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Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies

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Background—Genetic determinants of peripheral arterial disease (PAD) remain largely unknown. To identify genetic variants associated with the ankle-brachial index (ABI), a noninvasive measure of PAD, we conducted a meta-analysis of genome-wide association study data from 21 population-based cohorts.

Methods and Results—Continuous ABI and PAD (ABI ≤ 0.9) phenotypes adjusted for age and sex were examined. Each study conducted genotyping and imputed data to the ≈ 2.5 million single nucleotide polymorphisms (SNPs) in HapMap. Linear and logistic regression models were used to test each SNP for association with ABI and PAD using additive genetic models. Study-specific data were combined using fixed effects inverse variance weighted meta-analyses. There were a total of 41 692 participants of European ancestry ($\approx 60\%$ women, mean ABI 1.02 to 1.19), including 3409 participants with PAD and with genome-wide association study data available. In the discovery meta-analysis, rs10757269 on chromosome 9 near *CDKN2B* had the strongest association with ABI ($\beta = -0.006$, $P = 2.46 \times 10^{-8}$). We sought replication of the 6 strongest SNP associations in 5 population-based studies and 3 clinical samples ($n = 16\,717$). The association for rs10757269 strengthened in the combined discovery and replication analysis ($P = 2.65 \times 10^{-9}$). No other SNP associations for ABI or PAD achieved genome-wide significance. However, 2 previously reported candidate genes for PAD and 1 SNP associated with coronary artery disease were associated with ABI: *DAB2IP* (rs13290547, $P = 3.6 \times 10^{-5}$), *CYBA* (rs3794624, $P = 6.3 \times 10^{-5}$), and rs1122608 (*LDLR*, $P = 0.0026$).

Conclusions—Genome-wide association studies in more than 40 000 individuals identified 1 genome wide significant association on chromosome 9p21 with ABI. Two candidate genes for PAD and 1 SNP for coronary artery disease are associated with ABI. (*Circ Cardiovasc Genet.* 2012;5:100-112.)

Key Words: cohort study ■ genetic association ■ genome-wide association study ■ meta-analysis
■ peripheral vascular disease

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Peripheral arterial disease (PAD) affects approximately 27 million people in Europe and North America,¹ and is associated with increased risk for myocardial infarction, stroke, and mortality.^{2–6} Measurement of ankle and arm blood pressures with a Doppler device and calculation of the ankle-brachial index (ABI) is a simple and reliable method to detect PAD. An ABI ≤ 0.90 is indicative of definite PAD.⁷ In previous work, the Ankle-Brachial Index Collaboration demonstrated a reverse J-shaped relationship of ABI with mortality and coronary events, with a low risk ABI ranging from 1.11 to 1.40.⁸

Clinical Perspective on p 112

Little is known about genetic susceptibility to PAD, but familial aggregation and heritability estimates suggest a significant genetic component.^{9–13} A study of 112 biological candidate genes identified only 2 single nucleotide polymorphisms (SNPs) in *NOS3* significantly associated with ABI.¹⁴ The candidate gene approach to identify novel genetic variants for PAD has been limited by modest study sample size, relatively small number of genes examined, and lack of replication in independent samples.¹³

Genome-wide association studies (GWAS) have led successfully to the discovery of novel genetic variants for several common diseases, including coronary artery disease (CAD).¹⁵ The association between genetic variants on chromosome 9p21 and CAD has demonstrated replication,^{16,17} persistent association across race or ethnicity,¹⁸ and association with other vascular diseases.^{19–21} Notably, GWAS of subclinical atherosclerosis phenotypes, such as intima-medial thickness or ABI, are sparse. Therefore, we conducted a meta-analysis of GWAS findings for ABI within an international consortium of 21 population-based cohort studies that included 41 692 participants of European ancestry, among whom 3409 participants had PAD (ABI ≤ 0.90). We conducted replication analyses of our strongest findings in over 16 000 individuals from population-based cohort studies and clinically based samples of PAD. We hypothesized that this approach would lead to the unbiased identification of genetic variants associated with ABI. Further, we hypothesized that some genetic variants for ABI would be identical to those reported to be associated with CAD or its risk factors given shared underlying biological pathways, while some genetic variants would be associated uniquely with PAD.

Methods

Discovery Studies

Our analyses were conducted within the international Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium,²² and included 4 of the 5 original CHARGE cohorts: Atherosclerosis Risk in Communities Study (ARIC, $n=7630$), the Cardiovascular Health Study (CHS, $n=3193$), the Framingham Heart Study (FHS, $n=3572$), and the Rotterdam Study (RS-I, $n=5169$ and RS-II, $n=1642$). Ten additional population-based cohorts joined the collaboration for analysis of ABI phenotypes: the Family Heart Study (FamHS, $n=1736$), Genetic Epidemiology Network of Arteriopathy Study (GENOA, $n=991$), Gutenberg Heart Study (GHS, $n=3122$), Health, Aging, and Body Composition (Health ABC, $n=1564$), the Invecchiare in Chianti Study (InCHIANTI, $n=1130$), Cooperative Health Research in the Region of Augsburg (KORA F3, $n=1581$ and KORA F4, $n=1407$), Netherlands Study of Anxiety and Depression (NESDA, $n=1612$), Nijmegen

Biomedical Study (NBS, $n=544$), and the Study of Health in Pomerania (SHIP, $n=543$). A further 6 studies derived from population isolates also were available for the analyses: Amish Study (Amish, $n=1183$), Croatia-Vis ($n=897$), Croatia-Korcula ($n=851$), Croatia-Split ($n=499$), Erasmus Rucphen Family Study (ERF, $n=2133$), and the Orkney Complex Disease Study (ORCADES, $n=693$). For all studies participating in the meta-analyses, each participant self-identified as European or European-American and provided written informed consent, and the Institutional Review Board at the parent institution for each respective cohort approved the study protocols. More detailed study-specific information is provided in the online-only Data Supplement Methods.

Ankle-Brachial Index Phenotypes

Ankle and brachial blood pressure measurements for each participating study were obtained from the baseline examination or the first examination in which the measurement was obtained. Details on the ABI protocol used and the calculation performed in each study are provided in online-only Data Supplement Table I. To calculate the ABI for each leg, the systolic blood pressure at each ankle was divided by the systolic blood pressure in the arm. If the systolic blood pressure was measured in both arms, the higher arm reading was used in the ABI calculation. If replicate readings were obtained, the mean of the 2 measurements for each limb was used to calculate the ABI, with the exception of InCHIANTI, which used the higher of the 2 readings of each measurement set to calculate the ABI. The lower of the ABIs from the 2 legs was used for analysis. In ARIC and FamHS, the ABI was measured in only 1 leg, chosen at random. Participants with an ABI >1.40 were excluded because this high ABI may represent medial sclerosis, fibrocalcific disease secondary to diabetes mellitus, or other causes of noncompressible vessels.

To maximize the sample size and the power to detect genetic variants with modest effects, and to examine the entire range of ABI values given the recent evidence of increased cardiovascular disease risk associated with ABI values up to 1.1,⁸ we examined the continuous range of ABI <1.40 . As a secondary analysis to provide a clinical phenotype, we defined PAD as ABI ≤ 0.90 and conducted a case (ABI ≤ 0.9)/control; ABI >0.90 and <1.40 comparison analysis.

Genotyping and Imputation

Different genotyping platforms were used by the 21 studies (online-only Data Supplement Table II). Each study imputed the genotype “dosage” (0 to 2) for the expected number of alleles for ≈ 2.5 million Phase II HapMap CEU SNPs for each participant using currently available imputation methods.²³ CHS used BIMBAM (available at <http://stephenslab.uchicago.edu/software.html>),²⁴ GHS, InCHIANTI, NESDA, and SHIP used IMPUTE,²⁵ and all other cohorts used MACH (<http://www.sph.umich.edu/csg/abecasis/MaCH/>).

Statistical Analysis

We devised a GWAS analysis plan for the ABI and PAD phenotypes that each study independently implemented. Sex-specific and age-adjusted residuals of ABI were created from linear regression models and used as phenotypes in the analysis. No transformation of the ABI measure was performed before analysis. In FHS, residuals also were obtained separately in the original and offspring cohorts. Multi-site studies (ARIC, CHS, and FamHS) additionally adjusted for field study site. Each SNP was tested for association with ABI in additive genetic models using linear regression. The Amish Study, FamHS, FHS, and GENOA cohorts used linear mixed effects models to account for familial correlations. Croatia-Vis, Croatia-Korcula, Croatia-Split, ERF, and ORCADES used the “mmscore” function of the GenABEL package for R statistical software for the association test under an additive model. This score test for a family-based association takes into account pedigree structure and allows unbiased estimations of SNP allelic effect when relatedness is present between examinees. Logistic regression adjusting for age and sex was used to test each SNP for association with the PAD phenotype. The FamHS,

FHS, and GENOA cohorts used generalized estimating equations clustering on family to account for family correlations.

A genome-wide meta-analysis using a fixed effects approach with inverse variance weighting was then conducted in METAL²⁶ [www.sph.umich.edu/csg/abecasis/metal] for 2 669 158 SNPs in the meta-analysis, excluding the population isolates (2 670 732 SNPs including the population isolates) that met imputation and quality control criteria (online-only Data Supplement Table II). Before meta-analysis, genomic control was applied to each study. The association of ABI per each additional risk allele was quantified by the regression slope (β), its standard error [SE(β)], and the corresponding probability value. We calculated a meta-analysis odds ratio for each of the most significant SNP associations for PAD. The meta-analysis odds ratio estimates the increase in odds of PAD for each additional copy of the risk allele of the SNP. SNP associations were considered to be significant on a genome-wide level at $P < 5 \times 10^{-8}$.^{27,28} Standardized gene and SNP annotations were created using a PERL script.²⁹ We also tested for heterogeneity of study specific regression parameters using Cochran Q statistic. Because of concerns about heterogeneity, we conducted analyses of nonisolate studies and of the full group of studies. We selected SNPs for replication using results from the meta-analysis, excluding the population isolates, because the available replication samples did not include isolates. We excluded SNP association results if the total meta-analysis sample was less than 20 000 and if the average minor allele frequency of the SNP was $< 5\%$.

Replication

We sought to replicate independent SNP associations for ABI that attained genome-wide significance (1 region), SNPs with suggestive associations (5 regions, $P < 10^{-5}$), and bioinformatics data supporting the signal. The bioinformatic analyses are described in detail in the online-only Data Supplement Material. In addition, we sought to replicate 1 SNP associated with both ABI and PAD at $P < 10^{-4}$. The replication studies included 5 population-based studies and 3 clinically-based studies, including a total of over 16 000 participants: the Bruneck Study ($n=786$), the Copenhagen City Heart Study (CCHS, $n=5330$), the Multi-Ethnic Study of Atherosclerosis (MESA, $n=2611$), the National Health and Nutrition Examination Surveys (NHANES 1999–2002, $n=2335$), Prevention of Renal and Vascular End-stage disease (PREVEND, $n=3691$) cohort, Cardiovascular Disease in Intermittent Claudication (CAVASIC, $n=443$) Study, Genetic Determinants of Peripheral Arterial Disease (GenePAD, $n=850$), and the Linz Peripheral Arterial Disease (LIPAD, $n=671$) Study. Each collaborating study was provided with a SNP list and a detailed analysis plan. MESA and PREVEND used *in silico* genotyping (online-only Data Supplement Table II), and the remaining studies genotyped the SNPs using Taqman assays or Sequenom. Relative excess heterozygosity analysis demonstrated that all genotyped SNPs were compatible with Hardy-Weinberg equilibrium at the nominal 5% test-level (online-only Data Supplement Table III).³⁰

Examination of Candidate Genes Associated With Peripheral Artery Disease and Coronary Artery Disease/Myocardial Infarction

We selected candidate genes for ABI or PAD from the published literature using PubMed search terms “([ankle-brachial index] OR [peripheral arterial disease]) AND polymorphism.” Association studies with at least 100 cases and 100 controls were included regardless of whether the original study results were positive or negative. Using the discovery meta-analysis results for ABI, we then identified the most strongly associated SNPs based on probability values within the gene region ± 100 kb upstream or downstream of the candidate gene. Because of the high correlation of imputed genotypes, the effective number of loci were calculated for each gene region³¹ using the genotype scores from the KORA F4 Study (online-only Data Supplement Methods). Bonferroni correction of probability values then was applied in each region using the effective number of loci. Subsequently, false discovery rates (FDR) were calculated using these corrected probability values, accounting for the number of gene

regions examined (online-only Data Supplement Methods). Lastly, we examined the association with ABI of 30 SNPs strongly associated with CAD in recent GWAS.^{32–34} Our ABI discovery meta-analysis did not include 2 of the 30 SNPs (rs17465637 and rs3798220), and we were unable to identify proxy SNPs available in our data. Using the probability values for the 28 SNPs in our discovery meta-analysis, we then calculated the FDR for each CAD SNP, accounting for the 28 regions examined.

Results

Study Sample

The study sample included 41 692 participants of European ancestry (56% women, 6256 from population isolates) with ABI data and genome-wide genotyping. Participant characteristics at the time of ABI measurement for each cohort are provided in online-only Data Supplement Table IV. Across the studies the mean age ranged from 41.8 years to 73.8 years, the mean ABI ranged from 1.02 to 1.19, and 8.2% ($n=3409$) had PAD (ABI < 0.9). Characteristics of the replication samples were similar to the discovery set (online-only Data Supplement Table V).

ABI-SNP Associations

We conducted a meta-analysis with ($n=41 692$) and without ($n=35 434$) the population isolates (online-only Data Supplement Figures I and II, QQ-plots and Manhattan plots, and study-specific lambdas ranged from 0.997 to 1.044). Our primary meta-analysis excluded studies from population isolates because of concern for study heterogeneity and the lack of availability of replication samples from isolates. The strongest SNP association for ABI was rs10757269 on chromosome 9 near *CDKN2B* ($\beta = -0.006$, $P = 2.46 \times 10^{-8}$, P for heterogeneity = 0.23, Table 1; meta-analysis results, including the population isolates, online-only Data Supplement Table VII). Among the 96 SNP associations for ABI with $P < 10^{-5}$, 79 were located in the chromosome 9p21 region (online-only Data Supplement Table VI). The ABI SNP rs10757269 is in strong linkage disequilibrium (LD), with several SNPs in the region previously reported to be associated with CAD or myocardial infarction ($r^2 > 0.8$), but this ABI SNP is not in LD with SNPs previously associated with the type 2 diabetes mellitus (Figure 1). We repeated the meta-analysis to examine the association between ABI and rs10757269, first adjusting for CAD and then excluding individuals with CAD among the nonisolate studies. The association remained but was no longer genome-wide significant (adjusting for CAD: $P = 5.56 \times 10^{-6}$; excluding CAD: $P = 3.79 \times 10^{-5}$). Next, we sought to replicate the association between rs10757269 and ABI in both population-based and clinically-based samples ($n=16 717$). The magnitude and direction of the association in the replication studies was similar to the discovery set ($\beta = -0.0035$, $P = 0.0176$), providing evidence of replication. In the combined stage 2 discovery plus replication meta-analysis, the ABI-rs10757269 association became stronger ($P = 2.65 \times 10^{-9}$). The study-specific estimates of effect for the discovery studies, population isolates, replication studies, and overall discovery plus replication meta-analyses are presented in Figure 2. Two studies among the population isolates (the Amish Study and Croatia-Split) had effect estimates in the

Table 1. Meta-Analysis Results: ABI-SNP Associations with $P < 10^{-5}$ in the Primary Discovery Analysis With Population Isolates Excluded

SNP	Chr	Physical Position	Closest Gene	Risk/Non-Risk Allele	Risk Allele Frequency	Meta-Analysis	N	Beta	SE	P Value	P_{het}
rs10757269	9	22062264	<i>CDKN2B</i>	G/A	0.49	ABI discovery	35 036	-0.0056	0.001	2.46E-08	0.23
						ABI replication	16 672	-0.0035	0.0015	1.76E-02	0.67
						ABI combined	51 708	-0.0049	0.0008	2.65E-09	0.38
						PAD† discovery	34 555	0.0849	0.0296	4.15E-03	0.32
rs4659996	1	238912747	<i>GREM2</i>	A/G	0.48	ABI discovery	28 087	-0.006	0.0012	4.44E-07	0.34
						ABI replication	16 658	-0.0018	0.0016	2.67E-01	0.65
						ABI combined	44 745	-0.0045	0.001	2.12E-06	0.32
						PAD discovery	27 574	0.0725	0.0319	2.31E-02	0.52
rs7003385	8	41705907	<i>ANKK1</i> ‡	T/C	0.67	ABI discovery	35 375	-0.0053	0.0011	5.24E-07	0.49
						ABI replication	16 690	-0.002	0.0016	2.20E-01	0.52
						ABI combined	52 065	-0.0043	0.0009	1.11E-06	0.43
						PAD discovery	34 903	0.0838	0.0314	7.57E-03	0.24
rs819750	1	99469651	<i>LPPR4</i> ‡	G/T	0.12	ABI discovery	35 278	-0.007	0.0015	3.64E-06	0.51
						ABI replication	16 660	0.0022	0.0023	3.22E-01	0.99
						ABI combined	51 938	-0.0041	0.0013	1.01E-03	0.31
						PAD discovery	34 780	0.1068	0.0437	1.45E-02	0.06
rs9485528	6	102221473	<i>GRIK2</i> ‡	A/G	0.17	ABI discovery	35 339	-0.0061	0.0013	4.63E-06	0.78
						ABI replication	16 679	0.0002	0.002	9.24E-01	0.63
						ABI combined	52 018	-0.0041	0.0011	1.77E-04	0.48
						PAD discovery	34 850	0.1172	0.0380	2.02E-03	0.80
rs722453	7	84037497	<i>SEMA3A</i>	G/A	0.42	ABI discovery	26 200	-0.0054	0.0012	6.43E-06	0.69
						ABI replication	6300	-0.0046	0.0025	5.74E-02	0.08
						ABI combined	32 500	-0.0052	0.0011	1.02E-06	0.59
						PAD discovery	25 706	0.0575	0.0318	7.05E-02	0.63
rs16824978	2	211380306	<i>CPS1</i>	T/C	0.25	ABI discovery	34 950	-0.0054	0.0012	7.77E-06	0.37
						ABI replication	14 340	0.0000	0.0019	9.94E-01	0.22
						ABI combined	49 290	-0.0039	0.001	1.48E-04	0.11
						PAD discovery	34 518	0.0760	0.0343	2.65E-02	0.39

P_{het} indicates P value for heterogeneity; ‡, SNP is located within the gene; rs819750 is within 60kb of the gene; †, PAD discovery: ABI <0.9 vs ABI >0.9. Chr indicates chromosome.

opposite direction to the other studies. None of the other SNP associations for ABI achieved genome-wide significance. The significance of the associations for the additional SNPs chosen for replication diminished in the discovery plus replication meta-analysis (Table 1, online-only Data Supplement Table VII).

PAD-SNP Associations

None of the SNP associations for the PAD phenotype (defined by an ABI ≤ 0.9) achieved genome-wide significance (Table 2; for meta-analysis results including population isolates see online-only Data Supplement Table VIII). The strongest association was found for rs6584389 on chromosome 10 near the *PAX2* gene (odds ratio 1.17, 95% confidence interval 1.10, 1.25, $P=2.34 \times 10^{-6}$). Of note, the chromosome 9 SNP rs10757269 association with PAD was in a direction consistent with the ABI association but did not achieve statistical significance (Table 1, $\beta=0.0849$, $P=0.004$, increasing the odds of PAD).

Overlap in SNP Associations for ABI and PAD

While the directions of effect for the ABI SNPs in Table 1 were consistent with the PAD association result (lower ABI, increased odds of PAD), there was little overlap in the top associations for the 2 phenotypes. Only 3 regions marked by SNPs in or near *IDE* (10q23-q25), *DAB2IP* (9q33.2), and *GRAMD1C* (3q13.31), in addition to the chromosome 9p21 region, showed association with both ABI and PAD at the $P < 10^{-4}$ level (online-only Data Supplement Table IX). SNP rs7100623 in *IDE* demonstrated the strongest novel association with both ABI ($\beta=-0.005$, $P=1.89 \times 10^{-5}$) and PAD ($\beta=0.139$, $P=8.39 \times 10^{-5}$) at $P < 10^{-4}$; however, the association probability value was not significant in the replication stage, and diminished in the combined discovery plus replication meta-analysis.

Examination of PAD Candidate Genes

Among the 55 candidate genes or regions previously tested for association with ABI or PAD, 8 regions showed nominally significant probability values ($P < 0.05$) after correction

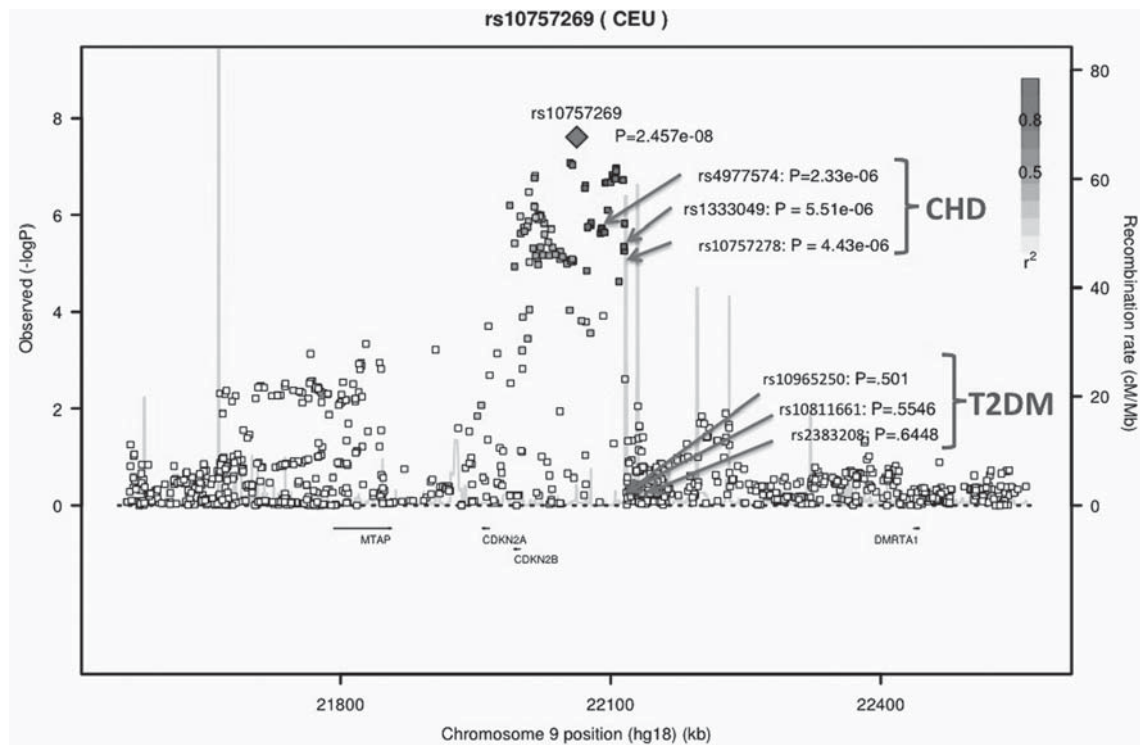


Figure 1. Genomic context of the genome-wide significant signal at chromosome 9p21 plotted against the $-\log_{10} P$ values. r^2 is between the top signal (rs10757269) and each SNP is shown. SNPs previously reported from genome-wide association studies (GWAS) to be associated with coronary artery disease (CHD, arrows), type 2 diabetes (T2DM, arrows), and P value for association with ankle-brachial index are shown. Chromosome positions are based on build hg18.

for the number of effective loci for each gene region. After accounting for the number of regions examined using a false discovery rate (FDR < 0.10), we found evidence of association between ABI and *CYBA* (rs3794624, uncorrected $P = 6.3 \times 10^{-5}$, corrected $P = 0.0036$, FDR = 0.0665) and *DAB2IP* (rs13290547, uncorrected $P = 3.6 \times 10^{-5}$, corrected $P = 0.0035$, FDR = 0.0665), in addition to the chromosome 9p21 locus (rs1333049) reported to be associated with ABI (Table 3).³⁵ We found no evidence of association between ABI and any of the other candidate genes previously tested for association with ABI or PAD (online-only Data Supplement Table X).

Examination of Coronary Artery Disease/Myocardial Infarction Candidate Genes

Among the 30 SNPs previously reported by GWAS to be associated with CAD or myocardial infarction, 28 SNPs were available in our discovery meta-analysis of ABI, and 2 of these SNPs demonstrated an association (FDR < 0.10) with ABI, including rs4977574 near *CDKN2B* ($P = 2.33 \times 10^{-6}$) and rs1122608 in *LDLR* ($P = 0.0026$) (Table 3, online-only Data Supplement Table XI).

Discussion

Our GWAS meta-analysis for ABI conducted in more than 40 000 adults of European ancestry has several notable findings. First, we identified and replicated 1 genome-wide significant association between a SNP in the chromosome 9p21 region and ABI. No other ABI-SNP associations achieved genome-wide significance. Second, in our discovery

sample, over 3000 adults had PAD (ABI ≤ 0.9); however, none of the SNP associations were significant. Third, the directions of effect were consistent across the 2 phenotypes for the most significant ABI SNPs (lower ABI, increased odds of PAD): however, we observed minimal overlap in the top SNP associations for ABI and PAD. Finally, the effect size for the 9p21 SNP was modest. The association itself is, however, intriguing, and may provide insights into the biological mechanisms contributing to generalized atherosclerosis.

Chromosome 9p21 Locus and Atherosclerosis Susceptibility

Common genetic variants in the 9p21 locus are associated strongly with myocardial infarction and CAD,^{17,33,36} and confer risk for other atherosclerotic diseases including stroke,¹⁹ cerebral and abdominal aortic aneurysm,^{20,21} and clinically diagnosed PAD; however, the relation with PAD was diminished when coronary artery disease cases were excluded.²⁰ SNP associations at the 9p21 locus with subclinical measures of atherosclerosis have been conflicting. Initially, no association was observed with carotid intima-medial thickness or flow mediated dilation in young or older adults;^{37,38} however, more recent reports demonstrate an association with the development and progression of carotid atherosclerosis³⁹ and with the suggestion of a stronger effect in men.⁴⁰ To further investigate the ABI-9p21 SNP association noted in this study, we conducted the meta-analysis after adjusting for CAD and after exclusion of individuals with CAD. Not surprisingly, the association persisted but was no

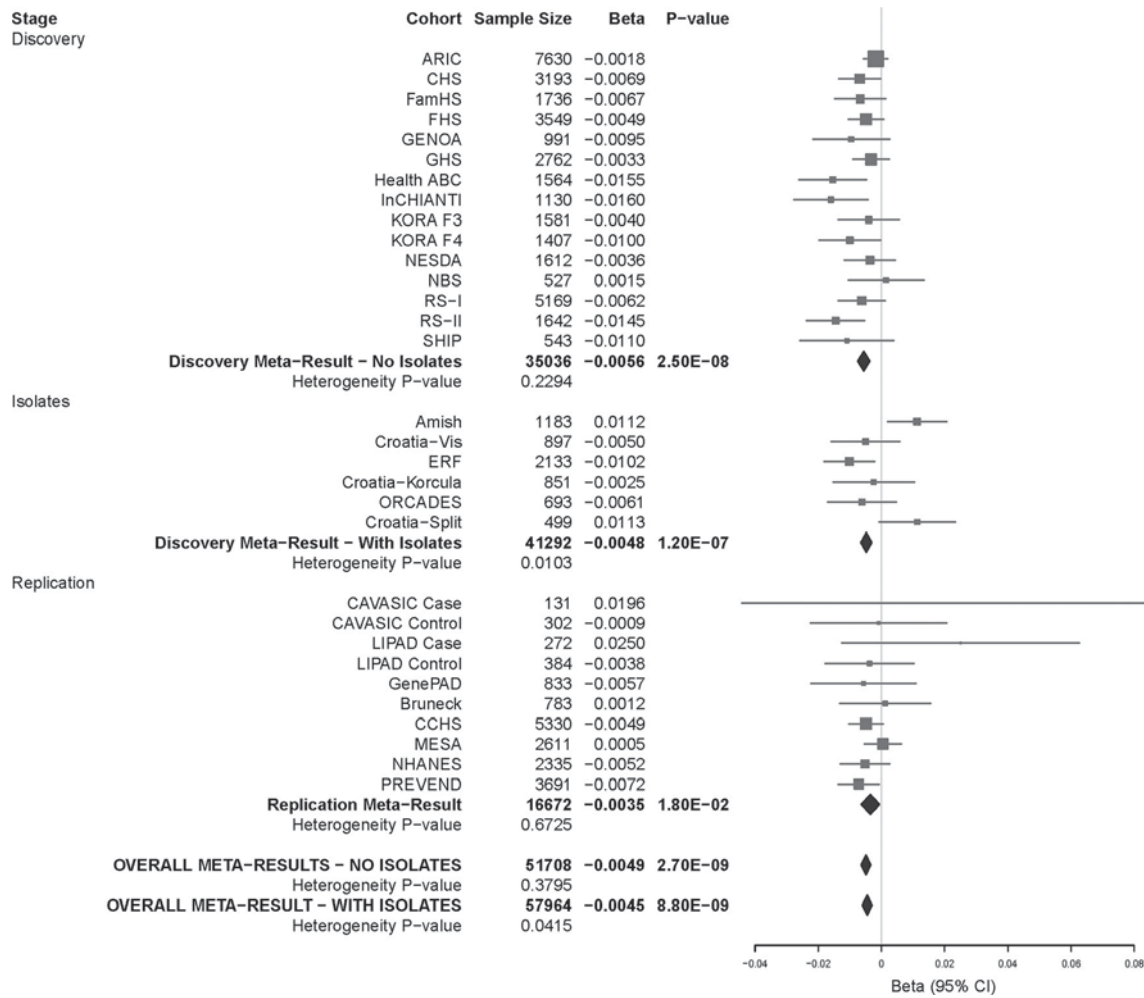


Figure 2. Ankle-brachial index-chromosome 9p21 (rs10757269) association: study-specific estimates of effect for the discovery studies, population isolates, replication studies, and overall discovery and replication meta-analyses.

longer genome-wide significant. Both CAD and PAD are manifestations of underlying atherosclerosis, and nearly two thirds of individuals with PAD have coexisting coronary or cerebrovascular disease.⁴¹ One previous report conducted in 3 studies of older adults identified an association between a variant at 9p21 and lower ABI, as well as an increased risk for PAD.³⁵ The primary effect of the chromosome 9p21 region may be on the atherosclerotic process itself, and there are likely to be many other factors, both genetic and environmental, that determine whether it manifests as CAD, PAD, or

another clinical atherosclerotic phenotype. The primary biological mechanism underlying the association with ABI is unknown but appears to be independent of 2 major PAD risk factors, diabetes and smoking, as the ABI SNP in the 9p21 region we identified is not in linkage disequilibrium with the SNPs in the region associated with diabetes risk^{42,43} or smoking-related behaviors.⁴⁴ The mechanism may be related to modulation of platelet reactivity,⁴⁵ atheroma formation, plaque instability, thrombosis, or biological processes not yet identified.⁴⁶ The SNP associated with ABI is nearest to

Table 2. Meta-Analysis Results: SNP Associations for PAD (ABI ≤0.9 vs ABI >0.9) With P < 10⁻⁵ With Population Isolates Excluded

SNP	Chr	Physical Position	Closest Gene	Risk/Non-Risk Allele	Risk Allele Frequency	N	OR	95% Confidence Interval	P Value	P _{het}
rs6584389	10	102459392	PAX2	C/A	0.50	24 474	1.17	(1.10, 1.25)	2.34E-06	0.37
rs9998941	4	162544312	FSTL5*	A/G	0.23	34 670	1.18	(1.10, 1.27)	2.34E-06	0.61
rs11751656	6	42751046	UBR2*	G/A	0.07	27 470	1.61	(1.32, 1.96)	2.46E-06	0.75
rs4535726	8	68938371	DEPDC2	T/C	0.20	34 915	1.18	(1.10, 1.26)	3.79E-06	0.01
rs2090205	17	73897869	PGS1*	A/C	0.24	34 912	1.16	(1.09, 1.24)	5.01E-06	0.17
rs11933540	4	25729099	RBPJ	C/T	0.30	34 830	1.15	(1.08, 1.23)	9.86E-06	0.08

P_{het} indicates P value for heterogeneity.

*SNP is located within the gene. Chr indicates chromosome.

Table 3. Literature-Reported Candidate Genes for Peripheral Artery Disease and Coronary Artery Disease and Their Association With Ankle-Brachial Index in the CHARGE GWAS Discovery Sample (Population Isolates Excluded) With FDR <0.10†

SNP	Chr	Physical Position	Closest Gene	Risk/Non-Risk Allele	Risk Allele Frequency	N	Beta	SE	P Value*	# of effective loci‡	P Value Corrected‡	False Discovery Rate‡
PAD genes												
rs10757269	9	22 062 264	<i>CDKN2B</i>	G/A	0.51	35036	-0.006	0.001	2.50E-08	69	1.70E-06	9.32E-05
rs3794624	16	87 244 575	<i>CYBA</i>	G/A	0.34	31035	-0.005	0.001	6.30E-05	58	3.60E-03	0.0665
rs13290547	9	123 527 316	<i>DAB2IP</i>	T/C	0.06	32135	-0.009	0.002	3.60E-05	97	3.50E-03	0.0665
CAD genes												
rs4977574	9	22 088 574	<i>CDKN2B</i>	G/A	0.49	35411	-0.0047	0.001	2.33E-06	6.52E-05
rs1122608	19	11 024 601	<i>LDLR</i>	G/T	0.74	35384	-0.0035	0.001	2.56E-03	0.036

*P value from Discovery GWAS of ABI. Chr indicates chromosome.

†Candidate genes for PAD were selected for testing with ABI if an association study with at least 100 cases and 100 controls was available in the literature, independent of whether the study was positive or negative. Genes for CAD were considered only for testing with ABI if they were identified by recent GWAS to be genome-wide significantly associated with CAD. The table shows only the genes which showed an experiment-wise significant association with ABI after correction for multiple testing. The entire list of genes can be seen in online-only Data Supplement Table X and XI for PAD and CAD genes, respectively.

‡Due to the high correlation of imputed genotype scores, the effective number of loci was calculated for each PAD gene region (31) using the genotype scores from the KORA F4 Study. Bonferroni correction of P values then was applied in each region using this number. Furthermore, the corrected P value thresholds of significance for 28 CAD loci (tested in online-only Data Supplement Table XI, $\alpha=0.05/28$, 1.85×10^{-3}) and 55 PAD loci (tested in online-only Data Supplement Table X, $\alpha=0.05/\text{effective number of loci}$) were calculated. We also calculated a false discovery rate (FDR) using the corrected P values accounting for the number of gene regions examined. An FDR <0.10 defined evidence of a significant association.

CDKN2B, a well recognized tumor-suppressor gene that encodes a cyclin-dependent kinase inhibitor and is involved in regulation of the cell cycle. *CDKN2B* is abundantly expressed in human atherosclerotic lesions,⁴⁷ and animal models suggest that altered *CDKN2A/B* expression results in abnormal regulation of vascular cell proliferation.⁴⁸ Functional studies reveal a long noncoding RNA at this locus named ANRIL, and a mouse model has confirmed the essential role of ANRIL in regulation of *CDKN2B* expression through a cis-acting mechanism.^{49,50} ANRIL is implicated in proliferation and senescence.

PAD Candidate Genes

We performed a literature search to identify all candidate gene regions previously investigated for association with PAD or ABI, irrespective of whether the association was reported to be positive or negative. This approach revealed 2 further associated gene regions: *DAB2IP* and *CYBA*. *DAB2IP* rs13290547 was not only associated with ABI, but also with PAD ($P=3.62 \times 10^{-5}$ and 2.2×10^{-5} , respectively; online-only Data Supplement Table X). The *DAB2IP* gene encodes an inhibitor that is involved in the regulation of cell survival and proliferation. One variant in the *DAB2IP* gene (rs70254486) recently has been detected in a GWAS of abdominal aortic aneurysm.⁵¹ That study also detected an association with PAD as a secondary end point in 3690 cases versus 12 271 controls ($P=3.9 \times 10^{-5}$). The same SNP showed an association with CVD within a meta-analysis of case control studies.⁵² The *CYBA* gene is involved in NADPH oxidase regulation, which contributes to oxidative stress and plays a key role in the pathophysiology of coronary disease. Only 1 report investigated a SNP (rs4673) in this gene for association with PAD among 324 cases and 295 controls, but did not find an association.⁵³ Our study found an association of rs3794624 ($r^2=0.5$ with rs4673) with continuous ABI, which may indicate that the earlier study likely lacked power

to find this association. None of the other gene regions had sufficient evidence for association with continuous ABI in our meta-analysis. Another very wide-reaching approach designed to systematically examine a large number of genes related to intermediate phenotypes of atherosclerosis, such as blood pressure regulation, lipoprotein metabolism, inflammation, oxidative stress, vascular wall biology, obesity, and diabetes, found only eNOS to be significantly associated with ABI.¹⁴ This gene could not be confirmed by our candidate gene examination.

