	intergenic	C/T	0.6117	2.52*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	1.74*10 ⁻⁰²	1.07 (1.01 - 1.14)
rs1530345	8	33651668	intergenic	G/C	0.6153	6.07*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	4.01*10 ⁻⁰¹	1.02 (0.98 - 1.05)
rs4733163	8	33653826	intergenic	C/T	0.6154	5.74*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	3.95*10 ⁻⁰¹	1.02 (0.98 - 1.05)
rs1026217	8	35090459	intergenic	A/G	0.3613	9.96*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	9.97*10 ⁻⁰¹	1.00 (0.96 - 1.04)
rs1451355	8	35123428	intergenic	A/G	0.3382	1.51*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	4.41*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs10958811	8	38891319	PLEKHA2	A/C	0.1843	8.38*10 ⁻⁰⁴	1.19 (1.07 - 1.31)	6.47*10 ⁻⁰¹	1.01 (0.96 - 1.07)
rs6989571	8	40105536	intergenic	T/G	0.6158	3.08*10 ⁻⁰⁵	1.2 (1.1 - 1.3)	6.31*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs3906806	8	53538312	intergenic	A/G	0.4256	9.31*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	3.39*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs10958322	8	53539789	intergenic	T/C	0.4333	3.01*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	2.02*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs12544654	8	66265324	intergenic	T/C	0.7066	7.66*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	1.44*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs16939078	8	76554139	HNF4G	A/T	0.2639	4.03*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	5.54*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs2977942	8	76628378	HNF4G	G/T	0.0544	3.18*10 ⁻⁰⁵	1.44 (1.21 - 1.71)	5.40*10 ⁻⁰¹	1.03 (0.95 - 1.11)
rs2922778	8	76664902	intergenic	T/C	0.1216	3.83*10 ⁻⁰⁴	1.24 (1.1 - 1.4)	1.73*10 ⁻⁰²	1.09 (1.01 - 1.17)
rs7818923	8	76705115	intergenic	T/C	0.1213	4.22*10 ⁻⁰⁴	1.24 (1.1 - 1.4)	9.53*10 ⁻⁰¹	1.00 (0.94 - 1.07)
rs16886892	8	87202047	ATP6V0D2	G/A	0.1336	7.04*10 ⁻⁰⁴	1.22 (1.09 - 1.38)	6.19*10 ⁻⁰²	1.06 (1.00 - 1.12)
rs13282617	8	90099093	intergenic	C/G	0.9306	1.72*10 ⁻⁰⁴	1.36 (1.16 - 1.61)	9.88*10 ⁻⁰¹	1.00 (0.93 - 1.07)
rs6994748	8	97165066	intergenic	A/T	0.0658	3.67*10 ⁻⁰⁴	1.33 (1.14 - 1.56)	6.16*10 ⁻⁰¹	1.02 (0.94 - 1.10)
rs2704261	8	97672009	SDC2	G/A	0.7671	1.35*10 ⁻⁰⁴	1.18 (1.07 - 1.3)	2.50*10 ⁻⁰¹	1.03 (0.98 - 1.07)
rs2028086	8	97673354	SDC2	G/C	0.7708	1.70*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	2.85*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs2704259	8	97675483	SDC2	G/A	0.7649	2.46*10 ⁻⁰⁴	1.18 (1.07 - 1.3)	3.04*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs2981220	8	107902953	intergenic	T/C	0.9254	8.17*10 ⁻⁰⁴	1.31 (1.12 - 1.54)	8.52*10 ⁻⁰²	1.07 (0.99 - 1.15)
rs2981218	8	107904720	intergenic	T/G	0.9258	7.77*10 ⁻⁰⁴	1.32 (1.12 - 1.54)	8.66*10 ⁻⁰²	1.07 (0.99 - 1.15)
rs12542215	8	123571823	intergenic	G/C	0.8791	7.41*10 ⁻⁰⁴	1.24 (1.09 - 1.4)	3.90*10 ⁻⁰³	1.11 (1.03 - 1.19)
rs263239	8	131934200	ADCY8	A/G	0.1712	8.13*10 ⁻⁰⁴	1.2 (1.08 - 1.34)	6.72*10 ⁻⁰³	1.11 (1.03 - 1.19)
rs2597348	8	133541123	KCNQ3	C/T	0.3152	3.23*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	1.59*10 ⁻⁰²	1.06 (1.01 - 1.11)
rs2403775	8	133541544	KCNQ3	A/G	0.3145	3.36*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	3.97*10 ⁻⁰¹	1.02 (0.98 - 1.06)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs2673556	8	133546112	KCNQ3	G/C	0.2864	3.80*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	4.17*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs17617902	8	137187961	intergenic	A/G	0.3913	8.26*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.53*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs3936181	8	139775446	COL22A1	G/T	0.1789	2.86*10 ⁻⁰⁴	1.2 (1.08 - 1.33)	1.01*10 ⁻⁰¹	1.04 (0.99 - 1.09)
rs13282061	8	141369559	TRAPPC9	T/C	0.0532	3.33*10 ⁻⁰⁴	1.36 (1.15 - 1.63)	6.61*10 ⁻⁰²	1.09 (0.99 - 1.20)
rs7865812	9	4160979	GLIS3	A/C	0.4958	9.21*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	2.17*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs4326470	9	14684536	ZDHHC21, AL159169.14	C/A	0.1808	2.77*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	7.37*10 ⁻⁰¹	1.01 (0.96 - 1.06)
rs9650683	9	15447801	SNAPC3	G/C	0.0873	6.16*10 ⁻⁰⁴	1.27 (1.11 - 1.46)	1.59*10 ⁻⁰²	1.10 (1.02 - 1.18)
rs6475535	9	21440474	AL353732.14-201	C/G	0.1391	1.49*10 ⁻⁰⁴	1.25 (1.11 - 1.4)	1.49*10 ⁻⁰³	1.14 (1.05 - 1.23)
rs1889680	9	21685460	AL355679.20, RP11-473O3.1	T/C	0.4785	2.13*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	1.14*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs1452658	9	21690795	AL355679.20, RP11-473O3.1	G/A	0.4744	2.42*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	4.54*10 ⁻⁰⁴	1.07 (1.03 - 1.11)
rs10811584	9	21691005	AL355679.20, RP11-473O3.1	T/G	0.4748	3.07*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	3.48*10 ⁻⁰⁴	1.07 (1.03 - 1.11)
rs7848524	9	21691432	AL355679.20, RP11-473O3.1	T/C	0.4793	7.25*10 ⁻⁰⁵	1.18 (1.09 - 1.28)	6.97*10 ⁻⁰⁵	1.08 (1.04 - 1.12)
rs6475552	9	21691674	AL355679.20, RP11-473O3.1	G/A	0.4739	4.65*10 ⁻⁰⁴	1.15 (1.07 - 1.25)	3.52*10 ⁻⁰⁴	1.07 (1.03 - 1.11)
rs643319	9	22007836	MTAP	C/A	0.5302	7.11*10 ⁻⁰⁵	1.16 (1.07 - 1.25)	1.92*10 ⁻¹⁴	1.17 (1.13 - 1.22)
rs7044859	9	22008781	MTAP	A/T	0.4586	2.03*10 ⁻⁰⁵	1.17 (1.08 - 1.27)	7.02*10 ⁻²⁴	1.21 (1.16 - 1.25)
rs523096	9	22009129	MTAP	A/G	0.5653	4.05*10 ⁻⁰⁵	1.18 (1.09 - 1.28)	5.18*10 ⁻²²	1.20 (1.16 - 1.24)
rs518394	9	22009673	MTAP	G/C	0.5677	4.43*10 ⁻⁰⁵	1.18 (1.08 - 1.28)	1.16*10 ⁻¹⁸	1.18 (1.14 - 1.23)
rs10757264	9	22009732	MTAP	G/A	0.4957	6.99*10 ⁻⁰⁶	1.17 (1.08 - 1.27)	1.82*10 ⁻¹⁹	1.18 (1.14 - 1.23)
rs10965212	9	22013795	MTAP	A/T	0.4897	1.03*10 ⁻⁰⁴	1.17 (1.08 - 1.26)	1.39*10 ⁻²⁵	1.21 (1.17 - 1.26)
rs496892	9	22014351	MTAP	C/T	0.5346	1.75*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	6.45*10 ⁻⁰⁸	1.17 (1.10 - 1.23)
rs10965215	9	22019445	MTAP	A/G	0.4862	1.85*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	1.32*10 ⁻²⁵	1.21 (1.17 - 1.26)
rs564398	9	22019547	MTAP	T/C	0.5948	1.82*10 ⁻⁰⁴	1.17 (1.08 - 1.27)	1.77*10 ⁻²⁴	1.21 (1.17 - 1.26)
rs7865618	9	22021005	MTAP	A/G	0.5854	6.25*10 ⁻⁰⁵	1.18 (1.09 - 1.28)	3.94*10 ⁻²⁵	1.22 (1.17 - 1.26)
rs10965219	9	22043687	intergenic	G/A	0.4966	2.36*10 ⁻⁰⁵	1.18 (1.09 - 1.27)	2.02*10 ⁻²⁵	1.23 (1.18 - 1.27)
rs10120688	9	22046499	intergenic	A/G	0.4951	7.24*10 ⁻⁰⁵	1.16 (1.07 - 1.26)	1.57*10 ⁻²⁵	1.23 (1.18 - 1.27)
rs8181047	9	22054465	intergenic	G/A	0.6913	6.18*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	4.79*10 ⁻¹²	1.18 (1.13 - 1.24)
rs10757270	9	22062719	intergenic	G/A	0.4428	4.52*10 ⁻⁰⁵	1.16 (1.07 - 1.25)	2.30*10 ⁻¹³	1.23 (1.17 - 1.30)
rs6475606	9	22071850	intergenic	T/C	0.4947	9.49*10 ⁻⁰⁷	1.21 (1.12 - 1.31)	1.23*10 ⁻⁴³	1.29 (1.25 - 1.34)
rs10757272	9	22078260	intergenic	T/C	0.4955	4.56*10 ⁻⁰⁶	1.19 (1.1 - 1.29)	1.68*10 ⁻⁴³	1.29 (1.25 - 1.34)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs4977574	9	22088574	intergenic	G/A	0.4973	2.41*10 ⁻⁰⁶	1.2 (1.1 - 1.3)	1.04*10 ⁻⁴⁵	1.30 (1.26 - 1.35)
rs2891168	9	22088619	intergenic	G/A	0.4971	2.29*10 ⁻⁰⁶	1.2 (1.1 - 1.3)	1.48*10 ⁻⁴⁵	1.30 (1.26 - 1.35)
rs1333042	9	22093813	intergenic	G/A	0.5131	2.60*10 ⁻⁰⁷	1.22 (1.12 - 1.32)	7.30*10 ⁻⁴⁰	1.30 (1.25 - 1.35)
rs1333048	9	22115347	intergenic	C/A	0.5058	1.08*10 ⁻⁰⁶	1.2 (1.11 - 1.3)	8.78*10 ⁻⁴⁴	1.30 (1.25 - 1.34)
rs1333049	9	22115503	intergenic	C/G	0.4858	4.28*10 ⁻⁰⁷	1.22 (1.12 - 1.32)	1.80*10 ⁻⁴⁴	1.30 (1.25 - 1.35)
rs7871745	9	23299087	intergenic	G/C	0.0697	5.31*10 ⁻⁰⁴	1.22 (1.13 - 1.54)	9.31*10 ⁻⁰²	1.08 (0.99 - 1.19)
rs2210292	9	23351805	intergenic	A/G	0.1498	9.78*10 ⁻⁰⁴	1.2 (1.08 - 1.34)	3.01*10 ⁻⁰²	1.06 (1.01 - 1.13)
rs1360380	9	23368488	intergenic	G/T	0.4391	5.43*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	5.23*10 ⁻⁰⁴	1.10 (1.04 - 1.17)
rs1414030	9	29716239	intergenic	T/C	0.5198	6.83*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	6.49*10 ⁻⁰²	1.03 (1.00 - 1.07)
rs10813159	9	29728493	intergenic	T/A	0.5262	2.81*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	9.47*10 ⁻⁰²	1.03 (0.99 - 1.07)
rs11143665	9	75506161	intergenic	G/A	0.5415	1.18*10 ⁻⁰⁴	1.17 (1.08 - 1.27)	1.11*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs11143677	9	75525136	intergenic	A/G	0.5443	1.80*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	4.74*10 ⁻⁰⁶	1.14 (1.08 - 1.20)
rs11143678	9	75527223	intergenic	G/T	0.5473	1.64*10 ⁻⁰⁴	1.17 (1.08 - 1.26)	1.03*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs11143679	9	75527334	intergenic	T/C	0.5502	1.67*10 ⁻⁰⁴	1.17 (1.08 - 1.26)	1.92*10 ⁻⁰¹	1.02 (0.99 - 1.06)
rs11143683	9	75532226	intergenic	C/T	0.5476	1.21*10 ⁻⁰⁴	1.17 (1.08 - 1.27)	1.05*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs7029105	9	75534759	intergenic	C/T	0.5482	1.52*10 ⁻⁰⁴	1.17 (1.08 - 1.26)	1.01*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs1327827	9	76444930	RORB	C/T	0.9492	4.02*10 ⁻⁰⁴	1.4 (1.16 - 1.69)	1.45*10 ⁻⁰¹	1.08 (0.98 - 1.19)
rs6560438	9	77086652	intergenic	C/A	0.1065	1.20*10 ⁻⁰⁴	1.28 (1.13 - 1.46)	6.87*10 ⁻⁰²	1.05 (1.00 - 1.12)
rs12342299	9	77832048	PCSK5	T/C	0.0702	1.09*10 ⁻⁰⁵	1.38 (1.19 - 1.61)	5.79*10 ⁻⁰⁴	1.17 (1.07 - 1.27)
rs1027384	9	78122513	PCSK5	G/A	0.4665	7.36*10 ⁻⁰⁵	1.16 (1.07 - 1.26)	3.27*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs11144827	9	78123694	PCSK5	G/A	0.1635	9.12*10 ⁻⁰⁴	1.2 (1.08 - 1.33)	7.78*10 ⁻⁰³	1.08 (1.02 - 1.14)
rs10780688	9	86636264	NTRK2	G/A	0.4750	6.06*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.36*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs10868228	9	86637366	NTRK2	G/A	0.4801	7.66*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.24*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs10115908	9	86813205	NTRK2	A/G	0.4482	3.60*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	6.84*10 ⁻⁰¹	1.01 (0.97 - 1.04)
rs2200968	9	86841932	intergenic	C/T	0.3030	3.26*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	9.97*10 ⁻⁰¹	1.00 (0.96 - 1.04)
rs3012352	9	106165626	intergenic	C/T	0.2850	8.26*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	6.54*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs7865150	9	106252156	intergenic	A/G	0.3185	4.79*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	6.01*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs698458	9	106273931	intergenic	G/A	0.3020	8.77*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	5.06*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs698459	9	106273979	intergenic	G/T	0.3009	5.06*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	3.11*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs698460	9	106274039	intergenic	T/C	0.3018	6.15*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	3.49*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs1916675	9	106286225	intergenic	G/A	0.3366	6.20*10 ⁻⁰⁵	1.19 (1.09 - 1.29)	1.36*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs7032725	9	106290026	intergenic	C/G	0.6750	6.43*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	6.17*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs10820650	9	106297227	intergenic	C/T	0.3182	5.59*10 ⁻⁰⁵	1.19 (1.09 - 1.3)	2.20*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs10820656	9	106300420	intergenic	T/C	0.3246	1.10*10 ⁻⁰⁴	1.18 (1.08 - 1.28)	2.47*10 ⁻⁰³	1.10 (1.03 - 1.16)
rs2515616	9	106721816	ABCA1	G/A	0.8017	4.61*10 ⁻⁰⁵	1.22 (1.1 - 1.35)	2.07*10 ⁻⁰²	1.06 (1.01 - 1.11)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs9299183	9	112021093	intergenic	C/T	0.4358	8.38*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	2.11*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs4979224	9	115022099	FKBP15, SLC31A1	G/A	0.3030	7.80*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	4.96*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs10981693	9	115025238	FKBP15, SLC31A1	C/T	0.3011	6.24*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	3.41*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs10121565	9	118865058	ASTN2	A/G	0.2544	5.39*10 ⁻⁰⁴	1.17 (1.07 - 1.29)	7.71*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs1329053	9	119415942	intergenic	A/G	0.8023	2.71*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	2.31*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs7046909	9	122803701	C5	C/T	0.0801	2.85*10 ⁻⁰⁴	1.29 (1.11 - 1.49)	1.79*10 ⁻⁰³	1.22 (1.08 - 1.38)
rs10985712	9	124379320	intergenic	T/C	0.3959	9.81*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	5.53*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs7867785	9	124380085	intergenic	T/C	0.4168	9.23*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	2.04*10 ⁻⁰¹	1.04 (0.98 - 1.10)
rs2384794	9	137472427	intergenic	C/T	0.6278	9.16*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	6.18*10 ⁻⁰³	1.07 (1.02 - 1.12)
rs7093049	10	2583077	intergenic	G/A	0.1363	5.45*10 ⁻⁰⁴	1.22 (1.08 - 1.37)	3.65*10 ⁻⁰²	1.06 (1.00 - 1.13)
rs11252934	10	5124416	AKR1C3, AL391427.9	T/C	0.6498	3.99*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	2.18*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs1937843	10	5126915	AKR1C3, AL391427.9	A/G	0.6478	5.57*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	4.57*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs7741	10	5128607	AKR1C3, AL391427.9	G/A	0.6487	3.25*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	1.56*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs1937920	10	5151955	RP11-499O7.5	G/A	0.2420	7.67*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	8.75*10 ⁻⁰¹	1.00 (0.96 - 1.05)
rs12776280	10	5158153	RP11-499O7.5	G/A	0.5748	4.45*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.58*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs4448597	10	5164475	RP11-499O7.5	A/G	0.6516	3.00*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	4.38*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs1781935	10	5189934	AKR1CL1	C/G	0.4109	6.93*10 ⁻⁰⁵	1.16 (1.07 - 1.26)	8.64*10 ⁻⁰¹	1.00 (0.96 - 1.05)
rs11253019	10	5190076	AKR1CL1	A/G	0.6854	3.40*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	8.37*10 ⁻⁰¹	1.00 (0.96 - 1.05)
rs1334467	10	5191219	AKR1CL1	G/A	0.6506	9.04*10 ⁻⁰⁴	1.15 (1.06 - 1.26)	5.32*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs4881406	10	5193296	AKR1CL1	A/G	0.6528	2.34*10 ⁻⁰⁴	1.17 (1.08 - 1.28)	2.78*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs11253022	10	5196049	AKR1CL1	C/T	0.6507	7.47*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	5.25*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs2398103	10	5196096	AKR1CL1	C/T	0.4087	1.35*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	9.20*10 ⁻⁰¹	1.00 (0.96 - 1.05)