Coronary Candidate Genes

Besides the chromosome 9 locus, 1 other SNP reported to be associated with coronary disease in recent GWAS also showed an association with ABI in our study; rs1122608 in *LDLR*. The *LDLR* gene plays an important role in cholesterol homeostasis, and mutations at this gene have been shown to influence LDL cholesterol levels and the subsequent risk for coronary disease.⁵⁴ The association of *LDLR* gene with ABI in our study is a confirmation of the shared biological pathways underlying both subclinical and clinically apparent disease.

Strengths/Limitations

Our meta-analysis represents the largest collaborative effort to date to identify genome-wide SNP associations for variation in ABI and PAD (ABI ≤ 0.90), and our findings suggest the absence of common variants with large effects on ABI. Use of ABI as our primary phenotype has major advantages of detecting asymptomatic PAD, as the ABI is an objective measurement, whereas clinical PAD requires subjective symptoms of exertional leg discomfort and mobility of the individual. However, several limitations of our meta-analysis merit comment. The blood pressure measurement protocol and ABI calculation was heterogeneous across participating studies. While protocols were standardized within each study,

the studies were not designed to be fully standardized and comparable across studies (online-only Data Supplement Table I). This phenotype heterogeneity may have impacted our ability to detect associations. Furthermore, for many studies, information about a previous revascularization intervention was not available. This lack of data may have resulted in the misclassification of some of the most affected persons by placing them into an ABI range of unaffected individuals and consequently reducing our power to detect true associations. Our sample was restricted to individuals of European ancestry, and thus our findings cannot yet be generalized to individuals of other race or ethnic groups. Furthermore, some PAD susceptibility variants may be race or ethnic specific and only can be uncovered through the study of non-Europeans. For example, African-Americans have a higher prevalence of PAD that cannot be attributed to traditional or novel risk factors.⁵⁵ This observation raises the hypothesis that polymorphisms unique to African-Americans partially may be responsible for the higher prevalence of PAD.⁵⁵ We did not evaluate gene by environment interactions, which may be especially relevant for cigarette smoking, a strong risk factor for PAD,⁵⁶ and a factor known to interact with other genes to modulate atherosclerosis.⁵⁷

Conclusions

In conclusion, a common variant near the *CDKN2B* gene in the chromosome 9p21 locus is associated with a lower ABI. PAD represents a diffuse form of atherosclerosis associated with increased risk for death and incident CVD events. Thus, the identification of genetic variants associated with ABI may provide an important opportunity not only to unravel the biological basis of PAD, but also to improve our understanding of the causes of the variation in degree of atherosclerosis from 1 arterial bed to another. Additional studies are warranted to identify the causal variants in the 9p21 locus and to characterize their functional significance. The search for genes influencing predilection to PAD remains elusive, and alternative approaches are warranted.

Appendix

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See online-only Data Supplement Material.

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Disclosures

None.

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CLINICAL PERSPECTIVE

Little is known about the genetic susceptibility to peripheral arterial disease (PAD). We conducted a meta-analysis of genome-wide association study findings for the ankle-brachial index (ABI), a noninvasive measure of PAD, within an international consortium of 21 population-based cohort studies that included over 40 000 participants of European descent, and conducted replication analyses in over 16 000 individuals from population-based cohorts and clinically-based studies of PAD. We identified and replicated 1 genome-wide significant association between a genetic variant in the chromosome 9p21 region and a lower ABI. Common genetic variants in the 9p21 locus are associated strongly with coronary artery disease and confer risk for other atherosclerotic diseases. Therefore, the primary effect of the 9p21 region may be on the atherosclerotic process itself, and there are likely many other factors, both genetic and environmental, that determine whether it manifests as coronary disease, PAD, or another clinical atherosclerotic phenotype. The primary biological mechanism underlying the association with ABI is unknown but appears independent of 2 major PAD risk factors, diabetes and smoking, as the ABI single nucleotide polymorphisms (SNP) in the 9p21 region we identified is not in linkage disequilibrium with the SNPs in the region associated with diabetes or smoking-related behaviors. PAD represents a diffuse form of atherosclerosis associated with increased risk for death and incident CVD events. Identification of genetic variants associated with ABI may provide an opportunity to unravel the biological basis of PAD.

Supplemental Material

Association between chromosome 9p21 variants and the Ankle-brachial Index identified by a meta-analysis of 21 genome-wide association studies

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1. Study Specific Phenotype and Genotype Information

1.1 Discovery cohorts: non-isolated populations

1.1.1 *Atherosclerosis Risk in Communities Study (ARIC)*

The ARIC study is a predominantly bi-racial prospective study of the etiology and natural history of subclinical and clinical atherosclerosis among 15,792 middle-aged men and women, aged 45 to 64 years old at recruitment in 1987 to 1989 ⁽¹⁾. Study participants were selected as a probability sample from four US communities: Forsyth Co, NC; Jackson, MS; seven northwestern suburbs of Minneapolis, MN; and Washington Co, MD. African-Americans were over-sampled in Forsyth CO and were exclusively sampled in Jackson. Participants were examined at baseline with collection of medical, social, and demographic data and at three triennial follow-up exams, the last of which occurred in 1999. Annual follow-up continues to ascertain vital status as well as CHD and stroke, including hospitalizations and deaths. GWAS data are available from 8,861 self-identified white ARIC participants.

1.1.2 *Cardiovascular Health Study (CHS)*

The CHS is a population-based cohort study of risk factors for CHD and stroke in adults age 65 years and older conducted across four field centers in the United States ⁽²⁾. The original predominantly Caucasian cohort of 5201 persons was recruited in 1989-1990 from a random sample of people on Medicare eligibility lists and an additional 687 African-Americans were enrolled subsequently for a total sample of 5,888.

DNA was extracted from blood samples drawn on all participants at their baseline examination in 1989 to 1990. Genotyping was performed from 2007 to 2008 at the General Clinical Research Center's Phenotyping/Genotyping Laboratory at Cedars- Sinai on the 3,980 CHS participants who had consented to genetic testing and were free of CVD at baseline. A total of 1,908 persons were excluded for lack of available DNA or prevalent coronary heart disease, congestive heart failure, peripheral vascular disease, valvular heart disease, stroke, or transient ischemic attack. Because the other cohorts were predominantly white, the African-American participants were excluded from this analysis to limit the potential for false positive associations due to population stratification, leaving 3397 Caucasians successfully genotyped, 3291 had measures of ABI.

1.1.3 *Family Heart Study (FamHS)*

The Family Heart Study (<https://dsgweb.wustl.edu/PROJECTS/MP1.html>) was begun in 1992 with the ascertainment of 1,200 families, half randomly sampled, and half selected because of an excess of coronary heart disease (CHD) or risk factor abnormalities as compared with age- and sex-specific population rates ⁽³⁾. The families, with approximately 6,000 individuals, were sampled on the basis of information on probands from four population-based parent studies: the Framingham Heart Study, the Utah Family Tree Study, and two ARIC centers (Minneapolis, and Forsyth County, NC). A broad range of phenotypes were assessed at a clinic examination (exam 1) in broad domains of CHD, atherosclerosis, cardiac and vascular function, inflammation and hemostasis, lipids and lipoproteins, blood pressure, diabetes and insulin resistance, pulmonary function, and anthropometry. Approximately 8 years later, study participants belonging to the largest pedigrees were invited for a second clinical exam. A total of 2,767 Caucasian subjects in 510 extended families were examined. This sample is the focus of the genome-wide association study (GWAS).

A two-stage design was adopted for the GWAS. In the first stage, 1016 subjects were chosen, equally distributed between the upper and lower quartile of age- and sex-adjusted values for coronary artery calcification, assessed by CT scan. These subjects were chosen to be largely unrelated; 34% of the subjects were from unique families, while 200 other subjects had 1 or more siblings selected into the sample, yielding a sample of 465 unrelated subjects. The remaining family members (n=1,753) will be genotyped in the second stage for replication of the top hits from the first stage.

1.1.4 Framingham Heart Study (FHS)

The FHS is a National Heart Lung and Blood Institute contract-funded observational cohort study initiated in 1948 to examine the determinants of cardiovascular disease and its risk factors (<http://www.framinghamheartstudy.org/>). The Original Cohort comprised 5,209 men and women, aged 28-62 years at enrollment who have undergone routine biennial examinations ^(4,5). In 1971, 5,124 Offspring of the Original Cohort participants and Offspring spouses, aged 5 to 70 years, were enrolled into the Framingham Offspring Study and have been examined approximately every 4 years ^(6,7). In the 1990s, DNA was obtained for genetic studies from surviving Original cohort and Offspring participants. Routine examinations for all FHS cohorts included a standardized physician administered medical history interview and physical examination, direct measurement of cardiovascular risk factors, laboratory assessment, and various questionnaires and noninvasive cardiovascular tests specific to the given examination cycle. Cardiovascular events were adjudicated by a panel of senior investigators using previously reported criteria. FHS examinations were approved by the Institutional Review Board of the Boston University Medical Center and all participants provided written informed consent.

1.1.5 Genetic Epidemiology Network of Arteriopathy Study (GENOA)

The Family Blood Pressure Program (FBPP), established by the National Heart Lung and Blood Institute in 1996, joined existing research networks that were investigating hypertension and cardiovascular diseases (<http://public.nhlbi.nih.gov/GeneticsGenomics/home/fbpp.aspx>). One of the four FBPP networks is the Genetic Epidemiology Network of Arteriopathy (GENOA), which recruited hypertensive, Caucasian sibships for linkage and association studies to investigate genetic contributions to hypertension and hypertension-related target organ damage. Sibships containing at least two individuals with clinically-diagnosed essential hypertension before age 60 years were recruited from Rochester, Minnesota. After identifying each hypertensive sibship, all members of the sibship were invited to participate regardless of their hypertension status. Informed consent was obtained from all subjects and approval was granted by participating institutional review boards. Participants were diagnosed with hypertension if they had either 1) a previous clinical diagnosis of hypertension by a physician with current anti-hypertensive treatment, or 2) an average systolic blood pressure (SBP) ≥ 140 or diastolic blood pressure (DBP) ≥ 90 on the second and third clinic visit as stipulated by the Joint National Committee-7 guidelines ⁽⁸⁾. Exclusion criteria were secondary hypertension, alcoholism or drug abuse, pregnancy, insulin-dependent diabetes mellitus, or active malignancy.

1.1.6 Gutenberg Heart Study (GHS)

The Gutenberg Health 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. It also investigates cancer, eye diseases, diseases of the immune system

and the metabolism. 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. All participants underwent a five hour examination including a biobanking in the study center. Follow-up examinations are carried out after 2.5 and 5 years. The study protocol was approved by the local ethics committee and the local data safety commissioner and the sampling design by the federal data safety commissioners. All subjects gave written informed consent.

1.1.7 Health, Aging, and Body Composition(Health ABC) Study

The Health Aging and Body Composition (Health ABC) Study is a NIA-sponsored ongoing cohort study of the factors that contribute to incident disability and the decline in function of healthier older persons, with a particular emphasis on changes in body composition in old age. Health ABC enrolled well-functioning, community-dwelling black (n=1281) and white (n=1794) men and women aged 70-79 years between April 1997 and June 1998. Participants were recruited from a random sample of white and all black Medicare eligible residents in the Pittsburgh, PA, and Memphis, TN, metropolitan areas. The key components of Health ABC include a baseline exam, annual follow-up clinical exams, and phone contacts every 6 months to identify major health events and document functional status between clinic visits. GWAS data are available from 1663 white participants.

1.1.8 Invecchiare in Chianti (InCHIANTI) Study

The InCHIANTI study is a population based longitudinal study designed to investigate the causes of decline in mobility in older subjects ⁽⁹⁾. The study sample comprises 1,453 individuals of white European descent and is representative of the older population aged 65 years and older supplemented with at least 30 men and 30 women for each 10 year age group from 20 to 70 years from two small towns from the Chianti region in Tuscany, Italy. Interviews were conducted at the participants' homes by three experienced interviewers. Within three weeks, participants attended a study clinic for blood drawing tests, having fasted for at least 8 and just concluded the 24-hour urine collection. On the same day, the participants received a series of medical examinations, including an assessment of the ankle-brachial index. On the second appointment a clinical evaluation and a comprehensive motor and cognitive performances session were performed by an experienced geriatrician and a trained physical therapist, respectively. INRCA Ethical Committee approved the entire study protocol.

1.1.9 and 1.1.10 Cooperative Health Research in the Region of Augsburg, Kooperative Gesundheitsforschung in der region Augsburg (KORA F3, KORA F4)

The KORA surveys S3 and S4 (Kooperative Gesundheitsforschung in der Region Augsburg ⁽¹⁰⁾) are population-based samples drawn from the general population of the South-German city of Augsburg and surrounding counties stratified by age (25 to 74 years) and sex. The follow-ups of these surveys were conducted in 2004/05 (KORA F3) and 2006-2008 (KORA F4). All participants had a German passport, were of European origin and underwent a standardized face-to-face interview by certified medical staff and a standardized medical examination. Genome-wide data are available for a subset of 1,644 subjects randomly chosen from

KORA F3 and for 1814 subjects from KORA F4. ABI-measures were additionally available for n=1,581 (KORA F3) and n=1,407 (KORA F4).

1.1.11. Netherlands Study of Depression and Anxiety (NESDA)

The Netherlands Study of Depression and Anxiety (NESDA) ⁽¹¹⁾, is a multi-centre study designed to examine the long-term course and consequences of depressive and anxiety disorders (<http://www.nesda.nl>). NESDA included both individuals with depressive and/or anxiety disorders and controls without psychiatric conditions. Inclusion criteria were age 18-65 years and self-reported western European ancestry, exclusion criteria were not being fluent in Dutch and having a primary diagnosis of another psychiatric condition (psychotic disorder, obsessive compulsive disorder, bipolar disorder, or severe substance use disorder).

For all participants DNA was isolated from the baseline blood sample. Through funding from the fNIH GAIN program (www.fnih.gov/gain), whole genome scan analysis was conducted for 1,859 NESDA (1,702 depressed cases and 157 controls) participants. A hundred subjects were excluded because of various quality control issues ⁽¹²⁾.

1.1.12 Nijmegen Biomedical Study (NBS)

The Nijmegen Biomedical Study is a population-based cross-sectional study conducted by the Radboud University Nijmegen Medical Centre ⁽¹³⁾. Nijmegen is a town in the eastern part of The Netherlands with 156,000 inhabitants, approximately 87% of Caucasian descent. Age and sex stratified randomly selected adult (age 18 years and older) inhabitants of Nijmegen (N=22,452) received an invitation to fill out a postal questionnaire on lifestyle and medical history. A total of 6,434 participants donated blood for DNA-isolation. GWA-data were available for 1,832 participants ⁽¹⁴⁾. We invited participants aged 50–70 yrs to come to the hospital and performed ABI at rest and after exercise. In total 1517 participants from the Nijmegen Biomedical Study were included ⁽¹⁵⁾. For 544 participants both ABI and GWA-data were available. Approval to conduct the study was obtained from the Institutional Review Board.

1.1.13 and 1.1.14 The Rotterdam Study I and II (RS-I and RS-II)

The Rotterdam Study is a prospective population-based cohort study to investigate the determinants of chronic diseases among participants aged 55 years and older ⁽¹⁶⁾. Briefly, residents of Ommoord, a district of Rotterdam, in the Netherlands, 55 years of age or older, were asked to participate, of whom 7,983 participated (RS-I). The baseline examination was conducted in 1990 -1993 and consisted of a home interview and research center visit for blood samples. In 1999, inhabitants who turned 55 years of age or moved into the study district since the start of the study were invited of whom 3,011 participated (RS-II). In total, at the time of the current Analyses, ABI data were available for 5,169 participants with GWA study data for RS-I and for 1,642 participants from RS-II. The Medical Ethics Committee of Erasmus MC approved the study, and all participants gave informed consent.

1.1.15 Study of Health in Pomerania (SHIP)

The Study of Health in Pomerania (SHIP) is a population-based survey in West Pomerania, the north-east area of Germany ^(17,18). A sample from the population aged 20 to 79 years was drawn from population registries. First, the three cities of the region (with 17,076 to 65,977 inhabitants) and the 12 towns (with 1,516 to 3,044 inhabitants) were selected, and then 17 out of 97 smaller towns (with less than 1,500 inhabitants), were drawn at random. Second, from each of the selected communities, subjects were drawn

at random, proportional to the population size of each community and stratified by age and gender. Only individuals with German citizenship and main residency in the study area were included. Finally, 7,008 subjects were sampled, with 292 persons of each gender in each of the twelve five-year age strata. In order to minimize drop-outs by migration or death, subjects were selected in two waves. The net sample (without migrated or deceased persons) comprised 6,267 eligible subjects. Selected persons received a maximum of three written invitations. In case of non-response, letters were followed by a phone call or by home visits if contact by phone was not possible. The SHIP population finally comprised 4,308 participants (corresponding to a final response of 68.7%). Baseline examinations were performed between 1997 and 2001 (SHIP-0). Follow-up examinations were conducted between 2002 and 2006 (SHIP-1) as well as between 2008 and 2012 (SHIP-2). Data for the present analyses were taken from a sample of SHIP-2.

1.2 Discovery cohorts: isolated populations

1.2.1 *The Old Order Amish Study (Amish)*

The Old Order Amish individuals included in this study were participants of several ongoing studies of cardiovascular health carried out at the University of Maryland ^(19,20). Participants were relatively healthy volunteers from the Old Order Amish community of Lancaster County, PA. and their family members. Examinations were conducted at the Amish Research Clinic in Strasburg, PA. All protocols were approved by the Institutional Review Board at the University of Maryland and informed consent was obtained, including permission to use their DNA for genetic studies.

1.2.2, 1.2.3 and 1.2.4 *CROATIA-Vis, CROATIA-Korcula and CROATIA-Split*

The CROATIA studies recruited adult individuals within each community irrespective of any specific phenotype. Fasting blood samples were collected, biochemical and physiological measurements taken and questionnaire data for medical history as well as lifestyle and environmental exposures were collected following similar protocols. The CROATIA study conformed to the ethical guidelines of the 1975 Declaration of Helsinki and were approved by appropriate ethics boards with all participants signing informed consent prior to participation.

The CROATIA-Vis study includes 1008 Croatians, aged 18–93 years, who were recruited from the villages of Vis and Komiza on the Dalmatian island of Vis during 2003 and 2004 within a larger genetic epidemiology program. The CROATIA-Korcula study includes 969 Croatians between the ages of 18 and 98. The field work was performed in 2007 and 2008 in the eastern part of the island, targeting healthy volunteers from the town of Korčula and the villages of Lumbarda, Žrnovo and Račišće. The CROATIA-Split study includes 499 Croatians between the ages of 18 and 85 recruited in 2009 from the city of Split.

1.2.5 *Erasmus Rucphen Family Study (ERF)*

The Erasmus Rucphen Family study (ERF) is a cross-sectional family-based study. The study population essentially consists of one extended family of descendants from 20 related couples who lived between 1850 and 1900 and had at least 6 children baptized in the community church. The detailed information about ERF can be found elsewhere ⁽²¹⁾. The Medical Ethical Committee of the Erasmus Medical Center, Rotterdam approved the study and informed consent was obtained from all participants.

1.2.6 Orkney Complex Disease Study (ORCADES)

The Orkney Complex Disease Study (ORCADES) is an ongoing family-based, cross-sectional study in the isolated Scottish archipelago of Orkney. Genetic diversity in this population is decreased compared to Mainland Scotland, consistent with the high levels of endogamy historically. Data for participants aged 18-91 years, from a subgroup of ten islands, were used for this analysis. Fasting blood samples were collected and over 300 health-related phenotypes and environmental exposures were measured in each individual. All participants gave informed consent and the study was approved by Research Ethics Committees in Orkney and Aberdeen.

1.3 Replication studies

1.3.1 Bruneck Study

The Bruneck Study is a prospective, population-based survey on the epidemiology, pathophysiology and prevention of cardiovascular and cerebrovascular disease ⁽²²⁻²⁶⁾. In 1990, 1000 individuals aged 40-79 years were randomly chosen from the inhabitants of the town of Bruneck (South Tyrol, Italy) on the basis of an age- and sex-stratified strategy (125 persons per sex and decade). The population of Bruneck is exclusively Caucasian and of heterogeneous geographic origin with sizeable segments of Austro-German or Italian background. Population mobility within the survey area was low at 0.2% per year. Follow-up examinations were performed in 1995, 2000 and 2005 with participation rates exceeding 90%. Analyses for the current investigation focused on the 1995 evaluation. The study protocol was approved by the pertinent ethics committee, and all participants gave their written informed consent.

1.3.2 Copenhagen City Heart Study (CCHS)

CCHS is a prospective cardiovascular study of the Danish general population initiated in 1976-1978 with follow-up examinations in 1981-1983, 1991-1994 and 2001-03 ⁽²⁷⁻²⁹⁾. Individuals were selected based on the Central Population Register Code to reflect the adult Danish general population aged 20-80+ years. Blood samples for DNA extraction are available for 10,594 participants. For 5,467 participants of this study ABI measurements are available from the 2001-03 examination.

1.3.3 Multi-Ethnic Study of Atherosclerosis (MESA)

MESA is an NHLBI-sponsored population-based, prospective, multi-center cohort study including participants recruited from six field sites in the United States – Forsyth County, NC (Wake Forest University), Northern Manhattan/Bronx, NY (Columbia University), Baltimore/Baltimore County, MD (Johns Hopkins University), St. Paul, MN (University of Minnesota, Twin Cities), Chicago, IL (Northwestern University), and Los Angeles County, CA (UCLA). Details of recruitment and study design have been previously published elsewhere ⁽³⁰⁾. Briefly, the MESA cohort comprises 6,814 men and women of diverse ethnic background who were 45 to 84 years old at the baseline exam and free of clinically overt cardiovascular disease (CVD) who were recruited to elucidate the determinants and natural history of subclinical CVD, and study progression of subclinical CVD. The cohort is 53% women with an ethnic composition of approximately 40% White, 30% African American, 20% Hispanic and 10% Asian primarily of Chinese descent. The MESA was approved by the Institutional Review Board of all participating field sites and reading centers and participants gave informed consent for participation and use of DNA specimens. Genotyping took place

using the Affymetrix 6.0 array. There were n=2611 participants of European descent who consented the use of DNA for research studies and had imputed GWAS data for the contributed SNPs as well as ABI measurements.

1.3.4 National Health and Nutrition Examination Surveys (NHANES)

The National Health and Nutrition Examination Surveys (NHANES) are conducted by the National Center on Health Statistics (NCHS) at the Centers for Disease Control and Prevention (CDC). NHANES is a collection of diverse, population-based cross-sectional surveys of non-institutionalized Americans regardless of health status at the time of ascertainment (<http://www.cdc.gov/nchs/nhanes.htm>). NHANES is considered a complex survey given that specific age groups (such as the elderly) and racial/ethnic groups (non-Hispanic blacks and Mexican-Americans) are oversampled. The NHANES data accessed for this work includes NHANES 1999-2000 and NHANES 2000-2001. Collectively, these surveys contain 7,839 DNA samples linked to demographic, health, and lifestyle data. Participants were consented by the CDC at the time of the survey and sample collection, and consent included the storage of data and biological specimens such as blood for future research^(31,32). The present study was approved by the CDC Ethics Review Board. Because the study investigators did not have access to personal identifiers, this study was considered non-human subjects research by the Vanderbilt University Internal Review Board.

Race/ethnicity is self-described and was categorized as non-Hispanic white, non-Hispanic black, Mexican-American, and others. Only data for non-Hispanic whites were included here for replication efforts. The ankle brachial pressure index (ABPI), also referred to as the ankle arm blood pressure index (AAI), is a noninvasive technique to measure peripheral vascular disease in population-based and clinical studies. ABPI was defined as the ratio of the systolic blood pressure in the ankle compared with that in the arm. ABPI measurement was performed by a health technician on all adults ≥ 40 years of age at interview. Exclusions for these procedures were bilateral amputation, casts, ulcers, dressings, or other conditions which make blood pressure readings at these sites impossible. The presence of these conditions on one limb did not exclude the study participant, but they were excluded if they occurred bilaterally. Systolic pressure was measured in one arm (brachial vessel, right arm if accessible) and both ankles. ABI was defined as the ratio of the systolic blood pressure in the ankle compared with that in the arm. The lower ABI of the two legs was used in the analysis. ABI > 1.4 and equal to 0 were excluded from the analysis. Serum HDL-C, triglycerides, and total cholesterol were measured using standard enzymatic methods. LDL-C was calculated using the Friedewald equation, with missing values assigned for samples with triglyceride levels greater than 400 mg/dl. Fasting status was recorded at time of blood draw. Body mass index was calculated from height and weight measured in the Mobile Examination Center by CDC medical personnel. Current smoking was defined by “do you smoke cigarettes now?” or cotinine levels $> 15\text{ng/ml}$. Former smoking was defined among non-current smokers by the answer “yes” to the question “Smoked at least 100 cigarettes in life”. Participants were considered to have type 2 diabetes if they answered “yes” to “Ever been told you have sugar/diabetes?” or if they had fasting blood glucose levels $> 126\text{ mg/dL}$. Hypertension was defined if average systolic blood pressure was ≥ 140 or average diastolic blood pressure was ≥ 90 or if the study participant reported taking medication for high blood pressure. Prevalent cardiovascular disease was defined by “Ever told you had heart attack”. Lipid lowering medication use was defined by “now taking prescribed medicine” to lower cholesterol.

Genotyping was performed for nine SNPs in all of NHANES 1999-2002 (n=7,839) using Sequenom in the Vanderbilt DNA Resources Core. SNPs targeted for genotyping included rs10757269, rs16824978, rs4659996, rs7003385, rs7100623, rs819750, rs9485528. In addition to genotyping experimental NHANES samples, we genotyped blind duplicates provided by CDC. All SNPs reported here save for rs16824978 passed CDC quality control metrics and are available for secondary analyses through NCHS/CDC.

Tests of association were performed unweighted using linear regression, unadjusted and adjusted for covariates as specified in the analysis plan. All statistical analyses were conducted remotely in SAS v9.2 (SAS Institute, Cary, NC) using the Analytic Data Research by Email (ANDRE) portal of the CDC Research Data Center in Hyattsville, MD.

1.3.5 PREVEND

The Prevention of RENal and Vascular ENd stage Disease study is an ongoing prospective study investigating the natural course of increased levels of urinary albumin excretion and its relation to renal and cardiovascular disease. Inhabitants 28 to 75 years of age (N=85,421) in the city of Groningen, The Netherlands, were asked to complete a short questionnaire, 47% responded, and individuals were then selected with a urinary albumin concentration of at least 10 mg/L (N= 7,768) and a randomly selected control group with a urinary albumin concentration less than 10 mg/L (N=3,395). Details of the protocol have been described elsewhere (www.prevend.org). Genotyping was performed in a subset of subjects. All subjects provided written informed consent.

1.3.6 Cardiovascular Disease in Intermittent Claudication (CAVASIC) Study

The CAVASIC Study (CArdioVAscular disease in Intermittent Claudication) is a prospective case-control study which was initiated in 2002 to identify cardiovascular risk factors in patients with intermittent claudication⁽³³⁾. Patients and controls were enrolled in two clinical centers, the Department of Vascular Surgery, Medical University Innsbruck and the 3rd Medical Department of Metabolic Diseases and Nephrology, Hietzing Hospital, Vienna, Austria. Patients were consecutively included in the study when they presented with or had a history of intermittent claudication (PAD IIa or IIb according to the criteria of Fontaine), regardless of whether they had already undergone a treatment procedure (bypass surgery or intervention). Patients were excluded from the study for any of the following: presence of acute or critical limb ischemia (Fontaine III or IV); impaired liver function with elevated enzymes (AST>50U/L, ALT >25U/L, Gamma GT >60U/L); impaired kidney function with serum creatinine >1.5 mg/dL; malignancy; past organ transplantation; therapy with nicotinic acid or corticosteroids. Furthermore controls were recruited from the same geographical region matched for age and presence of type 2 diabetes mellitus (T2DM). All members of the control group volunteered to participate in the study following a public invitation in newspapers. We applied the same exclusion criteria to the control group as used for patients. Controls with symptomatic PAD were excluded, but those with a history of cardiovascular disease were allowed to participate.

Neither the patients nor the controls suffered from acute illnesses or clinically detectable inflammatory processes at the time of enrollment. All subjects provided written informed consent and the examination protocol was approved by the Ethical Committee of the participating study centers. To minimize interobserver bias all interviews and examinations were performed by one physician at each of the two clinical centers who was specially trained in vascular examinations and echocardiography.

1.3.7 GENEPAD

The GENEPAD study was approved by the Institutional Review Boards at Stanford University and Mount Sinai; and registered at <http://clinicaltrials.gov> (NCT 00380185). Participants were recruited from patients undergoing elective, non-emergent coronary angiogram for angina, shortness of breath, abnormal stress test, or known CAD at Stanford University and Mount Sinai Medical Centers between April 2004 and February 2008, for whom the PAD status was not known to the investigators at the time of informed consent and recruitment into the study. This cross-sectional design allowed for two sharply defined phenotypes to emerge (i.e., patients with hemodynamically significant CAD alone, versus those with hemodynamically significant CAD and PAD). Cases were defined as patients with CAD and PAD while controls were defined as subjects with CAD alone. Furthermore, with this study design, confounding clinical covariates (e.g., traditional cardiovascular risk factors) would contribute minimally to the difference between the two phenotypes. This design would maximize our chances for discovery of novel factors that affect the distribution of atherosclerotic plaque. All participants provided written informed consent. Patients admitted for emergent catheterizations, or screening catheterizations prior to organ transplants were excluded. Additional exclusions included being younger than 40 years of age and having a history of radiation treatment, known chronic infectious diseases such as HIV, hepatitis B or C, or a language barrier.

1.3.8 Linz Peripheral Arterial Disease (LIPAD) Study

The LIPAD Study was performed from April 2000 to April 2002 at the St. John of God Hospital, Department of Surgery, Linz, Austria. Of the patients admitted for inpatient evaluation of suspected or definite PAD during the given time interval, all patients with chronic atherosclerotic occlusive disease of the lower extremities associated with typical symptoms were included into this study on the basis of the final clinical diagnosis established by the attending vascular surgeons. The diagnosis was verified by interview, physical examination, noninvasive techniques, and angiography, as detailed below. All cases with acute ischemia were excluded. Further exclusion criteria were PAD caused by nonatherosclerotic causes (cardioembolic disease, thromboangiitis obliterans, vasculitis, or congenital or metabolic vascular disease) and the history or presence of any malignancy. Doppler segmental blood pressure of the lower limbs, including continuous-wave spectral analysis and resting ankle-brachial index (ABI) measurements were performed in all patients with symptomatic PAD and control subjects as previously described⁽³⁴⁾. In addition to these measurements, intra-arterial aortofemoral angiography was performed in all patients to confirm the presence of PAD and to determine the location and extent of wall changes.

Control subjects were matched to the patients with PAD in a 1:1 design by sex, age (± 2 years), and diabetes mellitus status. All control subjects were patients in our hospital and fulfilled the following criteria: no clinical indication of PAD by history and physical examination; ABI ≥ 1.0 ; no pathologic pattern of pulse waves in lower limbs by continuous-wave spectral analysis; no CAD; no CVD; no previous vascular surgery or stenting of the internal carotid arteries; no stenosis of the internal carotid artery greater than 50% by color duplex ultrasound scans; no history of venous thromboembolism; and no history or presence of any malignancy. All control subjects were generally in good health and were admitted for treatment of minor health problems, such as cataract surgery, vertebrogenic pain, or nonvascular surgery. The study protocol was approved by the local ethics committee in accordance with the Declaration of Helsinki, and all study participants gave informed consent.

2. Bioinformatic Analysis

Data mining in publicly available databases was used to search for biological support for the signals selected for replication. Transcript structure and functional descriptions for every gene located +/- 50 kb from each SNP (+/- 200 kb for intergenic SNPs) were automatically retrieved from different bioinformatic databases (NCBI Entrez RefSeq, EBI SRS, and the UCSC Genome Browser) using Genowatch (now named Variowatch)⁽³⁵⁾ and further supplemented for interesting candidates by ad-hoc searches in OMIM and Pubmed. Additionally, the Genetic Association Database, the NHGRI GWAS Catalog⁽³⁶⁾ and the HuGE Navigator⁽³⁷⁾ database were mined for already known phenotype associations. Finally, in order to refine the functions of genes without clearly associated functions in the public databases pathway, we evaluated the pathway assignments in NCBI Entrez Gene were and used Genomatix Bibliosphere Software (Genomatix GmbH, Munich, Germany) to perform an automated literature and pathway analysis. The generated gene networks were then inspected for relevant tissue types and disease associations using build-in filter functions. However, this approach was inconclusive, probably due to the little data available in PubMed, and was thus not further pursued.

3. Statistical methods used for the candidate gene look-up

In the following, the statistical methods used for the look-up of PAD/ABI and CAD candidate genes will be explained in detail, exemplified on the *CYBA* gene region:

1. All SNPs were identified, which lie in the chromosomal region defined by each of the candidate genes ±100 kb upstream or downstream of the gene. In the case of *CYBA*, 138 SNPs lie within this defined region.
2. We then identified the most strongly associated SNP in each gene region using the discovery meta-analysis results for ABI (excluding isolates): for *CYBA* this was rs3794624 with a p-value of 6.30E-05.
3. Since the lowest p-value within each gene region was selected adjusting for multiple testing within each gene region is necessary. Neighboring and densely spaced SNPs are likely to be in high LD. Furthermore, the SNPs are given as genotype scores (allelic dosages between 0 and 2) derived from an imputation algorithm using HapMap. In this situation with high correlation between SNPs, simple Bonferroni correction with the number of SNPs would be too conservative. Therefore, the effective number of loci was calculated for each gene region using an algorithm by Gao et al⁽³⁸⁾. This method reduces the dimension of the parameter space. In the case of *CYBA*, the 138 SNPs could be explained sufficiently by a linear combination of 58 independent variables. Now, this so called effective number of loci can be used as the denominator in the Bonferroni correction formula. This leads to a corrected p-value of $6.30E-05 / 58 = 3.60E-03$ for the *CYBA* gene region.
4. So far, we have applied the Bonferroni correction within each gene region separately resulting in gene-region-wide corrected p-values. Since we have looked at 55 independent gene regions, further correction, however, is needed. The False Discovery Rate (FDR⁽³⁹⁾) was calculated on the 55 corrected p-values. This approach accounts for the multiple comparisons problem. Traditional methods like Bonferroni control the Family-wise error rate, the probability for at least one false positive among all tests. The False discovery rate on the contrary is the expected proportion of false positives amongst all rejected null hypothesis. It has a greater power than the methods controlling the Family-wise error rate

with the higher risk of false positives, however. In our analysis we have set the FDR threshold to 0.1, meaning that we are tolerating 10% of false positives out of the resulting list of significant findings. Since we are only including former PAD/ABI candidate gene regions, we are convinced that the prior knowledge outweighs the higher risk of false positives. For *CYBA*, a FDR of 0.0665 has been calculated.

5. For the CAD candidate genes, we have been looking at the specific reported SNPs rather than complete gene regions. In conclusion, we are sparing us the step of accounting for the number of SNPs within each gene region. Therefore, we are calculating the FDR directly on the p-values derived from the discovery meta-analysis results for ABI.

Supplementary Table 1. ABI Protocol and Calculation for Discovery Cohorts and Replication Studies

Cohort (ABI measurement date)	ABI protocol	ABI calculation
Discovery Cohorts		
ARIC (1987-1989)	Systolic blood pressures were measured with Dinamap 846 Sx automated oscillometric device in one arm and one ankle (posterior tibial artery). ⁽⁹⁶⁾ The ankle was randomly selected and measurement was taken in the supine position. Arm blood pressure was measured in the seated position and usually taken in the right arm. Repeat measures were obtained for the ankle about 5 to 8 minutes apart and for the arm about 5 minutes apart.	Mean systolic blood pressure in the ankle / mean of the seated arm systolic blood pressure
CHS (1989-1990)	Systolic blood pressure obtained with Doppler stethoscope (8 MHz, Parks Electronics, Aloha, OR) in right arm and both ankles (posterior tibial artery) and duplicate measures obtained for each location. ⁽⁹⁷⁾	The minimum of the mean systolic blood pressure in each ankle / mean of the right arm systolic blood pressure
FamHS (1994-1995)	Systolic blood pressures were measured with Dinamap 1846 Sx automated oscillometric device (Critikon, Inc., Tampa, FL). The ankle was randomly selected and a single systolic blood pressure was taken over the posterior tibial artery with the participant resting in the supine position. After three arm blood pressures were taken over the brachial artery, usually in the right arm, about 5 minutes apart.	Single systolic blood pressure in the ankle / mean of the three right arm systolic blood pressures.
FHS (Cohort:1994-1995; Offspring 1995-1998)	Participants rested for a minimum of five minutes in the supine position on the examining table prior to blood pressure measurement. Systolic blood pressure obtained with Doppler device (Parks Medical Electronics, Inc) in both arms and both ankles (posterior tibial artery) and repeat measurement in each limb obtained. ^(98,99) Dorsalis pedis pressure was measured if posterior tibial artery pressure could not be obtained.	Mean systolic blood pressure in each ankle site / higher of the two brachial systolic blood pressures
GENOA (1996)	ABI was measured in the supine position following 5 minutes of rest. Single systolic blood pressure obtained with Doppler device (Medisonics, Minneapolis MN) in both arms and both ankles (posterior tibial artery and dorsalis pedis). ⁽¹⁰⁰⁾	Systolic blood pressure in each ankle site (posterior tibial and dorsalis pedis/ higher of the two arm pressures. Lowest of the four ABI ratios was used for analysis. ²⁰
GHS (2007-2008)	ABI was measured in supine position after 10 minutes of rest. Systolic blood pressure was measured at the left arm with a Omron HEM 705-CP II. The peripheral systolic blood pressure was measured at the posterior tibial artery at both ankles with a hand-held 8-MHz Doppler probe (handydop, Elcat) and a conventional aneroid sphygmomanometer.	To calculate the ABI, the mean systolic blood pressure of the posterior tibial artery at both ankles was divided by the systolic blood pressure of the left arm.
Health ABC (1997-1998)	Arterial systolic blood pressure (SBP) was measured by a hand-held, 8-MHz Doppler probe (Huntleigh Technology, Inc., Manalapan, NJ, USA) placed directly over the artery and a conventional mercury sphygmomanometer. ⁽⁴²⁾	Means of the first and second SBP measurements for each leg and right arm were used to attain ABI. ABI was defined as the lowest ratio of SBP of either the right ankle to the right upper-arm or the left ankle to the right upper-arm.

InCHIANTI (1998)	Systolic blood pressure was obtained with a hand-held Doppler stethoscope (Parks Electronics model 41-A, Aloha, OR) in the right brachial and both posterior tibial arteries with duplicate measurements. ⁽¹⁰¹⁾	The highest systolic pressure at each site was used. The ABI was calculated using the lower of the right and left posterior tibial pressures / brachial artery pressure.
KORA F3 (2004-2005)	Systolic blood pressure obtained with Doppler device (HNE Healthcare, Mini Doppler Modell Nr. D 900) in the right arm and both ankles (posterior tibial artery). We generally performed two measurements and used the mean of the two measurements for further calculations. If we observed a difference of 10 mmHg or more for the two measurements, we performed a third measurement and calculated the mean of the two measurements which were closest to each other.	Mean systolic blood pressure of that ankle side which was lowest / mean of the two brachial systolic blood pressures of the right arm
KORA F4 (2006-2008)	Systolic blood pressure obtained with Doppler device (HNE Healthcare, Mini Doppler Modell Nr. D 900) in the right arm and both ankles (posterior tibial artery). We generally performed two measurements and used the mean of the two measurements for further calculations. If we observed a difference of 10 mmHg or more for the two measurements, we performed a third measurement and calculated the mean of the two measurements which were closest to each other.	Mean systolic blood pressure of that ankle side which was lowest / mean of the two brachial systolic blood pressures of the right arm
NESDA (2004-2007)	Both ankle and arm systolic blood pressure was measured by an ultrasound Doppler device at 8-MHz (UltraTech PD1v, Ultrasound Technologies Ltd, Itton, Chepstow, UK) in combination with an ordinary blood pressure cuff, as previously described. Blood pressure was assessed with the respondent in supine position.	Ankle-brachial index was calculated as the mean of two consecutive systolic right posterior tibial artery blood pressures divided by the mean of two consecutive systolic right humeral artery blood pressures.
NBS (2005-2008)	To measure ABI appropriately sized cuffs were placed around both arms above the elbow and around both legs just above the ankle. Resting blood pressures were measured at the left and right brachial artery, the left and right posterior tibial, and dorsalis pedis arteries using an 8-MHz hand-held Doppler probe (IMEXDOPCT; Biomedic, Almere, The Netherlands).	The highest of the two arm pressures was used to calculate ABI at rest for the posterior tibial and dorsalis pedis arteries. The lowest of the four ABI's was used in the analysis.
RS-I (1990-1993) RS-II (1999-2001)	Two seated blood pressures measured in right arm and a single systolic blood pressure obtained in each leg in supine position (posterior tibial) using Doppler device (Huntleigh 500 D, Huntleigh Technology) ⁽¹⁰²⁾ and random-zero manometer.	Systolic blood pressure in each ankle / mean of the seated right arm systolic blood pressure. The lowest ABI in either leg was used in the analysis.
SHIP (2008-2009)	Systolic blood pressure was measured with a "Dopplex D900" (Huntleigh Healthcare Ltd.) doppler ultrasound probe and a blood pressure cuff (Welch Allyn) in both arms and both ankles (anterior and posterior tibial artery). Measurements were taken in the supine position after at least 10 minutes rest.	The highest systolic pressure at each ankle site was used. The ABI was calculated using the lower of the right and left tibial pressures / higher of the two brachial artery pressures.

Discovery Cohorts Population Isolates		
Amish (2001-2009)	Systolic blood pressure was measured with a Doppler ultrasound probe (Hokanson, MD6 Bidirectional Doppler) and a blood pressure cuff (Hokanson blood pressure cuff in two sizes, SC10 and SC12) in both arms and both ankles (anterior and posterior tibial artery). Measurements were taken in the supine position after at least 15 minutes rest.	The ABI for each leg was calculated separately by dividing the ankle pressure in that leg by the mean brachial pressure of the two arms or the highest of the 2 arms if the difference between the two arms was ≥ 10 mmHg. Then the mean ABI for both legs was used for analysis.
Croatia-Vis (2003-2004) Croatia-Korcula (2007) Croatia-Split (2009-2010)	Participant asked to remove all tight clothing from arms and legs and lie flat for approx 5 min. Brachial measure: sphygmomanometer cuff placed around the right arm just above the elbow. Doppler probe placed over the brachial pulse. Cuff inflated until the Doppler sound disappears then cuff slowly deflated until the sound returns. Repeated on left arm. Ankle measure: Cuff placed around left leg just above the malleolus and Doppler used to locate the dorsalis pedis pulse. Cuff inflated until the Doppler sound disappears then cuff slowly deflated until the sound returns. Repeated for posterior tibial pulse. Both repeated for right leg.	The lowest posterior tibial systolic blood pressure at either ankle was divided by the highest systolic blood pressure in the arm
ERF (2002)	Two seated blood pressures measured in right arm and a single systolic blood pressure obtained in each leg (posterior tibial) using Doppler device (Huntleigh 500 D, Huntleigh Technology) ⁽¹⁰²⁾ and random-zero manometer.	Systolic blood pressure in each ankle/ mean of the seated right arm systolic blood pressure
Orcades (2005-2007)	Participant asked to remove all tight clothing from arms and legs and lie flat for approx 5 min. Brachial measure: sphygmomanometer cuff placed around the right arm just above the elbow. Doppler probe placed over the brachial pulse. Cuff inflated a further 10-20 mm Hg after the Doppler sound disappears then cuff slowly deflated until the pulse sound returns - measure recorded. Repeated on left arm. Ankle measure: Cuff placed around left leg just above the malleolus and Doppler used to locate the dorsalis pedis pulse. Cuff inflated a further 10-20 mm Hg after the Doppler sound disappears then cuff slowly deflated until the pulse sound returns - measure recorded. Repeated for posterior tibial pulse. Both repeated for right leg.	The lowest posterior tibial systolic blood pressure at either ankle was divided by the highest systolic blood pressure in the arm
Replication Studies		
Bruneck Study (1995)	The ankle-brachial index (ABI) was measured in a supine position. A cuff was inflated to 10 mmHg above systolic blood pressure and deflated at 2 mmHg/s. The first reappearance of the arterial signal at the ankle (posterior tibial artery) was taken as the systolic blood pressure (detected with a Doppler ultrasonic instrument).	To calculate the ABI for the right and left leg, the systolic blood pressure at each ankle was divided by the systolic blood pressure in the arm. The higher arm reading (right or left side) was used for ABI calculation. The lower ABI of the two legs was considered in the current analysis. Subjects with an ABI > 1.4 were

		excluded. There was no subject with an ABI of zero on both legs.
CCHS (2001-2003)	A standard brachial systolic and diastolic blood pressure was recorded on both arms, and systolic ankle blood pressure of the posterior tibial artery on both legs was obtained by Doppler (Huntleigh Mini Doppler D900, Huntleigh, United Kingdom).	The ABI was the lowest ankle systolic blood pressure divided by the highest brachial systolic blood pressure.
MESA (2000-2002)	Systolic blood pressure obtained with Nicolet Doppler apparatus (EN50 LE 100, Nicolet vascular, Golden, CO) in both arms and both ankles (posterior tibial and dorsalis pedis). Approximately 20 elapsed between each pressure.	ABI is the minimum of the right and left ABI. The right ABI is calculated as the (maximum of the right dorsalis pedis and right posterior tibial)/ (mean right and left brachial), and the left ABI is calculated as the (maximum of the left dorsalis pedis and left posterior tibial)/ (mean of the left and right brachial). For right ABI and left ABI, if the two brachial (arm) BPs differ by 10 mmHg or more, use the higher arm pressure as the denominator.
NHANES (1999-2002)	The ankle brachial pressure index (ABPI), also referred to as the ankle arm blood pressure index (AAI), is a noninvasive technique to measure peripheral vascular disease in population-based and clinical studies. ABPI was defined as the ratio of the systolic blood pressure in the ankle compared with that in the arm. ABPI measurement was performed by a health technician on all adults ≥ 40 years of age at interview. Exclusions for these procedures were bilateral amputation, casts, ulcers, dressings, or other conditions which make BP readings at these sites impossible. The presence of these conditions on one limb did not exclude the study participant, but they were excluded if they occurred bilaterally. Systolic pressure was measured in one arm (brachial vessel, right arm if accessible) and both ankles (posterior tibial vessels) for ages 40 and above.	ABI was defined as the ratio of the systolic blood pressure in the ankle compared with that in the arm. The lower ABI of the two legs was used in the analysis. ABI > 1.4 and equal to 0 were excluded from the analysis.
PREVEND (1997-1998)	At the first visit, while the participant was in a supine position, systolic blood pressure was measured each minute with an automatic Dynamap XL Model 9300 series device at the right brachial artery (ten times total). Within the first 5 min, systolic ankle pressure at each leg was measured at the same time a brachial pressure was performed. For ankle pressure measurements, the posterior tibial artery was measured using an 8-MHz continuous-wave Doppler probe (Huntleigh Model D900, Huntleigh Diagnostics) and a random-zero sphygmomanometer.	The ABI was calculated as the ratio of the systolic blood pressure of the ankle and arm for each leg. The lowest ankle-brachial index in either leg was used in the analysis.
CAVASIC (2002)	For the ABI measurement, the systolic blood pressure was measured in both arms and then two additional measures were obtained on the arm with the higher systolic blood pressure. The systolic blood pressure was obtained three times for both the posterior tibial and dorsalis pedis artery in each leg. ⁽³³⁾	The mean of the second and third systolic blood pressure measurement at each site was used to calculate the ABI for each of the 4 lower extremity sites. The ABI was calculated as the ratio of the mean systolic blood pressure at each of four sites to the mean systolic blood pressure in the arm.

		The lowest ABI from the four sites was used in analysis.
GenePAD (2004-2008)	The ABI (i.e. the ratio of ankle and arm systolic blood pressure) was measured using previously established methods. ^(103,104) In brief, prior to undergoing coronary angiogram, each participant rested in the supine position for 5 minutes, then, using a 5-MHz Doppler ultrasound (Nicolet Elite 5-MHz vascular model 110R Doppler; Nicolet Vascular, Golden, CO, USA), systolic pressures were measured in the posterior tibial, dorsalis pedis, and brachial arteries. Each pressure was measured twice in sequential and reverse order as listed. With an IV in one arm, only the contralateral arm was used for the brachial pressures. ⁽¹⁰⁵⁾	The ABI for each leg was calculated separately by dividing the higher of the two ankle pressures in that leg by the brachial pressure. If the ABI was less than 0.9 in either leg, the patient was considered to have PAD. The index leg was defined as the leg with the lower ABI.
LIPAD (2002)	ABI measurements in the LIPAD study were done according to ⁽³⁴⁾ : with the patient placed in a supine position, the brachial and ankle systolic pressure measurements are obtained.	The higher systolic pressure of the anterior tibial or posterior tibial measurement for each foot / the higher of the left and right brachial systolic blood pressure

Supplementary Table 2. Genotyping and Imputation Information for Discovery and Replication Samples (Part 1/3)

	ARIC	CHS	Family HS	FHS	GENOA	GHS	Health ABC	InCHIANTI
Genotyping platform	Affymetrix Genome-Wide Human SNP Array 6.0	Illumina 370CNV Duo® BeadChip	Illumina 550 array, Illumina 610 array, and Illumina 1M array	Affymetrix 250K Nsp and 250K Sty mapping arrays and the Affymetrix 50K supplemental gene-focused array	Affymetrix® Genome-Wide Human SNP Array 6.0	Affymetrix Genome-Wide Human SNP Array 6.0	Illumina Human1M-Duo Array	Illumina Infinium HumanHap550 array
Sample exclusions	1) Discordant with previous genotype data 2) sex mismatch 3) first-degree relative of an included individual based on genotype data; 4) genetic outlier as assessed by Identity by state (IBS); 5) > 8 SD along any of the first 10 principal components in EIGENSTRAT	1) call rate<95%; 2) sex mismatch; 3) other sample failure	1) sex mismatch; 2) outliers identified by the IBS clustering analysis	1) call rate <97%; 2) per subject heterozygosity±5 SDs from the mean; 3) per subject large Mendelian error rate	1) call rate <95%; 2) sex mismatch	1) call rate <97%; 2) per subject heterozygosity ±3 SDs from the mean	1) sample failure, 2) genotypic sex mismatch 3) first-degree relative	1) genotype call rate<98%; 2) sex mismatch
SNP exclusions	1) call rate <90%; 2) MAF<1%; 3) HWE p<10 ⁻⁶ ; 4) SNPs without chromosomal location; 5) monomorphic SNPs	1) call rate<0.97; 2) >2 replicate errors or Mendelian inconsistencies among reference CEPH trios; 3) HWE p<10 ⁻⁵ 4) no observed heterozygotes	1) MAF <1%; 2) HWE p<10 ⁻⁶ ; 3) SNP call rate <95%; 4) rsqhat<0.3	1) call rate < 97%; 2) Mishap p< 10 ⁻⁹ ; 3) HWE p < 10 ⁻⁶ ; 4) Mendelian errors > 100	1) call rate <95%; 2) monomorphic SNPs; 3) MAF<1%; 4) unknown chromosomal location	1) call rate < 98% 2) MAF < 1% 3) HWE p<10 ⁻⁴		1) MAF <1%; 2) HWE p<10 ⁻⁴ ; 3) SNP call rate <98%
Imputation method	MACH (version 1.0.16)	BIMBAM version 0.99	MACH 1.0	MACH (version 1.0.15)	MACH 1.0.16	IMPUTE v. 1.0.0	MACH 1.0.16	IMPUTE 3.1
Imputation backbone	BRLMM to Hapmap-V1 CEU from build 35	HapMap CEU using release 22, build 36	HapMap release 22 CEU	HapMap (release 22, build 36, CEU population	HapMap release 22, build 36, CEU	HapMap (rel. 22, build 36, CEU pop.	HapMap II (rel. 22, build 36) CEU	HapMap II (rel. 22, build 36) CEU
Imputation SNP exclusions	SNPs with <95% data completeness, MAF <1%, HWE P<0.00005		1) MAF <1%; 2) HWE p<10 ⁻⁶ ; 3) SNP not in HapMap	1) MAF<0.01; 2) HWE p<10 ⁻⁶ ; 3) callrate >0.97; 4) mishap test of non-random missingness p>10 ⁻⁹ ; 5) <100 Mendelian errors			MAF<0.01; HWE P<10 ⁻⁶ ; callrate<97%	
Statistical software	PLINK, Mach2QTL	R	SAS proc mixed and GEE	R packages kinship, GEE	R packages nlme, MASS	SNPTEST	R	SNPTEST

Supplementary Table 2. Genotyping and Imputation Information for Discovery and Replication Samples (Part 2/3)

	KORA F3	KORA F4	NESDA	NBS	RS-I	RS-II	SHIP
Genotyping platform	Affymetrix GeneChip Human Mapping 500K	Affymetrix Genome-Wide Human SNP Array 6.0	Perlegen	Illumina HumanHapCNV370-Duo-Beadchip	Illumina 550K array	Illumina 550K array	Affymetrix Genome-Wide Human SNP Array 6.0
Sample exclusions	1) sample call rate<93%; 2) sex mismatch	1) sample call rate<93%; 2) sex mismatch	call rate<95%, ethnic outliers, XO and XXY samples, high genome-wide homo- or heterozygosity, excess IBS	1) call rate < 96%; 2) <90% Caucasian ancestry as identified by Structure analysis	1) excess autosomal heterozygosity; 2) sex mismatch; 3) outliers identified by the IBS clustering analysis	1) excess autosomal heterozygosity; 2) sex mismatch; 3) outliers identified by the IBS clustering analysis	1) call rate<92%; 2) sex mismatch;
SNP exclusions			callrate <95%, MAF<1%		1) MAF <1%; 2) HWE p<10 ⁻⁶ ; 3) SNP call rate <98%	1) MAF <1%; 2) HWE p<10 ⁻⁵ ; 3) SNP call rate <90%	NA
Imputation method	Mach 1.0.10	Mach 1.0.16	Impute 0.4.2	Impute 0.5.0	MACH 1.0	MACH 1.0.15	IMPUTE 0.5.0
Imputation backbone	HapMap (release 21, build 35, CEU)	HapMap (release 22, build 36, CEU)	HapMap Phase II - release 22 build 36, CEU	HapMap Phase II - release 22 build 36, CEU	HapMap release 22 CEU	HapMap release 22 CEU	HapMap release 22 CEU
Imputation SNP exclusions	MAF <5%	genotype callrate<93%	MAF<0.01; HWE P<10 ⁻⁶ ; callrate<95%	1) call rate <96% 2) MAF <1% 3) HWE p<10 ⁻⁶	1) MAF <1%; 2) HWE p<10 ⁻⁶ ; 3) SNP call rate <98%	1) MAF <1%; 2) HWE p<10 ⁻⁶ ; 3) SNP call rate <98%	NA
Statistical software	Mach2QTL	Mach2QTL	SNPTEST v1.1.4; R	SNPTEST v 1.1.5	ProbABEL (version 1.1) *	ProbABEL (version 1.1) *	QUICKTEST version 0.95

* (<http://mga.bionet.nsc.ru/~yurii/ABEL/>).

Supplementary Methods Table 2. Genotyping and Imputation Information for Discovery and Replication Samples (Part 3/3)

	Population Isolates						Replication Studies*	
	Amish	Croatia-Vis	Croatia-Korcula	Croatia- Split	ERF	Orcades	MESA	PREVEND
Genotyping platform	Affymetrix GeneChip Human Mapping 500K	Illumina HumanHap300v1	Illumina 370CNV	Illumina 370CNV	Illumina 6K (n=3000), 318K (n=1200), 370K (n=100), Affymetrix 250K (n=200)	Illumina HumanHap300v2	Affymetrix 6.0 1M	Illumina CytoSNP12 V2
Sample exclusions	1) sample call rate <93%; 2) sex mismatch 3) excess Mendelian error rate	discrepancies between sex in phenotype file and genotyping; too high autosomal heterozygosity (FDR<1%); too high IBS sharing (>=95%); call rate (<97%)	discrepancies between sex in phenotype file and genotyping; too high autosomal heterozygosity (FDR<1%); too high IBS sharing (>=95%); call rate (<97%)	discrepancies between sex in phenotype file and genotyping; too high autosomal heterozygosity (FDR<1%); too high IBS sharing (>=95%); call rate (<97%)	1) excess autosomal heterozygosity; 2) sex mismatch; 3) outliers identified by the IBS clustering analysis	discrepancies between sex in phenotype file and genotyping; too high autosomal heterozygosity (FDR<1%); too high IBS sharing (>=95%); call rate (<97%)	1) gender mismatches and 2) cryptic duplicates	3SD phenotypic outliers, duplicates, contaminated, relatedness, gender mismatch
SNP exclusions	1) MAF <1%; 2) HWE p<10 ⁻⁶ ; 3) SNP call rate <95%	MAF<0.02, Call Rate 98%, pHWE < 1E-10	MAF<0.02, Call Rate 98%, pHWE <1E-10	MAF<0.02, Call Rate 98%, pHWE <1E-10	1) MAF <1%; 2) HWE p<10 ⁻⁶ ; 3) SNP call rate <95%	MAF<0.02, Call Rate 98%, pHWE <1E-10	None required for 7 SNPs requested	SNP call rate <95%; MAF < 0.01; HWE p< 1 x 10 ⁻⁵
Imputation method	MACH v-1.0.16	MACH (1.0.16)	MACH (1.0.16)	MACH (1.0.16)	MACH 1.0	MACH (1.0.16)	IMPUTE V2.1.0	BEAGLE v3.1.0
Imputation backbone	HapMap (release 22, build 36, CEU population)	HapMap r22 CEU	HapMap r22 CEU	HapMap r22 CEU	HapMap release 22 CEU	HapMap r22 CEU	HapMap Phase I and II - CEU, rel. 24 - Build 36 (dbSNP b126)	Hapmap rel 23a CEU
Imputation SNP exclusions	1) MAF <1%; 2) HWE p<10 ⁻⁶ ; 3) SNP call rate <95%	MAF<0.01, Call Rate 98%, pHWE < 1E-06	MAF<0.01, Call Rate 98%, pHWE < 1E-06	MAF<0.01, Call Rate 98%, pHWE < 1E-06	MAF<0.01, Call Rate 98%, pHWE < 1E-06	None required for 7 SNPs requested		1) MAF <1%; 2) HWE p<10 ⁻⁶ ; 3) SNP call rate <95%
Statistical software	MMAP	GenABEL/ProbABEL	GenABEL/ProbABEL	GenABEL/ProbABEL	PROBabel: with mmscore	GenABEL/ProbABEL	SNPTEST	PLINK v1.07

*Genotyping of the replication samples from the Bruneck Study, Copenhagen City Heart Study, CAVASIC Study and LIPAD Study was performed using 5' nuclease allelic discrimination (Taqman) assays. Genotyping of the replication samples from NHANES was performed using Sequenom.

Supplementary Table 3: Relative excess heterozygosity analysis of SNPs in replication studies

SNP	lnREH_Fixed	P_Fixed	CI_Fixed	lnREH_Random	P_Random	CI_Random	I2	I2_CI
rs10757269	0.0138	0.4582	[-0.02, 0.05]	-0.0027	0.9281	[-0.06, 0.06]	0.4675	[0.00, 0.79]
rs4659996	-0.0154	0.4073	[-0.05, 0.02]	-0.0297	0.2695	[-0.08, 0.02]	0.3645	[0.00, 0.75]
rs7003385	0.0049	0.8142	[-0.04, 0.05]	0.0049	0.8142	[-0.04, 0.05]	0.0000	[0.00, 0.07]
rs9485528	0.0184	0.5797	[-0.05, 0.08]	0.0184	0.5797	[-0.05, 0.08]	0.0000	[0.00, 0.71]
rs819750	-0.0262	0.5384	[-0.11, 0.06]	-0.0262	0.5384	[-0.11, 0.06]	0.0000	[0.00, 0.48]
rs16824978	0.0018	0.9443	[-0.05, 0.05]	0.0018	0.9443	[-0.05, 0.05]	0.0000	[0.00, 0.68]
rs7100623	-0.0952	0.0014	[-0.15, -0.04]	-0.0773	0.1140	[-0.17, 0.02]	0.5305	[0.00, 0.81]

Supplementary Table 4. Characteristics of Discovery Cohort Participants at time of Ankle-brachial Index Measurement (Part 1/3)

Characteristic, Mean (SD) or N (%)	ARIC	CHS	FamHS	FHS	GENOA	GHS	Health ABC	InCHIANTI
N	7630	3193	1736	3572	991	3122	1562	1130
Years ABI obtained	1987-1989	1989 - 1990	1994 - 1995	1994-1998	2001-2004	2007-2008	1997-1998	1998-2000
Age, years, mean (SD)	54.3 (5.7)	72.3 (5.4)	50.0 (12.9)	61.6 (11.8)	58.6 (10.1)	55.8 (10.9)	73.8 (2.8)	67.6 (15.3)
Women, n (%)	4073(53.4)	1950 (61.1)	941 (54.2)	1950 (54.6)	564 (56.9)	1533 (49.1)	743 (47.6)	613 (55.0)
ABI, mean (SD)	1.12 (0.13)	1.08 (0.14)	1.19 (0.12)	1.1 (0.13)	1.1 (0.14)	1.02 (0.12)	1.09 (0.16)	1.04 (0.15)
PAD = ABI \leq 0.9, n (%)	287 (3.8)	264 (8.3)	41 (2.4)	194 (5.4)	66 (6.7)	405 (13.0)	148 (9.5)	116 (10.4)
ABI = 0.91 to 1.10, n (%)	2886 (37.8)	1345 (42.1)	309 (18.7)	1214 (34.0)	387 (39.1)	1941 (62.2)	593 (42.0)	670 (60.1)
Hypertension, n (%)	1693 (22.3)	1011 (31.7)	400 (23.0)	1607 (45.0)	717 (72.4)	1640 (52.5)	727 (46.8)	338 (30.8)
Diabetes, n (%)	646 (8.5)	370 (11.7)	89 (5.2)	334 (9.4)	148 (14.9)	220 (7.0)	163 (10.5)	73 (6.7)
Current smoker, n (%)	1924 (25.2)	361 (11.3)	223 (13.2)	507 (14.3)	103 (10.4)	574 (18.4)	101 (6.5)	214 (19.2)
Former smoker, n (%)	2700 (35.4)	1306 (40.9)	734 (42.5)	1683 (47.5)	389 (39.3)	1096 (35.2)	796 (51.0)	282 (25.2)
Total cholesterol, mg/dL	214.9 (40.7)	213.2 (38.9)	202.4 (40.0)	206.0 (39.3)	197.1 (33.8)	224.5 (41.3)	201.4 (37.6)	216.0 (39.9)
HDL cholesterol, mg/dL	50.7 (16.9)	55.4 (15.9)	50.1 (14.6)	51.0 (16.2)	51.8 (15.1)	57.0 (16.0)	52.1 (16.4)	56.1 (15.1)
Triglyceride, mg/dL	137.2 (91.7)	139.9 (75.7)	148.7 (102.8)	141.7 (135.4)	157.0 (98.1)	125.6 (73.9)	152.8 (86.8)	126.3 (78.6)
BMI, kg/m ²	27.0 (4.8)	26.3 (4.4)	27.3 (5.1)	27.7 (5.0)	30.7 (6.2)	27.1 (4.7)	26.6 (4.1)	27.1 (4.1)
Claudication, n (%)	63 (0.8)	37 (1.2)	NA	131 (3.7)	NA	249 (8.0)	293 (18.9)	87 (7.9)
Prevalent CVD, n (%)	381 (5.1)	0	155 (8.9)	217 (6.1)	86 (8.7)	214 (6.9)	404 (26.3)	63 (5.7)

NA, not available

Supplementary Table 4. Characteristics of Discovery Cohort Participants at time of Ankle-brachial Index Measurement (Part 2/3)

Characteristic, Mean (SD) or N (%)	KORA F3	KORA F4	NESDA	NBS	RS-I	RS-II	SHIP
N	1581	1407	1612	544	5169	1642	543
Years ABI obtained	2004-2005	2006-2008	2004-2007	2005-2008	1991-1993	2000-2001	2008-2009
Age, years, mean (SD)	62.2 (10.1)	63.4 (7.2)	41.8 (12.4)	62.8 (5.4)	69.1 (9.0)	64.3 (7.7)	58.6 (13.0)
Women, n (%)	821 (51.9)	730 (51.9)	1112 (69.0)	279 (51.3)	3091 (59.8)	885 (53.9)	280 (51.6)
ABI, mean (SD)	1.12 (0.13)	1.14 (0.14)	1.14 (0.12)	1.09 (0.10)	1.05 (0.21)	1.06 (0.14)	1.12 (0.13)
PAD = ABI ≤ 0.9, n (%)	81 (5.1)	75 (5.3)	36 (2.2)	17 (3.13)	959 (18.6)	176 (10.7)	18 (3.32)
ABI = 0.91 to 1.10, n (%)	621 (39.3)	397 (28.2)	581 (36.9)	295 (56.0)	1786 (34.6)	808 (49.2)	225 (41.4)
Hypertension, n (%)	950 (60.4)	696 (49.6)	614 (38.1)	220 (40.4)	2912 (56.3)	935 (56.9)	299 (55.1)
Diabetes, n (%)	166 (10.5)	140 (10.0)	45 (2.8)	42 (7.7)	528 (10.2)	166 (10.1)	57 (10.5)
Current smoker, n (%)	214 (13.6)	195 (13.9)	670 (41.6)	83 (15.3)	1150 (22.2)	330 (20.1)	77 (14.2)
Former smoker, n (%)	569 (36.0)	583 (41.5)	512 (31.8)	273 (50.3)	2118 (41.0)	820 (49.9)	243 (44.8)
Total cholesterol, mg/dL	221.5 (40.4)	224.1 (39.6)	198.9 (41.4)	228.2 (38.7)	255.5 (47.0)	224.7 (37.9)	212.3 (42.2)
HDL cholesterol, mg/dL	58.2 (17.0)	56.5 (14.4)	63.1 (16.9)	54.5 (14.7)	51.9 (14.3)	53.4 (14.3)	54.5 (14.1)
Triglyceride, mg/dL	171.2 (121.9)	135.6 (96.1)	114.6 (77.6)	127.5 (67.3)	NA	NA	161.2 (111.7)
BMI, kg/m ²	28.1 (4.5)	28.5 (4.8)	25.5 (4.9)	26.9 (3.9)	26.3 (3.7)	27.2 (4.2)	28.16 (4.4)
Claudication, n (%)	63 (3.99)	56 (3.98)	333 (20.7)*	N/A	88 (1.7)	19 (1.2%)	50 (9.2)
Prevalent CVD, n (%)	173 (10.94)	163 (11.58)	50 (3.1)	19 (3.5)	833 (16.1)	149 (9.1%)	75 (13.8)

NA, not available

* Question asked was: "Do you have pain in one or both calves during walking?"

Supplementary Table 4. Characteristics of Discovery Cohort Participants from population isolates at time of Ankle-brachial Index Measurement (Part 3/3)

Characteristic, Mean (SD) or N (%)	Amish	ERF	CROATIA-Vis	CROATIA-Korcula	Orcades	CROATIA-Split
N	1183	2133	897	851	693	499
Years ABI obtained	2001-2009	2002	2003-2004	2007	2005-2007	2009-2010
Age, years, mean (SD)	49.0 (16.5)	49.7 (15.2)	56.1 (15.4)	55.93 (13.33)	53.74(15.31)	49.04 (14.65)
Women, n (%)	577 (48.8)	1309 (56.9)	518 (57.7)	542 (63.7)	372(53.7)	286 (57.3)
ABI, mean (SD)	1.09 (0.11)	1.05 (0.13)	1.10 (0.12)	1.02 (0.14)	1.03 (0.11)	1.03 (0.10)
PAD = ABI<0.9, n (%)	54 (4.6)	180 (8.5)	37 (4.1)	146 (17.2)	59 (8.5)	50 (10)
ABI = 0.91 to 1.10, n (%)	553 (46.8)	1195 (56.0)	464 (51.7)	494 (58.0)	468 (67.5)	346 (69.3)
Hypertension, n (%)	153 (12.9)	637 (29.0)	196 (21.9)	328 (38.5)	153 (22.1)	122 (24.4)
Diabetes, n (%)	19 (1.6)	108 (5.0)	55 (6.1)	83 (9.8)	15 (2.2)	16 (3.2)
Current smoker, n (%)	111 (9.7)	869 (39.8)	212 (23.6)	179 (21.0)	60 (8.7)	126 (25.3)
Former smoker, n (%)	162 (14.2)	653 (29.9)	229 (25.5)	224 (26.3)	233 (33.6)	138 (27.7)
Total cholesterol, mg/dL	211 (47.7)	214.5 (42.7)	197.2 (37.9)	229.3 (47.6)	224.3 (45.2)	227.4 (48.8)
HDL cholesterol, mg/dL	55.6 (14.6)	49.4 (14.1)	42.9 (6.2)	56.5 (13.5)	64.6 (15.5)	53.4 (12.9)
Triglyceride, mg/dL	75.6 (47.3)	119.3 (68.9)	150.6 (87.7)	126.7 (73.5)	117.8 (58.5)	133.5 (93.1)
BMI, kg/m ²	27.0 (4.7)	26.9 (4.8)	27.3 (4.3)	28.0 (4.1)	27.8 (4.9)	26.9 (4.2)
Claudication, n (%)	NA	43 (2.0)	NA	NA	NA	NA
Prevalent CVD, n (%)	50 (4.4)	48 (2.1)	27 (3.0)	11 (1.3)	52 (7.5)	4 (0.8)

NA, not available

Supplementary Table 5. Characteristics of the Replication Samples at the time of Ankle Brachial Index Measurement

Characteristic, Mean (SD) or N (%)	Bruneck Study	CCHS	NHANES	MESA	PREVEND	CAVASIC cases	CAVASIC controls	GenePAD	LIPAD cases	LIPAD controls
N	786	5330	2375	2611	3691	136	307	850	279	392
Years ABI obtained	1995	2001-2003	1999-2002	2000-2002	1997-1998	2002-2006	2002-2006	2004-2008	2000-2002	2000-2002
Age, years, mean (SD)	62.4 (11.0)	59.1 (16.0)	61.95(13.53)	62.7 (10.2)	49.4 (12.5)	59 (7)	57 (10)	68 (11)	68 (11)	67 (11)
Women, n (%)	397 (50.5)	57.5	1128(47.49)	1360 (52.1)	1791 (48.5)	0 (0)	0 (0)	258 (30)	87 (31)	121 (31)
ABI, mean (SD)	1.10 (0.15)	1.01 (0.15)	1.09(0.14)	1.11 (0.12)	1.16 (0.14)	0.7 (0.3)	1.1 (0.1)	1.0 (0.2)	0.7 (0.2)	1.2 (0.1)
PAD = ABI<0.9, n (%)	79 (10.1)	959 (18.0)	202 (8.5%)	82 (3.1)	135 (3.7)	106 (78)	19 (6)	153 (18)	239 (86)	0 (0)
ABI = 0.91 to 1.10, n (%)	321 (40.8)	2974 (55.8)	917(38.6)	926 (35.5)	802 (21.7)	15 (11)	161 (52)		22 (8)	121 (31)
Hypertension, n (%)	535 (68.1)	2703 (50.7)	1162(49.6%)	1000 (38.3)	1232 (33.4)	119 (88)	195 (64)	445 (52)	165 (59)	159 (41)
Diabetes, n (%)	80 (10.2)	327 (6.1)	188(8.01%)	116 (4.4)	139 (3.8)	15 (11)	97 (32)	125 (15)	89 (32)	105 (27)
Current smoker, n (%)	158 (20.1)	1736 (32.7)	529(22.3%)	296 (11.3)	1335 (36.1)	73 (55)	39 (13)	NA	125 (45)	51 (13)
Former smoker, n (%)	203 (25.8)	1847 (51.9)	908(38.2%)	1156 (44.3)	1327 (36.0)	54 (40)	140 (46)	NA	20 (7)	24 (6)
Ever smoker, n (%)	361 (45.9)		1361(57.3%)	1451 (55.6)	NA	127 (95)	179 (58)	511 (60)	145 (52)	75 (19)
Total cholesterol, mg/dL	223.2 (44.6)	212.9 (45.3)	208.71(39.18)	195.7 (35.5)	217.6 (42.5)	208 (43)	205 (35)	117 (40)	232 (52)	214 (44)
HDL cholesterol, mg/dL	56.6 (13.7)	57.1 (18.6)	52.44(16.35)	52.4 (15.7)	50.3 (15.2)	50 (13)	59 (17)	40 (12)	52 (16)	54 (17)
Triglyceride, mg/dL	135.6 (90.1)	137.9 (118.9)	162.95(154.84)	132.3 (89.1)	131.2 (89.5)	165 (98)	131 (74)	108 (68)	163 (102)	134 (76)
Lipid lowering meds, n (%)	24 (3.1)	296 (5.6)	415(17.5%)	488 (18.7)	(4.1)	51 (38)	60 (20)	689 (81)	56 (20)	0 (0)
BMI, kg/m ²	25.6 (3.8)	25.8 (4.3)	27.94(5.45)	27.8 ± 5.1	26.1 (4.2)	27 (4)	27 (4)	29 (6)	26 (4)	27 (4)
Claudication, n (%)	35 (4.5)	NA	NA	10 (0.38)	NA	136 (100)	0 (0)	85 (10)	236 (85)	0 (0)
Prevalent CVD, n (%)	109 (13.9)	702 (13.1)	169(7.2)	0 (0)	143 (3.9)	39 (29)	29 (9)	520 (61)	116 (42)	0 (0)

NA, not available

Supplementary Table 6: Overall Meta-analysis Results and Study Specific Results: ABI-SNP Associations with $p < 10^{-5}$, population isolates excluded
Table is at the end of this document

Supplementary Table 7. Meta-analysis results: ABI-SNP associations with $p < 10^{-5}$ in the primary discovery analysis with population isolates included.