rs11253036	10	5216718	AKR1CL1	T/C	0.6537	3.43*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	1.68*10 ⁻⁰³	1.10 (1.04 - 1.16)
rs12357686	10	5540673	intergenic	G/A	0.7560	5.41*10 ⁻⁰⁴	1.17 (1.07 - 1.29)	1.12*10 ⁻⁰¹	1.04 (0.99 - 1.08)
rs11816050	10	5547041	AL732437.12	C/T	0.7703	9.32*10 ⁻⁰⁴	1.18 (1.07 - 1.29)	1.48*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs2791408	10	6962346	intergenic	G/A	0.0622	1.11*10 ⁻⁰⁴	1.38 (1.17 - 1.63)	3.97*10 ⁻⁰¹	1.03 (0.96 - 1.12)
rs546899	10	6969151	intergenic	T/C	0.0598	5.98*10 ⁻⁰⁵	1.38 (1.17 - 1.63)	2.22*10 ⁻⁰²	1.14 (1.02 - 1.28)
rs2038922	10	9907914	intergenic	T/C	0.9499	4.36*10 ⁻⁰⁴	1.4 (1.16 - 1.69)	1.30*10 ⁻⁰¹	1.07 (0.98 - 1.16)
rs2815627	10	12637496	CAMK1D	G/T	0.6795	5.78*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	9.22*10 ⁻⁰³	1.06 (1.01 - 1.10)
rs11257888	10	12641510	CAMK1D	T/C	0.5740	9.61*10 ⁻⁰⁴	1.14 (1.05 - 1.24)	5.18*10 ⁻⁰³	1.08 (1.02 - 1.15)
rs928337	10	12875051	CAMK1D	A/G	0.5863	3.29*10 ⁻⁰⁴	1.14 (1.05 - 1.24)	1.77*10 ⁻⁰¹	1.03 (0.99 - 1.07)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs11258005	10	12893468	CAMK1D	G/A	0.0095	4.95*10 ⁻⁰⁴	2.03 (1.35 - 3.05)	3.11*10 ⁻⁰¹	1.11 (0.91 - 1.36)
rs11253924	10	16423777	intergenic	T/G	0.1840	9.98*10 ⁻⁰⁴	1.18 (1.07 - 1.31)	2.40*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs7090427	10	16423937	intergenic	G/A	0.1850	8.37*10 ⁻⁰⁴	1.19 (1.07 - 1.31)	6.42*10 ⁻⁰²	1.05 (1.00 - 1.11)
rs10827805	10	37934266	AL121927.24, RP11-175J10.2	C/A	0.7862	2.48*10 ⁻⁰⁵	1.24 (1.12 - 1.36)	1.97*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs17660144	10	37983220	intergenic	T/C	0.1794	2.50*10 ⁻⁰⁴	1.22 (1.1 - 1.36)	6.68*10 ⁻⁰¹	1.01 (0.96 - 1.06)
rs4595495	10	53343292	PRKG1	A/G	0.5872	7.59*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	2.77*10 ⁻⁰²	1.07 (1.01 - 1.13)
rs2893663	10	57263103	intergenic	C/T	0.7276	2.90*10 ⁻⁰⁴	1.18 (1.08 - 1.3)	1.12*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs11005987	10	59402438	intergenic	C/T	0.0125	1.65*10 ⁻⁰⁵	1.97 (1.38 - 2.81)	8.83*10 ⁻⁰¹	1.01 (0.85 - 1.20)
rs16911440	10	59403275	intergenic	C/A	0.0122	6.88*10 ⁻⁰⁵	1.88 (1.31 - 2.7)	6.79*10 ⁻⁰¹	1.04 (0.86 - 1.26)
rs7897320	10	59403324	intergenic	G/A	0.0122	1.56*10 ⁻⁰⁴	1.88 (1.31 - 2.69)	5.98*10 ⁻⁰¹	1.05 (0.87 - 1.29)
rs12355784	10	64791571	JMJD1C	A/C	0.5083	8.77*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	5.71*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs736883	10	65441008	intergenic	G/A	0.0228	7.53*10 ⁻⁰⁴	1.57 (1.2 - 2.04)	2.69*10 ⁻⁰²	1.22 (1.02 - 1.46)
rs2671507	10	65444020	intergenic	A/G	0.0230	7.27*10 ⁻⁰⁴	1.57 (1.21 - 2.03)	2.31*10 ⁻⁰³	1.21 (1.07 - 1.37)
rs1249149	10	79650731	intergenic	C/T	0.5502	2.52*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	6.79*10 ⁻⁰⁴	1.07 (1.03 - 1.11)
rs1149731	10	79658086	intergenic	G/A	0.6824	2.95*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	1.80*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs2448388	10	79658589	intergenic	A/G	0.6823	2.98*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	1.61*10 ⁻⁰⁴	1.08 (1.04 - 1.12)
rs16936710	10	80443378	intergenic	A/G	0.0413	1.33*10 ⁻⁰⁴	1.46 (1.2 - 1.78)	6.09*10 ⁻⁰²	1.09 (1.00 - 1.20)
rs16936718	10	80449010	intergenic	A/G	0.0400	6.15*10 ⁻⁰⁴	1.4 (1.15 - 1.71)	9.17*10 ⁻⁰²	1.10 (0.98 - 1.23)
rs10762836	10	80463875	intergenic	T/G	0.0470	5.28*10 ⁻⁰⁴	1.38 (1.15 - 1.66)	3.82*10 ⁻⁰²	1.12 (1.01 - 1.25)
rs3910578	10	80465384	intergenic	A/G	0.0476	2.92*10 ⁻⁰⁴	1.37 (1.14 - 1.64)	1.07*10 ⁻⁰²	1.13 (1.03 - 1.24)
rs10824708	10	80467529	intergenic	A/G	0.0483	2.39*10 ⁻⁰⁴	1.37 (1.15 - 1.65)	1.24*10 ⁻⁰²	1.13 (1.03 - 1.24)
rs1946843	10	80467583	intergenic	C/A	0.0475	2.41*10 ⁻⁰⁴	1.39 (1.16 - 1.67)	1.35*10 ⁻⁰²	1.13 (1.03 - 1.24)
rs1946844	10	80467608	intergenic	C/G	0.0478	3.04*10 ⁻⁰⁴	1.37 (1.14 - 1.64)	1.40*10 ⁻⁰²	1.13 (1.02 - 1.24)
rs1439034	10	80468979	intergenic	C/A	0.0483	2.39*10 ⁻⁰⁴	1.37 (1.15 - 1.65)	1.20*10 ⁻⁰²	1.13 (1.03 - 1.24)
rs7911085	10	81675250	MBL1P1	G/A	0.8580	9.56*10 ⁻⁰⁵	1.19 (1.06 - 1.33)	9.07*10 ⁻⁰²	1.06 (0.99 - 1.13)
rs1412444	10	90992907	LIPA	T/C	0.3245	6.29*10 ⁻⁰⁴	1.13 (1.04 - 1.23)	4.12*10 ⁻⁰⁵	1.11 (1.05 - 1.16)
rs2246833	10	90995834	LIPA	T/C	0.3270	6.78*10 ⁻⁰⁴	1.13 (1.04 - 1.23)	2.24*10 ⁻⁰⁵	1.10 (1.05 - 1.15)
rs701866	10	95201576	FER1L3	A/G	0.9201	6.77*10 ⁻⁰⁴	1.3 (1.12 - 1.52)	4.26*10 ⁻⁰²	1.08 (1.00 - 1.17)
rs10491067	10	97972230	BLNK	T/C	0.7522	5.17*10 ⁻⁰⁵	1.2 (1.09 - 1.32)	1.91*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs11193503	10	109223312	intergenic	C/T	0.0101	3.86*10 ⁻⁰⁴	2.02 (1.36 - 2.99)	9.14*10 ⁻⁰¹	1.01 (0.80 - 1.28)
rs7917932	10	115758167	intergenic	A/G	0.9735	8.57*10 ⁻⁰⁴	1.58 (1.21 - 2.07)	9.19*10 ⁻⁰³	1.17 (1.04 - 1.33)
rs11198060	10	119404884	intergenic	C/T	0.1701	8.54*10 ⁻⁰⁴	1.2 (1.08 - 1.33)	7.83*10 ⁻⁰²	1.04 (1.00 - 1.10)
rs2210604	10	119991181	C10orf84	G/A	0.6045	5.29*10 ⁻⁰⁵	1.16 (1.07 - 1.26)	1.16*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs11198334	10	120011676	C10orf84	T/C	0.1651	3.00*10 ⁻⁰⁴	1.22 (1.1 - 1.36)	2.07*10 ⁻⁰²	1.06 (1.01 - 1.11)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs6599671	10	124985297	intergenic	A/G	0.1988	5.28*10 ⁻⁰⁴	1.19 (1.08 - 1.32)	8.74*10 ⁻⁰³	1.10 (1.02 - 1.18)
rs4980271	10	125005696	intergenic	C/A	0.1958	5.32*10 ⁻⁰⁴	1.19 (1.08 - 1.32)	2.70*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs12254965	10	127287028	intergenic	A/G	0.8742	6.43*10 ⁻⁰⁴	1.24 (1.1 - 1.41)	1.09*10 ⁻⁰¹	1.05 (0.99 - 1.12)
rs17153404	10	127365853	C10orf122	C/G	0.0529	5.29*10 ⁻⁰⁴	1.37 (1.15 - 1.63)	5.63*10 ⁻⁰³	1.14 (1.04 - 1.25)
rs2229599	10	129097419	DOCK1	T/C	0.0698	7.53*10 ⁻⁰⁴	1.3 (1.12 - 1.51)	8.49*10 ⁻⁰¹	1.01 (0.94 - 1.08)
rs2260876	10	134008306	LRRC27	C/A	0.4089	5.53*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	4.84*10 ⁻⁰²	1.06 (1.00 - 1.12)
rs16925378	11	3633672	ART1	G/C	0.0205	7.82*10 ⁻⁰⁵	1.73 (1.31 - 2.28)	1.22*10 ⁻⁰²	1.22 (1.04 - 1.42)
rs16908350	11	10792454	intergenic	T/C	0.6970	2.55*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	6.47*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs7937695	11	10802693	intergenic	T/C	0.6961	1.65*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	5.95*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs2132521	11	10807098	intergenic	G/A	0.6967	1.79*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	7.10*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs1908705	11	10811298	intergenic	A/T	0.6965	2.16*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	4.95*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs10160217	11	12978400	intergenic	A/G	0.2878	3.84*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	2.17*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs4483574	11	12978980	intergenic	A/G	0.2882	3.51*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	2.48*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs4506627	11	12979394	intergenic	T/C	0.2882	3.25*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	2.21*10 ⁻⁰¹	1.03 (0.98 - 1.07)
rs4757085	11	12980219	intergenic	C/T	0.2884	3.19*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	1.86*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs1540157	11	15145985	INSC	A/G	0.8300	8.41*10 ⁻⁰⁴	1.2 (1.08 - 1.34)	1.97*10 ⁻⁰²	1.07 (1.01 - 1.13)
rs1627802	11	15148537	INSC	G/A	0.8333	2.97*10 ⁻⁰⁴	1.22 (1.1 - 1.36)	2.90*10 ⁻⁰²	1.07 (1.01 - 1.13)
rs905553	11	19039555	MRGPRX2	G/A	0.3159	5.30*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	3.13*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs1503502	11	19040053	MRGPRX2	T/C	0.3851	2.44*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	4.09*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs12222200	11	19040692	MRGPRX2	T/C	0.3874	1.47*10 ⁻⁰⁴	1.17 (1.08 - 1.27)	1.86*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs11024975	11	19048646	intergenic	A/G	0.3163	3.17*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	3.11*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs878256	11	19051010	intergenic	A/C	0.3154	8.68*10 ⁻⁰⁴	1.15 (1.06 - 1.26)	4.96*10 ⁻⁰⁴	1.08 (1.03 - 1.13)
rs1429778	11	20821407	NELL1	T/G	0.0555	8.48*10 ⁻⁰⁵	1.33 (1.12 - 1.58)	1.33*10 ⁻⁰²	1.11 (1.02 - 1.20)
rs10833429	11	20969470	NELL1	A/G	0.7744	3.82*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	3.04*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs7927234	11	27392932	LGR4	C/G	0.1074	8.42*10 ⁻⁰⁴	1.24 (1.1 - 1.41)	6.11*10 ⁻⁰³	1.09 (1.03 - 1.17)
rs473241	11	30451981	MPPED2	C/T	0.9348	2.00*10 ⁻⁰⁴	1.38 (1.16 - 1.63)	2.23*10 ⁻⁰²	1.11 (1.02 - 1.22)
rs7942782	11	38252542	intergenic	T/G	0.0365	5.32*10 ⁻⁰⁴	1.44 (1.17 - 1.78)	6.24*10 ⁻⁰¹	1.03 (0.92 - 1.14)
rs10836958	11	38302620	intergenic	C/T	0.0437	7.11*10 ⁻⁰⁴	1.39 (1.14 - 1.68)	4.97*10 ⁻⁰²	1.14 (1.00 - 1.31)
rs10501200	11	38439360	intergenic	T/C	0.0293	6.29*10 ⁻⁰⁴	1.49 (1.18 - 1.88)	7.37*10 ⁻⁰¹	1.02 (0.91 - 1.15)
rs1913033	11	38826444	intergenic	T/A	0.6261	1.11*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	6.00*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs994587	11	39357202	intergenic	A/G	0.3590	4.59*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	7.34*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs12420372	11	48454179	intergenic	T/G	0.6252	5.33*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	9.29*10 ⁻⁰³	1.05 (1.01 - 1.09)
rs7395662	11	48475469	intergenic	G/A	0.6257	2.74*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	8.61*10 ⁻⁰³	1.05 (1.01 - 1.09)
rs11039819	11	48518757	intergenic	T/G	0.6277	2.62*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	1.78*10 ⁻⁰³	1.07 (1.02 - 1.11)
rs11039820	11	48518828	intergenic	G/A	0.6258	2.81*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	7.58*10 ⁻⁰³	1.05 (1.01 - 1.09)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs4882017	11	48526758	intergenic	G/A	0.6255	2.99*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	8.28*10 ⁻⁰³	1.05 (1.01 - 1.09)
rs10838954	11	48535899	intergenic	A/G	0.6259	2.99*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	8.54*10 ⁻⁰³	1.05 (1.01 - 1.09)
rs6485872	11	48536286	intergenic	G/T	0.6256	2.88*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	7.58*10 ⁻⁰³	1.05 (1.01 - 1.09)
rs6485882	11	48549011	intergenic	G/C	0.6236	4.61*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	9.11*10 ⁻⁰³	1.05 (1.01 - 1.09)
rs4882132	11	48549701	intergenic	T/C	0.6261	3.44*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	1.80*10 ⁻⁰⁴	1.10 (1.04 - 1.15)
rs11039871	11	48583196	intergenic	C/T	0.6244	3.75*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	1.16*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs11040016	11	48740073	intergenic	T/C	0.6256	3.91*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	2.28*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs8188975	11	48848453	intergenic	A/G	0.6221	7.38*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.03*10 ⁻⁰³	1.10 (1.04 - 1.17)
rs612040	11	73815199	intergenic	A/C	0.4645	4.75*10 ⁻⁰⁵	1.17 (1.08 - 1.27)	8.29*10 ⁻⁰²	1.03 (1.00 - 1.07)
rs11236106	11	73828072	intergenic	G/A	0.4613	7.97*10 ⁻⁰⁵	1.17 (1.08 - 1.27)	1.17*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs10793085	11	73830656	intergenic	T/C	0.4636	1.54*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	7.72*10 ⁻⁰²	1.03 (1.00 - 1.07)
rs17412370	11	80404012	intergenic	T/G	0.7834	1.18*10 ⁻⁰⁴	1.22 (1.1 - 1.34)	9.36*10 ⁻⁰⁵	1.11 (1.05 - 1.17)
rs4944277	11	80435550	intergenic	A/G	0.4993	3.00*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	2.49*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs4945476	11	80435774	intergenic	C/G	0.4991	5.79*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	3.05*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs1533866	11	80440791	intergenic	C/T	0.5022	9.31*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	3.39*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs12789328	11	82497967	intergenic	A/C	0.0501	9.56*10 ⁻⁰⁴	1.35 (1.12 - 1.61)	1.11*10 ⁻⁰¹	1.07 (0.99 - 1.16)
rs515718	11	82617399	ANKRD42	C/T	0.6483	1.70*10 ⁻⁰⁴	1.17 (1.08 - 1.27)	9.19*10 ⁻⁰²	1.04 (0.99 - 1.08)
rs506321	11	82641936	ANKRD42	A/G	0.6392	1.41*10 ⁻⁰⁴	1.17 (1.08 - 1.28)	1.53*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs1278402	11	82649745	CCDC90B	A/G	0.7389	4.22*10 ⁻⁰⁴	1.18 (1.08 - 1.3)	5.86*10 ⁻⁰¹	1.01 (0.96 - 1.07)
rs673850	11	82690410	intergenic	G/C	0.6424	6.71*10 ⁻⁰⁵	1.18 (1.09 - 1.29)	3.92*10 ⁻⁰²	1.04 (1.00 - 1.09)
rs17517294	11	82726203	intergenic	C/T	0.0974	6.81*10 ⁻⁰⁴	1.26 (1.1 - 1.44)	2.22*10 ⁻⁰²	1.08 (1.01 - 1.15)
rs6592113	11	82743548	intergenic	G/A	0.6052	2.59*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	1.91*10 ⁻⁰¹	1.02 (0.99 - 1.06)
rs7124362	11	82743579	intergenic	C/T	0.6453	5.11*10 ⁻⁰⁶	1.21 (1.12 - 1.32)	9.12*10 ⁻⁰³	1.08 (1.02 - 1.15)
rs2512674	11	82839423	DLG2	C/T	0.6374	3.82*10 ⁻⁰⁵	1.19 (1.1 - 1.29)	2.94*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs2507847	11	82839996	DLG2	T/C	0.6313	1.17*10 ⁻⁰⁴	1.18 (1.08 - 1.28)	3.42*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs2507848	11	82840048	DLG2	G/C	0.6336	1.04*10 ⁻⁰⁴	1.18 (1.08 - 1.28)	3.62*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs2507850	11	82843293	DLG2	G/A	0.6490	8.98*10 ⁻⁰⁶	1.21 (1.11 - 1.32)	3.19*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs1075719	11	82852684	DLG2	T/C	0.7178	6.30*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	1.79*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs891773	11	82853427	DLG2	T/C	0.7196	3.59*10 ⁻⁰⁴	1.17 (1.08 - 1.28)	2.03*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs7108874	11	82856041	DLG2	C/T	0.7326	6.68*10 ⁻⁰⁵	1.2 (1.1 - 1.31)	3.27*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs1939105	11	86254742	intergenic	A/G	0.5996	4.07*10 ⁻⁰⁵	1.19 (1.1 - 1.3)	3.76*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs12801237	11	86279076	intergenic	A/T	0.5882	1.06*10 ⁻⁰⁴	1.18 (1.09 - 1.28)	2.99*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs17149491	11	86283707	intergenic	G/A	0.1234	5.30*10 ⁻⁰⁴	1.24 (1.1 - 1.4)	2.55*10 ⁻⁰¹	1.03 (0.98 - 1.09)