SNP	Chr	Physical Position	Closest Gene	Risk / Non-risk Allele	Risk Allele frequency	Meta-analysis	N	Beta	SE	P value	P _{het}
rs10757269	9	22062264	CDKN2B	G/A	0.50	ABI Discovery	41292	-0.0048	0.0009	1.22E-07	0.01
						ABI Replication	16672	-0.0035	0.0015	1.76E-02	0.67
						ABI Combined	57964	-0.0045	0.0008	8.82E-09	0.04
						PAD [†] Discovery	39600	0.0686	0.0274	1.23E-02	0.14
rs819750	1	99469651	LPPR4	G/T	0.12	ABI Discovery	41534	-0.0065	0.0014	2.79E-06	0.5
						ABI Replication	16660	0.0022	0.0023	3.22E-01	0.99
						ABI Combined	58194	-0.0041	0.0012	5.11E-04	0.36
						PAD Discovery	39825	0.0766	0.0407	5.97E-02	0.04
rs4659996	1	238912747	GREM2	A/G	0.48	ABI Discovery	33160	-0.005	0.0011	3.48E-06	0.34
						ABI Replication	16658	-0.0018	0.0016	2.67E-01	0.65
						ABI Combined	49818	-0.004	0.0009	7.27E-06	0.4
						PAD Discovery	32619	0.0467	0.0295	1.14E-01	0.33
rs11580768*	1	2789340	ACTRT2	C/T	0.53	ABI Discovery	34252	-0.0053	0.0012	3.85E-06	0.99
						PAD Discovery	33735	0.0832	0.0314	0.008095	0.4367
rs4366776*	17	216763	RPH3AL [‡]	C/T	0.51	ABI Discovery	37127	-0.0047	0.001	4.52E-06	0.78
						PAD Discovery	35398	0.061	0.0304	0.04508	0.4154
rs10509665*	10	95518432	LGI1 [‡]	A/G	0.61	ABI Discovery	41665	-0.0042	0.0009	5.99E-06	0.33
						PAD Discovery	39958	0.0454	0.0281	0.1058	0.1607
rs10507044*	12	93774126	NDUFA12	T/C	0.41	ABI Discovery	41596	-0.0041	0.0009	7.25E-06	0.91
						PAD Discovery	39910	0.0386	0.0277	0.1629	0.3781

P_{het} = p value for heterogeneity

* Not chosen for replication

[‡] SNP is located within the gene; rs819750 and rs4366776 are within 60kb of the gene [†]PAD defined as ABI_{≤0.9} vs ABI_{>0.9}

Supplementary Table 8. Meta-analysis results: SNP associations for PAD (ABI ≤0.9 vs ABI >0.9) with $p < 10^{-5}$ with population isolates† included.

SNP	Chr	Physical Position	Closest Gene	Risk / Non-risk Allele	Risk Allele frequency	N	OR	95% Confidence Interval	P value	P _{het}
rs9998941	4	162544312	<i>FSTL5</i> *	A/G	0.22	39715	1.18	(1.11, 1.27)	6.00E-07	0.49
rs11751656	6	42751046	<i>UBR2</i> *	G/A	0.07	29586	1.61	(1.33, 1.97)	1.72E-06	0.81
rs12772949	10	82698704	<i>SH2D4B</i>	G/A	0.17	38786	1.21	(1.12, 1.31)	2.14E-06	0.94
rs6426183	1	245079347	<i>AHCTF1</i> *	C/T	0.09	39959	1.24	(1.13, 1.36)	4.60E-06	0.54
rs11715199	3	178757173	<i>TBL1XR1</i>	G/C	0.28	39960	1.15	(1.08, 1.22)	4.89E-06	0.43
rs7696128	4	18697484	<i>LCORL</i>	G/T	0.52	39960	1.13	(1.07, 1.20)	5.02E-06	0.88
rs3119311	6	160613097	<i>SLC22A2</i>	C/T	0.12	39958	1.2	(1.11, 1.30)	5.54E-06	0.47

P_{het} = p value for heterogeneity

* SNP is located within the gene

† The Amish Study did not participate in the meta-analysis

Supplementary Table 9. SNP associations for both ABI and PAD (ABI<0.9) with $p < 10^{-4}$, excluding population isolates.

SNP	Chr	Closest Gene	Risk Allele	Non-risk Allele	Risk Alle Frequency	Ankle-brachial index (ABI)			Peripheral arterial disease (PAD)		
						Beta	P value	N	Beta	P value	N
rs615552	9	<i>CDKN2B</i>	t	c	0.5665	-0.0053	1.52E-07	35397	0.1176	8.69E-05	34903
rs523096	9	<i>CDKN2B</i>	a	g	0.5615	-0.0052	3.36E-07	35401	0.1165	9.99E-05	34915
rs518394	9	<i>CDKN2B</i>	g	c	0.5989	-0.0047	9.38E-06	35252	0.1256	8.60E-05	34904
rs7100623	10	<i>IDE</i> *	t	c	0.1992	-0.0054	1.89E-05	35412	0.1394	8.39E-05	34914
rs7908111	10	<i>IDE</i> *	a	g	0.2011	-0.0052	3.22E-05	35377	0.1384	7.90E-05	34879
rs13290547	9	<i>DAB2IP</i> *	t	c	0.0625	-0.0093	3.62E-05	32135	0.2797	2.20E-05	31720
rs7898493	10	<i>IDE</i> *	c	g	0.2032	-0.0051	3.67E-05	35346	0.1414	5.78E-05	34852
rs11187074	10	<i>IDE</i> *	c	g	0.2001	-0.0058	5.64E-05	27783	0.1380	8.77E-05	34915
rs1855916	10	<i>IDE</i> *	a	g	0.2022	-0.0050	5.87E-05	35320	0.1491	2.60E-05	34828
rs7084090	10	<i>IDE</i> *	a	t	0.2022	-0.0050	5.93E-05	35321	0.1490	2.62E-05	34829
rs6438172	3	<i>GRAMD1C</i> *	a	g	0.2165	-0.0048	6.56E-05	35413	0.1359	8.69E-05	34915
rs2245830	3	<i>GRAMD1C</i> *	g	t	0.2163	-0.0048	6.62E-05	35400	0.1364	8.83E-05	34902
rs4682143	3	<i>GRAMD1C</i> *	t	g	0.2162	-0.0048	6.64E-05	35402	0.1360	8.78E-05	34904
rs7093418	10	<i>IDE</i> *	t	g	0.2023	-0.0050	6.69E-05	35320	0.1497	2.43E-05	34828
rs2566973	3	<i>GRAMD1C</i> *	t	c	0.2161	-0.0048	6.99E-05	35400	0.1368	8.10E-05	34904
rs2566977	3	<i>GRAMD1C</i> *	c	a	0.2158	-0.0048	9.04E-05	35398	0.1366	9.90E-05	34901
rs1887922	10	<i>IDE</i> *	c	t	0.2005	-0.0049	9.74E-05	35320	0.1467	4.27E-05	34827

SNPs ordered by strength of the ABI association p value

* SNP is located within the gene

Supplementary Table 10: Literature-reported candidate genes for ankle-brachial-index (ABI) and/or peripheral arterial disease (PAD) and their association with ABI in the CHARGE GWAS discovery sample (population isolates excluded). The table reports the most strongly associated SNP (according to p-value) within the gene region ± 100 kb upstream and downstream of the candidate gene. We selected a candidate gene only if an association study with at least 100 cases and 100 controls was available independent whether the study was positive or negative. This decision was made on the basis that most of the negative studies were largely underpowered to exclude an association.

Candidate gene	Investigated markers as reported	Ref.	Chr.	Coding strand	Gene region		Most strongly associated SNP within the gene region ± 100 kb upstream and downstream of the candidate gene						# of loci (eff. loci)*	corr. P-value**	False discovery rate‡
					5' start 3' end	Top hit rs number	Position (bp)	Nearest gene	Ref./ coded allele	Coded allele freq.	Effect	P-value			
ACE	rs4340 (I/D), rs4291	^(40,45)	17	(+)	58,808,166	rs4459609	58,902,680	ACE	C/A	0.650	-0.002	0.0907	87 (31)	1.0000	1.0000
ADD1	G460W	⁽⁴⁶⁾	4	(+)	2,715,382	rs11947904	2,774,570	SH3BP2	G/T	0.052	0.007	0.0150	183 (63)	0.9463	1.0000
ADRB2	Two polymorphisms	⁽⁴⁷⁾	5	(+)	148,086,349	rs1432628	148,231,861	ADRB2	C/T	0.054	-0.007	0.0012	249 (70)	0.0860	0.4298
AGT	G-6A, T174M, M235T, rs699	^(41,42, 44)	1	(-)	228,804,892	rs4847000	228,848,364	COG2	G/A	0.219	0.003	0.0369	373 (109)	1.0000	1.0000
AGTR1	573C/T (exon 5), rs5186	^(41,44)	3	(+)	149,798,348	rs1492094	150,028,691	CPB1	G/A	0.392	0.003	0.0151	334 (88)	1.0000	1.0000
BRAP	rs11066001	⁽⁴⁸⁾	12	(-)	110,466,279	rs2051792	110,596,100	BRAP	C/T	0.024	0.008	0.0399	55 (18)	0.7173	1.0000
CDKN2B	rs1333049	⁽⁴⁹⁾	9		22,015,503	rs10757269	22,062,264	CDKN2B	G/A	0.506	0.006	2.5E-08	213 (69)	1.7E-06	9.32e-05
Chr 11 region***	rs9665943, rs1042602	⁽⁵⁰⁾	11		82,027,366	rs4144290	84,208,186	DLG2	G/A	0.126	-0.005	0.0058	7014 (1577)	1.0000	1.0000
CHRNA3	rs1051730	^(51,52)	15	(-)	76,574,707	rs1878399	76,699,058	CHRNA3	G/C	0.575	-0.003	0.0047	191 (40)	0.1869	0.5943
CRP	1059 G/C	⁽⁵³⁾	1	(-)	157,848,704	rs2808627	157,935,964	CRP	T/A	0.237	0.003	0.0197	221 (74)	1.0000	1.0000
GJA4 (CX37)	1019C>T Pro319Ser rs1764391	^(54,55)	1	(+)	34,931,186	rs12127690	35,077,856	C1orf212	G/C	0.689	0.003	0.0229	124 (40)	0.9176	1.0000
CX3CR1	V249I, T280M	⁽⁵⁶⁾	3	(-)	39,179,990	rs2669845	39,296,222	CX3CR1	C/T	0.133	-0.004	0.0073	192 (65)	0.4767	1.0000

to be continued

Supplementary Table 10: continued

Candidate gene	Investigated markers as reported	Ref.	Chr.	Coding strand	Gene region		Most strongly associated SNP within the gene region ± 100 kb upstream and downstream of the candidate gene								False discovery rate‡
					5' start 3' end	Top hit rs number	Position (bp)	Nearest gene	Ref./ coded allele	Coded allele freq.	Effect	P-value	# of loci (eff. loci)*	corr. P-value**	
CYBA (p22 phox)	C242T	⁽⁵⁷⁾	16	(-)	87,137,199	rs3794624	87,244,575	CYBA	G/A	0.340	0.005	6.3E-05	138 (58)	0.0036	0.0665
CYP2C9	rs1799853, rs1057910	⁽⁵⁸⁾	10	(+)	96,588,430	rs9332235	96,737,895	CYP2C9	G/A	0.025	-0.011	0.0043	204 (44)	0.1887	0.5943
DAB2IP	rs7025486	⁽⁵⁹⁾	9	(+)	123,269,220	rs1290547	123,527,316	DAB2IP	C/T	0.063	-0.009	3.6E-05	363 (97)	0.0035	0.0665
ENPP1	K121Q	⁽⁶⁰⁾	6	(+)	132,070,853	rs11154647	132,254,445	ENPP1	G/T	0.052	-0.007	0.0034	324 (86)	0.2897	0.7598
SELE (E- selectin)	S128R	^(53,61)	1	(-)	167,858,406	rs7531806	167,917,668	SELL	G/A	0.561	-0.003	0.0045	348 (65)	0.2901	0.7598
F13A1	V34L	⁽⁶²⁾	6	(-)	5,989,310	rs11756027	6,077,751	F13A1	C/T	0.756	0.003	0.0109	638 (211)	1.0000	1.0000
F2	Prothrombin G20210A	⁽⁶³⁻⁶⁶⁾	11	(+)	46,597,331	rs7109698	46,629,920	KIAA0652	C/T	0.170	-0.004	0.0009	83 (17)	0.0155	0.2132
F5	G1691A (Leiden)	⁽⁶³⁻⁶⁶⁾	1	(-)	167,647,816	rs2040444	167,749,060	F5	G/A	0.525	0.003	0.0024	441 (105)	0.2534	0.7334
F7	AA I/D at 11293, R353q	⁽⁶⁷⁻⁶⁹⁾	13	(+)	112,708,106	rs2993312	112,731,466	MCF2L	G/A	0.645	-0.003	0.0106	179 (71)	0.7491	1.0000
FGB (FBG)	Bcl I digestion; T1689G; G- 455A	^(67,69- 72)	4	(+)	155,603,596	rs6054	155,709,058	FGB	C/T	0.006	-0.048	0.0007	174 (57)	0.0384	0.2740
FGG	10034C>T, rs2066865	⁽⁷³⁾	4	(-)	155,644,737	rs6054	155,709,058	FGB	C/T	0.006	-0.048	0.0007	163 (55)	0.0371	0.2740
F12 (FXII)	rs17876008 (4C>T)	⁽⁷⁴⁾	5	(-)	176,661,747	rs335467	176,823,248	DBN1	G/A	0.457	0.003	0.0455	65 (24)	1.0000	1.0000
GNB3	825C>T	⁽⁴⁶⁾	12	(+)	6,719,636	rs729751	6,924,611	C12orf57	C/T	0.039	-0.010	0.0034	137 (57)	0.1945	0.5943
GSTM1		⁽⁷⁵⁾	1	(+)	109,931,965	rs655315	110,016,701	GSTM2	G/A	0.497	0.005	0.0004	163 (63)	0.0277	0.2740
GSTT1		⁽⁷⁵⁾	22	(-)	22,606,141	rs9624387	22,750,128	CABIN1	C/T	0.075	-0.004	0.0269	64 (24)	0.6444	1.0000

to be continued

Supplementary Table 10: continued

Candidate gene	Investigated markers as reported	Ref.	Chr.	Coding strand	Gene region		Most strongly associated SNP within the gene region ± 100 kb upstream and downstream of the candidate gene							# of loci (eff. loci)*	corr. P-value**	False discovery rate‡
					5' start 3' end	Top hit rs number	Position (bp)	Nearest gene	Ref./ coded allele	Coded allele freq.	Effect	P-value				
HFE	C282Y, H63D	⁽⁷⁶⁾	6	(+)	26,095,488 26,305,035	rs11751812	26,295,313	HIST1H4D	G/T	0.095	0.004	0.0177	183 (48)	0.8472	1.0000	
HIF1A	P582S, rs11549465 A588T, rs11549467	⁽⁷⁷⁾	14	(+)	61,131,992 61,384,729	rs17098997	61,171,460	HIF1A	G/C	0.192	0.004	0.0010	206 (51)	0.0509	0.3113	
HP (hapto-globin)	Hp1, Hp2	⁽⁷⁸⁾	16	(+)	70,546,009 70,752,458	rs16973520	70,553,792	KIAA0174	G/T	0.748	0.004	0.0007	204 (54)	0.0399	0.2740	
ICAM1	K469E	^(52,53,61)	19	(+)	10,142,779 10,358,291	rs281419	10,277,842	GLP-1	G/A	0.149	-0.003	0.1610	113 (43)	1.0000	1.0000	
IL1B	+3953	⁽⁷⁹⁾	2	(-)	113,203,808 113,410,827	rs12472089	113,371,320	IL1F7	C/T	0.326	0.003	0.0168	192 (34)	0.5705	1.0000	
IL6	-174 G/C	^(52,53,80)	7	(+)	22,633,345 22,838,141	rs7796691	22,768,932	IL6	C/T	0.797	-0.003	0.0089	261 (73)	0.6516	1.0000	
ITGB3	PLA1/A2; P1 ^A	^(71,81)	17	(+)	42,586,207 42,845,075	rs11871477	42,783,505	C17orf57	G/A	0.985	0.012	0.0173	206 (53)	0.9164	1.0000	
LIPC	rs2070895 (G-250A)	⁽⁸²⁾	15	(+)	56,411,467 56,748,364	rs261292	56,468,196	LIPC	G/A	0.004	0.047	0.0027	500 (178)	0.4758	1.0000	
LPA	K-IV repeats; rs1853021 (C93T)	^(83,84)	6	(-)	160,772,506 161,107,397	rs10455872	160,930,108	LPA	G/A	0.936	0.007	0.0062	268 (74)	0.4615	1.0000	
CCL2 (MCP1)	-2518 A/G	⁽⁵³⁾	17	(+)	29,506,409 29,708,331	rs2368697	29,522,313	ACCN1	G/A	0.257	-0.002	0.0447	236 (64)	1.0000	1.0000	
MIF	-173 G/C	⁽⁵³⁾	22	(+)	22,466,565 22,667,409	rs17004046	22,570,304	MIF	G/T	0.145	-0.003	0.0580	211 (57)	1.0000	1.0000	
MMP1	-1607 1G/2G	⁽⁵³⁾	11	(-)	102,065,861 102,274,104	rs11225443	102,248,161	MMP12	C/T	0.033	-0.011	0.0081	329 (90)	0.7254	1.0000	
MMP3	-1171 5A/6A	⁽⁵³⁾	11	(-)	102,111,738 102,319,552	rs11225443	102,248,161	MMP12	C/T	0.033	-0.011	0.0081	257 (79)	0.6367	1.0000	
MMP9	-1563 C/T	⁽⁵³⁾	20	(+)	43,970,954 44,178,606	rs11698938	44,171,037	CD40	C/T	0.010	-0.026	0.0026	174 (53)	0.1389	0.5877	

to be continued

Supplementary Table 10: continued

Candidate gene	Investigated markers as reported	Ref.	Chr.	Coding strand	Gene region		Most strongly associated SNP within the gene region ± 100 kb upstream and downstream of the candidate gene							# of loci (eff. loci)*	corr. P-value**	False discovery rate‡
					5' start 3' end	Top hit rs number	Position (bp)	Nearest gene	Ref./ coded allele	Coded allele freq.	Effect	P-value				
MTHFR	C677T	^(65,66,85)	1	(-)	11,668,374 11,888,702	rs2050265	11,802,286	CLCN6	G/A	0.840	0.003	0.0286	221 (62)	1.0000	1.0000	
MTTP (MTP)	-493G>T	⁽⁸⁶⁾	4	(+)	100,615,004 100,863,649	rs11730739	100,859,020	MTTP	C/T	0.291	-0.003	0.0163	216 (46)	0.7480	1.0000	
NOS3	14 SNPs; -786T>C, - 894G>T, 4a/4b	^(43,87)	7	(+)	150,219,080 150,442,608	rs11763819	150,247,598	KCNH2	T/A	0.975	-0.010	0.0175	127 (47)	0.8239	1.0000	
P2RY12	H2 haplotype	⁽⁸⁸⁾	3	(-)	152,438,066 152,685,234	rs3821665	152,616,506	MED12L	G/A	0.514	0.003	0.0391	294 (60)	1.0000	1.0000	
PLA2G7 (PAF-AH)	G994T in exon 9	⁽⁸⁹⁾	6	(-)	46,680,238 46,911,055	rs1833460	46,885,336	MEP1A	C/T	0.112	0.006	0.0037	205 (47)	0.1719	0.5943	
SERPINE1 (PAI1)	HindIII	⁽⁶⁷⁾	7	(+)	100,457,172 100,669,026	rs4727479	100,552,387	SERPINE1	G/C	0.130	-0.005	0.0039	131 (47)	0.1851	0.5943	
PPARG	rs1801282 (Pro12Ala)	⁽⁹⁰⁾	3	(+)	12,204,349 12,550,854	rs310766	12,208,482	SYN2	G/A	0.254	-0.002	0.0515	314 (82)	1.0000	1.0000	
SCARB1	rs4238001, intron 5 (C>T at intron pos.55), rs5888	⁽⁹¹⁾	12	(-)	123,728,129 124,014,287	rs11057830	123,873,006	SCARB1	G/A	0.154	-0.004	0.0069	265 (99)	0.6828	1.0000	
SLC2A10	10 SNPs	⁽⁹²⁾	20	(+)	44,671,686 44,898,390	rs11550540	44,749,176	TP53RK	C/T	0.898	0.005	0.0081	230 (77)	0.6208	1.0000	
SRD5A1	Hinfl SNP	⁽⁹³⁾	5	(+)	6,586,500 6,822,673	rs12522035	6,819,185	POLS	C/A	0.926	-0.004	0.0318	346 (101)	1.0000	1.0000	
SRD5A2	(V89L	⁽⁹³⁾	2	(-)	31,503,160 31,759,544	rs7424544	31,625,875	SRD5A2	C/T	0.977	-0.007	0.0441	127 (25)	1.0000	1.0000	
UGT1A1	-53 TA-repeat	⁽³³⁾	2	(+)	234,233,658 234,446,684	rs11690786	234,357,356	UGT1A1	C/T	0.315	0.003	0.0036	597 (137)	0.4924	1.0000	
VKORC1		⁽⁹⁴⁾	16	(-)	30,909,677 31,113,777	rs17708638	31,078,675	PRSS36	C/T	0.310	0.003	0.0061	54 (12)	0.0736	0.4048	
ZNF202	rs10893081 (- 660A>G)	⁽⁹⁵⁾	11	(-)	123,000,207 123,217,573	rs1148107	123,020,997	SCN3B	C/A	0.969	0.011	0.0015	308 (70)	0.1064	0.4877	

to be continued

PubMed search terms "((ankle-brachial index) OR (peripheral arterial disease)) AND polymorphism"

For all candidate genes the official HGNC-approved gene names are reported and, where needed, the alias names used in the publications are provided in brackets. The chromosomal coordinates refer to the plus-strand according to HapMap Rel 24 (based on NCBI Genome Build 36 and dbSNP b.126). In the case that more than one RefSeq transcript is known, the +/- 100 kb gene region was defined starting from the coordinates which comprised all known transcripts (i.e. starting from the beginning of the outmost 5' exon to the end of the outmost 3' exon). The strand actually encoding the candidate gene is reported in the column "coding strand".

* Effective number of independent loci calculated using the function reported by Gao⁽³⁸⁾ based on imputed genotype data in KORA F4

** P-value Bonferroni corrected within each gene region using the effective number of loci

*** Chromosome 11 region: Chromosomal region identified by admixture mapping

‡ Using the corrected p-values of the SNP in association to ABI, we calculated a false discovery rate (FDR) to account for the number of gene regions examined. An FDR <0.10 defined evidence of a significant association.

Supplementary Table 11: Candidate SNPs for myocardial infarction and /or coronary artery disease and their association with ABI in the CHARGE GWAS discovery sample (population isolates excluded) †.

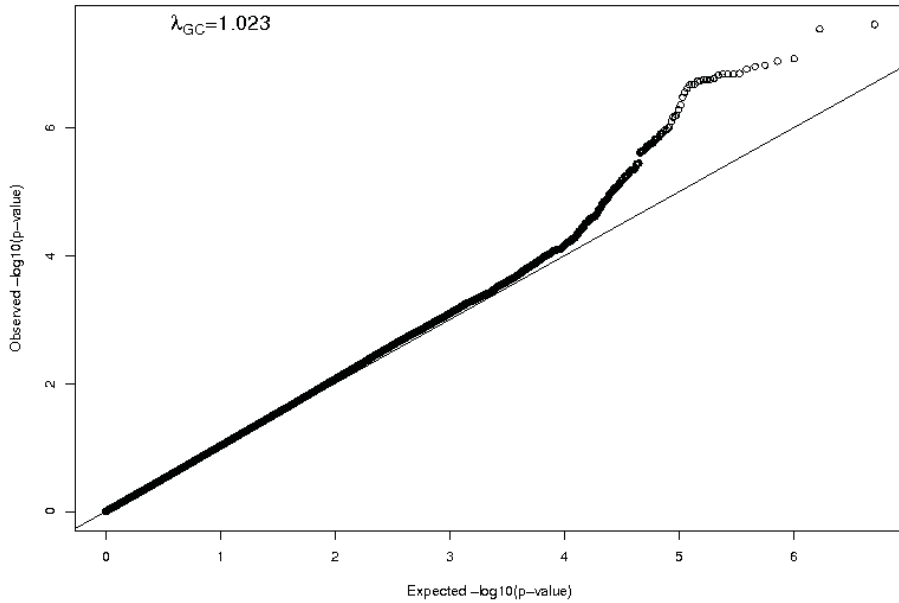
SNP	Chr	Physical Position	Closest Gene	Risk / Non-risk Allele	Risk Allele frequency	N	Beta	SE	P value	False discovery rate‡
rs4977574	9	22,088,574	<i>CDKN2A, CKDN2B</i>	G/A	0.49	35411	-0.0047	0.001	2.33E-06	6.52E-05
rs1122608	19	11,024,601	<i>LDLR</i>	G/T	0.74	35384	-0.0035	0.001	2.56E-03	0.036
rs1412444	10	90,992,907	<i>LIPA</i>	C/T	0.67	26195	0.0027	0.001	3.05E-02	0.284
rs2505083	10	30,375,128	<i>KIAA1462</i>	C/T	0.42	35411	0.0018	0.001	8.28E-02	0.58
rs46522	17	44,343,596	<i>UBE2Z,GIP,ATP5G1,SNF8</i>	T/C	0.54	35364	-0.0015	0.001	1.17E-01	0.594
rs12936587	17	17,484,447	<i>RASD1, SMCR3, PEMT</i>	G/A	0.55	35346	0.0016	0.001	1.27E-01	0.594
rs2895811	14	99,203,695	<i>HHIPL1</i>	C/T	0.42	35396	0.0014	0.001	1.76E-01	0.69
rs964184	11	116,154,127	<i>ZNF259,APOA5-A4-C3-A1</i>	G/C	0.14	35384	0.0019	0.002	1.97E-01	0.69
rs3184504	12	110,368,991	<i>SH2B3</i>	T/C	0.5	35359	-0.0011	0.001	2.70E-01	0.762
rs2306374	3	139,602,642	<i>MRAS</i>	C/T	0.16	35410	0.0015	0.001	2.81E-01	0.762
rs6903956	6	11,882,569	<i>C6orf105</i>	G/A	0.63	30183	0.0012	0.001	2.99E-01	0.762
rs12413409	10	104,709,086	<i>CYP17A1,CNNM2,NT5C2</i>	G/A	0.91	35413	0.0016	0.002	3.61E-01	0.843
rs10953541	7	107,031,781	<i>7q22</i>	C/T	0.75	35369	0.0009	0.001	4.52E-01	0.886
rs974819	11	103,165,777	<i>PDGFD</i>	C/T	0.71	35280	0.0007	0.001	5.05E-01	0.886
rs4773144	13	109,758,713	<i>COL4A1, COL4A2</i>	A/G	0.55	33491	-0.0007	0.001	5.06E-01	0.886
rs12190287	6	134,256,218	<i>TCF21</i>	G/C	0.38	35168	0.0007	0.001	5.32E-01	0.886
rs6725887	2	203,454,130	<i>WDR12</i>	C/T	0.13	35399	0.0009	0.002	5.54E-01	0.886
rs17114036	1	56,735,409	<i>PPAP2B</i>	A/G	0.9	35187	-0.001	0.002	5.91E-01	0.886
rs9982601	21	34,520,998	<i>MRPS6</i>	T/C	0.14	35343	-0.0008	0.002	6.01E-01	0.886
rs17609940	6	35,142,778	<i>ANKS1A</i>	G/C	0.8	35382	0.0006	0.001	6.51E-01	0.911
rs216172	17	2,073,254	<i>SMG6, SRR</i>	G/C	0.65	26051	0.0004	0.001	7.42E-01	0.927
rs1746048	10	44,095,830	<i>CXCL12</i>	T/C	0.13	35403	-0.0004	0.002	7.59E-01	0.927
rs3825807	15	76,876,166	<i>ADAMTS7</i>	G/A	0.44	35338	0.0003	0.001	7.61E-01	0.927
rs579459	9	135,143,989	<i>ABO</i>	C/T	0.22	35371	0.0002	0.001	8.72E-01	0.98
rs12526453	6	13,035,530	<i>PHACTR1</i>	C/G	0.65	35353	-0.0001	0.001	9.09E-01	0.98
rs11206510	1	55,268,627	<i>PCSK9</i>	T/C	0.81	35174	-0.0001	0.001	9.54E-01	0.98
rs599839	1	109,623,689	<i>SORT1</i>	G/A	0.23	35379	0	0.001	9.75E-01	0.98
rs11556924	7	129,450,732	<i>ZC3HC1</i>	C/T	0.61	35217	0	0.001	9.80E-01	0.98

† Candidate genes for look-up of association with ABI were identified by recent GWAS to be genome-wide significantly associated with CAD.

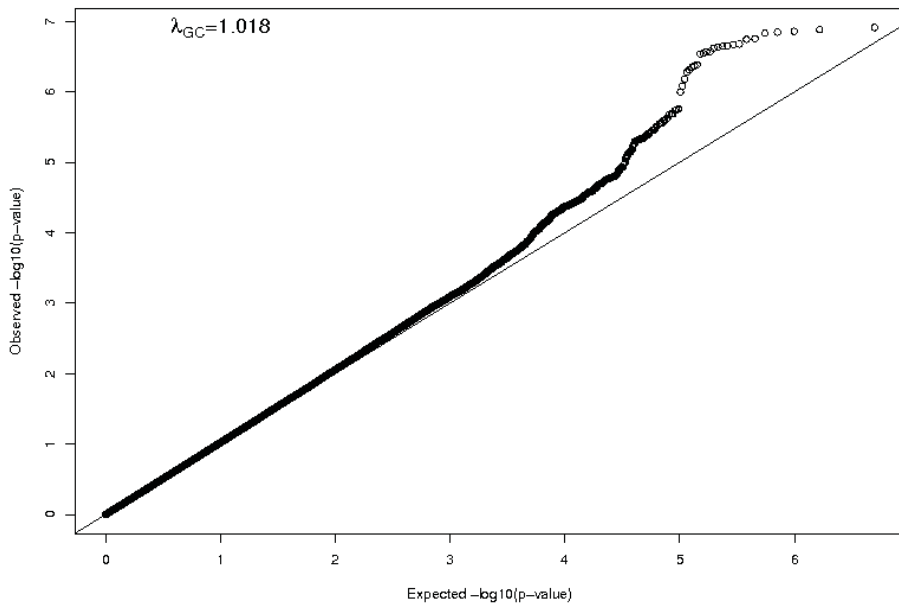
‡ Using the p-values of the SNP in association to ABI, we calculated a false discovery rate (FDR) to account for the number of gene regions examined. An FDR <0.10 defined evidence of a significant association.

Suppl Figure 1: Quantile-quantile plots of the meta-analysis of GWAS of ABI. The dots represent the observed $-\log_{10}$ p-values associated with ABI. The expected distribution of $-\log_{10}$ p-values under the null hypothesis is shown by the straight line. A) excluding the population isolates; B) including the population isolates

A

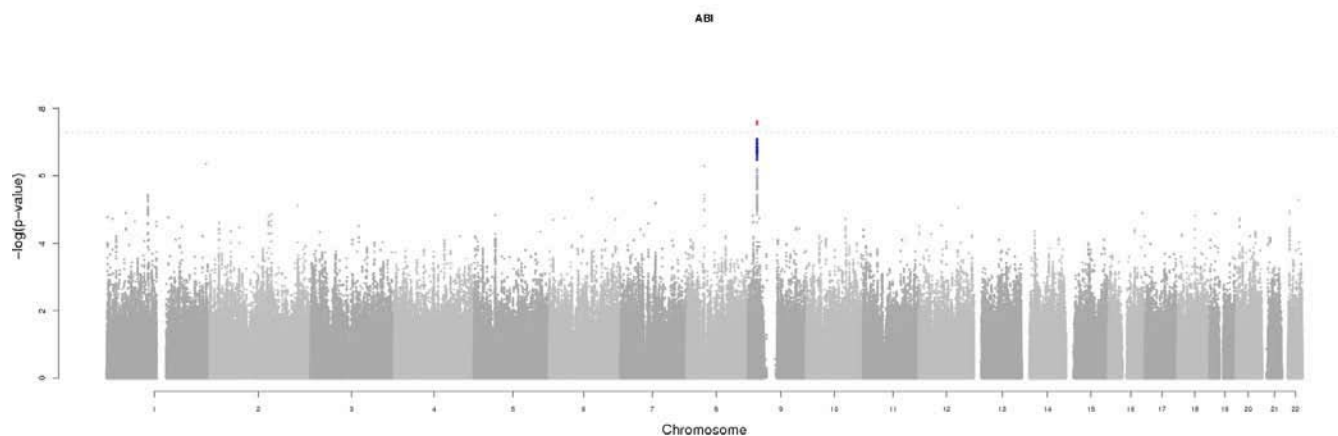


B

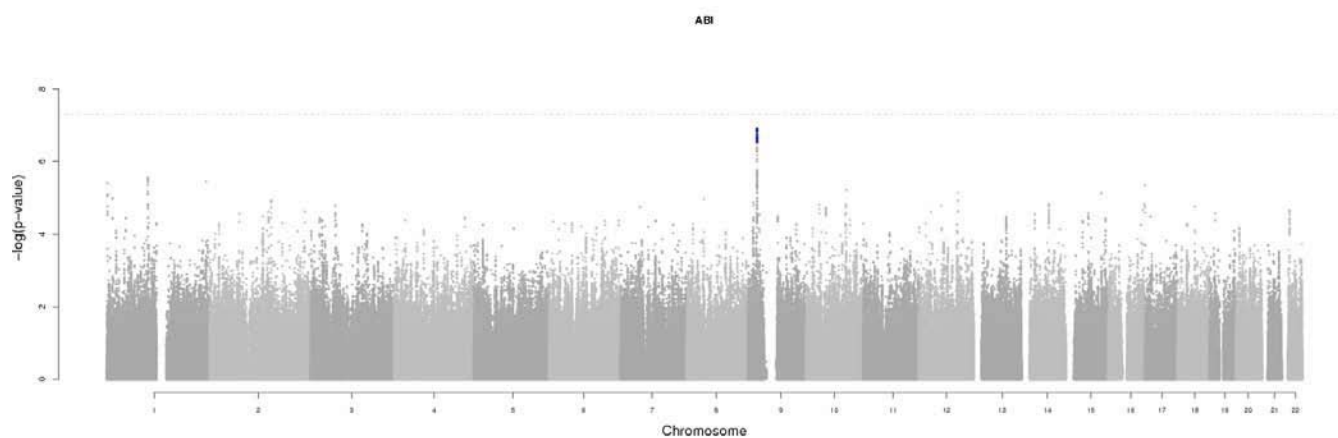


Suppl Figure 2: Manhattan plots of the meta-analysis of GWAS of ABI. X-axis represents the chromosomal position for each SNP, and the y-axis the $-\log_{10}$ p-value for association with ABI. The horizontal dotted line represents the genome-wide significance level of $P < 5 \times 10^{-8}$. A) excluding the population isolates; B) including the population isolates

A



B



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Supplementary Table 6: Overall Meta-analysis Results and Study Specific Results: ABI-SNP Associations with $p < 10^{-5}$

SNP	Chr	Physical Position	Allele1	Allele2	Meta-analysis results, population isolates excluded						Closest gene
					Allele 1 frequency	Beta	SE	P value	P_{het} value	Total N	
rs10757269	9	22062264	a	g	0.5057	0.0056	0.001	2.46E-08	0.2294	35036	CDKN2B
rs9632884	9	22062301	c	g	0.4945	-0.0055	0.001	2.89E-08	0.2555	35035	CDKN2B
rs10811647	9	22055002	c	g	0.5692	0.0054	0.001	8.39E-08	0.3306	35306	CDKN2B
rs10811650	9	22057593	a	g	0.569	0.0054	0.001	9.17E-08	0.323	35305	CDKN2B
rs1537375	9	22106071	t	c	0.4831	0.0053	0.001	1.06E-07	0.05722	35303	CDKN2B
rs2383207	9	22105959	a	g	0.4827	0.0053	0.001	1.12E-07	0.05728	35308	CDKN2B
rs1537374	9	22106046	a	g	0.4829	0.0053	0.001	1.22E-07	0.05755	35303	CDKN2B
rs1004638	9	22105589	a	t	0.4836	0.0053	0.001	1.43E-07	0.06191	35303	CDKN2B
rs944797	9	22105286	t	c	0.484	0.0053	0.001	1.45E-07	0.06293	35303	CDKN2B
rs10511701	9	22102599	t	c	0.4795	0.0053	0.001	1.46E-07	0.07575	35274	CDKN2B
rs7341786	9	22102241	a	c	0.4796	0.0053	0.001	1.46E-07	0.07571	35274	CDKN2B
rs615552	9	22016077	t	c	0.5665	-0.0053	0.001	1.52E-07	0.8319	35397	CDKN2B
rs10738604	9	22015493	a	g	0.3618	-0.0055	0.0011	1.71E-07	0.6335	35364	CDKN2B
rs2383206	9	22105026	a	g	0.4841	0.0052	0.001	1.77E-07	0.07524	35304	CDKN2B
rs10738609	9	22104495	a	g	0.4843	0.0052	0.001	1.79E-07	0.07523	35304	CDKN2B
rs10733376	9	22104469	c	g	0.5156	-0.0052	0.001	1.79E-07	0.0751	35304	CDKN2B
rs10738610	9	22113766	a	c	0.489	0.0053	0.001	1.87E-07	0.0537	35330	CDKN2B
rs1333046	9	22114123	a	t	0.5111	-0.0053	0.001	1.91E-07	0.0535	35330	CDKN2B
rs7859362	9	22095927	t	c	0.4849	0.0052	0.001	2.10E-07	0.07804	35305	CDKN2B
rs1412834	9	22100131	t	c	0.4847	0.0052	0.001	2.10E-07	0.07823	35304	CDKN2B
rs1333042	9	22093813	a	g	0.499	0.0052	0.001	2.15E-07	0.0905	35354	CDKN2B
rs6475606	9	22071850	t	c	0.4873	-0.0051	0.001	2.43E-07	0.229	35411	CDKN2B
rs10116277	9	22071397	t	g	0.4871	-0.0051	0.001	2.80E-07	0.2044	35236	CDKN2B
rs523096	9	22009129	a	g	0.5615	-0.0052	0.001	3.36E-07	0.891	35401	CDKN2B
rs4659996	1	238912747	a	g	0.4846	-0.006	0.0012	4.44E-07	0.3354	28087	GREM2
rs7003385	8	41705907	t	c	0.6656	-0.0053	0.0011	5.24E-07	0.4894	35375	ANK1
rs3218020	9	21987872	a	g	0.3485	-0.0054	0.0011	6.36E-07	0.6896	35095	CDKN2A
rs10811644	9	22015067	a	t	0.542	0.005	0.001	6.63E-07	0.3091	35394	CDKN2B
rs7035484	9	22015240	c	g	0.5421	0.005	0.001	6.86E-07	0.3098	35395	CDKN2B
rs1333043	9	22096731	a	t	0.5036	-0.0049	0.001	8.00E-07	0.04727	35314	CDKN2B
rs564398	9	22019547	t	c	0.582	-0.0049	0.001	9.83E-07	0.8683	35407	CDKN2B
rs634537	9	22022152	t	g	0.5834	-0.0049	0.001	1.01E-06	0.897	35400	CDKN2B
rs7865618	9	22021005	a	g	0.5725	-0.0049	0.001	1.08E-06	0.8914	35411	CDKN2B
rs2069418	9	21999698	c	g	0.542	-0.005	0.001	1.08E-06	0.8796	35224	CDKN2B
rs543830	9	22016639	a	t	0.5849	-0.0049	0.001	1.14E-06	0.8487	35401	CDKN2B
rs2157719	9	22023366	t	c	0.5739	-0.0049	0.001	1.21E-06	0.9112	35382	CDKN2B
rs679038	9	22019080	a	g	0.4156	0.0049	0.001	1.26E-06	0.8549	35409	CDKN2B
rs7044859	9	22008781	a	t	0.4537	-0.0049	0.001	1.36E-06	0.3891	35394	CDKN2B
rs10757272	9	22078260	t	c	0.4904	-0.0048	0.001	1.45E-06	0.06182	35411	CDKN2B
rs1008878	9	22026112	t	g	0.5803	-0.0049	0.001	1.49E-06	0.9102	35196	CDKN2B
rs1333048	9	22115347	a	c	0.4997	0.0049	0.001	1.50E-06	0.03292	35369	CDKN2B
rs10738607	9	22078094	a	g	0.5079	0.0048	0.001	1.60E-06	0.06705	35409	CDKN2B
rs2106120	9	22007101	t	g	0.4538	-0.0048	0.001	1.75E-06	0.3937	35391	CDKN2B
rs2106119	9	22007550	a	g	0.5461	0.0048	0.001	1.76E-06	0.3926	35393	CDKN2B
rs1537370	9	22074310	t	c	0.4894	-0.0048	0.001	1.79E-06	0.1455	35241	CDKN2B
rs10811640	9	22003411	t	g	0.4519	-0.0048	0.001	1.83E-06	0.4239	35350	CDKN2B
rs1556516	9	22090176	c	g	0.4909	-0.0047	0.001	1.91E-06	0.05805	35406	CDKN2B
rs1537371	9	22089568	a	c	0.4909	-0.0047	0.001	1.93E-06	0.05815	35406	CDKN2B
rs1412829	9	22033926	a	g	0.582	-0.0048	0.001	1.95E-06	0.911	35355	CDKN2B
rs10811641	9	22004137	c	g	0.6318	0.0049	0.001	2.14E-06	0.7504	35356	CDKN2B

rs7859727	9	22092165	t	c	0.4892	-0.0047	0.001	2.19E-06	0.05953	35406	CDKN2B
rs1537373	9	22093341	t	g	0.5112	0.0047	0.001	2.28E-06	0.05976	35406	CDKN2B
rs2891168	9	22088619	a	g	0.5095	0.0047	0.001	2.32E-06	0.0655	35410	CDKN2B
rs4977574	9	22088574	a	g	0.5094	0.0047	0.001	2.33E-06	0.06531	35411	CDKN2B
rs2069416	9	22000004	a	t	0.3576	-0.005	0.0011	2.37E-06	0.744	35254	CDKN2B
rs1556515	9	22026367	t	c	0.5815	-0.0048	0.001	2.48E-06	0.9065	35196	CDKN2B
rs1333037	9	22030765	t	c	0.5741	-0.0047	0.001	3.60E-06	0.9059	35356	CDKN2B
rs2099861	8	41700444	t	c	0.3664	-0.0048	0.001	3.64E-06	0.1513	35386	ANK1
rs819750	1	99469651	t	g	0.8772	0.007	0.0015	3.65E-06	0.5103	35278	LPPR4
rs1063192	9	21993367	a	g	0.5676	-0.0047	0.001	3.82E-06	0.9158	35268	CDKN2B
rs819748	1	99467756	a	c	0.8762	0.007	0.0015	4.19E-06	0.5079	35291	LPPR4
rs10757278	9	22114477	a	g	0.5167	0.0047	0.001	4.43E-06	0.0157	35348	CDKN2B
rs1333047	9	22114504	a	t	0.5166	0.0047	0.001	4.47E-06	0.01568	35348	CDKN2B
rs10115049	9	22022119	a	g	0.5233	0.0046	0.001	4.61E-06	0.5317	35383	CDKN2B
rs1360589	9	22035317	t	c	0.5746	-0.0046	0.001	4.62E-06	0.8514	35355	CDKN2B
rs9485528	6	102221473	a	g	0.1699	-0.0061	0.0013	4.63E-06	0.7808	35339	GRIK2
rs1872877	8	41704728	t	c	0.6336	0.0047	0.001	4.66E-06	0.167	35391	ANK1
rs10965212	9	22013795	a	t	0.4768	-0.0046	0.001	4.85E-06	0.3242	35405	CDKN2B
rs819746	1	99466332	a	c	0.8757	0.0069	0.0015	5.04E-06	0.4729	35316	LPPR4
rs4977575	9	22114744	c	g	0.5166	0.0046	0.001	5.47E-06	0.01628	35348	CDKN2B
rs1333049	9	22115503	c	g	0.483	-0.0046	0.001	5.51E-06	0.01224	35358	CDKN2B
rs7030641	9	22044040	t	c	0.573	-0.0046	0.001	5.68E-06	0.8398	35394	CDKN2B
rs2279437	8	41707343	a	g	0.3652	-0.0047	0.001	5.69E-06	0.1507	35368	ANK1
rs819797	1	99459990	a	g	0.866	0.0069	0.0015	5.74E-06	0.3963	35101	LPPR4
rs944801	9	22041670	c	g	0.5739	-0.0046	0.001	5.80E-06	0.8418	35396	CDKN2B
rs722453	7	84037497	a	g	0.5771	0.0054	0.0012	6.43E-06	0.6902	26200	SEMA3A
rs7780912	7	84110129	a	g	0.5769	0.0053	0.0012	6.57E-06	0.7077	26171	SEMA3D
rs7028570	9	22038683	a	g	0.4808	-0.0045	0.001	6.60E-06	0.4655	35342	CDKN2B
rs2151280	9	22024719	a	g	0.4825	-0.0045	0.001	6.73E-06	0.529	35205	CDKN2B
rs1360590	9	22031443	t	c	0.5207	0.0045	0.001	6.81E-06	0.4601	35359	CDKN2B
rs1591136	9	22016834	c	g	0.4767	-0.0045	0.001	6.85E-06	0.3436	35401	CDKN2B
rs10120688	9	22046499	a	g	0.4881	-0.0045	0.001	7.19E-06	0.5001	35408	CDKN2B
rs16824978	2	211380306	t	c	0.2501	-0.0054	0.0012	7.77E-06	0.3732	34950	CPS1
rs7049105	9	22018801	a	g	0.5234	0.0045	0.001	7.88E-06	0.3545	35404	CDKN2B
rs10965224	9	22057276	a	t	0.5993	-0.0045	0.001	8.13E-06	0.5374	35394	CDKN2B
rs10965219	9	22043687	a	g	0.5199	0.0045	0.001	8.19E-06	0.3665	35390	CDKN2B
rs7530667	1	99464320	t	c	0.3874	-0.0045	0.001	8.43E-06	0.1114	35391	LPPR4
rs1537378	9	22051614	a	g	0.3994	0.0045	0.001	8.49E-06	0.6196	35376	CDKN2B
rs8181050	9	22054391	a	g	0.5995	-0.0045	0.001	8.75E-06	0.5883	35405	CDKN2B
rs4977756	9	22058652	a	g	0.6006	-0.0045	0.001	8.82E-06	0.5672	35405	CDKN2B
rs1333039	9	22055657	c	g	0.5995	-0.0045	0.001	8.86E-06	0.5856	35405	CDKN2B
rs7311009	12	94859134	c	g	0.9711	0.0152	0.0034	8.94E-06	0.965	30436	CCDC38
rs10811651	9	22057830	a	g	0.5997	-0.0045	0.001	9.22E-06	0.5821	35404	CDKN2B
rs518394	9	22009673	c	g	0.4011	0.0047	0.0011	9.38E-06	0.8702	35252	CDKN2B
rs819756	1	99474518	t	c	0.8961	0.0074	0.0017	9.71E-06	0.5301	35257	LPPR4
rs2241896	8	41674630	t	c	0.6369	0.0047	0.0011	9.99E-06	0.1807	35243	ANK1

Atherosclerosis Risk in Communities Study

af	oevar_aric	coded_aric	noncoded_aric	beta_aric	se_aric	p_aric	n_aric	maf_aric
0.4879	0.9945	G	A	-0.00183463	0.00200732	0.36068207	7630	0.4879
0.488	0.9955	C	G	-0.00183487	0.00200629	0.36037386	7630	0.488
0.5733	0.9732	C	G	0.00319315	0.0020569	0.12054388	7630	0.4267
0.5732	0.9729	A	G	0.00318621	0.00205763	0.12148582	7630	0.4268
0.5128	0.9759	C	T	-5.76E-05	0.00203077	0.97735436	7630	0.4872
0.5124	0.9753	G	A	-4.98E-05	0.00203108	0.98043457	7630	0.4876
0.5126	0.9756	G	A	-5.31E-05	0.00203097	0.97913034	7630	0.4874
0.5123	0.9753	T	A	-4.81E-05	0.00203109	0.98108634	7630	0.4877
0.5122	0.9752	C	T	-4.64E-05	0.00203108	0.98176423	7630	0.4878
0.5144	0.9656	C	T	-8.89E-05	0.00203988	0.96523633	7630	0.4856
0.5143	0.9656	C	A	-8.82E-05	0.00203976	0.96551416	7630	0.4857
0.5582	0.9978	T	C	-0.0031378	0.0020047	0.11751214	7630	0.4418
0.3568	0.9858	A	G	-0.00397774	0.00210414	0.05869572	7630	0.3568
0.5121	0.9752	G	A	-4.42E-05	0.00203104	0.98264733	7630	0.4879
0.512	0.9752	G	A	-4.26E-05	0.002031	0.98327579	7630	0.488
0.5119	0.9752	C	G	-4.00E-05	0.00203085	0.98427083	7630	0.4881
0.5086	0.9879	C	A	-0.00043888	0.00202089	0.82805345	7630	0.4914
0.5087	0.9881	A	T	-0.00043936	0.00202062	0.82784477	7630	0.4913
0.5112	0.9757	C	T	-2.75E-05	0.00202968	0.98918975	7630	0.4888
0.5114	0.9754	C	T	-3.22E-05	0.00203018	0.98734162	7630	0.4886
0.5007	0.9932	G	A	-2.91E-06	0.00201531	0.99884963	7630	0.4993
0.4811	0.9985	T	C	-0.00101356	0.0019989	0.6120711	7630	0.4811
0.4809	0.9934	T	G	-0.00105318	0.0020046	0.59927153	7630	0.4809
0.5536	0.9997	A	G	-0.0026719	0.00200147	0.18185367	7630	0.4464
0.5166	0.8771	G	A	0.00185897	0.00212836	0.38237946	7630	0.4834
0.6666	0.9984	T	C	-0.00504406	0.00212636	0.01769082	7630	0.3334
0.3409	0.9395	A	G	-0.00326476	0.00218813	0.13566875	7630	0.3409
0.4512	0.9981	T	A	-0.00254969	0.00201594	0.20592022	7630	0.4512
0.4512	0.998	G	C	-0.00253295	0.00201604	0.20893363	7630	0.4512
0.4976	0.9816	A	T	0.00023452	0.00201663	0.90740828	7630	0.4976
0.5756	0.9997	T	C	-0.0028059	0.00201974	0.16473219	7630	0.4244
0.5753	0.9967	T	G	-0.00288453	0.00202053	0.15337896	7630	0.4247
0.5668	0.9979	A	G	-0.00259143	0.00201473	0.19832451	7630	0.4332
0.5346	0.9718	C	G	-0.00196773	0.00203216	0.33284865	7630	0.4654
0.5772	0.9994	A	T	-0.00274235	0.00201929	0.17440808	7630	0.4228
0.567	0.9961	T	C	-0.00256224	0.00201604	0.20372039	7630	0.433
0.5767	0.9983	G	A	-0.0027566	0.00202022	0.17237802	7630	0.4233
0.4466	0.9996	A	T	-0.00209805	0.00201716	0.29824611	7630	0.4466
0.4848	0.9977	T	C	0.00035805	0.00200593	0.85831437	7630	0.4848
0.5762	0.9661	T	G	-0.00266527	0.00204774	0.19303248	7630	0.4238
0.4958	0.999	C	A	-0.00018765	0.00200289	0.92534493	7630	0.4958
0.4847	0.9929	G	A	0.00030927	0.00201038	0.87772422	7630	0.4847
0.4464	0.9984	T	G	-0.00210092	0.00201877	0.29796941	7630	0.4464

0.4465	0.9989	G	A	-0.00209888	0.0020181	0.29828183	7630	0.4465
0.4837	0.9696	T	C	-2.58E-05	0.00203274	0.98988367	7630	0.4837
0.4442	0.9892	T	G	-0.00213926	0.00203169	0.29232119	7630	0.4442
0.4866	0.9995	C	G	0.00036765	0.00200258	0.85431714	7630	0.4866
0.4865	0.9998	A	C	0.00037253	0.00200233	0.8523868	7630	0.4865
0.5731	0.9879	A	G	-0.00263971	0.00202643	0.19266374	7630	0.4269
0.3587	0.9889	G	C	-0.00271476	0.00210413	0.19694572	7630	0.3587
0.4866	0.9991	T	C	0.00036118	0.00200292	0.85687916	7630	0.4866
0.4866	0.9991	G	T	0.00035985	0.00200299	0.85740336	7630	0.4866
0.4865	0.9999	G	A	0.00037458	0.00200223	0.85157869	7630	0.4865
0.4865	0.9999	G	A	0.00037366	0.00200222	0.85193679	7630	0.4865
0.3504	0.9757	A	T	-0.00239867	0.00213083	0.26025124	7630	0.3504
0.5765	0.9628	T	C	-0.00252026	0.00205112	0.21913909	7630	0.4235
0.5662	0.989	T	C	-0.00229685	0.0020215	0.25582692	7630	0.4338
0.367	0.9975	T	C	-0.00470226	0.00206081	0.02250919	7630	0.367
0.8766	0.9602	T	G	0.00949865	0.00306533	0.00194718	7630	0.1234
0.5602	0.9858	A	G	-0.00194817	0.00203368	0.33803723	7630	0.4398
0.8749	0.973	A	C	0.00925206	0.00302879	0.0022568	7630	0.1251
0.4795	0.9875	G	A	0.00053336	0.00201649	0.79137114	7630	0.4795
0.4797	0.9882	T	A	0.00053025	0.00201571	0.79247952	7630	0.4797
0.4738	0.9959	G	A	-0.00256005	0.00201271	0.20335971	7630	0.4738
0.566	0.9955	T	C	-0.0014943	0.00201459	0.45819596	7630	0.434
0.8405	0.9736	G	A	0.00598268	0.00269535	0.02644875	7630	0.1595
0.3678	0.9982	C	T	-0.00474185	0.00205868	0.02126491	7630	0.3678
0.4701	0.9998	A	T	-0.00212833	0.00200796	0.28912529	7630	0.4701
0.8746	0.9763	A	C	0.00920232	0.00302111	0.00232309	7630	0.1254
0.4798	0.9889	G	C	0.00052789	0.00201488	0.79329864	7630	0.4798
0.4796	0.9948	C	G	0.00062719	0.00201003	0.75498597	7630	0.4796
0.5652	0.9967	T	C	-0.0014528	0.00201292	0.4704035	7630	0.4348
0.3676	0.9979	A	G	-0.00484375	0.00205939	0.01867719	7630	0.3676
0.8624	0.8951	A	G	0.00868779	0.00303747	0.00423886	7630	0.1376
0.5657	0.9975	C	G	-0.00145724	0.00201248	0.46895425	7630	0.4343

Cardiovascular Health Study

af_chs	oevar_chs	coded_chs	noncoded_c		beta_chs	se_chs	p_chs	n_chs	maf_chs
			hs						
0.47619073	0.93163899	A	G		0.00688849	0.00339263	0.04231299	3193	0.47619073
0.47615143	0.93186249	G	C		0.00688602	0.0033922	0.04236097	3193	0.47615143
0.43995866	0.98017303	G	C		-0.00460375	0.00334966	0.16932005	3193	0.43995866
0.44000266	0.98019466	G	A		-0.00460657	0.0033496	0.16905017	3193	0.44000266
0.46460179	0.98269811	T	C		0.00543526	0.00334237	0.10391326	3193	0.46460179
0.46799092	1.00475623	A	G		0.00535525	0.00330539	0.10519916	3193	0.46799092
0.46724225	0.99264554	A	G		0.00538876	0.003325	0.1050862	3193	0.46724225
0.47253868	0.98847442	A	T		0.0052339	0.00333005	0.11601603	3193	0.47253868
0.47552067	0.98341614	T	C		0.00521381	0.0033371	0.11819953	3193	0.47552067
0.45960492	0.91913763	T	C		0.00549199	0.00344926	0.11133459	3193	0.45960492
0.45958284	0.91844525	A	C		0.00549058	0.00345039	0.11154356	3193	0.45958284
0.4140642	0.85768652	C	T		0.00606861	0.00360725	0.09250298	3193	0.4140642
0.34580629	0.73440757	A	G		-0.00664051	0.00404949	0.10103832	3193	0.34580629
0.47610085	0.98181345	A	G		0.00517855	0.00333915	0.1209355	3193	0.47610085
0.47706044	0.97938435	A	G		0.00510229	0.00334188	0.12681833	3193	0.47706044
0.47758926	0.97805503	G	C		0.00509845	0.00334373	0.12731361	3193	0.47758926
0.47062026	0.90384121	A	C		0.00558813	0.00346506	0.10680841	3193	0.47062026
0.46966708	0.90054547	T	A		0.00557733	0.00347125	0.10811526	3193	0.46966708
0.47518822	0.95985821	T	C		0.0052924	0.0033725	0.11658255	3193	0.47518822
0.47459395	0.96081271	T	C		0.005273	0.00337124	0.11779056	3193	0.47459395
0.52002114	0.95431687	A	G		0.00592529	0.0033536	0.07725448	3193	0.479979
0.5013705	0.99732119	C	T		0.00657617	0.00325919	0.04361916	3193	0.49863
0.49939712	1.01003772	T	G		-0.00670693	0.00323948	0.03841743	3193	0.49939712
0.42033432	0.86356124	G	A		0.00622611	0.00359893	0.08363193	3193	0.42033432
0.48953696	0.97817916	A	G		-0.0071575	0.00341608	0.03614992	3193	0.48953696
0.35147087	0.74960305	C	T		0.00556292	0.0040051	0.16484488	3193	0.35147087
0.36293846	0.98399398	A	G		-0.00639755	0.00345063	0.06373542	3193	0.36293846
0.52303304	0.84457689	A	T		0.0074032	0.00361997	0.04084512	3193	0.476967
0.52451769	0.84425702	C	G		0.00735993	0.0036214	0.04211865	3193	0.475482
0.502443	0.87453154	T	A		0.00533974	0.00351843	0.1291033	3193	0.497557
0.4226746	0.91389175	C	T		0.00521765	0.00350143	0.13618504	3193	0.4226746
0.40220952	0.97376389	G	T		0.00520125	0.00342372	0.12871714	3193	0.40220952
0.43391575	0.92426587	G	A		0.00545496	0.00346878	0.11581415	3193	0.43391575
0.45653727	0.86946078	G	C		0.00643676	0.00356576	0.07104975	3193	0.45653727
0.39945412	0.88399562	T	A		0.00587369	0.00357222	0.10012097	3193	0.39945412
0.41525321	0.98792437	C	T		0.0053248	0.00336926	0.11401375	3193	0.41525321
0.40445803	0.90029984	A	G		0.00552049	0.00354139	0.11903271	3193	0.40445803
0.47357172	0.86093229	A	T		-0.0076699	0.00358862	0.03257474	3193	0.47357172
0.50445725	0.96349096	C	T		0.00636697	0.00331902	0.0550697	3193	0.495543
0.41612606	0.97776287	G	T		0.00546894	0.00338701	0.10638036	3193	0.41612606
0.49081992	0.79874005	A	C		0.00557985	0.0036674	0.12814182	3193	0.49081992
0.50287363	0.96630408	A	G		0.00638104	0.00331304	0.05409942	3193	0.497126
0.52554244	0.86140044	G	T		0.00767844	0.00358726	0.03231609	3193	0.474458

0.52554322	0.86139719	A	G	0.00767829	0.00358726	0.03231992	3193	0.474457
0.50023223	0.96879241	C	T	0.00647096	0.00330849	0.05048141	3193	0.499768
0.46146774	0.90708127	T	G	-0.00725322	0.00351486	0.03905719	3193	0.46146774
0.48435343	0.89305765	C	G	-0.00641169	0.00345436	0.06343714	3193	0.48435343
0.48516411	0.89443313	A	C	-0.00638951	0.00345079	0.06408182	3193	0.48516411
0.40386893	0.99322843	G	A	0.00573334	0.00340083	0.09182257	3193	0.40386893
0.38296821	0.8195557	G	C	-0.00611346	0.00374023	0.10215111	3193	0.38296821
0.53625744	0.90208384	C	T	0.00602395	0.00344272	0.08015857	3193	0.463743
0.4581508	0.90751773	G	T	-0.00590263	0.00343653	0.08586657	3193	0.4581508
0.51939211	0.90910282	A	G	0.00636452	0.00342129	0.06284728	3193	0.480608
0.51801676	0.9105468	A	G	0.00639234	0.00341783	0.06144295	3193	0.481983
0.35873974	0.82350797	A	T	-0.00629036	0.00378829	0.09681871	3193	0.35873974
0.40686988	0.95479807	C	T	0.00555421	0.00343211	0.10559598	3193	0.40686988
0.40867836	0.95718608	C	T	0.00564112	0.0034349	0.10052877	3193	0.40867836
0.34295161	0.7625445	T	C	-0.00667154	0.00404341	0.09894737	3193	0.34295161
0.11465878	1.02855338	G	T	-0.0089047	0.00510546	0.08113237	3193	0.11465878
0.42177889	0.9854606	G	A	0.00618952	0.00337143	0.06637631	3193	0.42177889
0.11589821	0.94777648	C	A	-0.00950566	0.00528459	0.07205815	3193	0.11589821
0.47202897	0.73894179	G	A	-0.00432705	0.00378431	0.25286432	3193	0.47202897
0.47203758	0.73891842	T	A	-0.00432702	0.00378434	0.25287169	3193	0.47203758
0.51234028	0.96262635	A	G	0.00591505	0.00339423	0.08139019	3193	0.48766
0.40722127	0.91984761	C	T	0.00551321	0.00350048	0.11525955	3193	0.40722127
0.17786439	0.72694677	A	G	-0.00636832	0.00525899	0.22591838	3193	0.17786439
0.34022675	0.74826656	C	T	-0.0068743	0.00408413	0.09234099	3193	0.34022675
0.50601049	0.87266629	T	A	0.0071088	0.00354895	0.04516951	3193	0.49399
0.11523505	0.93153156	C	A	-0.00955237	0.00534274	0.07378982	3193	0.11523505
0.47204995	0.73888869	G	C	-0.00432702	0.00378444	0.25288402	3193	0.47204995
0.47208988	0.73879111	C	G	-0.00432851	0.00378452	0.25273098	3193	0.47208988
0.41445944	0.90096971	C	T	0.00571738	0.00352198	0.10451569	3193	0.41445944
0.33333636	0.74162621	A	G	-0.00729095	0.00412523	0.07716027	3193	0.33333636
0.12394159	0.81307176	G	A	-0.0105103	0.00554024	0.05781687	3193	0.12394159
0.40734591	0.91841393	G	C	0.00552373	0.00350138	0.11466036	3193	0.40734591
0.43618212	0.98678838	G	A	-0.00997384	0.00335105	0.00291716	3193	0.43618212
0.42606389	0.98781614	G	A	-0.00957766	0.00335615	0.00432044	3193	0.42606389
0.50458801	0.93410068	G	A	0.00616011	0.00344202	0.07350556	3193	0.495412
0.48017444	0.99662926	A	G	-0.0052702	0.00335759	0.11649936	3193	0.48017444
0.50501206	0.95617204	T	C	0.00602889	0.00340763	0.07685549	3193	0.494988
0.50532524	0.88919568	G	C	0.00660862	0.00351643	0.06019612	3193	0.494675
0.49609756	1.00802829	A	G	-0.00505888	0.00332674	0.12834269	3193	0.49609756
0.28297714	0.76069416	T	C	-0.01211976	0.00424259	0.00428081	3193	0.28297714
0.50745803	0.90132606	A	G	0.00634113	0.00349897	0.06994204	3193	0.492542
0.39341325	0.97036766	T	A	0.00656648	0.00340892	0.05407159	3193	0.39341325
0.50413514	0.90046898	A	G	0.00611493	0.00350442	0.08099882	3193	0.495865
0.37948309	0.93475383	T	C	-0.00857897	0.00355796	0.01589985	3193	0.37948309
0.38823974	0.95621341	A	G	0.00667086	0.0034426	0.05265475	3193	0.38823974
0.39333182	0.9697676	G	A	0.00656451	0.00341011	0.05422789	3193	0.39333182
0.38758268	0.99392834	G	A	0.00641695	0.0033747	0.05723811	3193	0.38758268

0.39341967	0.97034506	G	C	0.00656557	0.00340895	0.05410666	3193	0.39341967
0.03742452	0.1798872	G	C	-0.01350262	0.02471886	0.58489552	3193	0.03742452
0.39230817	0.97415835	G	A	0.00655946	0.0034045	0.05401669	3193	0.39230817
0.36855105	0.65881478	C	G	0.00739739	0.0042007	0.07823982	3193	0.36855105
0.08911697	0.57027126	C	T	-0.01536755	0.00764962	0.04454455	3193	0.08911697
0.34480066	0.64922581	C	T	-0.00307645	0.00445638	0.48997656	3193	0.34480066

Rotterdam Study II

af_eplus	oevar_eplus	coded_eplus	noncoded_e		beta_eplus	se_eplus	p_eplus	n_eplus	maf_eplus
			plus						
0.465425	0.9828	G	A		-0.0145255	0.00469681	0.00200146	1642	0.465425
0.465443	0.9829	C	G		-0.0145092	0.00469633	0.00202275	1642	0.465443
0.583946	0.9933	C	G		0.0151418	0.00473399	0.0013959	1642	0.416054
0.583789	0.9933	A	G		0.0151214	0.00473386	0.00141641	1642	0.416211
0.482092	0.994	C	T		-0.01482	0.00463816	0.00141189	1642	0.482092
0.484354	0.9996	G	A		-0.0150682	0.00462101	0.00112386	1642	0.484354
0.483223	0.9961	G	A		-0.0149556	0.00463135	0.00125505	1642	0.483223
0.483833	0.9985	T	A		-0.0150147	0.00462604	0.00118493	1642	0.483833
0.483441	0.9989	C	T		-0.0149565	0.00462706	0.00124119	1642	0.483441
0.488976	0.9781	C	T		-0.0152647	0.00467531	0.00110763	1642	0.488976
0.488942	0.9779	C	A		-0.0152631	0.00467574	0.00111015	1642	0.488942
0.562711	0.9727	T	C		-0.00452235	0.00475321	0.34115745	1642	0.437289
0.358371	0.9563	A	G		-0.0167126	0.00499561	0.00083238	1642	0.358371
0.483405	0.9987	G	A		-0.0149551	0.00462743	0.00124368	1642	0.483405
0.483357	0.9985	G	A		-0.0149514	0.00462796	0.00124867	1642	0.483357
0.483321	0.9983	C	G		-0.0149502	0.00462836	0.00125111	1642	0.483321
0.475855	0.9559	C	A		-0.0149356	0.00474763	0.00167174	1642	0.475855
0.475823	0.953	A	T		-0.0149587	0.00475489	0.00167149	1642	0.475823
0.482878	0.9959	C	T		-0.0149226	0.00463349	0.0012932	1642	0.482878
0.482953	0.9963	C	T		-0.0149292	0.00463259	0.00128406	1642	0.482953
0.469639	0.983	G	A		-0.0134829	0.00469501	0.00410598	1642	0.469639
0.458942	0.9989	T	C		-0.0122774	0.00467777	0.00870369	1642	0.458942
0.458943	0.9991	T	G		-0.0122756	0.00467739	0.00870807	1642	0.458943
0.556484	0.9707	A	G		-0.00409128	0.0047576	0.38958305	1642	0.443516
0.530285	0.9929	G	A		0.00485961	0.0047631	0.30738464	1642	0.469715
0.653729	0.9999	T	C		-0.00665627	0.00485232	0.16999811	1642	0.346271
0.336983	0.9215	A	G		-0.0175588	0.00518962	0.00072583	1642	0.336983
0.455511	0.9723	T	A		-0.0118925	0.00475131	0.01234482	1642	0.455511
0.455473	0.9725	G	C		-0.0118913	0.0047507	0.01234259	1642	0.455473
0.47866	0.9857	A	T		-0.0148727	0.00466037	0.00143101	1642	0.47866
0.57066	0.9946	T	C		-0.00465588	0.00470929	0.32260774	1642	0.42934
0.568938	0.9986	T	G		-0.00451543	0.00469878	0.3363367	1642	0.431062
0.558149	0.9948	A	G		-0.00608508	0.00467028	0.19244106	1642	0.441851
0.530856	0.9599	C	G		-0.00537446	0.00473921	0.25658122	1642	0.469144
0.572089	0.9977	A	T		-0.00477581	0.00470359	0.30971986	1642	0.427911
0.556438	0.9993	T	C		-0.0059306	0.00465881	0.20285909	1642	0.443562
0.572059	0.9977	G	A		-0.00476572	0.00470365	0.31074657	1642	0.427941
0.450091	0.968	A	T		-0.0114994	0.0047719	0.01598912	1642	0.450091
0.459536	0.9859	T	C		-0.0125143	0.00470698	0.00787396	1642	0.459536
0.556497	0.9988	T	G		-0.00591184	0.00466016	0.20442294	1642	0.443503
0.471586	0.931	C	A		-0.0149792	0.00481525	0.00188288	1642	0.471586
0.459504	0.9865	G	A		-0.0125027	0.0047056	0.00791348	1642	0.459504
0.450315	0.9673	T	G		-0.0114986	0.00477362	0.01603456	1642	0.450315