rs1789158	11	106877275	ALKBH8	C/A	0.9112	7.15*10 ⁻⁰⁴	1.28 (1.11 - 1.48)	8.70*10 ⁻⁰¹	1.01 (0.94 - 1.07)
rs10892117	11	116830688	DSCAML1	C/T	0.0718	1.63*10 ⁻⁰⁴	1.34 (1.15 - 1.57)	1.46*10 ⁻⁰¹	1.07 (0.98 - 1.17)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs12098917	11	117221361	FXVD6	C/T	0.1595	7.62*10 ⁻⁰⁴	1.2 (1.08 - 1.34)	4.58*10 ⁻⁰³	1.09 (1.03 - 1.16)
rs530291	11	119494779	TRIM29	T/C	0.0321	8.48*10 ⁻⁰⁴	1.45 (1.16 - 1.81)	5.57*10 ⁻⁰¹	1.05 (0.90 - 1.21)
rs10790424	11	120642730	intergenic	T/C	0.2817	3.31*10 ⁻⁰⁴	1.17 (1.08 - 1.28)	3.70*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs10790443	11	120739341	AP002959.2	C/A	0.3106	3.38*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	1.59*10 ⁻⁰²	1.08 (1.01 - 1.14)
rs72991	11	120748926	intergenic	C/T	0.2674	2.82*10 ⁻⁰⁴	1.18 (1.08 - 1.29)	2.69*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs985421	11	120867526	SORL1	G/A	0.9837	1.23*10 ⁻⁰⁴	1.98 (1.39 - 2.83)	4.98*10 ⁻⁰²	1.19 (1.00 - 1.41)
rs11218351	11	120958917	SORL1	T/C	0.0802	9.35*10 ⁻⁰⁴	1.28 (1.11 - 1.48)	6.65*10 ⁻⁰¹	1.02 (0.94 - 1.09)
rs7126620	11	122247638	CRTAM	G/T	0.1684	9.75*10 ⁻⁰⁴	1.19 (1.07 - 1.33)	1.20*10 ⁻⁰¹	1.04 (0.99 - 1.10)
rs3107635	11	122286766	C11orf63	G/A	0.1604	3.39*10 ⁻⁰⁴	1.22 (1.1 - 1.36)	2.56*10 ⁻⁰²	1.07 (1.01 - 1.14)
rs2512284	11	123591632	OR8G2	A/G	0.4978	8.53*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	3.86*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs954838	11	126834560	intergenic	G/T	0.3798	9.70*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	4.07*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs11221362	11	127955429	intergenic	C/A	0.9617	9.27*10 ⁻⁰⁴	1.44 (1.16 - 1.8)	2.73*10 ⁻⁰¹	1.06 (0.96 - 1.17)
rs1395504	11	132234377	OPCML	G/T	0.4647	6.59*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.42*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs4937883	11	133798653	intergenic	G/A	0.9315	9.00*10 ⁻⁰⁴	1.32 (1.12 - 1.56)	4.35*10 ⁻⁰¹	1.04 (0.95 - 1.13)
rs10773979	12	1659125	intergenic	A/C	0.1615	1.57*10 ⁻⁰⁴	1.21 (1.09 - 1.35)	3.45*10 ⁻⁰²	1.06 (1.00 - 1.11)
rs1863657	12	22892233	intergenic	T/C	0.5318	2.15*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	9.67*10 ⁻⁰¹	1.00 (0.96 - 1.04)
rs1861932	12	67172800	intergenic	T/C	0.8637	5.68*10 ⁻⁰⁴	1.23 (1.1 - 1.39)	2.35*10 ⁻⁰²	1.07 (1.01 - 1.13)
rs10878977	12	68085957	SRP_euk_arch	T/C	0.7525	1.04*10 ⁻⁰⁴	1.21 (1.1 - 1.32)	2.39*10 ⁻⁰⁴	1.08 (1.04 - 1.13)
rs11177666	12	68111378	intergenic	A/G	0.8649	5.28*10 ⁻⁰⁴	1.24 (1.1 - 1.4)	1.58*10 ⁻⁰²	1.08 (1.01 - 1.15)
rs2707126	12	77433783	intergenic	C/T	0.8241	8.51*10 ⁻⁰⁴	1.2 (1.08 - 1.33)	6.80*10 ⁻⁰¹	1.01 (0.96 - 1.06)
rs17691177	12	80654496	PPFIA2	T/G	0.8255	4.25*10 ⁻⁰⁴	1.21 (1.09 - 1.35)	2.07*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs10506852	12	80687070	intergenic	G/A	0.6258	4.93*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	2.29*10 ⁻⁰¹	1.02 (0.99 - 1.06)
rs12307959	12	80757555	intergenic	G/A	0.8292	4.08*10 ⁻⁰⁴	1.21 (1.09 - 1.35)	2.05*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs10777699	12	94445392	USP44	C/G	0.5351	3.05*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	2.53*10 ⁻⁰²	1.04 (1.01 - 1.08)
rs2373455	12	100417052	intergenic	T/C	0.4724	8.20*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	1.41*10 ⁻⁰²	1.06 (1.01 - 1.11)
rs733328	12	100417290	intergenic	C/A	0.3751	5.39*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	7.42*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs733327	12	100417446	intergenic	A/G	0.4412	4.59*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	8.76*10 ⁻⁰³	1.06 (1.01 - 1.11)
rs11614937	12	100417857	intergenic	A/G	0.4720	6.49*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.18*10 ⁻⁰²	1.06 (1.01 - 1.11)
rs11112867	12	105020976	NUAK1	G/T	0.7762	2.68*10 ⁻⁰⁴	1.19 (1.07 - 1.31)	3.93*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs2062906	12	116732449	KSR2	T/A	0.8789	3.09*10 ⁻⁰⁴	1.26 (1.11 - 1.43)	3.59*10 ⁻⁰¹	1.03 (0.97 - 1.10)
rs4767629	12	116739460	KSR2	G/T	0.8798	3.60*10 ⁻⁰⁴	1.26 (1.11 - 1.42)	3.82*10 ⁻⁰¹	1.03 (0.96 - 1.11)
rs7299238	12	119546133	intergenic	A/G	0.3175	7.57*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	6.52*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs10846531	12	122664565	DDX55, SNORA9	G/C	0.1526	2.94*10 ⁻⁰⁴	1.23 (1.1 - 1.37)	2.18*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs4765195	12	124022458	DHX37	T/C	0.2511	2.94*10 ⁻⁰⁴	1.19 (1.08 - 1.3)	1.94*10 ⁻⁰¹	1.04 (0.98 - 1.11)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs619302	12	129086627	AC055717.36	T/C	0.3842	8.74*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.02*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs7299940	12	129956707	Y_RNA	G/C	0.5670	4.26*10 ⁻⁰⁴	1.12 (1.03 - 1.21)	7.91*10 ⁻⁰¹	1.00 (0.97 - 1.04)
rs11061560	12	130537457	intergenic	C/T	0.8489	8.63*10 ⁻⁰⁴	1.21 (1.08 - 1.36)	8.77*10 ⁻⁰¹	1.00 (0.95 - 1.06)
rs12716699	13	21677237	intergenic	T/C	0.7348	7.66*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	6.20*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs4262814	13	28945180	intergenic	A/T	0.1195	9.35*10 ⁻⁰⁴	1.23 (1.09 - 1.39)	8.13*10 ⁻⁰¹	1.01 (0.94 - 1.08)
rs17076673	13	31279039	RXFP2	A/G	0.1449	4.15*10 ⁻⁰⁴	1.22 (1.09 - 1.36)	7.90*10 ⁻⁰²	1.05 (0.99 - 1.10)
rs10492606	13	31281225	intergenic	C/T	0.1473	5.28*10 ⁻⁰⁴	1.22 (1.09 - 1.36)	6.32*10 ⁻⁰²	1.05 (1.00 - 1.11)
rs594679	13	36400102	RP11-421P11.8	C/G	0.4182	6.44*10 ⁻⁰⁴	1.13 (1.04 - 1.23)	6.39*10 ⁻⁰³	1.08 (1.02 - 1.15)
rs9549168	13	39784355	intergenic	C/T	0.4410	4.70*10 ⁻⁰⁵	1.16 (1.07 - 1.26)	7.16*10 ⁻⁰²	1.05 (1.00 - 1.11)
rs13378575	13	43825384	intergenic	C/T	0.9351	2.02*10 ⁻⁰⁴	1.37 (1.16 - 1.63)	5.90*10 ⁻⁰³	1.12 (1.03 - 1.21)
rs1041711	13	44004018	TSC22D1	C/T	0.9603	4.42*10 ⁻⁰⁴	1.45 (1.17 - 1.8)	6.79*10 ⁻⁰²	1.10 (0.99 - 1.22)
rs9534145	13	44908470	RP11-38J6.1	A/C	0.5844	7.55*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.98*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs7324600	13	45245355	intergenic	G/A	0.0653	1.24*10 ⁻⁰⁴	1.37 (1.17 - 1.61)	2.02*10 ⁻⁰²	1.10 (1.01 - 1.19)
rs17068501	13	46113908	LRCH1	A/G	0.8915	8.74*10 ⁻⁰⁵	1.31 (1.14 - 1.49)	7.79*10 ⁻⁰¹	1.01 (0.95 - 1.07)
rs6561324	13	46142405	LRCH1	G/A	0.8883	3.27*10 ⁻⁰⁴	1.27 (1.12 - 1.45)	5.68*10 ⁻⁰¹	1.02 (0.96 - 1.08)
rs9645940	13	46143992	LRCH1	T/C	0.8890	5.64*10 ⁻⁰⁴	1.26 (1.11 - 1.44)	8.36*10 ⁻⁰¹	1.01 (0.95 - 1.07)
rs17068595	13	46144505	LRCH1	G/T	0.9283	7.05*10 ⁻⁰⁴	1.32 (1.13 - 1.55)	6.25*10 ⁻⁰¹	1.02 (0.95 - 1.09)
rs4942931	13	50072312	intergenic	T/C	0.5481	3.35*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.04*10 ⁻⁰³	1.07 (1.02 - 1.12)
rs6562437	13	65609441	intergenic	A/G	0.5799	1.75*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	5.54*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs891643	13	67744600	intergenic	T/C	0.3663	7.18*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	9.55*10 ⁻⁰²	1.04 (0.99 - 1.08)
rs9541316	13	67754079	intergenic	A/G	0.3707	6.35*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.94*10 ⁻⁰¹	1.03 (0.99 - 1.06)
rs9541317	13	67761954	RP11-520F24.2	G/A	0.3643	6.85*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.70*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs6562522	13	67769430	RP11-520F24.1	C/G	0.3606	9.46*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.95*10 ⁻⁰¹	1.03 (0.99 - 1.06)
rs7332897	13	67773416	RP11-520F24.1	A/G	0.3645	7.85*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.88*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs9529327	13	67796857	intergenic	A/C	0.3708	8.56*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	3.21*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs9541322	13	67805872	RP11-520F24.3	G/A	0.3650	7.93*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.40*10 ⁻⁰¹	1.02 (0.99 - 1.06)
rs17086847	13	69824408	intergenic	T/C	0.0854	6.84*10 ⁻⁰⁴	1.28 (1.11 - 1.47)	9.16*10 ⁻⁰²	1.06 (0.99 - 1.14)
rs17086923	13	69835751	intergenic	T/C	0.0833	4.29*10 ⁻⁰⁴	1.29 (1.12 - 1.49)	3.91*10 ⁻⁰¹	1.03 (0.96 - 1.10)
rs9600699	13	75857025	intergenic	T/G	0.0784	2.96*10 ⁻⁰⁴	1.31 (1.13 - 1.52)	3.82*10 ⁻⁰¹	1.03 (0.96 - 1.12)
rs16955846	13	98233139	intergenic	C/T	0.7191	4.31*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	5.72*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs1821542	13	109146713	intergenic	G/A	0.9574	8.19*10 ⁻⁰⁴	1.42 (1.15 - 1.74)	8.05*10 ⁻⁰⁴	1.20 (1.08 - 1.34)
rs9587963	13	109150490	intergenic	A/C	0.9685	6.50*10 ⁻⁰⁵	1.65 (1.29 - 2.12)	1.84*10 ⁻⁰²	1.17 (1.03 - 1.34)
rs8001174	13	109254227	intergenic	T/G	0.3963	5.83*10 ⁻⁰⁴	1.16 (1.06 - 1.25)	2.70*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs8001629	13	113134783	ADPRHL1	C/T	0.0473	7.38*10 ⁻⁰⁴	1.37 (1.14 - 1.65)	7.24*10 ⁻⁰²	1.22 (0.98 - 1.50)
rs977123	14	29053877	intergenic	G/A	0.8981	2.99*10 ⁻⁰⁴	1.29 (1.12 - 1.48)	8.34*10 ⁻⁰³	1.08 (1.02 - 1.15)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs977122	14	29054049	intergenic	C/A	0.8794	7.59*10 ⁻⁰⁴	1.24 (1.1 - 1.41)	6.62*10 ⁻⁰²	1.05 (1.00 - 1.11)
rs4981191	14	32986367	NPAS3	A/G	0.1531	3.53*10 ⁻⁰⁴	1.21 (1.08 - 1.34)	5.16*10 ⁻⁰²	1.07 (1.00 - 1.13)
rs12434640	14	47970228	intergenic	G/T	0.1610	3.98*10 ⁻⁰⁶	1.22 (1.09 - 1.36)	3.66*10 ⁻⁰²	1.06 (1.00 - 1.13)
rs10083389	14	47989758	intergenic	G/A	0.1448	2.13*10 ⁻⁰⁵	1.21 (1.08 - 1.36)	1.41*10 ⁻⁰²	1.07 (1.01 - 1.14)
rs10873099	14	56230692	intergenic	A/G	0.4637	7.07*10 ⁻⁰⁴	1.14 (1.05 - 1.24)	1.99*10 ⁻⁰¹	1.02 (0.99 - 1.06)
rs17779877	14	65840963	intergenic	G/C	0.0946	5.55*10 ⁻⁰⁵	1.31 (1.14 - 1.5)	2.01*10 ⁻⁰²	1.08 (1.01 - 1.15)
rs7160622	14	65870632	intergenic	T/C	0.1213	1.55*10 ⁻⁰⁴	1.26 (1.11 - 1.42)	9.80*10 ⁻⁰²	1.05 (0.99 - 1.12)
rs7149488	14	65893425	intergenic	T/C	0.1239	3.34*10 ⁻⁰⁴	1.23 (1.09 - 1.38)	1.22*10 ⁻⁰¹	1.05 (0.99 - 1.12)
rs12589479	14	65963473	intergenic	A/G	0.1236	2.56*10 ⁻⁰⁴	1.23 (1.09 - 1.38)	1.08*10 ⁻⁰¹	1.05 (0.99 - 1.12)
rs735957	14	65965477	intergenic	A/G	0.1235	3.12*10 ⁻⁰⁴	1.23 (1.09 - 1.38)	1.02*10 ⁻⁰¹	1.05 (0.99 - 1.12)
rs933039	14	65973000	intergenic	G/A	0.1230	1.23*10 ⁻⁰⁴	1.25 (1.11 - 1.4)	7.43*10 ⁻⁰²	1.06 (0.99 - 1.13)
rs7146723	14	66038848	C14orf53	T/A	0.1193	1.90*10 ⁻⁰⁵	1.28 (1.14 - 1.45)	1.32*10 ⁻⁰²	1.07 (1.01 - 1.14)
rs7146849	14	66101823	GPHN	C/T	0.1242	1.69*10 ⁻⁰⁴	1.24 (1.1 - 1.4)	7.81*10 ⁻⁰²	1.06 (0.99 - 1.12)
rs9783601	14	66218692	GPHN	C/T	0.1239	3.12*10 ⁻⁰⁴	1.23 (1.09 - 1.39)	7.84*10 ⁻⁰²	1.06 (0.99 - 1.12)
rs6573706	14	66220517	GPHN	A/T	0.1235	2.72*10 ⁻⁰⁴	1.23 (1.09 - 1.39)	7.76*10 ⁻⁰²	1.06 (0.99 - 1.12)
rs7157740	14	66231094	GPHN	G/A	0.1242	2.19*10 ⁻⁰⁴	1.24 (1.1 - 1.39)	7.06*10 ⁻⁰²	1.06 (1.00 - 1.13)
rs7154017	14	66233836	GPHN	C/A	0.1241	2.69*10 ⁻⁰⁴	1.23 (1.09 - 1.39)	7.66*10 ⁻⁰²	1.06 (0.99 - 1.12)
rs1885198	14	66234513	GPHN	T/C	0.1228	4.03*10 ⁻⁰⁴	1.22 (1.09 - 1.38)	1.09*10 ⁻⁰¹	1.05 (0.99 - 1.12)
rs17836572	14	66262776	GPHN	G/A	0.1238	1.36*10 ⁻⁰⁴	1.24 (1.1 - 1.4)	6.09*10 ⁻⁰²	1.06 (1.00 - 1.13)
rs6573719	14	66278401	GPHN	C/T	0.1242	2.14*10 ⁻⁰⁴	1.24 (1.1 - 1.39)	6.96*10 ⁻⁰²	1.06 (1.00 - 1.13)
rs17247749	14	66292836	GPHN	G/A	0.1243	2.67*10 ⁻⁰⁴	1.24 (1.1 - 1.39)	6.81*10 ⁻⁰²	1.06 (1.00 - 1.13)
rs17765625	14	69721366	SLC8A3, COX16	G/A	0.9476	1.76*10 ⁻⁰⁴	1.43 (1.18 - 1.73)	2.58*10 ⁻⁰¹	1.05 (0.96 - 1.14)
rs11466414	14	75517603	C14orf179, TGFB3, C14orf159	G/A	0.9385	8.70*10 ⁻⁰⁴	1.35 (1.13 - 1.6)	7.66*10 ⁻⁰³	1.12 (1.03 - 1.23)
rs4903711	14	77683970	intergenic	T/C	0.1543	3.46*10 ⁻⁰⁴	1.21 (1.09 - 1.36)	1.83*10 ⁻⁰²	1.07 (1.01 - 1.12)
rs10444740	14	77741579	intergenic	C/G	0.5518	5.01*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	5.91*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs7152994	14	82706270	intergenic	C/G	0.7206	9.89*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	2.99*10 ⁻⁰⁴	1.12 (1.05 - 1.20)
rs1457011	14	82719963	intergenic	G/C	0.7808	4.79*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	4.42*10 ⁻⁰⁴	1.08 (1.04 - 1.13)
rs10484152	14	82720294	intergenic	T/C	0.7820	3.90*10 ⁻⁰⁴	1.19 (1.08 - 1.32)	8.14*10 ⁻⁰⁴	1.08 (1.03 - 1.13)
rs7155433	14	87237928	intergenic	T/C	0.0097	1.29*10 ⁻⁰⁴	2.15 (1.44 - 3.22)	2.29*10 ⁻⁰¹	1.26 (0.87 - 1.83)
rs17259751	14	87256973	intergenic	C/T	0.0096	3.90*10 ⁻⁰⁴	2.06 (1.37 - 3.08)	1.27*10 ⁻⁰¹	1.33 (0.92 - 1.92)
rs17128893	14	92685360	intergenic	A/G	0.9641	1.47*10 ⁻⁰⁴	1.55 (1.23 - 1.95)	2.95*10 ⁻⁰³	1.17 (1.06 - 1.30)
rs748752	14	94358391	intergenic	A/G	0.3675	5.21*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	2.47*10 ⁻⁰¹	1.03 (0.98 - 1.07)
rs10130003	14	94452633	intergenic	T/C	0.8585	9.36*10 ⁻⁰⁴	1.22 (1.08 - 1.37)	3.03*10 ⁻⁰¹	1.03 (0.97 - 1.10)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs1350277	14	97562596	intergenic	T/C	0.7271	6.24*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	2.02*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs2183623	14	97621009	intergenic	T/G	0.4501	4.55*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	5.33*10 ⁻⁰⁴	1.07 (1.03 - 1.11)
rs11625944	14	98653124	intergenic	C/A	0.9166	7.38*10 ⁻⁰⁴	1.29 (1.11 - 1.49)	8.39*10 ⁻⁰²	1.08 (0.99 - 1.17)
rs1958956	14	101200280	intergenic	T/C	0.4589	5.71*10 ⁻⁰⁵	1.18 (1.09 - 1.28)	7.13*10 ⁻⁰⁴	1.10 (1.04 - 1.17)
rs11625483	14	101321490	PPP2R5C	C/G	0.6489	1.94*10 ⁻⁰⁴	1.17 (1.08 - 1.28)	9.11*10 ⁻⁰²	1.03 (0.99 - 1.07)
rs4779824	15	29191586	intergenic	T/C	0.4018	4.98*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	9.02*10 ⁻⁰²	1.04 (0.99 - 1.08)
rs2338853	15	29193335	intergenic	A/G	0.3771	5.55*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	2.59*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs4779592	15	30938399	FMN1	G/A	0.2051	3.06*10 ⁻⁰⁴	1.2 (1.09 - 1.32)	4.36*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs4780050	15	30938452	FMN1	C/T	0.1797	7.27*10 ⁻⁰⁴	1.2 (1.08 - 1.32)	5.87*10 ⁻⁰³	1.08 (1.02 - 1.14)
rs4780051	15	30938654	FMN1	C/G	0.2053	4.98*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	4.88*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs10519759	15	30939107	FMN1	A/G	0.2057	3.93*10 ⁻⁰⁴	1.19 (1.08 - 1.32)	4.41*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs542036	15	41328431	TGM5, Y_RNA	T/C	0.7503	8.70*10 ⁻⁰⁴	1.17 (1.07 - 1.29)	1.36*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs17779494	15	41366515	TGM7	C/T	0.7554	1.82*10 ⁻⁰⁴	1.2 (1.09 - 1.32)	2.20*10 ⁻⁰³	1.07 (1.02 - 1.12)
rs514438	15	41407735	ADAL, LCMT2	T/C	0.7895	2.13*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	1.44*10 ⁻⁰²	1.06 (1.01 - 1.12)
rs10518812	15	41440229	ZNF690	A/C	0.7872	2.49*10 ⁻⁰⁴	1.21 (1.09 - 1.33)	7.02*10 ⁻⁰²	1.04 (1.00 - 1.09)
rs17780920	15	41449654	ELL3, TUBGCP4, ZNF690	C/T	0.7870	2.50*10 ⁻⁰⁴	1.21 (1.09 - 1.33)	7.43*10 ⁻⁰²	1.04 (1.00 - 1.09)
rs16957715	15	41496029	TP53BP1, TUBGCP4	T/G	0.7876	1.22*10 ⁻⁰⁴	1.22 (1.1 - 1.35)	5.35*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs12899865	15	41528309	TP53BP1	G/A	0.7880	2.11*10 ⁻⁰⁴	1.21 (1.09 - 1.34)	2.35*10 ⁻⁰²	1.06 (1.01 - 1.11)
rs17795279	15	41716670	CATSPER2, HISPPD2A, U6	C/T	0.8036	1.81*10 ⁻⁰⁴	1.21 (1.1 - 1.35)	4.37*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs11070411	15	41845926	PDIA3	C/G	0.8037	1.19*10 ⁻⁰⁴	1.22 (1.1 - 1.36)	2.18*10 ⁻⁰²	1.06 (1.01 - 1.11)
rs2930531	15	41908862	WDR76, MFAP1	A/G	0.8013	1.82*10 ⁻⁰⁴	1.22 (1.1 - 1.35)	9.07*10 ⁻⁰²	1.06 (0.99 - 1.14)
rs7183100	15	45008657	intergenic	T/C	0.2833	2.07*10 ⁻⁰⁴	1.18 (1.08 - 1.29)	5.76*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs12443493	15	45077010	intergenic	G/A	0.3051	7.65*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	4.64*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs10431773	15	45080767	intergenic	C/T	0.3061	4.74*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	4.04*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs1515744	15	45122962	intergenic	A/G	0.3068	8.41*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	4.01*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs281299	15	45473373	intergenic	C/T	0.3791	2.44*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	1.00*10 ⁻⁰²	1.05 (1.01 - 1.09)
rs8036806	15	46926246	SHC4	A/T	0.9755	5.09*10 ⁻⁰⁴	1.63 (1.23 - 2.15)	9.33*10 ⁻⁰¹	1.01 (0.89 - 1.14)
rs16961743	15	46936551	SHC4	C/T	0.9754	5.07*10 ⁻⁰⁴	1.63 (1.23 - 2.15)	9.62*10 ⁻⁰¹	1.00 (0.88 - 1.14)
rs9672326	15	46944898	SHC4	T/G	0.9745	1.41*10 ⁻⁰⁴	1.66 (1.26 - 2.18)	6.87*10 ⁻⁰¹	1.03 (0.91 - 1.16)
rs10519195	15	46950476	SHC4	C/T	0.9754	6.99*10 ⁻⁰⁴	1.6 (1.22 - 2.12)	9.08*10 ⁻⁰¹	1.01 (0.89 - 1.14)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs10519196	15	46951793	SHC4	C/T	0.9759	7.70*10 ⁻⁰⁵	1.77 (1.33 - 2.36)	7.24*10 ⁻⁰¹	1.02 (0.90 - 1.16)
rs577659	15	47248540	GALK2	T/C	0.2049	8.21*10 ⁻⁰⁴	1.18 (1.07 - 1.31)	3.98*10 ⁻⁰³	1.11 (1.03 - 1.19)
rs7167041	15	47542036	FGF7, C15orf33	G/C	0.2490	6.29*10 ⁻⁰⁴	1.17 (1.07 - 1.29)	1.03*10 ⁻⁰³	1.07 (1.03 - 1.12)
rs7180653	15	48067540	ATP8B4	A/G	0.0349	1.68*10 ⁻⁰⁴	1.5 (1.21 - 1.85)	2.02*10 ⁻⁰¹	1.07 (0.97 - 1.18)
rs2413998	15	48077587	ATP8B4	G/A	0.0330	1.23*10 ⁻⁰⁴	1.53 (1.23 - 1.9)	5.56*10 ⁻⁰¹	1.03 (0.93 - 1.14)
rs7170142	15	48111352	ATP8B4	A/C	0.0329	1.47*10 ⁻⁰⁴	1.52 (1.22 - 1.89)	4.00*10 ⁻⁰¹	1.05 (0.94 - 1.16)
rs16963416	15	48299661	SLC27A2, Y_RNA	G/C	0.1659	9.68*10 ⁻⁰⁴	1.19 (1.07 - 1.32)	3.65*10 ⁻⁰¹	1.02 (0.97 - 1.07)
rs2165991	15	50888992	intergenic	G/A	0.2465	4.99*10 ⁻⁰⁴	1.18 (1.08 - 1.3)	1.65*10 ⁻⁰²	1.06 (1.01 - 1.11)
rs2440352	15	50932511	intergenic	G/T	0.2570	6.93*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	2.37*10 ⁻⁰²	1.06 (1.01 - 1.11)
rs4774822	15	53854963	intergenic	G/T	0.5317	9.13*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	1.78*10 ⁻⁰³	1.07 (1.03 - 1.12)
rs2635382	15	55652104	intergenic	T/C	0.3516	4.38*10 ⁻⁰⁵	1.19 (1.09 - 1.29)	1.26*10 ⁻⁰³	1.10 (1.04 - 1.17)
rs1666577	15	55654219	intergenic	T/G	0.3559	4.06*10 ⁻⁰⁵	1.19 (1.09 - 1.29)	2.46*10 ⁻⁰³	1.07 (1.02 - 1.12)
rs7181170	15	55655740	intergenic	A/T	0.3782	5.29*10 ⁻⁰⁵	1.18 (1.09 - 1.28)	3.84*10 ⁻⁰⁴	1.07 (1.03 - 1.12)
rs1690325	15	55667015	GRINL1A	T/C	0.4588	2.29*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	2.14*10 ⁻⁰³	1.09 (1.03 - 1.15)
rs1452455	15	85187845	AGBL1	A/C	0.9001	2.03*10 ⁻⁰⁴	1.3 (1.13 - 1.5)	4.33*10 ⁻⁰²	1.06 (1.00 - 1.13)
rs3087374	15	87660998	POLG, FANCI	C/A	0.9200	2.58*10 ⁻⁰⁴	1.33 (1.14 - 1.55)	5.23*10 ⁻⁰²	1.07 (1.00 - 1.16)
rs11634165	15	89710119	intergenic	T/G	0.9015	7.99*10 ⁻⁰⁴	1.26 (1.1 - 1.45)	1.50*10 ⁻⁰¹	1.06 (0.98 - 1.14)
rs4777989	15	90807744	ST8SIA2	A/G	0.5898	6.10*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	5.66*10 ⁻⁰³	1.05 (1.02 - 1.09)
rs2397805	15	93927621	intergenic	G/A	0.0934	1.34*10 ⁻⁰⁴	1.26 (1.1 - 1.44)	1.18*10 ⁻⁰³	1.14 (1.05 - 1.24)
rs1045763	16	664085	RHBDL1, RHOT2	C/T	0.9333	4.63*10 ⁻⁰⁴	1.34 (1.14 - 1.58)	8.09*10 ⁻⁰⁴	1.14 (1.06 - 1.23)
rs2005316	16	5313941	intergenic	T/C	0.1151	2.40*10 ⁻⁰⁴	1.27 (1.12 - 1.44)	1.53*10 ⁻⁰⁴	1.12 (1.06 - 1.19)
rs932233	16	15766780	MYH11	G/C	0.6992	6.30*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	6.49*10 ⁻⁰⁴	1.07 (1.03 - 1.12)
rs321472	16	26652877	intergenic	G/A	0.3258	8.04*10 ⁻⁰⁴	1.15 (1.06 - 1.26)	7.13*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs11649335	16	66993655	SMPD3	T/C	0.2004	7.62*10 ⁻⁰⁴	1.19 (1.07 - 1.31)	1.55*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs2278044	16	75812364	intergenic	G/C	0.0921	4.99*10 ⁻⁰⁴	1.28 (1.11 - 1.47)	1.90*10 ⁻⁰¹	1.05 (0.98 - 1.12)
rs8064066	16	77096616	WWOX	C/G	0.9660	7.96*10 ⁻⁰⁴	1.48 (1.17 - 1.87)	1.73*10 ⁻⁰²	1.14 (1.02 - 1.27)
rs4888920	16	77673432	WWOX	A/G	0.4837	2.00*10 ⁻⁰⁴	1.17 (1.08 - 1.26)	1.83*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs13339155	16	77676570	WWOX	A/G	0.4942	7.94*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	1.78*10 ⁻⁰³	1.07 (1.02 - 1.11)
rs2875784	16	81885663	CDH13	G/A	0.5160	3.65*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	2.45*10 ⁻⁰²	1.05 (1.01 - 1.10)
rs735675	16	82340018	CDH13	C/T	0.9613	4.30*10 ⁻⁰⁵	1.58 (1.27 - 1.97)	1.94*10 ⁻⁰¹	1.07 (0.97 - 1.18)
rs11641114	16	82342649	CDH13	C/T	0.9626	8.33*10 ⁻⁰⁵	1.56 (1.25 - 1.96)	2.11*10 ⁻⁰¹	1.06 (0.97 - 1.17)
rs11864540	16	82348766	CDH13	G/A	0.9623	5.50*10 ⁻⁰⁵	1.58 (1.26 - 1.97)	3.69*10 ⁻⁰¹	1.05 (0.95 - 1.16)
rs8058334	16	82383135	CDH13	T/C	0.8935	5.18*10 ⁻⁰⁵	1.32 (1.15 - 1.51)	1.48*10 ⁻⁰¹	1.05 (0.98 - 1.11)
rs7197423	16	82388190	CDH13	G/A	0.9495	3.56*10 ⁻⁰⁵	1.5 (1.23 - 1.82)	1.74*10 ⁻⁰¹	1.06 (0.97 - 1.16)
rs9940475	16	86714884	intergenic	T/G	0.1207	8.28*10 ⁻⁰⁵	1.27 (1.13 - 1.43)	8.42*10 ⁻⁰¹	1.01 (0.94 - 1.08)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs9936927	16	86720383	intergenic	A/G	0.1166	1.78*10 ⁻⁰⁴	1.26 (1.12 - 1.42)	9.24*10 ⁻⁰¹	1.00 (0.95 - 1.06)
rs4534894	17	9137020	STX8	A/G	0.6962	1.26*10 ⁻⁰⁴	1.19 (1.09 - 1.3)	8.68*10 ⁻⁰²	1.04 (0.99 - 1.08)
rs16946685	17	12686023	AC005277.1	A/G	0.0301	4.47*10 ⁻⁰⁴	1.51 (1.2 - 1.9)	3.11*10 ⁻⁰²	1.14 (1.01 - 1.28)
rs12938215	17	32887493	TADA2L	G/A	0.7646	6.24*10 ⁻⁰⁴	1.18 (1.08 - 1.3)	7.49*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs11574831	17	40703393	MAP3K14	C/T	0.8686	4.77*10 ⁻⁰⁴	1.24 (1.1 - 1.4)	6.92*10 ⁻⁰²	1.05 (1.00 - 1.11)
rs2873938	17	47110373	CA10	G/A	0.4564	7.15*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	9.30*10 ⁻⁰¹	1.00 (0.97 - 1.04)
rs2958933	17	50308029	intergenic	T/C	0.9350	7.72*10 ⁻⁰⁴	1.33 (1.13 - 1.58)	7.25*10 ⁻⁰³	1.13 (1.03 - 1.24)
rs8071484	17	50705097	HLF	C/T	0.9369	4.96*10 ⁻⁰⁴	1.35 (1.14 - 1.6)	7.22*10 ⁻⁰¹	1.02 (0.93 - 1.10)
rs10515149	17	53211049	intergenic	G/C	0.0716	5.86*10 ⁻⁰⁴	1.3 (1.12 - 1.52)	1.88*10 ⁻⁰¹	1.05 (0.98 - 1.13)
rs8077600	17	55968112	intergenic	C/T	0.0391	4.03*10 ⁻⁰⁴	1.44 (1.17 - 1.76)	5.06*10 ⁻⁰²	1.11 (1.00 - 1.22)
rs1197062	17	55995900	intergenic	G/T	0.0406	6.38*10 ⁻⁰⁴	1.4 (1.15 - 1.71)	3.54*10 ⁻⁰²	1.12 (1.01 - 1.26)
rs757558	17	60992054	AXIN2	T/G	0.1637	2.59*10 ⁻⁰⁵	1.25 (1.13 - 1.4)	4.56*10 ⁻⁰¹	1.02 (0.96 - 1.09)
rs734232	17	70277326	SLC9A3R1, NAT9	G/A	0.5759	3.58*10 ⁻⁰⁴	1.14 (1.05 - 1.23)	4.26*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs9908508	17	73201616	intergenic	C/T	0.9594	2.09*10 ⁻⁰⁴	1.49 (1.2 - 1.85)	3.92*10 ⁻⁰²	1.10 (1.00 - 1.21)
rs9901599	17	73207843	intergenic	A/C	0.6754	2.77*10 ⁻⁰⁴	1.17 (1.08 - 1.28)	7.59*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs9902073	17	73208038	intergenic	A/C	0.9582	2.49*10 ⁻⁰⁴	1.48 (1.2 - 1.83)	6.00*10 ⁻⁰²	1.09 (1.00 - 1.20)
rs9897643	17	73213171	intergenic	G/C	0.9059	1.65*10 ⁻⁰⁴	1.31 (1.14 - 1.51)	4.12*10 ⁻⁰³	1.10 (1.03 - 1.18)
rs7217176	17	73788078	AC087645.19-201	G/A	0.0531	2.18*10 ⁻⁰⁵	1.45 (1.22 - 1.72)	4.55*10 ⁻⁰²	1.10 (1.00 - 1.21)
rs9891371	17	78531117	B3GNTL1	A/G	0.0144	6.74*10 ⁻⁰⁴	1.75 (1.26 - 2.43)	9.31*10 ⁻⁰²	1.19 (0.97 - 1.45)
rs12606657	18	10448256	APCDD1	A/C	0.1789	9.83*10 ⁻⁰⁴	1.19 (1.07 - 1.32)	1.97*10 ⁻⁰¹	1.05 (0.98 - 1.13)
rs11663520	18	13420212	C18orf1	A/C	0.5137	6.24*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	1.56*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs12458775	18	13422341	C18orf1	T/C	0.4516	2.53*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	5.30*10 ⁻⁰²	1.04 (1.00 - 1.09)
rs9950714	18	21545098	intergenic	T/C	0.0898	4.82*10 ⁻⁰⁴	1.28 (1.11 - 1.47)	2.79*10 ⁻⁰¹	1.04 (0.97 - 1.10)
rs16941764	18	21560658	intergenic	A/G	0.0918	6.49*10 ⁻⁰⁴	1.27 (1.11 - 1.46)	2.64*10 ⁻⁰¹	1.04 (0.97 - 1.10)
rs10502876	18	42511420	ST8SIA5	A/G	0.0298	7.01*10 ⁻⁰⁴	1.48 (1.18 - 1.85)	2.38*10 ⁻⁰¹	1.06 (0.96 - 1.17)
rs16955291	18	48383321	DCC	G/A	0.9771	5.19*10 ⁻⁰⁴	1.66 (1.24 - 2.22)	3.55*10 ⁻⁰²	1.16 (1.01 - 1.34)
rs559998	18	52468021	WDR7	G/T	0.8505	7.93*10 ⁻⁰⁴	1.19 (1.06 - 1.33)	2.51*10 ⁻⁰²	1.06 (1.01 - 1.12)
rs477415	18	52470097	WDR7	A/T	0.8516	6.26*10 ⁻⁰⁴	1.2 (1.07 - 1.34)	1.47*10 ⁻⁰²	1.07 (1.01 - 1.12)
rs12953387	18	52516963	WDR7	T/C	0.8495	1.91*10 ⁻⁰⁴	1.21 (1.08 - 1.35)	1.47*10 ⁻⁰²	1.07 (1.01 - 1.12)
rs2080681	18	52539900	WDR7	G/T	0.8493	2.43*10 ⁻⁰⁴	1.2 (1.07 - 1.35)	1.67*10 ⁻⁰²	1.07 (1.01 - 1.12)
rs4800956	18	52854527	intergenic	C/T	0.6512	7.00*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	2.51*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs1426284	18	56889918	intergenic	A/G	0.9651	5.17*10 ⁻⁰⁵	1.62 (1.28 - 2.04)	3.34*10 ⁻⁰²	1.12 (1.01 - 1.24)
rs8090450	18	56903198	intergenic	G/A	0.9832	4.96*10 ⁻⁰⁵	2.06 (1.44 - 2.94)	1.25*10 ⁻⁰¹	1.13 (0.97 - 1.31)
rs17067791	18	56936463	intergenic	G/A	0.9812	1.02*10 ⁻⁰⁴	1.89 (1.36 - 2.62)	1.82*10 ⁻⁰²	1.30 (1.05 - 1.63)
rs10460149	18	56938911	intergenic	C/T	0.9803	3.60*10 ⁻⁰⁴	1.76 (1.29 - 2.42)	1.31*10 ⁻⁰¹	1.12 (0.97 - 1.30)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs1421521	18	60236486	intergenic	G/A	0.6498	4.29*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	9.03*10 ⁻⁰⁵	1.08 (1.04 - 1.13)
rs11151300	18	62549968	intergenic	G/A	0.2601	2.73*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	6.30*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs17754718	18	69411839	intergenic	T/C	0.4396	6.61*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	3.49*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs1943858	18	69444668	intergenic	T/C	0.3180	4.02*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	2.78*10 ⁻⁰²	1.07 (1.01 - 1.14)
rs17829352	18	69444962	intergenic	A/G	0.3162	6.13*10 ⁻⁰⁴	1.16 (1.07 - 1.27)	2.05*10 ⁻⁰¹	1.03 (0.99 - 1.07)
rs1943856	18	69445059	intergenic	T/C	0.3171	9.23*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	2.70*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs17762504	18	69459603	intergenic	A/T	0.3235	9.30*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	3.62*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs4892122	18	69473702	intergenic	G/A	0.3332	9.10*10 ⁻⁰⁴	1.15 (1.06 - 1.26)	4.51*10 ⁻⁰¹	1.02 (0.97 - 1.06)
rs9953978	18	69498407	intergenic	G/A	0.3470	5.76*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	5.64*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs1667918	18	72945946	MBP	G/A	0.2053	1.97*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	8.41*10 ⁻⁰¹	1.00 (0.96 - 1.05)
rs12957544	18	73371516	intergenic	A/G	0.6302	5.52*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	1.19*10 ⁻⁰¹	1.03 (0.99 - 1.08)
rs2168838	18	74319036	intergenic	A/T	0.1335	9.20*10 ⁻⁰⁴	1.21 (1.08 - 1.36)	1.08*10 ⁻⁰¹	1.04 (0.99 - 1.10)
rs10415811	19	11038408	SMARCA4	T/C	0.7081	7.20*10 ⁻⁰⁴	1.17 (1.07 - 1.28)	2.30*10 ⁻⁰⁴	1.13 (1.06 - 1.20)
rs1062958	19	11477807	ECSIT, ZNF653	A/G	0.9708	2.41*10 ⁻⁰⁴	1.61 (1.24 - 2.07)	4.06*10 ⁻⁰³	1.35 (1.10 - 1.66)
rs2361019	19	22521453	ZNF729	A/T	0.4326	3.27*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	3.50*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs1105167	19	33320637	intergenic	T/C	0.8546	2.00*10 ⁻⁰⁵	1.29 (1.15 - 1.45)	1.77*10 ⁻⁰¹	1.04 (0.98 - 1.09)
rs4805590	19	35810431	intergenic	T/C	0.4909	9.59*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	4.96*10 ⁻⁰¹	1.01 (0.97 - 1.06)
rs10417396	19	35817069	intergenic	T/A	0.4924	9.64*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	2.67*10 ⁻⁰¹	1.02 (0.98 - 1.07)
rs2867078	19	35827051	intergenic	A/G	0.4950	3.07*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	7.11*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs17714261	19	49669102	ZNF180, AC069278.1	C/T	0.2124	7.74*10 ⁻⁰⁴	1.18 (1.07 - 1.3)	7.93*10 ⁻⁰⁴	1.08 (1.03 - 1.13)
rs1399834	19	56489138	intergenic	A/G	0.4446	7.42*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	4.87*10 ⁻⁰³	1.07 (1.02 - 1.11)
rs299170	19	61008282	NLRP11	A/G	0.7091	4.29*10 ⁻⁰⁵	1.18 (1.08 - 1.29)	9.84*10 ⁻⁰¹	1.00 (0.96 - 1.04)
rs6052360	20	4039972	intergenic	C/T	0.1064	2.61*10 ⁻⁰⁴	1.26 (1.11 - 1.43)	4.91*10 ⁻⁰¹	1.02 (0.96 - 1.09)
rs13039424	20	38055505	intergenic	C/T	0.2129	2.44*10 ⁻⁰⁵	1.21 (1.1 - 1.33)	5.40*10 ⁻⁰²	1.05 (1.00 - 1.09)
rs10485664	20	38064192	intergenic	G/A	0.2105	2.62*10 ⁻⁰⁵	1.21 (1.1 - 1.34)	9.70*10 ⁻⁰³	1.06 (1.01 - 1.11)
rs4812422	20	38085300	intergenic	G/C	0.2077	1.36*10 ⁻⁰⁴	1.2 (1.09 - 1.32)	1.14*10 ⁻⁰¹	1.04 (0.99 - 1.10)
rs8122094	20	39115097	TOP1	G/C	0.2269	2.24*10 ⁻⁰⁵	1.23 (1.12 - 1.35)	6.23*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs2179680	20	42229264	JPH2	G/A	0.4631	3.44*10 ⁻⁰⁵	1.18 (1.09 - 1.28)	1.95*10 ⁻⁰²	1.07 (1.01 - 1.13)
rs4812790	20	42236111	JPH2	C/T	0.6175	5.58*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	6.90*10 ⁻⁰¹	1.01 (0.97 - 1.05)
rs4812791	20	42236175	JPH2	C/T	0.6154	2.58*10 ⁻⁰⁴	1.17 (1.07 - 1.27)	9.08*10 ⁻⁰¹	1.00 (0.96 - 1.04)
rs738498	20	42241323	JPH2	G/A	0.6174	7.84*10 ⁻⁰⁴	1.15 (1.06 - 1.25)	9.80*10 ⁻⁰¹	1.00 (0.96 - 1.04)
rs667008	20	47837871	intergenic	A/G	0.0175	4.57*10 ⁻⁰⁴	1.7 (1.26 - 2.29)	1.88*10 ⁻⁰¹	1.15 (0.93 - 1.43)
rs12479616	20	54854061	intergenic	T/C	0.6430	1.03*10 ⁻⁰⁴	1.18 (1.08 - 1.28)	3.40*10 ⁻⁰²	1.05 (1.00 - 1.10)
rs12481021	20	54855185	intergenic	A/G	0.5941	6.72*10 ⁻⁰⁵	1.17 (1.08 - 1.27)	1.41*10 ⁻⁰¹	1.04 (0.99 - 1.09)