0.450278	0.9674	G	A	-0.0114997	0.00477335	0.01601861	1642	0.450278
0.458972	0.9979	T	C	-0.0122962	0.00468025	0.00863719	1642	0.458972
0.450465	0.9667	T	G	-0.0114816	0.00477528	0.0162291	1642	0.450465
0.465009	0.9917	C	G	-0.0131286	0.00468252	0.00507696	1642	0.465009
0.464947	0.992	A	C	-0.0131195	0.00468221	0.00510461	1642	0.464947
0.571009	0.9978	A	G	-0.00423072	0.00471136	0.36896153	1642	0.428991
0.363925	0.9618	G	C	-0.014111	0.00498268	0.00465069	1642	0.363925
0.465145	0.9912	T	C	-0.0131493	0.00468318	0.00501437	1642	0.465145
0.465254	0.9908	G	T	-0.0131668	0.00468369	0.00496144	1642	0.465254
0.464897	0.9922	G	A	-0.0131114	0.00468196	0.00512963	1642	0.464897
0.464858	0.9923	G	A	-0.013106	0.00468177	0.00514606	1642	0.464858
0.351306	0.9533	A	T	-0.014129	0.00504732	0.00514723	1642	0.351306
0.556976	0.9967	T	C	-0.00598639	0.00466715	0.19944825	1642	0.443024
0.558446	0.9965	T	C	-0.00579713	0.00467405	0.21469969	1642	0.441554
0.369241	0.9994	T	C	0.00606699	0.00477462	0.20367981	1642	0.369241
0.872412	1	T	G	-0.00220322	0.00704311	0.75427654	1642	0.127588
0.545683	0.999	A	G	-0.00620274	0.00466538	0.1835257	1642	0.454317
0.872411	1	A	C	-0.0022026	0.0070431	0.75434293	1642	0.127589
0.459954	0.9132	G	A	-0.015191	0.00487398	0.00184532	1642	0.459954
0.459933	0.9118	T	A	-0.0152026	0.00487797	0.00184645	1642	0.459933
0.461189	0.9992	G	A	-0.0116514	0.00468266	0.01286864	1642	0.461189
0.558388	0.9898	T	C	-0.0055904	0.00469955	0.23403483	1642	0.441612
0.83711	0.9999	G	A	0.00311825	0.00626805	0.61864756	1642	0.16289
0.369112	0.9998	C	T	0.00598818	0.00477357	0.2095113	1642	0.369112
0.46493	0.9967	A	T	-0.0118836	0.00467944	0.01112989	1642	0.46493
0.87241	1	A	C	-0.00220252	0.00704308	0.75435155	1642	0.12759
0.459921	0.911	G	C	-0.0152138	0.00488016	0.00184084	1642	0.459921
0.45983	0.9043	C	G	-0.0152518	0.00489902	0.00186741	1642	0.45983
0.558332	0.9894	T	C	-0.00552529	0.00469984	0.23955342	1642	0.441668
0.368538	0.997	A	G	0.00593791	0.00478094	0.21406642	1642	0.368538
0.862253	0.9224	A	G	-0.00135591	0.00708063	0.84804708	1642	0.137747
0.558367	0.9897	C	G	-0.00556553	0.00469972	0.23613843	1642	0.441633
0.418647	0.9999	G	A	0.00404727	0.0048044	0.399323	1642	0.418647
0.419305	1	G	A	0.00415108	0.00480224	0.38713081	1642	0.419305
0.467556	0.9906	A	G	-0.01103	0.00470517	0.01909341	1642	0.467556
0.461122	0.9995	A	G	-0.0116321	0.00468196	0.01300507	1642	0.461122
0.464256	0.9946	C	T	-0.0115853	0.00468894	0.01351161	1642	0.464256
0.464661	0.9984	C	G	-0.0118743	0.00467568	0.01112838	1642	0.464661
0.4752	0.9962	A	G	-0.00977621	0.00467291	0.03643988	1642	0.4752
0.75216	0.9971	C	T	0.0138221	0.00523834	0.00835302	1642	0.24784
0.464589	0.9989	G	A	-0.0118709	0.00467452	0.0111312	1642	0.464589
0.416947	0.9971	T	A	0.00455732	0.00474609	0.3367152	1642	0.416947
0.463615	0.9791	G	A	-0.0120559	0.00472348	0.01073027	1642	0.463615
0.593284	0.9939	C	T	0.00897128	0.00475543	0.05920557	1642	0.406716
0.583497	0.9934	G	A	-0.00503299	0.00475273	0.28940226	1642	0.416503
0.417108	0.9962	G	A	0.00457507	0.00474759	0.3349895	1642	0.417108
0.416744	0.9981	G	A	0.00453523	0.00474416	0.33886542	1642	0.416744

0.416987	0.9968	G	C	0.00456153	0.00474646	0.33630586	1642	0.416987
0.967328	0.8988	C	G	0.0101079	0.0140318	0.47107084	1642	0.032672
0.416772	0.998	G	A	0.00453922	0.00474445	0.3384697	1642	0.416772
0.607156	0.8204	G	C	-0.00289013	0.00524028	0.58106319	1642	0.392844
0.892022	0.9696	T	C	-0.00376301	0.00768726	0.62427979	1642	0.107978
0.362713	0.8209	C	T	0.00105613	0.00537832	0.84422909	1642	0.362713

Family Heart Study

af_famhs	oevar_famhs	coded_famhs	ncoded_famhs	beta_famhs	se_famhs	p_famhs	n_famhs	maf_famhs
0.5144	0.9627	A	G	0.006716	0.004168	0.10736016	1736	0.4856
0.4856	0.9632	C	G	-0.0067	0.004168	0.10820111	1736	0.4856
0.5798	0.9946	C	G	0.007404	0.004133	0.07347037	1736	0.4202
0.5798	0.995	A	G	0.007415	0.004132	0.07296254	1736	0.4202
0.5244	0.9897	C	T	-0.00803	0.004109	0.05101198	1736	0.4756
0.4708	0.9992	A	G	0.00798	0.004099	0.05178223	1736	0.4708
0.4737	0.9914	A	G	0.008021	0.004108	0.05112133	1736	0.4737
0.4733	0.9967	A	T	0.007914	0.004095	0.05351406	1736	0.4733
0.526	0.9988	C	T	-0.00788	0.004089	0.05422653	1736	0.474
0.5357	0.9625	C	T	-0.00779	0.004193	0.06338047	1736	0.4643
0.4643	0.9622	A	C	0.007795	0.004194	0.06328012	1736	0.4643
0.4399	0.9899	C	T	0.01009	0.004136	0.01485334	1736	0.4399
0.3523	0.995	A	G	-0.0096	0.004234	0.02349133	1736	0.3523
0.4741	0.9983	A	G	0.007884	0.00409	0.05411029	1736	0.4741
0.4741	0.9978	A	G	0.007887	0.004091	0.05408672	1736	0.4741
0.5258	0.9976	C	G	-0.00789	0.004091	0.05404816	1736	0.4742
0.4837	0.9652	A	C	0.007377	0.004152	0.07581954	1736	0.4837
0.5163	0.964	A	T	-0.00739	0.004154	0.07564577	1736	0.4837
0.5246	0.9909	C	T	-0.00795	0.004105	0.0529997	1736	0.4754
0.5248	0.9921	C	T	-0.00794	0.004103	0.05314592	1736	0.4752
0.4945	0.9742	A	G	0.007049	0.004121	0.08742494	1736	0.4945
0.5177	0.9978	C	T	0.005345	0.004087	0.1911306	1736	0.4823
0.5173	0.9977	G	T	0.005314	0.004088	0.19383488	1736	0.4827
0.5545	0.9907	A	G	-0.01018	0.004153	0.01431974	1736	0.4455
0.4909	0.996	A	G	-0.00367	0.004133	0.37461227	1736	0.4909
0.3295	0.9994	C	T	0.000352	0.004169	0.93264816	1736	0.3295
0.3462	0.9975	A	G	-0.01048	0.004258	0.01394803	1736	0.3462
0.5521	0.9923	A	T	0.007497	0.004136	0.07009121	1736	0.4479
0.5521	0.9926	C	G	0.00749	0.004135	0.07032631	1736	0.4479
0.518	0.9771	A	T	-0.00805	0.004133	0.05173598	1736	0.482
0.4184	0.9983	C	T	0.008942	0.004093	0.02908529	1736	0.4184
0.4183	0.9988	G	T	0.008923	0.004092	0.02942418	1736	0.4183
0.5708	0.999	A	G	-0.00814	0.004106	0.04779036	1736	0.4292
0.5346	0.9795	C	G	-0.00896	0.004158	0.03128112	1736	0.4654
0.5818	0.9968	A	T	-0.00917	0.004108	0.02581541	1736	0.4182
0.4292	0.9996	C	T	0.008114	0.004106	0.04836752	1736	0.4292
0.4182	0.9972	A	G	0.009152	0.004107	0.02605562	1736	0.4182
0.4439	0.9912	A	T	-0.00767	0.004166	0.06591506	1736	0.4439
0.5045	0.9947	C	T	0.006845	0.004088	0.09430636	1736	0.4955
0.429	0.9987	G	T	0.008179	0.004111	0.0468475	1736	0.429
0.4912	0.9207	A	C	0.00777	0.004257	0.06818866	1736	0.4912
0.5036	0.9937	A	G	0.007157	0.004084	0.07996042	1736	0.4964
0.5561	0.9931	G	T	0.007499	0.004157	0.07150495	1736	0.4439
0.5562	0.9935	A	G	0.007481	0.004157	0.07219413	1736	0.4438

0.5183	0.9988	C	T	0.005405	0.004084	0.18598291	1736	0.4817
0.5559	0.9919	G	T	0.007591	0.004156	0.06802409	1736	0.4441
0.4967	0.9937	C	G	-0.00693	0.004083	0.08969196	1736	0.4967
0.4966	0.9941	A	C	-0.00693	0.004082	0.08974031	1736	0.4966
0.5834	0.9968	A	G	-0.00868	0.004094	0.03411268	1736	0.4166
0.6441	0.9949	C	G	0.01053	0.004256	0.01344365	1736	0.3559
0.5031	0.9923	C	T	0.006938	0.004085	0.08968342	1736	0.4969
0.497	0.992	G	T	-0.00694	0.004086	0.08966676	1736	0.497
0.5035	0.9944	A	G	0.006928	0.004081	0.08985034	1736	0.4965
0.5036	0.995	A	G	0.006926	0.00408	0.08984471	1736	0.4964
0.3504	0.9739	A	T	-0.01078	0.004311	0.01255035	1736	0.3504
0.428	0.9925	C	T	0.008047	0.004121	0.05106787	1736	0.428
0.4278	0.995	C	T	0.007852	0.004106	0.05603583	1736	0.4278
0.6097	0.9989	C	T	0.003148	0.004133	0.4462965	1736	0.3903
0.1268	1	G	T	-0.00717	0.006042	0.23524773	1736	0.1268
0.5629	0.9986	A	G	-0.00814	0.004115	0.04819188	1736	0.4371
0.8732	1	A	C	0.007175	0.006042	0.23524773	1736	0.1268
0.497	0.9359	A	G	0.007969	0.004209	0.05856344	1736	0.497
0.4971	0.9334	A	T	0.007998	0.004215	0.05802156	1736	0.4971
0.5344	0.9983	A	G	0.00575	0.004102	0.16123042	1736	0.4656
0.4313	0.9894	C	T	0.007726	0.004104	0.05997402	1736	0.4313
0.1673	0.9998	A	G	-0.00743	0.005495	0.17655057	1736	0.1673
0.3906	0.9992	C	T	-0.00314	0.004131	0.44696475	1736	0.3906
0.4702	0.9948	A	T	-0.00665	0.004103	0.10553328	1736	0.4702
0.8732	1	A	C	0.007175	0.006042	0.23526788	1736	0.1268
0.4981	0.9173	C	G	0.008188	0.004254	0.05447115	1736	0.4981
0.5011	0.905	C	G	-0.00834	0.004284	0.05178666	1736	0.4989
0.4319	0.9887	C	T	0.007678	0.004103	0.06154363	1736	0.4319
0.387	0.9955	A	G	-0.00257	0.004152	0.53600811	1736	0.387
0.8627	0.924	A	G	0.004546	0.006058	0.45314912	1736	0.1373
0.5683	0.9897	C	G	-0.00771	0.004102	0.06047336	1736	0.4317
0.5808	0.9997	A	G	0.004295	0.004122	0.29764094	1736	0.4192
0.5801	0.9997	A	G	0.004789	0.004119	0.24517144	1736	0.4199
0.4725	0.9907	A	G	-0.00676	0.004104	0.09992396	1736	0.4725
0.4657	0.9978	A	G	-0.00581	0.004105	0.15745608	1736	0.4657
0.475	0.9918	C	T	-0.00632	0.004098	0.12358667	1736	0.475
0.469	0.9974	C	G	-0.00653	0.004105	0.11185839	1736	0.469
0.4828	0.995	A	G	-0.00616	0.00406	0.1296977	1736	0.4828
0.7455	0.9996	C	T	0.007147	0.004684	0.12732665	1736	0.2545
0.5315	0.9994	A	G	0.00647	0.004105	0.11518703	1736	0.4685
0.5957	0.9954	A	T	-0.00671	0.004155	0.10672656	1736	0.4043
0.5302	0.9833	A	G	0.006446	0.004118	0.1177556	1736	0.4698
0.6026	0.9949	C	T	-0.00425	0.004146	0.30546344	1736	0.3974
0.4029	0.9923	A	G	0.006771	0.004169	0.10456591	1736	0.4029
0.5957	0.9946	A	G	-0.00669	0.004157	0.10767824	1736	0.4043
0.5999	0.9993	A	G	-0.0076	0.004158	0.06785587	1736	0.4001
0.5957	0.9953	C	G	-0.0067	0.004155	0.10688339	1736	0.4043

0.9647	0.9462	C	G	0.01668	0.01195	0.16286949	1736	0.0353
0.5958	0.9954	A	G	-0.00673	0.004155	0.10573157	1736	0.4042
0.4037	0.8171	C	G	0.005112	0.005397	0.34377563	1736	0.4037
0.1023	0.9672	C	T	-0.00649	0.006674	0.33064496	1736	0.1023
0.3678	0.924	C	T	-0.00429	0.004218	0.30901759	1736	0.3678

Framingham Heart Study

af_framhs2	oevar_framhs2	coded_framhs2	noncoded_framhs2	beta_framhs2	se_framhs2	p_framhs2	n_framhs2	af_genoa
0.466703	0.997683	A	G	0.004905069	0.002858255	0.0861426	3549	0.4863
0.466639	0.998217	G	C	0.004897496	0.002857536	0.08654938	3549	0.4873
0.455599	0.920944	G	C	-0.003855664	0.002989724	0.19717613	3549	0.5697
0.455712	0.920072	G	A	-0.003835981	0.002990884	0.19964704	3549	0.5698
0.449397	0.958738	T	C	0.004396344	0.002918468	0.13196766	3549	0.5107
0.4495	0.958574	A	G	0.004404341	0.00291861	0.13128484	3549	0.5105
0.449449	0.95865	A	G	0.004400584	0.002918543	0.13160533	3549	0.5107
0.449534	0.958527	A	T	0.004407311	0.002918645	0.13102973	3549	0.5104
0.449656	0.958372	T	C	0.004415748	0.00291875	0.13030751	3549	0.5102
0.448106	0.95202	T	C	0.004483664	0.002929153	0.12584272	3549	0.5121
0.448141	0.952006	A	C	0.004486314	0.002929145	0.12561813	3549	0.512
0.411342	0.998398	C	T	0.005979733	0.0029383	0.04184087	3549	0.5532
0.377222	0.993649	A	G	-0.002344397	0.002978229	0.43117752	3549	0.3681
0.449708	0.958314	A	G	0.004419984	0.002918792	0.12994473	3549	0.5101
0.449828	0.958199	A	G	0.00442874	0.002918843	0.12919274	3549	0.51
0.44988	0.958149	G	C	0.004432532	0.002918868	0.12886845	3549	0.5099
0.4535	0.977938	A	C	0.004029132	0.002895102	0.16401125	3549	0.5067
0.453431	0.978199	T	A	0.00402496	0.002894803	0.16440466	3549	0.5069
0.450361	0.957942	T	C	0.004465039	0.00291874	0.12607042	3549	0.5091
0.450241	0.957956	T	C	0.004456452	0.002918827	0.12681181	3549	0.5093
0.46108	0.981933	A	G	0.004518751	0.002886832	0.11751317	3549	0.4986
0.470976	0.991977	C	T	0.003865274	0.002866203	0.17747534	3549	0.4829
0.471348	0.988808	G	T	0.003902746	0.002870874	0.17401106	3549	0.4825
0.415136	0.999605	G	A	0.005870188	0.002929993	0.0451256	3549	0.5497
0.450191	0.069315	A	G	-0.012246108	0.010964361	0.26403654	3549	0.5258
0.333296	0.963527	C	T	0.010622616	0.003105571	0.00062505	3549	0.6339
0.35709	0.938903	A	G	-0.003034314	0.003097915	0.32734796	3549	0.3565
0.530102	1.00501	A	T	0.003550696	0.002892502	0.21961519	3549	0.4469
0.530113	1.005015	C	G	0.003551996	0.002892446	0.21943748	3549	0.447
0.466229	0.970623	T	A	0.003828443	0.002894915	0.18601111	3549	0.5014
0.388888	0.998091	C	T	0.00690759	0.002963121	0.01974348	3549	0.5654
0.389781	0.992495	G	T	0.006906015	0.002971304	0.02011277	3549	0.5642
0.39697	1.003092	G	A	0.00706545	0.002953205	0.01673547	3549	0.5577
0.436893	0.972533	G	C	0.006670763	0.002967709	0.0245901	3549	0.5382
0.387628	0.999586	T	A	0.006645419	0.002960919	0.02480816	3549	0.5659
0.398066	0.997607	C	T	0.006966644	0.00295976	0.01858326	3549	0.5575
0.387718	0.999754	A	G	0.006686441	0.002960233	0.02389862	3549	0.566
0.533653	1.004195	T	A	0.003438015	0.002893469	0.2347553	3549	0.4432
0.522836	0.994388	T	C	-0.003628264	0.002866581	0.20561648	3549	0.4898
0.392538	0.963575	G	T	0.00689074	0.003025975	0.02277449	3549	0.5674
0.468581	0.994921	A	C	0.003374079	0.002866863	0.23922597	3549	0.5001
0.528497	0.977801	G	A	-0.003882686	0.002887983	0.17880996	3549	0.4895
0.534252	0.999805	G	T	0.003515687	0.002901158	0.22558053	3549	0.4432
0.465827	1.000331	G	A	-0.003505773	0.002900221	0.22674154	3549	0.4432
0.471174	0.985317	C	T	0.003863648	0.002876423	0.17920309	3549	0.4865
0.464681	0.996104	T	G	-0.003615923	0.002906528	0.21347392	3549	0.4431
0.477462	0.995308	G	C	0.00390356	0.002864428	0.17295464	3549	0.491
0.477488	0.995764	C	A	0.003902902	0.002863872	0.17294367	3549	0.491
0.396824	0.984211	G	A	0.006277096	0.002979029	0.03510938	3549	0.5632
0.381607	0.987415	G	C	-0.002507419	0.002980842	0.40024826	3549	0.3724

0.522677	0.993528	T	C	-0.003904727	0.002866637	0.1731574	3549	0.4909
0.477272	0.993152	T	G	0.003903843	0.002867085	0.17332199	3549	0.4908
0.522461	0.996781	G	A	-0.003901233	0.002862587	0.17293461	3549	0.491
0.522339	0.996895	G	A	-0.003888573	0.00286269	0.17434844	3549	0.491
0.366731	0.978936	A	T	-0.002900952	0.003021388	0.33698541	3549	0.3682
0.392023	0.959906	C	T	0.006419964	0.003029127	0.03405578	3549	0.5672
0.402068	0.989816	C	T	0.006120332	0.002965435	0.0390281	3549	0.5569
0.36449	0.9292	T	C	-0.011029536	0.003062245	0.00031604	3549	0.3423
0.123755	0.863486	G	T	-0.003003164	0.004597228	0.51359159	3549	0.8529
0.405376	0.984303	G	A	0.007507584	0.002966938	0.01139278	3549	0.5534
0.123838	0.861833	C	A	-0.003014529	0.004600135	0.51226612	3549	0.8518
0.509436	0.983425	G	A	-0.00374517	0.002876468	0.1929154	3549	0.4876
0.509488	0.983702	T	A	-0.003741171	0.002876137	0.1933398	3549	0.4877
0.507096	0.997761	A	G	0.004436798	0.002882515	0.12375292	3549	0.4626
0.400548	1.002592	C	T	0.005783124	0.002945232	0.04958177	3549	0.5567
0.176637	0.997971	A	G	-0.004928936	0.003771491	0.19124899	3549	0.8327
0.364267	0.93116	C	T	-0.010928015	0.003058832	0.00035344	3549	0.3423
0.506264	1.001894	T	A	0.003968222	0.002874868	0.1674898	3549	0.4595
0.124512	0.850915	C	A	-0.003096821	0.004617825	0.50246056	3549	0.851
0.509521	0.983883	G	C	-0.003739164	0.002875919	0.19354499	3549	0.488
0.50953	0.985255	C	G	-0.003707415	0.002874341	0.19710919	3549	0.489
0.401086	1.004736	C	T	0.005723606	0.00294179	0.05170034	3549	0.5553
0.362017	0.921125	A	G	-0.010980243	0.003082647	0.00036811	3549	0.3423
0.135212	0.780571	G	A	-0.00338876	0.004652765	0.46641004	3549	0.841
0.400821	1.003897	G	C	0.00574951	0.002943177	0.05075987	3549	0.5558
0.418933	1.013299	G	A	-0.007354205	0.002870295	0.01040182	3549	0.4057
0.424478	1.015437	G	A	-0.007615966	0.002857745	0.00769824	3549	0.4022
0.50123	0.991152	G	A	0.004433182	0.002886716	0.12460745	3549	0.4632
0.497866	0.966175	G	A	0.004490948	0.002929679	0.12529689	3549	0.4725
0.502147	0.988425	T	C	0.004281555	0.002891187	0.13863358	3549	0.4623
0.506432	1.002265	G	C	0.004058601	0.002874317	0.15794332	3549	0.4598
0.485519	0.949425	G	A	0.004534653	0.002947117	0.12388379	3549	0.4687
0.245306	0.839369	T	C	-0.007918995	0.003620226	0.02871107	3549	0.7656
0.506479	1.002479	A	G	0.004082759	0.002873837	0.15541427	3549	0.46
0.365328	0.985371	T	A	0.006877507	0.003026207	0.02304735	3549	0.4071
0.498552	0.998731	A	G	0.004147073	0.002873766	0.14899804	3549	0.463
0.387225	0.910888	T	C	-0.00672056	0.003085659	0.02940614	3549	0.6044
0.364518	0.982477	A	G	0.00691069	0.003032621	0.02267988	3549	0.5937
0.36538	0.985834	G	A	0.006895828	0.003025464	0.02265143	3549	0.4067
0.365277	0.984626	G	A	0.006858445	0.003027312	0.02348061	3549	0.4069
0.365336	0.985507	G	C	0.0068811	0.003025989	0.02296596	3549	0.407
0.036004	0.773943	G	C	-0.025800581	0.008900193	0.00374499	3549	0.9694
0.365291	0.984796	G	A	0.006862013	0.003027082	0.02339792	3549	0.407
0.41123	0.985633	C	G	0.005723602	0.002948515	0.05223628	3549	0.6042
0.110229	0.888246	C	T	-0.000303995	0.004782559	0.94931804	3549	0.8794
0.363676	1.02407	C	T	-0.009152632	0.002933134	0.00180589	3549	0.3252

GENOA

af_genoa	oevar_genoa	coded_genoa	noncoded_genoa	beta_genoa	se_genoa	p_genoa	n_genoa	maf_genoa
0.4863	0.981759369	G	A	-0.009542862	0.00620261	0.1244874	991	0.4863
0.4873	0.988681355	C	G	-0.009479123	0.00618203	0.12575985	991	0.4873
0.5697	0.962113333	C	G	0.014537652	0.00622841	0.01994525	991	0.4303
0.5698	0.96250553	A	G	0.014560348	0.006226	0.01970631	991	0.4302
0.5107	0.99662403	C	T	-0.006133881	0.00613526	0.31785224	991	0.4893
0.5105	0.996349189	G	A	-0.006180971	0.00613673	0.31427044	991	0.4895
0.5107	0.996534959	G	A	-0.006149726	0.00613575	0.31664349	991	0.4893
0.5104	0.996278236	T	A	-0.006196835	0.00613717	0.31306644	991	0.4896
0.5102	0.996129369	C	T	-0.006232963	0.00613809	0.31032868	991	0.4898
0.5121	0.987623696	C	T	-0.006291712	0.00616262	0.30772145	991	0.4879
0.512	0.987654045	C	A	-0.006309808	0.00616283	0.30635018	991	0.488
0.5532	0.974664823	T	C	-0.006851864	0.00609122	0.26112534	991	0.4468
0.3681	0.950141706	A	G	-0.007129499	0.0063466	0.26176862	991	0.3681
0.5101	0.99609431	G	A	-0.006254734	0.00613846	0.30867201	991	0.4899
0.51	0.996043672	G	A	-0.006272175	0.00613888	0.30735913	991	0.49
0.5099	0.995997014	C	G	-0.006302068	0.00613946	0.30510729	991	0.4901
0.5067	1.0178619	C	A	-0.006657216	0.00607013	0.27323822	991	0.4933
0.5069	1.018193158	A	T	-0.006628104	0.00606885	0.27523769	991	0.4931
0.5091	0.996142806	C	T	-0.006452383	0.00614125	0.2938682	991	0.4909
0.5093	0.99602494	C	T	-0.006411272	0.00614095	0.29692854	991	0.4907
0.4986	1.030161383	G	A	-0.007929684	0.00605621	0.19095541	991	0.4986
0.4829	1.049148243	T	C	-0.008922056	0.00600216	0.13771847	991	0.4829
0.4825	1.04063442	T	G	-0.008996756	0.00602774	0.13611778	991	0.4825
0.5497	0.978463748	A	G	-0.006064883	0.00610303	0.32077589	991	0.4503
0.5258	0.583574908	G	A	0.008970029	0.00786643	0.25465386	991	0.4742
0.6339	0.98487417	T	C	-0.007876609	0.00636312	0.21629126	991	0.3661
0.3565	0.876746955	A	G	-0.006389075	0.00664383	0.33663935	991	0.3565
0.4469	0.963379076	T	A	-0.010233476	0.00607905	0.09285692	991	0.4469
0.447	0.963172909	G	C	-0.01024111	0.00607938	0.09263186	991	0.447
0.5014	1.020953815	A	T	-0.005599969	0.00606525	0.35625663	991	0.4986
0.5654	0.976530355	T	C	-0.007462287	0.00614478	0.2251048	991	0.4346
0.5642	0.979150639	T	G	-0.0072361	0.00613899	0.2390153	991	0.4358
0.5577	0.983301954	A	G	-0.00726093	0.00610515	0.23482281	991	0.4423
0.5382	0.959663973	C	G	-0.005742609	0.00614494	0.35043668	991	0.4618
0.5659	0.973909284	A	T	-0.007096312	0.00615266	0.24925123	991	0.4341
0.5575	0.982561719	T	C	-0.007232353	0.0061062	0.23674809	991	0.4425
0.566	0.973584247	G	A	-0.007132041	0.00615352	0.24694454	991	0.434
0.4432	0.963633804	A	T	-0.009275117	0.00610872	0.12949502	991	0.4432
0.4898	1.045988631	T	C	-0.007627454	0.0060044	0.20450305	991	0.4898
0.5674	0.950094544	T	G	-0.00807885	0.00620773	0.19365247	991	0.4326
0.5001	1.047122821	C	A	-0.005604953	0.00598261	0.34922829	991	0.4999
0.4895	1.040880369	G	A	-0.007725695	0.00601887	0.19982172	991	0.4895
0.4432	0.962886013	T	G	-0.009267582	0.00611122	0.12996289	991	0.4432
0.4432	0.963125879	G	A	-0.009270137	0.00611045	0.12980895	991	0.4432

0.4865	1.01637299	T	C	-0.008488613	0.00609124	0.1639999	991	0.4865
0.4431	0.960419465	T	G	-0.009237497	0.00611931	0.13172025	991	0.4431
0.491	1.056149526	C	G	-0.00731755	0.00598023	0.22161068	991	0.491
0.491	1.056392444	A	C	-0.007356491	0.00597902	0.21907187	991	0.491
0.5632	0.977157879	A	G	-0.007179545	0.00614014	0.24278992	991	0.4368
0.3724	0.961815082	G	C	-0.006855629	0.00628504	0.27583845	991	0.3724
0.4909	1.055566173	T	C	-0.007185697	0.00598329	0.23027618	991	0.4909
0.4908	1.055503224	G	T	-0.007161357	0.0059837	0.23188888	991	0.4908
0.491	1.056796941	G	A	-0.007416123	0.00597699	0.21520848	991	0.491
0.491	1.056796941	G	A	-0.007416123	0.00597699	0.21520848	991	0.491
0.3682	0.950345456	A	T	-0.006826133	0.00634301	0.28231796	991	0.3682
0.5672	0.949697511	T	C	-0.008055007	0.00620784	0.19497665	991	0.4328
0.5569	0.981589653	T	C	-0.007173985	0.00610623	0.24055034	991	0.4431
0.3423	0.95902294	T	C	-0.014702838	0.00646229	0.02327397	991	0.3423
0.8529	0.971694588	T	G	0.014964336	0.00886	0.09178257	991	0.1471
0.5534	0.957846425	A	G	-0.006094871	0.00619895	0.32593029	991	0.4466
0.8518	0.974176825	A	C	0.015172137	0.00881689	0.08584066	991	0.1482
0.4876	1.027478264	G	A	-0.008677053	0.00604169	0.15150659	991	0.4876
0.4877	1.027900793	T	A	-0.008648809	0.00604012	0.15273434	991	0.4877
0.4626	0.959211536	G	A	-0.010369677	0.00615149	0.0924094	991	0.4626
0.5567	0.981336985	T	C	-0.008229459	0.00610022	0.17787001	991	0.4433
0.8327	0.989721001	G	A	0.010040433	0.00807887	0.21446267	991	0.1673
0.3423	0.959213314	C	T	-0.014682644	0.00646177	0.02345212	991	0.3423
0.4595	0.961611957	A	T	-0.010451854	0.00611791	0.08811778	991	0.4595
0.851	0.977679412	A	C	0.015294845	0.00877848	0.08200498	991	0.149
0.488	1.028801707	G	C	-0.008588507	0.0060368	0.15538445	991	0.488
0.489	1.026798416	C	G	-0.009039627	0.00604214	0.13519386	991	0.489
0.5553	0.985024179	T	C	-0.008349062	0.00608664	0.17070702	991	0.4447
0.3423	0.959121894	A	G	-0.014745881	0.00646193	0.02286718	991	0.3423
0.841	0.918961991	A	G	0.015350795	0.0088113	0.08202943	991	0.159
0.5558	0.98508204	C	G	-0.008311062	0.00608691	0.17267755	991	0.4442
0.4057	1.035723921	G	A	-0.009042601	0.00615409	0.14229765	991	0.4057
0.4022	1.023301062	G	A	-0.008499748	0.00618823	0.17013814	991	0.4022
0.4632	0.956379819	A	G	-0.012002819	0.00613147	0.05077766	991	0.4632
0.4725	0.925190212	A	G	-0.011302016	0.00624673	0.07094726	991	0.4725
0.4623	0.955114774	C	T	-0.010340861	0.00615975	0.09375481	991	0.4623
0.4598	0.96043873	C	G	-0.010515078	0.00612	0.08632377	991	0.4598
0.4687	0.944465156	A	G	-0.014489293	0.00618557	0.01950885	991	0.4687
0.7656	0.868435534	C	T	0.010311953	0.00764507	0.17793658	991	0.2344
0.46	0.960358743	G	A	-0.010531966	0.00611985	0.08581384	991	0.46
0.4071	1.014870036	T	A	0.009577611	0.00615081	0.12000671	991	0.4071
0.463	0.958532439	G	A	-0.012013566	0.00612424	0.05030086	991	0.463
0.6044	1.031328457	C	T	0.010646792	0.00610245	0.08159215	991	0.3956
0.5937	1.01121449	G	A	-0.009466142	0.00615513	0.12463345	991	0.4063
0.4067	1.014959934	G	A	0.009508945	0.00615151	0.12272189	991	0.4067
0.4069	1.004238981	G	A	0.00968597	0.00618678	0.11801104	991	0.4069
0.407	1.014828139	G	C	0.009567811	0.00615164	0.12043516	991	0.407

0.9694	0.830894535	C	G	0.006508432	0.02048663	0.75083768	991	0.0306
0.407	1.011229147	G	A	0.009617301	0.00616318	0.11922163	991	0.407
0.6042	0.97072276	G	C	-0.007719134	0.00633031	0.22321013	991	0.3958
0.8794	0.946478265	T	C	0.014810571	0.0099366	0.13665607	991	0.1206
0.3252	0.896550839	C	T	-0.017106249	0.00673357	0.01134115	991	0.3252

Gutenberg Heart Study

af_guten	oevar_guten	coded_guten	noncoded_guten	beta_guten	se_guten	p_guten	n_guten	maf_guten
0.483345	0.949711	G	A	-0.00329573	0.00299794	0.271174	2762	0.483345
0.51648	0.949714	G	C	0.00329188	0.00299809	0.272534	2761	0.48352
0.430841	0.976687	G	C	-0.00459936	0.00298117	0.123381	3022	0.430841
0.430818	0.976581	G	A	-0.00458917	0.00298141	0.123783	3021	0.430818
0.500166	0.982863	T	C	0.00267697	0.00295265	0.364234	3018	0.499834
0.499834	0.983022	G	A	-0.00268304	0.00295254	0.363996	3018	0.499834
0.499834	0.982964	G	A	-0.0026777	0.00295258	0.364758	3018	0.499834
0.499834	0.983015	T	A	-0.00268446	0.00295253	0.363792	3018	0.499834
0.500166	0.982901	T	C	0.00268318	0.00295252	0.363055	3018	0.499834
0.499336	0.980314	T	C	0.00264877	0.00295529	0.369483	3013	0.499336
0.500664	0.980435	C	A	-0.00265082	0.00295527	0.370689	3013	0.499336
0.557395	0.998143	T	C	-0.00802581	0.00296013	0.00669655	3110	0.442605
0.636231	0.99057	G	A	0.0058553	0.00302364	0.0526642	3083	0.363769
0.499834	0.983019	G	A	-0.00268318	0.00295252	0.363922	3019	0.499834
0.499834	0.983036	G	A	-0.00268261	0.00295252	0.363839	3019	0.499834
0.500166	0.982901	G	C	0.00268261	0.00295252	0.363278	3019	0.499834
0.498534	0.992505	C	A	-0.00186827	0.00293835	0.524794	3069	0.498534
0.501466	0.992506	T	A	0.00186905	0.00293835	0.524982	3069	0.498534
0.500331	0.983102	T	C	0.00268665	0.00295221	0.362741	3020	0.499669
0.500166	0.982999	T	C	0.00268471	0.00295234	0.362747	3019	0.499834
0.496622	1	G	A	-0.002708	0.00293237	0.355755	3108	0.496622
0.478059	1	T	C	-0.00343934	0.00291202	0.237569	3122	0.478059
0.478106	0.97612	T	G	-0.002645	0.00294918	0.369473	2946	0.478106
0.44811	1	G	A	0.00699285	0.00296009	0.018158	3122	0.44811
0.512484	1	G	A	0.0110502	0.00302661	0.00026121	3084	0.487516
0.660289	0.996976	T	C	-0.00467105	0.00304432	0.124854	3110	0.339711
0.653435	0.926743	G	A	0.00432443	0.00317245	0.173581	2809	0.346565
0.450322	0.998302	T	A	-0.00769645	0.00292851	0.00858382	3110	0.450322
0.450322	0.998261	G	C	-0.00769546	0.00292861	0.00859451	3110	0.450322
0.509622	0.988908	T	A	0.00170317	0.00293707	0.561746	3066	0.490378
0.582745	1	T	C	-0.00688951	0.00298734	0.0210974	3118	0.417255
0.582663	0.997193	T	G	-0.00670866	0.00298332	0.0246039	3109	0.417337
0.42729	1	G	A	0.00658816	0.00296662	0.0263669	3122	0.42729
0.45664	0.968127	G	C	0.00697903	0.00298637	0.0197514	2952	0.45664
0.41664	0.99853	T	A	0.00680192	0.0029843	0.022653	3113	0.41664
0.572283	0.995896	T	C	-0.00672701	0.00296861	0.0234498	3092	0.427717
0.582906	0.999128	G	A	-0.00674789	0.00298322	0.0237006	3118	0.417094
0.554397	1	T	A	0.00671661	0.00294305	0.022478	3116	0.445603
0.480942	1	T	C	-0.00171138	0.00292488	0.558473	3122	0.480942
0.587599	0.962627	T	G	-0.00669981	0.00302306	0.026794	2911	0.412401
0.490391	1	C	A	-0.000635501	0.00291898	0.827653	3122	0.490391
0.482532	0.998653	G	A	-0.00160637	0.00292667	0.583174	3120	0.482532
0.446371	0.99657	T	G	-0.00665433	0.00293954	0.0235341	3114	0.446371
0.446406	0.997359	G	A	-0.00664759	0.00293876	0.0236497	3116	0.446406