SNP	Chr	Position (bp)	Gene	Risk/NonRisk Allele	Risk frequency	GWA		Pooled analysis	
						P Value	OR (95% CI)	P Value	OR (95% CI)
rs1537479	20	56260074	PPP4R1L, AL354776.15	T/C	0.5556	9.95*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	3.61*10 ⁻⁰²	1.04 (1.00 - 1.08)
rs531317	20	56324877	RAB22A	A/G	0.8246	7.92*10 ⁻⁰⁴	1.2 (1.08 - 1.34)	3.59*10 ⁻⁰³	1.09 (1.03 - 1.15)
rs718670	21	14570025	ABCC13	T/C	0.1548	2.34*10 ⁻⁰⁴	1.23 (1.1 - 1.37)	3.60*10 ⁻⁰¹	1.02 (0.97 - 1.08)
rs718671	21	14570050	ABCC13	G/A	0.1575	3.91*10 ⁻⁰⁴	1.22 (1.09 - 1.36)	6.55*10 ⁻⁰¹	1.01 (0.96 - 1.06)
rs17274722	21	15220401	intergenic	T/C	0.0918	8.85*10 ⁻⁰⁴	1.26 (1.1 - 1.45)	6.02*10 ⁻⁰²	1.07 (1.00 - 1.15)
rs9981313	21	29752264	intergenic	T/G	0.5790	9.52*10 ⁻⁰⁴	1.14 (1.06 - 1.24)	7.95*10 ⁻⁰³	1.06 (1.01 - 1.10)
rs2835327	21	36543972	DOPEY2	G/A	0.8493	7.25*10 ⁻⁰⁴	1.22 (1.09 - 1.37)	8.42*10 ⁻⁰⁴	1.10 (1.04 - 1.17)
rs8130834	21	42143203	PRDM15	T/C	0.2294	1.69*10 ⁻⁰⁴	1.19 (1.08 - 1.31)	2.73*10 ⁻⁰³	1.07 (1.02 - 1.12)
rs4346474	21	42146473	PRDM15	A/T	0.2293	2.93*10 ⁻⁰⁴	1.18 (1.08 - 1.3)	6.83*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs385674	21	45367098	ADARB1	G/A	0.3349	1.64*10 ⁻⁰⁴	1.18 (1.08 - 1.28)	2.80*10 ⁻⁰³	1.06 (1.02 - 1.10)
rs412626	21	45370468	ADARB1	A/G	0.1806	1.25*10 ⁻⁰⁴	1.22 (1.1 - 1.36)	2.10*10 ⁻⁰¹	1.03 (0.98 - 1.09)
rs391815	21	45373039	ADARB1	G/A	0.3356	1.35*10 ⁻⁰⁴	1.18 (1.08 - 1.28)	4.89*10 ⁻⁰³	1.06 (1.02 - 1.11)
rs5761704	22	25449061	intergenic	C/T	0.5012	4.82*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	1.61*10 ⁻⁰¹	1.03 (0.99 - 1.06)
rs6005150	22	25452480	intergenic	C/T	0.3701	1.03*10 ⁻⁰⁴	1.16 (1.07 - 1.26)	3.85*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs5761709	22	25453638	intergenic	G/T	0.3708	1.42*10 ⁻⁰⁴	1.16 (1.06 - 1.26)	3.21*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs5761710	22	25453944	intergenic	T/C	0.3748	7.63*10 ⁻⁰⁵	1.16 (1.07 - 1.26)	2.92*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs5761711	22	25459747	intergenic	A/G	0.5079	8.43*10 ⁻⁰⁶	1.18 (1.09 - 1.28)	2.73*10 ⁻⁰¹	1.02 (0.98 - 1.06)
rs7291420	22	34018623	HMG2L1	T/C	0.0372	3.06*10 ⁻⁰⁴	1.43 (1.16 - 1.76)	8.18*10 ⁻⁰²	1.09 (0.99 - 1.21)
rs133416	22	34136376	MCM5	T/C	0.2879	8.74*10 ⁻⁰⁴	1.16 (1.06 - 1.27)	2.82*10 ⁻⁰¹	1.03 (0.98 - 1.08)
rs9610322	22	34310119	intergenic	A/G	0.5367	3.85*10 ⁻⁰⁴	1.16 (1.07 - 1.25)	9.77*10 ⁻⁰²	1.03 (0.99 - 1.07)
rs989677	22	43147495	intergenic	G/C	0.2184	8.78*10 ⁻⁰⁴	1.18 (1.07 - 1.3)	9.43*10 ⁻⁰¹	1.00 (0.95 - 1.06)
rs4823354	22	43148331	intergenic	C/T	0.2172	6.13*10 ⁻⁰⁴	1.18 (1.08 - 1.3)	8.02*10 ⁻⁰¹	1.01 (0.96 - 1.06)
rs5766424	22	43881197	intergenic	A/G	0.4644	6.12*10 ⁻⁰⁴	1.15 (1.06 - 1.24)	7.84*10 ⁻⁰¹	1.01 (0.96 - 1.06)
rs2858642	22	48037941	intergenic	A/C	0.1501	3.71*10 ⁻⁰⁴	1.22 (1.1 - 1.37)	1.25*10 ⁻⁰¹	1.05 (0.99 - 1.12)
rs802637	23	154639046	intergenic	C/A	0.9575	9.49*10 ⁻⁰⁴	1.42 (1.15 - 1.74)	9.09*10 ⁻⁰¹	1.02 (0.77 - 1.34)
rs781716	23	154648189	SPRY3	T/C	0.2948	3.41*10 ⁻⁰⁷	1.26 (1.15 - 1.38)	7.39*10 ⁻⁰¹	1.02 (0.90 - 1.16)