0.477642	0.978838	T	C	-0.00196066	0.0029538	0.506125	2952	0.477642
0.445458	0.989954	T	G	-0.00663538	0.00294615	0.0241749	3071	0.445458
0.517485	0.99943	G	C	0.00131875	0.00292429	0.652015	3117	0.482515
0.517485	0.99943	C	A	0.00131875	0.00292429	0.652015	3117	0.482515
0.418081	0.990776	G	A	0.00677482	0.00298567	0.0232138	3064	0.418081
0.366753	0.989062	G	C	-0.0046312	0.00303179	0.126668	3077	0.366753
0.482515	0.99943	T	C	-0.00131875	0.00292429	0.652015	3117	0.482515
0.517485	0.99943	T	G	0.00131875	0.00292429	0.652015	3117	0.482515
0.481897	1	G	A	-0.00120561	0.00292304	0.680011	3121	0.481897
0.482223	1	G	A	-0.00118099	0.00292624	0.686518	3122	0.482223
0.644485	0.968986	T	A	0.00492175	0.00308321	0.11128	2983	0.355515
0.588458	0.962169	T	C	-0.0068063	0.00302531	0.0244193	2911	0.411542
0.57294	0.991634	T	C	-0.00684931	0.00297136	0.0211454	3071	0.42706
0.361958	0.998717	T	C	-0.00671244	0.0030382	0.0271905	3115	0.361958
0.885336	0.95836	T	G	0.00877027	0.00457112	0.0554806	2987	0.114664
0.423968	0.964599	G	A	0.00556912	0.00301998	0.0655882	2979	0.423968
0.117667	0.96343	C	A	-0.00866668	0.00454746	0.0566928	3000	0.117667
0.468991	0.996595	G	A	0.00038263	0.00293302	0.895683	3112	0.468991
0.468991	0.996595	T	A	0.00038263	0.00293302	0.895683	3112	0.468991
0.477523	0.994981	G	A	-0.00605932	0.00293004	0.0386459	3092	0.477523
0.577224	0.993559	T	C	-0.00742349	0.00296329	0.0122567	3069	0.422776
0.827936	0.982831	G	A	0.00389456	0.00390793	0.318038	3057	0.172064
0.637981	0.999475	T	C	0.0062398	0.00303229	0.0395878	3120	0.362019
0.522742	1	T	A	0.00657705	0.00292853	0.0247134	3122	0.477258
0.12	0.972212	C	A	-0.00854873	0.00451141	0.0580966	3025	0.12
0.468991	0.996595	G	C	0.000382981	0.00293303	0.895682	3112	0.468991
0.53075	1	G	C	-0.000382205	0.0029264	0.896087	3122	0.46925
0.573335	0.996035	T	C	-0.00746659	0.00295836	0.0115838	3109	0.426665
0.639704	1	G	A	0.00604796	0.00304655	0.0471239	3103	0.360296
0.12205	0.905476	G	A	-0.00743565	0.00451165	0.0990507	2839	0.12205
0.42623	0.996824	G	C	0.00744467	0.00295831	0.0118476	3111	0.42623
0.426603	0.999603	G	A	-0.00631136	0.00298904	0.0346744	3120	0.426603
0.429311	0.99587	G	A	-0.00616046	0.0029905	0.0393977	3091	0.429311
0.517179	0.992104	G	A	0.00670428	0.00293252	0.0222467	3056	0.482821
0.508408	0.963538	G	A	0.00593915	0.00297256	0.0457891	2914	0.491592
0.52082	0.992095	T	C	0.00610614	0.00293599	0.0375036	3074	0.47918
0.523771	0.998566	G	C	0.00637252	0.0029296	0.029584	3113	0.476229
0.516522	1	G	A	0.00707238	0.0029359	0.0159993	3117	0.483478
0.226308	0.909396	T	C	-0.00664467	0.00363747	0.0679219	2733	0.226308
0.476076	0.999097	G	A	-0.00631491	0.00292907	0.0310881	3114	0.476076
0.408535	1	T	A	0.00521936	0.00297997	0.0798627	3105	0.408535
0.483643	1	G	A	-0.0068524	0.00292742	0.0192442	3118	0.483643
0.38291	1	T	C	-0.00886497	0.00303062	0.00344307	3113	0.38291
0.593992	0.991206	G	A	-0.005417	0.00297144	0.0681959	3096	0.406008
0.406611	0.998796	G	A	0.00537775	0.0029668	0.0698445	3116	0.406611
0.406581	0.998757	G	A	0.00536501	0.00296695	0.070522	3115	0.406581
0.406611	0.998878	G	C	0.00537177	0.00296672	0.0701244	3116	0.406611

0.0106275	0.77367	G	C	-0.0110879	0.0104711	0.289678	2964	0.0106275
0.406581	0.998855	G	A	0.0053661	0.00296679	0.0704378	3115	0.406581
0.554484	1	G	C	-0.006276	0.00296811	0.0344744	3111	0.445516
0.9040522	0.949436	T	C	0.0127457	0.00489628	0.00930972	2986	0.0959478
0.643177	1	T	C	0.00536654	0.00301971	0.0755404	3122	0.356823

Health ABC

af_habc	oevar_habc	coded_habc	noncoded_habc	beta_habc	se_habc	p_habc	n_habc	maf_habc
0.4988	0.9767	A	G	0.015465851	0.00549687	0.00496083	1564	0.4988
0.5012	0.9768	C	G	-0.01547994	0.00549609	0.00491559	1564	0.4988
0.5601	0.9991	C	G	0.009774864	0.00548397	0.07487148	1564	0.4399
0.5602	0.9994	A	G	0.009818172	0.00548369	0.07357843	1564	0.4398
0.533	0.9962	C	T	-0.01697609	0.00544527	0.00185669	1564	0.467
0.466	0.9996	A	G	0.016939701	0.00543384	0.00185758	1564	0.466
0.4662	0.9988	A	G	0.016948715	0.00543632	0.00185609	1564	0.4662
0.4695	0.9991	A	T	0.016604412	0.00546383	0.00241333	1564	0.4695
0.5303	0.9995	C	T	-0.01658508	0.00546355	0.00244043	1564	0.4697
0.5357	0.9746	C	T	-0.01685806	0.00553179	0.00234639	1564	0.4643
0.4644	0.9743	A	C	0.01686088	0.00553258	0.00234579	1564	0.4644
0.4264	0.9976	C	T	0.006355011	0.00558542	0.25538495	1564	0.4264
0.3721	0.9989	A	G	-0.0058316	0.00571457	0.30765963	1564	0.3721
0.4698	0.999	A	G	0.016590823	0.00546499	0.00243841	1564	0.4698
0.47	0.9981	A	G	0.016600372	0.00546722	0.00243431	1564	0.47
0.53	0.9978	C	G	-0.01660268	0.00546778	0.0024334	1564	0.47
0.4785	0.9362	A	C	0.018451751	0.0056218	0.00105285	1564	0.4785
0.5215	0.9349	A	T	-0.01846562	0.0056257	0.00105215	1564	0.4785
0.5282	0.9908	C	T	-0.0166787	0.00548646	0.00240536	1564	0.4718
0.5284	0.9917	C	T	-0.01667059	0.00548407	0.00240657	1564	0.4716
0.4912	0.9786	A	G	0.017779993	0.00552786	0.00132454	1564	0.4912
0.504	0.9986	C	T	0.016088001	0.00544253	0.0031636	1564	0.496
0.5036	0.9989	G	T	0.016123886	0.00543717	0.00306787	1564	0.4964
0.5702	0.9971	A	G	-0.00621093	0.005564	0.2644784	1564	0.4298
0.4816	0.9962	A	G	-0.00736396	0.00546745	0.17821637	1564	0.4816
0.3328	0.9994	C	T	-0.00025898	0.00574764	0.96406663	1564	0.3328
0.3644	0.9981	A	G	-0.00338128	0.00568453	0.55204841	1564	0.3644
0.5298	0.9985	A	T	0.001368799	0.00554038	0.80489519	1564	0.4702
0.5298	0.9986	C	G	0.001379691	0.00553983	0.80335544	1564	0.4702
0.5225	0.9787	A	T	-0.01719536	0.00552333	0.00188417	1564	0.4775
0.4057	0.9995	C	T	0.004349059	0.00562649	0.43966253	1564	0.4057
0.4061	0.9994	G	T	0.004379425	0.00561818	0.4357976	1564	0.4061
0.5873	0.999	A	G	-0.00465772	0.00561084	0.40659248	1564	0.4127
0.5488	0.9828	C	G	-0.00455818	0.00554506	0.41118787	1564	0.4512
0.5954	0.9992	A	T	-0.00408965	0.00562809	0.46755017	1564	0.4046
0.4131	0.9999	C	T	0.00469813	0.00559852	0.40150048	1564	0.4131
0.4047	0.9995	A	G	0.004127227	0.00562752	0.46342404	1564	0.4047
0.4667	0.9987	A	T	-0.00126797	0.00551297	0.81812329	1564	0.4667
0.5021	0.9997	C	T	0.018319584	0.00550432	0.00089438	1564	0.4979
0.4131	0.9994	G	T	0.004658327	0.00560054	0.4056693	1564	0.4131
0.4881	0.8547	A	C	0.019448709	0.00588251	0.00096722	1564	0.4881
0.5021	0.9997	A	G	0.018319689	0.0055043	0.00089429	1564	0.4979
0.5334	0.9991	G	T	0.001271287	0.00551064	0.81758051	1564	0.4666
0.5332	0.9995	A	G	0.001237227	0.00551092	0.82239422	1564	0.4668
0.5045	0.9994	C	T	0.016048518	0.00545225	0.00329355	1564	0.4955

0.5341	0.9988	G	T	0.001343881	0.00550653	0.80722238	1564	0.4659
0.5016	0.9968	C	G	-0.0177827	0.00548721	0.00121728	1564	0.4984
0.5014	0.9977	A	C	-0.01776596	0.00548527	0.00122539	1564	0.4986
0.5942	0.9993	A	G	-0.00406598	0.00562273	0.46970684	1564	0.4058
0.6243	0.9985	C	G	0.005692442	0.00566271	0.31493181	1564	0.3757
0.4981	0.9954	C	T	0.017805304	0.00549004	0.00120693	1564	0.4981
0.502	0.9951	G	T	-0.01781139	0.00549073	0.001204	1564	0.498
0.4987	0.998	A	G	0.017760653	0.00548457	0.00122775	1564	0.4987
0.4988	0.9987	A	G	0.017748423	0.00548305	0.00123345	1564	0.4988
0.3689	0.9768	A	T	-0.00418291	0.00574109	0.46636088	1564	0.3689
0.4125	0.9971	C	T	0.004447637	0.00561187	0.42816589	1564	0.4125
0.4125	0.9982	C	T	0.004296833	0.00560619	0.44352783	1564	0.4125
0.6462	0.9971	C	T	-0.00227996	0.00568769	0.68857953	1564	0.3538
0.1064	1	G	T	-0.00064761	0.00904172	0.94291019	1564	0.1064
0.5806	0.9988	A	G	-0.00217403	0.00554394	0.69500396	1564	0.4194
0.8936	1	A	C	0.000647606	0.00904172	0.94291019	1564	0.1064
0.4951	0.8731	A	G	0.018571337	0.0057988	0.00138933	1564	0.4951
0.4953	0.8708	A	T	0.018584613	0.00580626	0.00139812	1564	0.4953
0.5123	0.9985	A	G	-0.00045822	0.00551594	0.93380552	1564	0.4877
0.4206	0.9979	C	T	0.006419806	0.00559373	0.2512772	1564	0.4206
0.1724	0.9991	A	G	-0.01209966	0.00735067	0.0999524	1564	0.1724
0.3548	1	C	T	0.002045112	0.00567544	0.7186384	1564	0.3548
0.4921	0.9981	A	T	0.000943139	0.00551726	0.86429048	1564	0.4921
0.8936	1	A	C	0.000647606	0.00904172	0.94291019	1564	0.1064
0.4959	0.8624	C	G	0.018617195	0.00583402	0.00144531	1564	0.4959
0.5028	0.8452	C	G	-0.01868205	0.00589226	0.00155078	1564	0.4972
0.421	0.9952	C	T	0.006395927	0.00560141	0.25369461	1564	0.421
0.354	0.9949	A	G	0.002544244	0.00568641	0.65462992	1564	0.354
0.8802	0.8479	A	G	-0.00046643	0.00926907	0.95987256	1564	0.1198
0.5792	0.9969	C	G	-0.00640714	0.00559663	0.25245859	1564	0.4208
0.5778	0.9992	A	G	0.006406946	0.0055641	0.24971125	1564	0.4222
0.5772	0.9996	A	G	0.006481399	0.00556258	0.24412459	1564	0.4228
0.4896	0.9996	A	G	-0.00112176	0.00550232	0.83848215	1564	0.4896
0.4877	0.999	A	G	0.000522401	0.00551393	0.92453187	1564	0.4877
0.4885	0.9971	C	T	0.000828704	0.00551375	0.88054916	1564	0.4885
0.4919	0.9991	C	G	0.00086663	0.00551649	0.87518783	1564	0.4919
0.5016	0.9989	A	G	-0.00311985	0.00548572	0.56962624	1564	0.4984
0.7574	0.9994	C	T	0.008832601	0.0063791	0.16636786	1564	0.2426
0.5081	0.9994	A	G	-0.00084858	0.00551622	0.87776138	1564	0.4919
0.6065	0.9989	A	T	-0.00863443	0.00559895	0.12323954	1564	0.3935
0.5128	0.9913	A	G	0.000690864	0.00552981	0.90059148	1564	0.4872
0.601	1	C	T	0.006349893	0.00554872	0.25263816	1564	0.399
0.3931	0.9951	A	G	0.008522789	0.00561009	0.1289174	1564	0.3931
0.6065	0.9986	A	G	-0.00864219	0.00559982	0.12296125	1564	0.3935
0.6142	0.9999	A	G	-0.00783177	0.00561768	0.163477	1564	0.3858
0.6065	0.9988	C	G	-0.00863543	0.00559913	0.12320834	1564	0.3935
0.9708	0.9655	C	G	0.008154465	0.0162193	0.61520187	1564	0.0292

0.6068	0.9975	A	G	-0.0086085	0.00560383	0.12469691	1564	0.3932
0.3688	0.8623	C	G	0.006167875	0.00607977	0.31050556	1564	0.3688
0.0882	0.9543	C	T	-0.00093303	0.01003655	0.92594438	1564	0.0882
0.3622	0.9959	C	T	0.005511626	0.00567552	0.33163749	1564	0.3622

InCHIANTI

af_inch2	oevar_inch2	coded_inch2	noncoded_inch2	beta_inch2	se_inch2	p_inch2	n_inch2	maf_inch2
0.567	0.9546	G	A	-0.016	0.006	0.01698	1130	0.433
0.4328	0.9548	G	C	0.015	0.006	0.01712	1130	0.4328
0.4952	0.9929	G	C	-0.015	0.006	0.01778	1130	0.4952
0.4956	0.9928	G	A	-0.015	0.006	0.01782	1130	0.4956
0.4068	0.9887	T	C	0.018	0.006	0.005233	1130	0.4068
0.596	0.9989	G	A	-0.018	0.006	0.005359	1130	0.404
0.5949	0.9946	G	A	-0.018	0.006	0.005301	1130	0.4051
0.5944	0.9971	T	A	-0.018	0.006	0.005741	1130	0.4056
0.4062	0.9981	T	C	0.018	0.006	0.005941	1130	0.4062
0.4009	0.9745	T	C	0.017	0.006	0.007205	1130	0.4009
0.5988	0.9731	C	A	-0.017	0.006	0.007494	1130	0.4012
0.6446	0.9562	T	C	-0.015	0.007	0.02304	1130	0.3554
0.5701	0.9408	G	A	0.015	0.007	0.0265	1130	0.4299
0.5938	0.9976	G	A	-0.017	0.006	0.006015	1130	0.4062
0.5936	0.997	G	A	-0.017	0.006	0.006118	1130	0.4064
0.4065	0.996	G	C	0.017	0.006	0.006292	1130	0.4065
0.5826	0.8922	C	A	-0.019	0.007	0.005144	1130	0.4174
0.4174	0.8913	T	A	0.019	0.007	0.005175	1130	0.4174
0.4073	0.9921	T	C	0.017	0.006	0.007056	1130	0.4073
0.4072	0.9926	T	C	0.017	0.006	0.006941	1130	0.4072
0.5781	0.9684	G	A	-0.016	0.006	0.01276	1130	0.4219
0.5604	0.9961	T	C	-0.016	0.006	0.01413	1130	0.4396
0.5606	0.9965	T	G	-0.016	0.006	0.01367	1130	0.4394
0.3593	0.9532	G	A	0.015	0.007	0.02223	1130	0.3593
0.5316	0.7745	G	A	0.015	0.007	0.03414	1130	0.4684
0.7134	0.9995	T	C	-0.014	0.007	0.04043	1130	0.2866
0.5888	0.904	G	A	0.013	0.007	0.05321	1130	0.4112
0.5304	0.9481	T	A	-0.018	0.006	0.0056	1130	0.4696
0.5303	0.9482	G	C	-0.018	0.006	0.005605	1130	0.4697
0.4137	0.9759	T	A	0.017	0.006	0.009999	1130	0.4137
0.6614	0.9963	T	C	-0.013	0.007	0.04915	1130	0.3386
0.661	0.9977	T	G	-0.013	0.007	0.05017	1130	0.339
0.3459	0.9966	G	A	0.014	0.007	0.03221	1130	0.3459
0.375	0.9454	G	C	0.016	0.007	0.01423	1130	0.375
0.3379	0.9963	T	A	0.013	0.007	0.04918	1130	0.3379
0.6537	0.9985	T	C	-0.014	0.007	0.0329	1130	0.3463
0.6619	0.9969	G	A	-0.013	0.007	0.04872	1130	0.3381
0.471	0.9475	T	A	0.018	0.006	0.004408	1130	0.471
0.5693	0.9714	T	C	-0.015	0.006	0.0221	1130	0.4307
0.6537	0.9981	T	G	-0.014	0.007	0.03321	1130	0.3463
0.5702	0.8096	C	A	-0.018	0.007	0.008654	1130	0.4298
0.5693	0.9708	G	A	-0.015	0.006	0.02204	1130	0.4307
0.5293	0.9479	T	G	-0.018	0.006	0.004395	1130	0.4707
0.5292	0.9478	G	A	-0.018	0.006	0.004394	1130	0.4708

0.5602	0.9918	T	C	-0.015	0.006	0.01545	1130	0.4398
0.5312	0.9544	T	G	-0.018	0.006	0.004375	1130	0.4688
0.4295	0.9793	G	C	0.015	0.006	0.02252	1130	0.4295
0.4296	0.9797	C	A	0.015	0.006	0.02284	1130	0.4296
0.339	0.9968	G	A	0.013	0.007	0.05012	1130	0.339
0.4314	0.9452	G	C	-0.015	0.007	0.02052	1130	0.4314
0.5707	0.9786	T	C	-0.015	0.006	0.02169	1130	0.4293
0.4292	0.9784	T	G	0.015	0.006	0.02162	1130	0.4292
0.5703	0.9802	G	A	-0.014	0.006	0.02335	1130	0.4297
0.5702	0.9805	G	A	-0.014	0.006	0.02361	1130	0.4298
0.5771	0.9374	T	A	0.015	0.007	0.01842	1130	0.4229
0.6544	0.9951	T	C	-0.014	0.007	0.03085	1130	0.3456
0.6543	0.9955	T	C	-0.014	0.007	0.03047	1130	0.3457
0.3835	0.9986	T	C	-0.007	0.006	0.2986	1130	0.3835
0.8492	1	T	G	0.025	0.009	0.004779	1130	0.1508
0.3508	0.9995	G	A	0.012	0.007	0.06272	1130	0.3508
0.1508	1	C	A	-0.025	0.009	0.004778	1130	0.1508
0.5564	0.8414	G	A	-0.018	0.007	0.008343	1130	0.4436
0.5558	0.8355	T	A	-0.018	0.007	0.008414	1130	0.4442
0.5461	0.9844	G	A	-0.015	0.006	0.01446	1130	0.4539
0.6534	0.9745	T	C	-0.013	0.007	0.05715	1130	0.3466
0.7823	0.993	G	A	0.004	0.008	0.6397	1130	0.2177
0.6158	0.9994	T	C	0.007	0.006	0.3018	1130	0.3842
0.452	0.9824	T	A	0.016	0.006	0.01376	1130	0.452
0.1508	1	C	A	-0.025	0.009	0.004778	1130	0.1508
0.5553	0.8302	G	C	-0.018	0.007	0.008565	1130	0.4447
0.4483	0.8002	G	C	0.018	0.007	0.00973	1130	0.4483
0.6528	0.9732	T	C	-0.013	0.007	0.05805	1130	0.3472
0.6175	0.9953	G	A	0.007	0.006	0.2965	1130	0.3825
0.1598	0.9304	G	A	-0.026	0.009	0.003281	1130	0.1598
0.3469	0.9738	G	C	0.013	0.007	0.05762	1130	0.3469
0.4748	0.9999	G	A	-0.004	0.006	0.4906	1130	0.4748
0.4748	1	G	A	-0.004	0.006	0.491	1130	0.4748
0.4471	0.975	G	A	0.015	0.006	0.02333	1130	0.4471
0.4541	0.9847	G	A	0.015	0.006	0.01481	1130	0.4541
0.4517	0.9825	T	C	0.016	0.006	0.01347	1130	0.4517
0.4527	0.9839	G	C	0.016	0.006	0.01387	1130	0.4527
0.4368	0.9806	G	A	0.013	0.006	0.03867	1130	0.4368
0.2863	0.9961	T	C	-0.001	0.007	0.8457	1130	0.2863
0.5471	0.9844	G	A	-0.016	0.006	0.01388	1130	0.4529
0.3268	0.9971	T	A	0.014	0.007	0.04286	1130	0.3268
0.5519	0.97	G	A	-0.015	0.006	0.02337	1130	0.4481
0.4105	0.9897	T	C	-0.004	0.006	0.5204	1130	0.4105
0.6729	0.9902	G	A	-0.013	0.007	0.05273	1130	0.3271
0.3273	0.9945	G	A	0.014	0.007	0.04245	1130	0.3273
0.3266	0.9985	G	A	0.014	0.007	0.04302	1130	0.3266
0.3269	0.9964	G	C	0.014	0.007	0.04274	1130	0.3269

0.0334	0.8181	G	C	-0.02	0.019	0.291	1130	0.0334
0.3266	0.9981	G	A	0.014	0.007	0.04295	1130	0.3266
0.6877	0.7822	G	C	-0.02	0.008	0.007989	1130	0.3123
0.8767	0.9466	T	C	0.022	0.01	0.02675	1130	0.1233
0.6227	0.7968	T	C	0.009	0.007	0.2111	1130	0.3773

KORA3

af_kora3	oevar_kora3	coded_kora3	noncoded_kora3	beta_kora3	se_kora3	p_kora3	n_kora3	maf_kora3
0.4954	0.9951	A	G	0.004	0.005	0.4389	1581	0.4954
0.4951	0.9981	G	C	0.004	0.005	0.4403	1581	0.4951
0.4182	0.8779	G	C	-0.008	0.005	0.1112	1581	0.4182
0.4184	0.8806	G	A	-0.008	0.005	0.1141	1581	0.4184
0.4425	0.9409	T	C	0.008	0.005	0.07597	1581	0.4425
0.444	0.9372	A	G	0.008	0.005	0.07985	1581	0.444
0.4438	0.9376	A	G	0.008	0.005	0.07853	1581	0.4438
0.4451	0.9356	A	T	0.008	0.005	0.08146	1581	0.4451
0.4453	0.9355	T	C	0.008	0.005	0.08426	1581	0.4453
0.4441	0.9244	T	C	0.007	0.005	0.1118	1581	0.4441
0.4442	0.9245	A	C	0.007	0.005	0.1185	1581	0.4442
0.425	0.9981	C	T	0.004	0.005	0.3823	1581	0.425
0.6258	0.9563	G	A	0.005	0.005	0.2782	1581	0.3742
0.4454	0.9354	A	G	0.008	0.005	0.08874	1581	0.4454
0.4455	0.9353	A	G	0.008	0.005	0.09687	1581	0.4455
0.4461	0.9352	G	C	0.008	0.005	0.1025	1581	0.4461
0.4447	0.9588	A	C	0.008	0.005	0.08662	1581	0.4447
0.4445	0.9598	T	A	0.008	0.005	0.0852	1581	0.4445
0.4497	0.941	T	C	0.007	0.005	0.1487	1581	0.4497
0.4489	0.9386	T	C	0.007	0.005	0.1331	1581	0.4489
0.4617	0.9756	A	G	0.006	0.005	0.2142	1581	0.4617
0.49	0.9991	C	T	0.006	0.005	0.1817	1581	0.49
0.4913	0.9867	G	T	0.006	0.005	0.207	1581	0.4913
0.43	1	G	A	0.005	0.005	0.3124	1581	0.43
0.4423	0.1112	A	G	-0.025	0.013	0.06518	1581	0.4423
0.3007	0.9392	C	T	0.001	0.005	0.9182	1581	0.3007
0.6435	0.6868	G	A	0.006	0.006	0.2765	1581	0.3565
0.555	0.9988	A	T	0.004	0.005	0.4335	1581	0.445
0.555	0.9982	C	G	0.004	0.005	0.4331	1581	0.445
0.4654	0.9488	T	A	0.007	0.005	0.1388	1581	0.4654
0.41	1	C	T	0.005	0.005	0.3137	1581	0.41
0.4105	0.995	G	T	0.005	0.005	0.2615	1581	0.4105
0.415	1	G	A	0.005	0.005	0.3164	1581	0.415
0.4441	0.8719	G	C	0.006	0.005	0.2665	1581	0.4441
0.4099	0.9994	T	A	0.005	0.005	0.2679	1581	0.4099
0.4158	0.9944	C	T	0.005	0.005	0.2592	1581	0.4158
0.4098	0.9993	A	G	0.005	0.005	0.2733	1581	0.4098
0.56	1	T	A	0.005	0.005	0.3361	1581	0.44
0.4651	0.9993	C	T	0.007	0.005	0.1321	1581	0.4651
0.4051	0.9522	G	T	0.005	0.005	0.2747	1581	0.4051
0.458	0.9936	A	C	0.008	0.005	0.06635	1581	0.458
0.4655	0.996	A	G	0.006	0.005	0.1711	1581	0.4655
0.5602	0.9779	G	T	0.004	0.005	0.3505	1581	0.4398
0.5601	0.9905	A	G	0.004	0.005	0.3451	1581	0.4399
0.4719	0.9566	C	T	0.007	0.005	0.1544	1581	0.4719
0.5607	0.9529	G	T	0.004	0.005	0.4114	1581	0.4393

0.4758	0.9924	G	C	0.006	0.005	0.1811	1581	0.4758
0.4751	0.9986	C	A	0.006	0.005	0.1797	1581	0.4751
0.4142	0.9773	G	A	0.005	0.005	0.2667	1581	0.4142
0.6176	0.9461	C	G	0.007	0.005	0.1606	1581	0.3824
0.4769	0.9844	C	T	0.006	0.005	0.1927	1581	0.4769
0.4771	0.9837	T	G	0.006	0.005	0.1979	1581	0.4771
0.475	1	A	G	0.006	0.005	0.1745	1581	0.475
0.475	0.9999	A	G	0.006	0.005	0.1746	1581	0.475
0.6269	0.8565	T	A	0.008	0.005	0.1444	1581	0.3731
0.4053	0.9504	C	T	0.005	0.005	0.2847	1581	0.4053
0.4177	0.9838	C	T	0.005	0.005	0.2588	1581	0.4177
0.6345	0.9136	C	T	-0.001	0.005	0.8149	1581	0.3655
0.109	0.9295	G	T	0.002	0.007	0.7614	1581	0.109
0.4199	0.8634	G	A	0.006	0.005	0.2349	1581	0.4199
0.1102	0.9375	C	A	0.002	0.007	0.7309	1581	0.1102
0.4753	0.9868	A	G	0.009	0.005	0.05197	1581	0.4753
0.4751	0.9882	A	T	0.009	0.005	0.04934	1581	0.4751
0.5408	0.9937	A	G	0.005	0.005	0.3143	1581	0.4592
0.4181	0.9832	C	T	0.006	0.005	0.2318	1581	0.4181
0.1459	0.974	A	G	0.003	0.006	0.5932	1581	0.1459
0.6363	0.9301	T	C	-0.001	0.005	0.8777	1581	0.3637
0.54	1	T	A	0.005	0.005	0.3146	1581	0.46
0.111	0.9435	C	A	0.003	0.007	0.6864	1581	0.111
0.4743	0.9944	C	G	0.009	0.005	0.04601	1581	0.4743
0.4744	0.9961	G	C	0.009	0.005	0.05242	1581	0.4744
0.4206	0.9896	C	T	0.006	0.005	0.2316	1581	0.4206
0.6384	0.9128	G	A	-0.001	0.005	0.8136	1581	0.3616
0.12	0.8606	G	A	0.001	0.007	0.8427	1581	0.12
0.4197	0.9886	G	C	0.006	0.005	0.2318	1581	0.4197
0.5391	0.9827	G	A	0.006	0.005	0.1957	1581	0.4609
0.5294	0.9497	G	A	0.005	0.005	0.3241	1581	0.4706
0.5415	0.9818	T	C	0.005	0.005	0.2396	1581	0.4585
0.5399	0.9994	G	C	0.005	0.005	0.3147	1581	0.4601
0.5198	0.9164	G	A	0.006	0.005	0.1728	1581	0.4802
0.2877	0.8573	T	C	-0.011	0.006	0.07039	1573	0.2877
0.5398	0.9992	A	G	0.005	0.005	0.3148	1581	0.4602
0.5984	0.9846	A	T	-0.005	0.005	0.3106	1581	0.4016
0.5396	0.9964	A	G	0.006	0.005	0.1867	1581	0.4604
0.3347	0.9827	T	C	0.001	0.005	0.8059	1581	0.3347
0.3964	0.9689	A	G	0.005	0.005	0.3167	1581	0.3964
0.5988	0.9705	A	G	-0.005	0.005	0.3129	1581	0.4012
0.5995	0.9769	A	G	-0.005	0.005	0.3221	1581	0.4005
0.5986	0.9763	C	G	-0.005	0.005	0.314	1581	0.4014
0.0284	0.7839	G	C	-0.018	0.013	0.1826	1581	0.0284
0.5987	0.9824	A	G	-0.005	0.005	0.3163	1581	0.4013
0.3906	0.9635	C	G	0.002	0.005	0.6632	1581	0.3906
0.0946	0.9163	C	T	0.003	0.007	0.7033	1581	0.0946
0.6294	0.9954	T	C	-0.003	0.005	0.4707	1581	0.3706

KORA4

af_kora4	oevar_kora4	coded_kora4	noncoded_kora4	beta_kora4	se_kora4	p_kora4	n_kora4	maf_kora4
0.4963	0.9842	G	A	-0.01	0.005	0.04198	1407	0.4963
0.5032	0.9893	G	C	0.01	0.005	0.04117	1407	0.4968
0.434	0.9476	G	C	-0.007	0.005	0.1405	1407	0.434
0.4344	0.9468	G	A	-0.007	0.005	0.1397	1407	0.4344
0.4854	0.9606	T	C	0.007	0.005	0.1559	1407	0.4854
0.5143	0.9604	G	A	-0.007	0.005	0.154	1407	0.4857
0.5145	0.9605	G	A	-0.007	0.005	0.155	1407	0.4855
0.5142	0.9604	T	A	-0.007	0.005	0.1535	1407	0.4858
0.486	0.9603	T	C	0.007	0.005	0.1523	1407	0.486
0.4839	0.9507	T	C	0.008	0.005	0.126	1407	0.4839
0.516	0.9509	C	A	-0.008	0.005	0.1256	1407	0.484
0.5746	0.9859	T	C	-0.008	0.005	0.1034	1407	0.4254
0.6358	0.9554	G	A	0.009	0.005	0.08848	1407	0.3642
0.5137	0.9604	G	A	-0.007	0.005	0.1504	1407	0.4863
0.5136	0.9605	G	A	-0.007	0.005	0.1496	1407	0.4864
0.4866	0.9605	G	C	0.007	0.005	0.149	1407	0.4866
0.5091	0.977	C	A	-0.008	0.005	0.1272	1407	0.4909
0.4903	0.9786	T	A	0.008	0.005	0.1305	1407	0.4903
0.4878	0.9631	T	C	0.007	0.005	0.1424	1407	0.4878
0.4875	0.9622	T	C	0.007	0.005	0.144	1407	0.4875
0.5025	0.9865	G	A	-0.008	0.005	0.09371	1407	0.4975
0.4903	0.9983	T	C	-0.007	0.005	0.1599	1407	0.4903
0.4894	0.974	T	G	-0.008	0.005	0.1305	1407	0.4894
0.4326	0.9959	G	A	0.007	0.005	0.1695	1407	0.4326
0.5124	0.9101	G	A	0.013	0.005	0.01157	1407	0.4876
0.6771	0.9883	T	C	-0.013	0.005	0.01582	1407	0.3229
0.6448	0.8068	G	A	0.009	0.006	0.1004	1407	0.3552
0.4587	0.9886	T	A	-0.008	0.005	0.09747	1407	0.4587
0.4589	0.9877	G	C	-0.008	0.005	0.09651	1407	0.4589
0.4964	0.9736	T	A	0.007	0.005	0.1798	1407	0.4964
0.5951	0.9899	T	C	-0.006	0.005	0.2174	1407	0.4049
0.5962	0.9931	T	G	-0.006	0.005	0.2119	1407	0.4038
0.4098	0.9973	G	A	0.005	0.005	0.2981	1407	0.4098
0.4422	0.8914	G	C	0.004	0.005	0.4866	1407	0.4422
0.4023	0.9863	T	A	0.006	0.005	0.2277	1407	0.4023
0.5898	0.994	T	C	-0.005	0.005	0.3145	1407	0.4102
0.5981	0.9864	G	A	-0.006	0.005	0.2226	1407	0.4019
0.5481	0.9949	T	A	0.007	0.005	0.1559	1407	0.4519
0.4932	0.9955	T	C	-0.007	0.005	0.1413	1407	0.4932
0.5977	0.9649	T	G	-0.005	0.005	0.333	1407	0.4023
0.5023	0.9984	C	A	-0.007	0.005	0.1735	1407	0.4977
0.4926	0.9748	G	A	-0.007	0.005	0.1411	1407	0.4926
0.4542	0.9815	T	G	-0.007	0.005	0.1546	1407	0.4542
0.4541	0.9837	G	A	-0.007	0.005	0.1546	1407	0.4541
0.492	0.9645	T	C	-0.007	0.005	0.1439	1407	0.492