Supplementary Table 5. SNPs previously reported to be associated with CAD and/or myocardial infarction in the literature used for eQTL analyses

	Chr	Gene	Reference
rs10755578	6q26-q27	LPA	15
rs11206510	1p32.3	PCSK9	6
rs1122608	19p13.2	SMARCA4, LDLR	6
rs12526453	6p24.1	PHACTR1	6
rs1333048	9p21.3	ANRIL	16
rs17228212	15q22.33	SMAD3	3
rs1746048	10q11.21	intergenic, CXCL12	6
rs17465637	1q41	MIA3	6
rs17672135	1q43	FMN2	7
rs2048327	6q26-q27	SLC22A3	15
rs2146807	10q11.21	intergenic, CXCL12	17
rs2259816	12q24.31	HNF1A, C12orf43	4
rs2439554	6p24.1	intergenic	18
rs2943634	2q36.3	intergenic	3
rs3127599	6q26-q27	LPAL2	15
rs4977574	9p21.3	ANRIL	6
rs599839	1p13.1	PSRC1, SORT1	3
rs629301*	1p13.1	CELSR2, PSRC1, SORT1	6
rs671765	10q11.21	intergenic, CXCL12	3
rs6725887	2q33.1	WDR12	6
rs688034	22q12	SEZ61	7
rs6922269	6q25.1	MTHFD1L	3
rs7767084	6q26-q27	LPA	15
rs8055236	16q23	CDH13	7
rs9818870	3q22.3	MRAS	4
rs9978407	21q22.11	SLC5A3, MRPS6, KCNE2	6

*The corresponding published tagSNP for rs629301 is rs646776

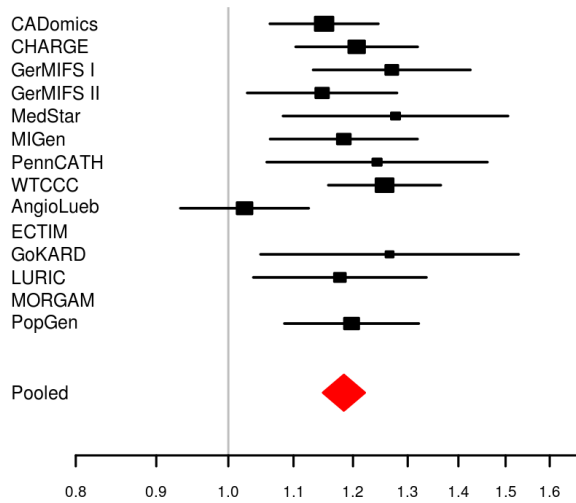
Part C – Supplementary Figures

Supplementary Figure 1. Meta-analysis of the association of the loci on chromosome 9p21.3 with coronary artery disease in a case-control design including 14 independent cohorts of European ancestry with n=59,789

Forest plots showing SNPs on chromosome 9p21.3 that reached genome-wide significance in the final meta-analysis ($P < 5 \times 10^{-8}$). The individual odds ratios (OR) with 95% confidence intervals and p-values are presented.

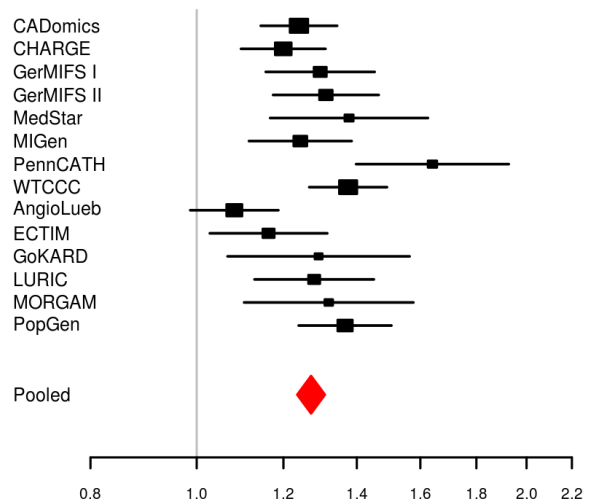
1 A.

rs1333049
 OR 1.27
 95% CI 1.23 - 1.31
 $P = 7.12 \times 10^{-58}$



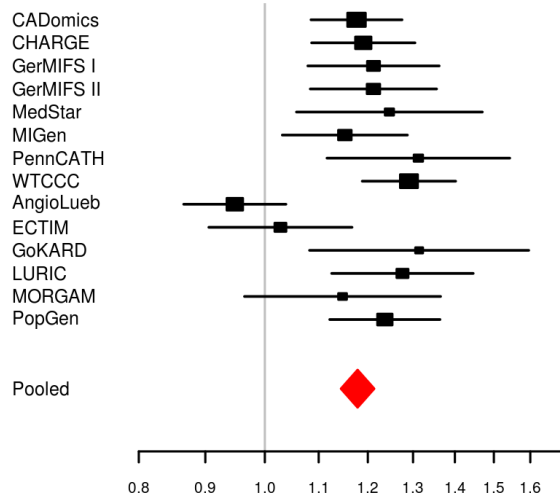
1 B.

rs7044859
 OR 1.18
 95% CI 1.15 - 1.22
 $P = 3.93 \times 10^{-27}$



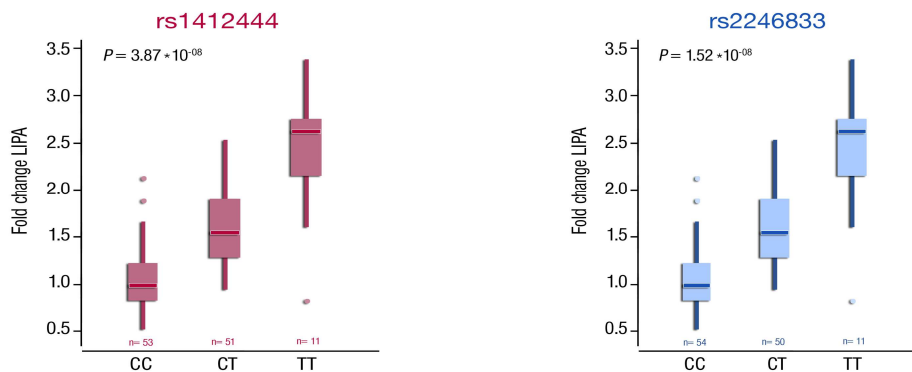
1 C.

rs7865618
 OR 1.18
 95% CI 1.14 – 1.21
 P = 1.72×10^{-27}



Supplementary Figure 2. Platform validation of *LIPA* eSNP - eQTL transcript analyses

For validation of association of *LIPA* eSNPs rs1412444 and rs2246833 with *LIPA* transcript, semi-quantitative RT-PCR was performed on 119 monocytic total RNA samples of the GHSExpress Study that were not used for global gene expression analysis, but for whom genotypes were available. Boxplots are shown for the fold change of *LIPA* expression depending on the genotype. Fold change of *LIPA* expression was calculated relative to median expression of the non-risk allele (C) genotype.



Part D. Supplementary References

1. Blankenberg S, Rupprecht HJ, Bickel C, Torzewski M, Hafner G, Tiret L, Smieja M, Cambien F, Meyer J, Lackner KJ. Glutathione peroxidase 1 activity and cardiovascular events in patients with coronary artery disease. *N Engl J Med.* 2003;349:1605-1613
2. Psaty BM, O'Donnell CJ, Gudnason V, Lunetta KL, Folsom AR, Rotter JI, Uitterlinden AG, Harris TB, Witteman JC, Boerwinkle E. Cohorts for heart and aging research in genomic epidemiology (charge) consortium: Design of prospective meta-analyses of genome-wide association studies from 5 cohorts. *Circ Cardiovasc Genet.* 2009;2:73-80
3. Samani NJ, Erdmann J, Hall AS, Hengstenberg C, Mangino M, Mayer B, Dixon RJ, Meitinger T, Braund P, Wichmann HE, Barrett JH, König IR, Stevens SE, Szymczak S, Tregouet DA, Iles MM, Pahlke F, Pollard H, Lieb W, Cambien F, Fischer M, Ouwehand W, Blankenberg S, Balmforth AJ, Baessler A, Ball SG, Strom TM, Braenne I, Gieger C, Deloukas P, Tobin MD, Ziegler A, Thompson JR, Schunkert H. Genomewide association analysis of coronary artery disease. *N Engl J Med.* 2007;357:443-453
4. Erdmann J, Grosshennig A, Braund PS, König IR, Hengstenberg C, Hall AS, Linsel-Nitschke P, Kathiresan S, Wright B, Tregouet DA, Cambien F, Bruse P, Aherrahrou Z, Wagner AK, Stark K, Schwartz SM, Salomaa V, Elosua R, Melander O, Voight BF, O'Donnell CJ, Peltonen L, Siscovick DS, Altshuler D, Merlino PA, Peyvandi F, Bernardinelli L, Ardissino D, Schillert A, Blankenberg S, Zeller T, Wild P, Schwarz DF, Tiret L, Perret C, Schreiber S, El Mokhtari NE, Schafer A, Marz W, Renner W, Bugert P, Kluter H, Schrezenmeir J, Rubin D, Ball SG, Balmforth AJ, Wichmann HE, Meitinger T, Fischer M, Meisinger C, Baumert J, Peters A, Ouwehand WH, Deloukas P, Thompson JR, Ziegler A, Samani NJ, Schunkert H. New susceptibility locus for coronary artery disease on chromosome 3q22.3. *Nat Genet.* 2009;41:280-282

5. Grant SF, Thorleifsson G, Reynisdottir I, Benediktsson R, Manolescu A, Sainz J, Helgason A, Stefansson H, Emilsson V, Helgadóttir A, Styrkarsdóttir U, Magnusson KP, Walters GB, Palsdóttir E, Jonsdóttir T, Gudmundsdóttir T, Gylfason A, Saemundsdóttir J, Wilensky RL, Reilly MP, Rader DJ, Bagger Y, Christiansen C, Gudnason V, Sigurdsson G, Thorsteinsdóttir U, Gulcher JR, Kong A, Stefansson K. Variant of transcription factor 7-like 2 (*tcf7l2*) gene confers risk of type 2 diabetes. *Nat Genet.* 2006;38:320-323
6. Kathiresan S, Voight BF, Purcell S, Musunuru K, Ardissino D, Mannucci PM, Anand S, Engert JC, Samani NJ, Schunkert H, Erdmann J, Reilly MP, Rader DJ, Morgan T, Spertus JA, Stoll M, Girelli D, McKeown PP, Patterson CC, Siscovick DS, O'Donnell CJ, Elosua R, Peltonen L, Salomaa V, Schwartz SM, Melander O, Altshuler D, Merlini PA, Berzuini C, Bernardinelli L, Peyvandi F, Tubaro M, Celli P, Ferrario M, Fève R, Marziliano N, Casari G, Galli M, Ribichini F, Rossi M, Bernardi F, Zonzin P, Piazza A, Yee J, Friedlander Y, Marrugat J, Lucas G, Subirana I, Sala J, Ramos R, Meigs JB, Williams G, Nathan DM, MacRae CA, Havulinna AS, Berglund G, Hirschhorn JN, Asselta R, Duga S, Sreafico M, Daly MJ, Nemes J, Korn JM, McCarroll SA, Surti A, Guiducci C, Gianniny L, Mirel D, Parkin M, Burt N, Gabriel SB, Thompson JR, Braund PS, Wright BJ, Balmforth AJ, Ball SG, Hall AS, Linsel-Nitschke P, Lieb W, Ziegler A, König I, Hengstenberg C, Fischer M, Stark K, Grosshennig A, Preuss M, Wichmann HE, Schreiber S, Ouwehand W, Deloukas P, Scholz M, Cambien F, Li M, Chen Z, Wilensky R, Matthai W, Qasim A, Hakonarson HH, Devaney J, Burnett MS, Pichard AD, Kent KM, Satler L, Lindsay JM, Waksman R, Epstein SE, Scheffold T, Berger K, Häge A, Martinelli N, Olivieri O, Corrocher R, McKeown P, Erdmann E, König IR, Holm H, Thorleifsson G, Thorsteinsdóttir U, Stefansson K, Do R, Xie C, Siscovick D. Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. *Nat Genet.* 2009;41:334-341
7. Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature.* 2007;447:661-678

8. Kee F, Morrison C, Evans AE, McCrum E, McMaster D, Dallongeville J, Nicaud V, Poirier O, Cambien F. Polymorphisms of the p-selectin gene and risk of myocardial infarction in men and women in the ectim extension study. Etude cas-temoin de l'infarctus myocarde. *Heart*. 2000;84:548-552
9. Parra HJ, Arveiler D, Evans AE, Cambou JP, Amouyel P, Bingham A, McMaster D, Schaffer P, Douste-Blazy P, Luc G, et al. A case-control study of lipoprotein particles in two populations at contrasting risk for coronary heart disease. The ectim study. *Arterioscler Thromb*. 1992;12:701-707
10. Winkelmann BR, Marz W, Boehm BO, Zotz R, Hager J, Hellstern P, Senges J. Rationale and design of the luric study--a resource for functional genomics, pharmacogenomics and long-term prognosis of cardiovascular disease. *Pharmacogenomics*. 2001;2:S1-73
11. Evans A, Salomaa V, Kulathinal S, Asplund K, Cambien F, Ferrario M, Perola M, Peltonen L, Shields D, Tunstall-Pedoe H, Kuulasmaa K. Morgam (an international pooling of cardiovascular cohorts). *Int J Epidemiol*. 2005;34:21-27
12. Krawczak M, Nikolaus S, von Eberstein H, Croucher PJ, El Mokhtari NE, Schreiber S. Popgen: Population-based recruitment of patients and controls for the analysis of complex genotype-phenotype relationships. *Community Genet*. 2006;9:55-61
13. Warnholtz A, Wild P, Ostad MA, Elsner V, Stieber F, Schinzel R, Walter U, Peetz D, Lackner K, Blankenberg S, Munzel T. Effects of oral niacin on endothelial dysfunction in patients with coronary artery disease: Results of the randomized, double-blind, placebo-controlled inef study. *Atherosclerosis*. 2009;204:216-221
14. Zeller T, Wild P, Szymczak S, Rotival M, Schillert A, Castagne R, Maouche S, Germain M, Lackner K, Rossmann H, Eleftheriadis M, Sinning CR, Schnabel RB, Lubos E, Mennerich D, Rust W, Perret C, Proust C, Nicaud V, Loscalzo J, Hubner N, Tregouet D, Munzel T, Ziegler A, Tiret L, Blankenberg S, Cambien F. Genetics and beyond--the transcriptome of human monocytes and disease susceptibility. *PLoS One*. 5:e10693

15. Tregouet DA, König IR, Erdmann J, Munteanu A, Braund PS, Hall AS, Grosshennig A, Linsel-Nitschke P, Perret C, DeSuremain M, Meitinger T, Wright BJ, Preuss M, Balmforth AJ, Ball SG, Meisinger C, Germain C, Evans A, Arveiler D, Luc G, Ruidavets JB, Morrison C, van der Harst P, Schreiber S, Neureuther K, Schafer A, Bugert P, El Mokhtari NE, Schrezenmeir J, Stark K, Rubin D, Wichmann HE, Hengstenberg C, Ouwehand W, Ziegler A, Tiret L, Thompson JR, Cambien F, Schunkert H, Samani NJ. Genome-wide haplotype association study identifies the *slc22a3-lpa2-lpa* gene cluster as a risk locus for coronary artery disease. *Nat Genet.* 2009;41:283-285
16. McPherson R, Pertsemlidis A, Kavaslar N, Stewart A, Roberts R, Cox DR, Hinds DA, Pennacchio LA, Tybjaerg-Hansen A, Folsom AR, Boerwinkle E, Hobbs HH, Cohen JC. A common allele on chromosome 9 associated with coronary heart disease. *Science.* 2007;316:1488-1491
17. Karvanen J, Silander K, Kee F, Tiret L, Salomaa V, Kuulasmaa K, Wiklund PG, Virtamo J, Saarela O, Perret C, Perola M, Peltonen L, Cambien F, Erdmann J, Samani NJ, Schunkert H, Evans A. The impact of newly identified loci on coronary heart disease, stroke and total mortality in the morgam prospective cohorts. *Genet Epidemiol.* 2009;33:237-246
18. Larson MG, Atwood LD, Benjamin EJ, Cupples LA, D'Agostino RB, Sr., Fox CS, Govindaraju DR, Guo CY, Heard-Costa NL, Hwang SJ, Murabito JM, Newton-Cheh C, O'Donnell CJ, Seshadri S, Vasan RS, Wang TJ, Wolf PA, Levy D. Framingham heart study 100k project: Genome-wide associations for cardiovascular disease outcomes. *BMC Med Genet.* 2007;8 Suppl 1:S5

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AngioLueb

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CHARGE

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ECTIM

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GerMIFS I und II

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MIGen

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MORGAM

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