0.4516	0.968	T	G	-0.007	0.005	0.1554	1407	0.4516
0.5074	0.9986	G	C	0.008	0.005	0.1113	1407	0.4926
0.5076	0.9996	C	A	0.008	0.005	0.1096	1407	0.4924
0.4059	0.9871	G	A	0.005	0.005	0.2754	1407	0.4059
0.3703	0.9581	G	C	-0.006	0.005	0.2025	1407	0.3703
0.493	0.9976	T	C	-0.008	0.005	0.1147	1407	0.493
0.5068	0.9975	T	G	0.008	0.005	0.116	1407	0.4932
0.4923	1	G	A	-0.008	0.005	0.109	1407	0.4923
0.4923	1	G	A	-0.008	0.005	0.1092	1407	0.4923
0.6339	0.9	T	A	0.005	0.005	0.3857	1407	0.3661
0.598	0.9629	T	C	-0.005	0.005	0.3478	1407	0.402
0.5889	0.9887	T	C	-0.004	0.005	0.3793	1407	0.4111
0.3713	0.9921	T	C	-0.01	0.005	0.06382	1407	0.3713
0.8745	0.9265	T	G	-0.001	0.008	0.8782	1407	0.1255
0.4128	0.8858	G	A	0.004	0.005	0.4376	1407	0.4128
0.1273	0.9355	C	A	0.001	0.008	0.885	1407	0.1273
0.4836	0.9795	G	A	-0.007	0.005	0.1942	1407	0.4836
0.484	0.9817	T	A	-0.007	0.005	0.1974	1407	0.484
0.4854	0.9919	G	A	-0.007	0.005	0.1434	1407	0.4854
0.5893	0.9949	T	C	-0.004	0.005	0.4789	1407	0.4107
0.8078	0.9525	G	A	0.009	0.006	0.1729	1407	0.1922
0.6285	0.9933	T	C	0.01	0.005	0.05774	1407	0.3715
0.5188	0.9911	T	A	0.006	0.005	0.2253	1407	0.4812
0.1286	0.9454	C	A	0.001	0.008	0.8906	1407	0.1286
0.4842	0.9827	G	C	-0.006	0.005	0.199	1407	0.4842
0.5182	0.9968	G	C	0.006	0.005	0.2152	1407	0.4818
0.5881	0.9929	T	C	-0.003	0.005	0.4989	1407	0.4119
0.6287	0.9954	G	A	0.01	0.005	0.05557	1407	0.3713
0.1377	0.8701	G	A	-0.001	0.008	0.9096	1407	0.1377
0.4109	0.9963	G	C	0.003	0.005	0.4895	1407	0.4109
0.4278	0.9961	G	A	0	0.005	0.9269	1407	0.4278
0.429	0.9873	G	A	0	0.005	0.9922	1407	0.429
0.514	0.994	G	A	0.005	0.005	0.2773	1407	0.486
0.5064	0.9642	G	A	0.007	0.005	0.1587	1407	0.4936
0.5144	0.9873	T	C	0.006	0.005	0.1974	1407	0.4856
0.5176	0.9858	G	C	0.006	0.005	0.2085	1407	0.4824
0.5077	0.9896	G	A	0.006	0.005	0.2211	1407	0.4923
0.244	0.8563	T	C	-0.009	0.006	0.1757	1407	0.244
0.4826	0.9857	G	A	-0.006	0.005	0.2048	1407	0.4826
0.3907	0.9894	T	A	0.008	0.005	0.1293	1407	0.3907
0.4864	0.9986	G	A	-0.005	0.005	0.2948	1407	0.4864
0.3784	0.9832	T	C	-0.002	0.005	0.7727	1407	0.3784
0.6123	0.9781	G	A	-0.008	0.005	0.1446	1407	0.3877
0.3909	0.9817	G	A	0.008	0.005	0.1384	1407	0.3909
0.3906	0.9825	G	A	0.008	0.005	0.1246	1407	0.3906
0.3907	0.9871	G	C	0.008	0.005	0.1306	1407	0.3907
0.0299	0.7459	G	C	-0.036	0.017	0.03782	1407	0.0299

0.3906	0.9853	G	A	0.008	0.005	0.1264	1407	0.3906
0.606	0.9575	G	C	-0.008	0.005	0.1173	1407	0.394
0.9004	0.92	T	C	0.006	0.009	0.48	1407	0.0996
0.6364	0.9687	T	C	0.013	0.005	0.01653	1407	0.3636

NESDA

af_nesda	oevar_nesda	coded_nesda	noncoded_nesda	beta_nesda	se_nesda	p_nesda	n_nesda	maf_nesda
0.46540881	0.971693	G	A	-0.00364498	0.00416633	0.381643	1612	0.46540881
0.46541718	0.971819	C	G	-0.00364973	0.00416606	0.380997	1612	0.46541718
0.40694789	1	G	C	-0.00185562	0.0041988	0.658531	1612	0.40694789
0.40888546	0.993784	G	A	-0.00162312	0.00420184	0.699281	1612	0.40888546
0.48632321	0.993663	C	T	-0.00508293	0.00408207	0.213064	1612	0.48632321
0.48636386	0.993944	G	A	-0.00507875	0.00408154	0.213377	1612	0.48636386
0.48634678	0.993825	G	A	-0.00508053	0.00408177	0.213244	1612	0.48634678
0.48636727	0.993971	T	A	-0.00507834	0.00408149	0.213409	1612	0.48636727
0.48637038	0.993992	C	T	-0.00507804	0.00408145	0.213436	1612	0.48637038
0.4918626	0.976989	C	T	-0.00530053	0.0041191	0.198158	1612	0.4918626
0.49186197	0.976979	C	A	-0.00530039	0.00411911	0.198174	1612	0.49186197
0.44843142	0.958411	C	T	0.00386948	0.00424978	0.362541	1612	0.44843142
0.35225456	0.94035	A	G	-0.00144509	0.00440674	0.742962	1612	0.35225456
0.48727498	1	G	A	-0.00497854	0.00407342	0.221632	1612	0.48727498
0.48637193	0.993997	G	A	-0.00507756	0.00408144	0.213476	1612	0.48637193
0.48637193	0.993996	C	G	-0.00507755	0.00408144	0.213479	1612	0.48637193
0.47213801	0.967259	C	A	-0.00601256	0.00413149	0.14559	1612	0.47213801
0.47213832	0.967238	A	T	-0.00601262	0.00413154	0.145587	1612	0.47213832
0.48635859	0.993773	C	T	-0.00507423	0.00408188	0.213383	1612	0.48635859
0.48636542	0.993882	C	T	-0.00507588	0.00408167	0.213657	1612	0.48636542
0.47252111	0.988101	G	A	-0.00543942	0.00409784	0.18438	1612	0.47252111
0.45838509	1	T	C	-0.00404998	0.00408827	0.321864	1612	0.45838509
0.4583978	0.994728	T	G	-0.0041752	0.00409659	0.308109	1612	0.4583978
0.45515289	0.953908	G	A	0.00526904	0.004255	0.215601	1612	0.45515289
0.34088089	1	C	T	-0.00160836	0.00425192	0.705232	1612	0.34088089
0.33293073	0.909614	A	G	-0.00392189	0.00453933	0.387591	1612	0.33293073
0.45169259	0.954399	T	A	-0.00333529	0.0041874	0.425737	1612	0.45169259
0.4517013	0.954508	G	C	-0.00333348	0.0041872	0.425962	1612	0.4517013
0.4841852	0.990073	A	T	-0.00548842	0.00408054	0.178619	1612	0.4841852
0.43854749	1	C	T	0.00388796	0.00418064	0.352375	1612	0.43854749
0.43798209	0.994125	G	T	0.00407638	0.00418374	0.329892	1612	0.43798209
0.45217391	1	G	A	0.00398595	0.00418865	0.341297	1612	0.45217391
0.48005954	0.94368	G	C	0.0050186	0.00429493	0.242609	1612	0.48005954
0.43822112	0.993433	T	A	0.00406778	0.00418317	0.330845	1612	0.43822112
0.451313	0.992712	C	T	0.00379446	0.00419757	0.366013	1612	0.451313
0.43814059	0.995043	A	G	0.00405289	0.00418101	0.332372	1612	0.43814059
0.44482658	0.950497	A	T	-0.0047643	0.00420553	0.257272	1612	0.44482658
0.45934202	1	T	C	-0.00593271	0.00405413	0.143365	1612	0.45934202
0.43935918	0.96884	G	T	0.00341889	0.00427464	0.423821	1612	0.43935918
0.46985699	0.970904	C	A	-0.00640033	0.00411615	0.119965	1612	0.46985699
0.47001533	0.992119	G	A	-0.00546821	0.00408401	0.180588	1612	0.47001533
0.44469851	0.950471	T	G	-0.00478357	0.00420547	0.255338	1612	0.44469851
0.44473287	0.950452	G	A	-0.00477857	0.00420554	0.255846	1612	0.44473287
0.46044933	0.981094	T	C	-0.00460696	0.00411272	0.262634	1612	0.46044933
0.44395875	0.952486	T	G	-0.0047709	0.00420301	0.256324	1612	0.44395875
0.4698534	0.992101	C	G	-0.00550222	0.00408325	0.177821	1612	0.4698534

0.46985311	0.992105	A	C	-0.00550205	0.00408324	0.177833	1612	0.46985311
0.43662996	0.991855	G	A	0.00418714	0.00419209	0.317881	1612	0.43662996
0.35714973	0.946334	G	C	-0.00254274	0.00439359	0.562762	1612	0.35714973
0.46985433	0.992086	T	C	-0.00550278	0.00408328	0.177772	1612	0.46985433
0.46985464	0.992077	G	T	-0.00550311	0.0040833	0.177755	1612	0.46985464
0.4698528	0.992112	G	A	-0.0055018	0.00408323	0.177842	1612	0.4698528
0.4698528	0.992112	G	A	-0.00550179	0.00408323	0.177843	1612	0.4698528
0.34627916	0.940473	A	T	-0.00263962	0.00443128	0.551383	1612	0.34627916
0.43846805	0.969096	C	T	0.00327542	0.00427481	0.443551	1612	0.43846805
0.44940022	0.994577	C	T	0.00370627	0.0041993	0.37746	1612	0.44940022
0.36339533	0.994703	T	C	0.00188323	0.00420029	0.653896	1612	0.36339533
0.12425786	0.980932	G	T	-0.0087608	0.00604846	0.147495	1612	0.12425786
0.46356855	0.985998	G	A	0.00572466	0.00419897	0.172774	1612	0.46356855
0.12280702	1	C	A	-0.00819891	0.0060495	0.175321	1612	0.12280702
0.45866375	0.985546	G	A	-0.00613478	0.00410022	0.134602	1612	0.45866375
0.45866375	0.985545	T	A	-0.00613476	0.00410023	0.134602	1612	0.45866375
0.46227885	0.990477	G	A	-0.00344849	0.00409752	0.40001	1612	0.46227885
0.44619693	0.986835	C	T	0.00344988	0.00421984	0.413624	1612	0.44619693
0.17207379	1	A	G	-0.0107712	0.00528017	0.0413563	1612	0.17207379
0.36379134	0.994318	C	T	0.00190236	0.00420126	0.650693	1612	0.36379134
0.46179805	0.98697	A	T	-0.00352669	0.00410336	0.390089	1612	0.46179805
0.12310367	0.970818	C	A	-0.00820939	0.0060995	0.17833	1612	0.12310367
0.45866375	0.985531	G	C	-0.00613476	0.00410025	0.134605	1612	0.45866375
0.45866437	0.985487	C	G	-0.00613489	0.00410034	0.134607	1612	0.45866437
0.44611104	0.982433	C	T	0.00346548	0.00422597	0.412187	1612	0.44611104
0.36290416	0.983552	A	G	0.00193309	0.00422706	0.647443	1612	0.36290416
0.13412024	0.874686	G	A	-0.0117459	0.00619443	0.0579326	1612	0.13412024
0.4461383	0.983722	G	C	0.00346086	0.00422425	0.412626	1612	0.4461383
0.4185047	0.996382	G	A	-0.00353274	0.00416261	0.39606	1612	0.4185047
0.41820724	0.996293	G	A	-0.00350373	0.00416633	0.400369	1612	0.41820724
0.46702725	0.984582	A	G	-0.00305485	0.00410718	0.457004	1612	0.46702725
0.47423418	0.968306	A	G	-0.0029966	0.00414103	0.469294	1612	0.47423418
0.47041985	1	C	T	-0.00300003	0.00416892	0.47176	1612	0.47041985
0.46196958	0.989026	C	G	-0.00349078	0.00409975	0.394515	1612	0.46196958
0.4772168	0.977349	A	G	-0.00235479	0.00415075	0.570501	1612	0.4772168
0.26330798	1	T	C	-0.00261836	0.00464875	0.573273	1612	0.26330798
0.46206948	0.990479	G	A	-0.00346888	0.00409716	0.397189	1612	0.46206948
0.42324425	1	T	A	0.00365438	0.004175	0.38141	1612	0.42324425
0.46301887	0.969831	G	A	-0.00299547	0.00413494	0.468805	1612	0.46301887
0.4016451	0.918573	T	C	-0.00307281	0.00424024	0.468645	1612	0.4016451
0.4222208	0.984295	A	G	0.00337048	0.00420717	0.423053	1612	0.4222208
0.42333193	0.99483	G	A	0.00346654	0.00418183	0.407131	1612	0.42333193
0.42316344	0.995808	G	A	0.00345157	0.00417921	0.408869	1612	0.42316344
0.42326828	0.995508	G	C	0.00345981	0.00418018	0.407861	1612	0.42326828
0.42314674	0.996062	G	A	0.0034434	0.00417877	0.409931	1612	0.42314674
0.40027978	0.842307	C	G	0.00495077	0.00451507	0.272863	1612	0.40027978
0.11309117	0.94838	C	T	-0.00937341	0.00643155	0.14501	1612	0.11309117
0.35357125	0.811326	C	T	-0.00364625	0.00463303	0.431275	1612	0.35357125

NBS								
af_nij	oevar_nij	coded_nij	noncoded_nij	beta_nij	se_nij	p_nij	n_nij	maf_nij
0.45825427	0.984754	G	A	0.00148322	0.00617125	0.810248	527	0.45825427
0.54174573	0.984789	G	C	-0.00147869	0.00617091	0.810431	527	0.458254
0.41340782	0.996125	G	C	0.00483875	0.00624649	0.438324	537	0.41340782
0.41340782	0.996218	G	A	0.00482706	0.00624575	0.439646	537	0.41340782
0.51301115	0.995284	T	C	0.00036301	0.00637473	0.953903	538	0.486989
0.48618785	1	G	A	-0.00074251	0.0063831	0.907396	543	0.48618785
0.48698885	0.995284	G	A	-0.00036301	0.00637473	0.955236	538	0.48698885
0.48698885	0.995284	T	A	-0.00036347	0.0063746	0.954804	538	0.48698885
0.51301115	0.995273	T	C	0.00036069	0.0063745	0.954241	538	0.486989
0.50194553	0.947626	T	C	0.00075124	0.00653716	0.906068	514	0.498054
0.49805447	0.947534	C	A	-0.00074428	0.00653734	0.912869	514	0.49805447
0.53240741	0.997515	T	C	0.00092474	0.00592598	0.876032	540	0.467593
0.66385768	0.996208	G	A	0.00163142	0.00656026	0.805108	534	0.336142
0.48698885	0.995239	G	A	-0.00035673	0.00637449	0.955478	538	0.48698885
0.48698885	0.995239	G	A	-0.00035673	0.00637449	0.955478	538	0.48698885
0.51301115	0.995239	G	C	0.00035673	0.00637449	0.955259	538	0.486989
0.4766537	0.957483	C	A	0.00010434	0.00649609	0.98282	514	0.4766537
0.5233463	0.957472	T	A	-0.00010657	0.00649598	0.991958	514	0.476654
0.51301115	0.994788	T	C	0.00033603	0.00637527	0.958667	538	0.486989
0.51301115	0.994902	T	C	0.00034368	0.00637569	0.956898	538	0.486989
0.46993988	0.957617	G	A	9.25E-05	0.00645856	0.98815	499	0.46993988
0.45664207	0.998999	T	C	0.00186096	0.00620334	0.764183	542	0.45664207
0.45488029	1	T	G	0.00218744	0.00621524	0.724878	543	0.45488029
0.47180451	0.99634	G	A	4.01E-05	0.00592141	0.994163	532	0.47180451
0.49722736	1	G	A	0.00194942	0.00594751	0.743085	541	0.49722736
0.66795367	0.975209	T	C	-0.0021921	0.00672948	0.744932	518	0.332046
0.67625232	1	G	A	0.00314993	0.00662684	0.634552	539	0.323748
0.43761639	0.997274	T	A	0.00059236	0.00598706	0.921134	537	0.43761639
0.43866171	0.997315	G	C	0.00059079	0.00598684	0.921422	538	0.43866171
0.5259481	0.95932	T	A	0.00032921	0.00644233	0.960016	501	0.474052
0.54704797	0.998527	T	C	0.00294295	0.00592023	0.620039	542	0.452952
0.546875	0.999291	T	G	0.00295493	0.00593417	0.619443	544	0.453125
0.46494465	0.999212	G	A	-0.00290239	0.00592788	0.624782	542	0.46494465
0.49238095	0.988323	G	C	-2.49E-05	0.00595735	0.99868	525	0.49238095
0.45378928	0.99801	T	A	-0.00297545	0.00593843	0.615944	541	0.45378928
0.53406998	1	T	C	0.00254301	0.00594724	0.668946	543	0.46593
0.546875	0.998579	G	A	0.00296675	0.00593653	0.618494	544	0.453125
0.56685499	0.996427	T	A	0.00031659	0.00597149	0.957718	531	0.433145
0.45664207	0.998979	T	C	0.00185821	0.0062034	0.764807	542	0.45664207
0.53531599	0.999323	T	G	0.00287307	0.0059332	0.628132	538	0.464684
0.47	0.947314	C	A	9.83E-05	0.00648741	0.984125	500	0.47
0.45664207	0.998999	G	A	0.00186088	0.00620321	0.764187	542	0.45664207
0.43301887	0.996282	T	G	-0.00028677	0.00597232	0.961174	530	0.43301887
0.43301887	0.99634	G	A	-0.00029182	0.00597201	0.960806	530	0.43301887
0.45664207	0.998999	T	C	0.00186088	0.00620321	0.764187	542	0.45664207

0.43045113	0.996451	T	G	-0.0002283	0.00596214	0.969354	532	0.43045113
0.54335793	0.998578	G	C	-0.00184225	0.00620522	0.766552	542	0.456642
0.54335793	0.998578	C	A	-0.00184225	0.00620522	0.766552	542	0.456642
0.44944853	1	G	A	-0.00263611	0.00587942	0.653892	544	0.44944853
0.34116541	0.995762	G	C	-0.00377765	0.00642383	0.55642	532	0.34116541
0.45664207	0.99849	T	C	0.00183331	0.00620566	0.767669	542	0.45664207
0.54335793	0.998359	T	G	-0.00182445	0.00620646	0.769078	542	0.456642
0.45664207	0.998679	G	A	0.00184825	0.00620477	0.765798	542	0.45664207
0.45664207	0.998679	G	A	0.00184825	0.00620477	0.765798	542	0.45664207
0.66698473	0.985361	T	A	0.00368344	0.00655837	0.571905	524	0.333015
0.53531599	0.998973	T	C	0.00285741	0.00593197	0.629788	538	0.464684
0.53531599	0.997612	T	C	0.00273246	0.00590769	0.643726	538	0.464684
0.36832061	0.976354	T	C	-0.00087591	0.00652769	0.894169	524	0.36832061
0.87775735	1	T	G	0.0118556	0.009584	0.216081	544	0.122243
0.48154982	1	G	A	-0.00187878	0.00590897	0.75052	542	0.48154982
0.12224265	0.997486	C	A	-0.0118691	0.00958849	0.215774	544	0.12224265
0.46319018	0.941521	G	A	-0.00059776	0.00647569	0.929568	489	0.46319018
0.46319018	0.941521	T	A	-0.00059776	0.00647569	0.929568	489	0.46319018
0.45404412	0.999295	G	A	0.0026037	0.0060045	0.664585	544	0.45404412
0.5380334	0.997256	T	C	0.0028188	0.00589522	0.631544	539	0.461967
0.84579439	0.987608	G	A	0.0188647	0.00861777	0.0285009	535	0.154206
0.63167939	0.97581	T	C	0.00084733	0.00652806	0.900391	524	0.368321
0.5494403	0.997345	T	A	-0.00270701	0.00601306	0.651753	536	0.45056
0.12224265	0.994657	C	A	-0.0119302	0.00959704	0.213607	544	0.12224265
0.46319018	0.941521	G	C	-0.00059776	0.00647569	0.929568	489	0.46319018
0.53680982	0.941521	G	C	0.00059776	0.00647569	0.922797	489	0.46319
0.53810409	0.996338	T	C	0.00281686	0.00589785	0.633258	538	0.461896
0.62065637	0.970023	G	A	0.00043608	0.00653312	0.949437	518	0.379344
0.12524272	0.919777	G	A	-0.0124523	0.00969249	0.198646	515	0.12524272
0.46189591	0.996828	G	C	-0.00280012	0.00589642	0.634815	538	0.46189591
0.39430147	1	G	A	-0.00785967	0.00627194	0.210152	544	0.39430147
0.39430147	1	G	A	-0.00785967	0.00627194	0.210152	544	0.39430147
0.54267161	0.996842	G	A	-0.00242388	0.00593935	0.681624	539	0.457328
0.55606618	1	G	A	-0.00282291	0.00601544	0.638871	544	0.443934
0.5464684	0.997615	T	C	-0.00237992	0.00596322	0.689756	538	0.453532
0.54805915	0.997992	G	C	-0.00267345	0.00601031	0.656114	541	0.451941
0.53584559	1	G	A	-0.00470841	0.00591635	0.42613	544	0.464154
0.24372385	0.912671	T	C	-0.00026907	0.0074579	0.970053	478	0.24372385
0.45395948	0.998344	G	A	0.00264858	0.00600832	0.659307	543	0.45395948
0.43081181	0.999772	T	A	-0.00424698	0.00598404	0.47788	542	0.43081181
0.4447619	0.986338	G	A	0.00289283	0.00601579	0.629495	525	0.4447619
0.37947269	0.994339	T	C	0.00202062	0.00618875	0.744048	531	0.37947269
0.56754221	0.996371	G	A	0.00445353	0.00598412	0.456832	533	0.432458
0.43081181	0.999542	G	A	-0.00426635	0.0059841	0.475999	542	0.43081181
0.43186004	1	G	A	-0.00455285	0.00600495	0.448341	543	0.43186004
0.43081181	0.99972	G	C	-0.00425152	0.00598418	0.477436	542	0.43081181
0.01886792	0.88365	G	C	-0.00787422	0.0207814	0.704733	530	0.01886792

0.43081181	0.999772	G	A	-0.00424698	0.00598404	0.47788	542	0.43081181
0.64340102	0.84269	G	C	0.00213481	0.00668969	0.751868	394	0.356599
0.89408397	0.985945	T	C	0.0119016	0.00983129	0.227288	524	0.105916
0.65508021	0.858921	T	C	-0.00393181	0.00675505	0.551012	374	0.34492

Rotterdam Study

af_rott	oevar_rott	coded_rott	noncoded_rott	beta_rott	se_rott	p_rott	n_rott	maf_rott
0.464583	0.975397	G	A	-0.0062218	0.00384133	0.10527406	5169	0.464583
0.464599	0.975617	C	G	-0.00624191	0.00384075	0.10410128	5169	0.464599
0.584212	0.995835	C	G	0.00356825	0.00387065	0.35652094	5169	0.415788
0.584053	0.996161	A	G	0.00355522	0.0038699	0.35818694	5169	0.415947
0.483684	0.989937	C	T	-0.00779184	0.00381492	0.04110721	5169	0.483684
0.488885	0.999582	G	A	-0.0072542	0.0037928	0.05579221	5169	0.488885
0.488682	0.998733	G	A	-0.00727865	0.00379449	0.05508008	5169	0.488682
0.488534	0.998581	T	A	-0.00728178	0.00379407	0.05494844	5169	0.488534
0.487831	0.998822	C	T	-0.00731994	0.00379215	0.05356769	5169	0.487831
0.49373	0.976933	C	T	-0.00739168	0.00383192	0.05373057	5169	0.49373
0.493713	0.976805	C	A	-0.00738675	0.00383217	0.05390625	5169	0.493713
0.55782	0.973453	T	C	-0.00070363	0.00386787	0.85562132	5169	0.44218
0.351445	0.957304	A	G	-0.00296968	0.00407763	0.46636396	5169	0.351445
0.487799	0.998606	G	A	-0.00731434	0.00379253	0.053775	5169	0.487799
0.487769	0.998387	G	A	-0.00730683	0.00379289	0.05404431	5169	0.487769
0.487736	0.998172	C	G	-0.00730062	0.00379328	0.05427373	5169	0.487736
0.477094	0.921396	C	A	-0.00766627	0.00395385	0.05250608	5169	0.477094
0.477081	0.920495	A	T	-0.00767008	0.00395568	0.05249792	5169	0.477081
0.487483	0.996492	C	T	-0.00724668	0.00379638	0.05627868	5169	0.487483
0.487563	0.997015	C	T	-0.00726394	0.00379538	0.05563004	5169	0.487563
0.473009	0.979077	G	A	-0.00733977	0.00384077	0.05599856	5169	0.473009
0.458239	0.998612	T	C	-0.00681728	0.0038045	0.07313851	5169	0.458239
0.458317	0.998812	T	G	-0.00684281	0.003804	0.07203236	5169	0.458317
0.553979	0.971172	A	G	-0.00118146	0.00386852	0.76001472	5169	0.446021
0.517925	0.993687	G	A	0.00570184	0.0038569	0.13928053	5169	0.482075
0.665569	0.999744	T	C	-0.00427619	0.00399781	0.28471819	5169	0.334431
0.333348	0.929186	A	G	-0.0042799	0.00419945	0.30805882	5169	0.333348
0.452536	0.972188	T	A	0.00180156	0.00388385	0.64268789	5169	0.452536
0.452486	0.972506	G	C	0.00178755	0.00388335	0.64523238	5169	0.452486
0.482296	0.983227	A	T	-0.00731517	0.00382446	0.05577781	5169	0.482296
0.568183	0.996129	T	C	-0.00111709	0.00383483	0.77077764	5169	0.431817
0.56793	0.998727	T	G	-0.00121311	0.00382897	0.75133099	5169	0.43207
0.55663	0.996553	A	G	-0.00158159	0.00383516	0.67999541	5169	0.44337
0.532004	0.955	C	G	-0.00183377	0.00390904	0.6389287	5169	0.467996
0.569979	0.997478	A	T	-0.00068313	0.00383183	0.85847811	5169	0.430021
0.556507	0.999471	T	C	-0.00165538	0.00382901	0.66544716	5169	0.443493
0.56989	0.997682	G	A	-0.00071414	0.00383143	0.8521104	5169	0.43011
0.449666	0.966873	A	T	0.00146798	0.00389673	0.70632839	5169	0.449666
0.465654	0.979408	T	C	-0.00707687	0.0038465	0.06578659	5169	0.465654
0.556593	0.998924	T	G	-0.00170254	0.00383058	0.65665044	5169	0.443407
0.472174	0.893183	C	A	-0.00770004	0.00401641	0.05521537	5169	0.472174
0.465393	0.977333	G	A	-0.00709026	0.00385053	0.06555914	5169	0.465393
0.449776	0.966551	T	G	0.00149872	0.00389725	0.70051179	5169	0.449776
0.449743	0.966644	G	A	0.00149014	0.00389709	0.70213246	5169	0.449743
0.464194	0.970138	T	C	-0.00713989	0.00386462	0.06466712	5169	0.464194

0.449302	0.966437	T	G	0.00141958	0.00389858	0.71571342	5169	0.449302
0.466893	0.990165	C	G	-0.0070277	0.0038254	0.06618455	5169	0.466893
0.466847	0.990406	A	C	-0.00701556	0.00382507	0.06663077	5169	0.466847
0.568967	0.998792	A	G	-0.00143739	0.00383078	0.7074434	5169	0.431033
0.360914	0.961208	G	C	-0.00234904	0.00404595	0.56144759	5169	0.360914
0.467049	0.989381	T	C	-0.00706694	0.00382651	0.0647628	5169	0.467049
0.467091	0.989165	G	T	-0.00707808	0.00382681	0.06436343	5169	0.467091
0.466824	0.990518	G	A	-0.00700985	0.0038249	0.06684108	5169	0.466824
0.466791	0.990697	G	A	-0.00700191	0.00382467	0.0671332	5169	0.466791
0.350803	0.945963	A	T	-0.00285839	0.00412229	0.48798554	5169	0.350803
0.557488	0.996489	T	C	-0.00157952	0.00383398	0.68029851	5169	0.442512
0.557864	0.996724	T	C	-0.00164435	0.00383449	0.66798854	5169	0.442136
0.378201	0.998692	T	C	-0.00536299	0.00391734	0.17094346	5169	0.378201
0.871735	0.999992	T	G	0.00775369	0.00570341	0.17394864	5169	0.128265
0.545898	0.998405	A	G	-0.00136893	0.00383203	0.72086753	5169	0.454102
0.871734	0.999992	A	C	0.0077538	0.00570342	0.17394282	5169	0.128266
0.462009	0.888256	G	A	-0.00803149	0.00402046	0.04575423	5169	0.462009
0.461965	0.883765	T	A	-0.00805124	0.00403037	0.04575558	5169	0.461965
0.462063	0.998608	G	A	0.00115867	0.003836	0.76256891	5169	0.462063
0.557194	0.987588	T	C	-0.00241727	0.00383927	0.52887326	5169	0.442806
0.823665	0.999836	G	A	0.00854046	0.00498245	0.08649262	5169	0.176335
0.377958	0.999155	C	T	-0.00509551	0.00391777	0.19334017	5169	0.377958
0.464761	0.995693	A	T	0.00177652	0.00383517	0.64314771	5169	0.464761
0.871734	0.99999	A	C	0.00775358	0.00570341	0.17395446	5169	0.128266
0.461952	0.882334	G	C	-0.00805321	0.00403347	0.04586897	5169	0.461952
0.461895	0.877154	C	G	-0.00807279	0.00404502	0.04596218	5169	0.461895
0.557249	0.987158	T	C	-0.002381	0.00383979	0.53512933	5169	0.442751
0.377229	0.994349	A	G	-0.00528464	0.00392814	0.17847225	5169	0.377229
0.860267	0.9176	A	G	0.00770625	0.00574192	0.17951556	5169	0.139733
0.557215	0.987397	C	G	-0.00240511	0.0038395	0.53097356	5169	0.442785
0.418045	0.999697	G	A	-0.00250572	0.00385213	0.51531235	5169	0.418045
0.418678	0.999895	G	A	-0.00251322	0.00385025	0.51385107	5169	0.418678
0.467949	0.988571	A	G	0.00081232	0.00383591	0.83225743	5169	0.467949
0.46185	0.999259	A	G	0.00109171	0.00383537	0.775876	5169	0.46185
0.463434	0.995756	C	T	0.00117277	0.00383622	0.7597825	5169	0.463434
0.464445	0.997807	C	G	0.00170291	0.00383184	0.65668702	5169	0.464445
0.477854	0.996228	A	G	-0.00051896	0.00381664	0.89182215	5169	0.477854
0.743318	0.999471	C	T	-0.00021943	0.00431823	0.95946623	5169	0.256682
0.464363	0.998439	G	A	0.00168212	0.00383087	0.66053365	5169	0.464363
0.415818	0.997987	T	A	0.0009358	0.00385118	0.80797623	5169	0.415818
0.463985	0.977887	G	A	0.00085479	0.003862	0.82480009	5169	0.463985
0.603234	0.994256	C	T	0.0114317	0.00389272	0.00332455	5169	0.396766
0.583851	0.993373	G	A	-0.00105243	0.00385864	0.78500758	5169	0.416149
0.416001	0.99687	G	A	0.00095535	0.00385258	0.80411709	5169	0.416001
0.415652	0.999052	G	A	0.00091802	0.00384982	0.81148982	5169	0.415652
0.415868	0.997675	G	C	0.0009411	0.00385158	0.80693112	5169	0.415868
0.970674	0.88263	C	G	0.00456312	0.0118828	0.70091669	5169	0.029326

0.415685	0.998825	G	A	0.00092143	0.00385008	0.81081577	5169	0.415685
0.614657	0.829946	G	C	-0.00166939	0.00427054	0.69581141	5169	0.385343
0.891477	0.98329	T	C	0.0101947	0.00615317	0.09753467	5169	0.108523
0.380196	0.817464	C	T	-0.0085947	0.00432185	0.04673787	5169	0.380196

SHIP

af_ship	oevar_ship	coded_ship	noncoded_ship	beta_ship	se_ship	p_ship	n_ship	maf_ship
0.459686	0.986475	G	A	-0.0109506	0.00759535	0.149372	543	0.459686
0.53622652	0.944519	G	C	0.0113383	0.00775203	0.14357	543	0.463773
0.42077293	0.978388	G	C	-0.0103203	0.00770528	0.180447	543	0.42077293
0.42080884	0.978243	G	A	-0.0103426	0.00770588	0.17954	543	0.42080884
0.51883425	0.973215	T	C	0.0107815	0.00774395	0.163846	543	0.481166
0.48113168	0.973312	G	A	-0.0107783	0.00774331	0.163936	543	0.48113168
0.48114457	0.973268	G	A	-0.0107797	0.00774363	0.163898	543	0.48114457
0.48112615	0.973318	T	A	-0.0107776	0.00774327	0.163964	543	0.48112615
0.51887753	0.973328	T	C	0.0107779	0.00774319	0.163948	543	0.481122
0.51775691	0.969361	T	C	0.0107533	0.00775465	0.165536	543	0.482243
0.48224217	0.969375	C	A	-0.0107543	0.00775452	0.165488	543	0.48224217
0.55870074	0.995808	T	C	-0.0111998	0.00786546	0.154469	543	0.441299
0.63335912	0.986561	G	A	0.00510464	0.00797095	0.521909	543	0.366641
0.48112339	0.973331	G	A	-0.0107772	0.00774318	0.163974	543	0.48112339
0.48111971	0.973348	G	A	-0.010777	0.00774307	0.163976	543	0.48111971
0.51887937	0.973348	G	C	0.0107767	0.00774307	0.163986	543	0.481121
0.47749816	0.991734	C	A	-0.0120101	0.00776407	0.121892	543	0.47749816
0.5224954	0.991775	T	A	0.0120109	0.00776403	0.121865	543	0.477505
0.51894843	0.97358	T	C	0.0107706	0.00774154	0.164142	543	0.481052
0.51891344	0.973463	T	C	0.0107738	0.0077423	0.16406	543	0.481087
0.47296869	0.939647	G	A	-0.0120372	0.00781749	0.123614	543	0.47296869
0.45464088	0.993633	T	C	-0.0120655	0.00765034	0.114768	543	0.45464088
0.44805157	0.983274	T	G	-0.0116322	0.00768985	0.130363	543	0.44805157
0.448907	0.994173	G	A	0.0104555	0.00781975	0.1812	543	0.448907
0.52776519	0.167303	G	A	-0.00196393	0.0185514	0.91569	543	0.472235
0.65126796	0.993325	T	C	-0.0103311	0.00792857	0.192567	543	0.348732
0.64657827	0.947161	G	A	0.00041351	0.00827237	0.960133	543	0.353422
0.46497053	0.995873	T	A	-0.00923825	0.00797478	0.246687	543	0.46497053
0.46497238	0.995857	G	C	-0.00923757	0.0079748	0.246723	543	0.46497238
0.5302081	0.977881	T	A	0.0111221	0.00768731	0.147951	543	0.469792
0.56971363	0.992749	T	C	-0.0132359	0.00785264	0.0918858	543	0.430286
0.57102486	0.993873	T	G	-0.012138	0.00784679	0.121893	543	0.428975
0.44087201	0.996213	G	A	0.0118147	0.00795893	0.137689	543	0.44087201
0.46384807	0.963607	G	C	0.00896057	0.00820423	0.27475	543	0.46384807
0.42659042	0.997072	T	A	0.0134643	0.00786656	0.0869739	543	0.42659042
0.56332689	0.992758	T	C	-0.0106475	0.00793568	0.179684	543	0.436673
0.57294199	0.996012	G	A	-0.0134089	0.00786356	0.0881584	543	0.427058
0.54107827	0.996873	T	A	0.00868325	0.00795221	0.274864	543	0.458922
0.45322007	0.970119	T	C	-0.0117252	0.00772981	0.129298	543	0.45322007
0.57121823	0.960638	T	G	-0.0104068	0.00821462	0.205203	543	0.428782
0.46614641	0.985924	C	A	-0.012706	0.00774329	0.100816	543	0.46614641
0.45753775	0.996347	G	A	-0.0113569	0.0076602	0.138183	543	0.45753775
0.45948435	0.993668	T	G	-0.00858144	0.00800685	0.283827	543	0.45948435
0.45948987	0.995636	G	A	-0.00869235	0.00798029	0.276053	543	0.45948987
0.45456262	0.975495	T	C	-0.0115877	0.00771876	0.133294	543	0.45456262

0.45908195	0.983047	T	G	-0.00764492	0.00814818	0.348123	543	0.45908195
0.54307919	0.997554	G	C	0.0113451	0.00764581	0.137852	543	0.456921
0.54307827	0.997558	C	A	0.0113445	0.00764579	0.137874	543	0.456922
0.4316779	0.988736	G	A	0.012126	0.00785497	0.122654	543	0.4316779
0.36804843	0.982422	G	C	-0.00272745	0.00812059	0.73697	543	0.36804843
0.45691897	0.997553	T	C	-0.0113456	0.00764581	0.137836	543	0.45691897
0.54308195	0.99755	T	G	0.0113462	0.00764582	0.137815	543	0.456918
0.45736924	0.99672	G	A	-0.0113819	0.00765368	0.136984	543	0.45736924
0.45737109	0.996717	G	A	-0.011382	0.00765367	0.136982	543	0.45737109
0.64137293	0.969265	T	A	0.00336041	0.00829215	0.685293	543	0.358627
0.57200092	0.959406	T	C	-0.0106185	0.00822669	0.196796	543	0.427999
0.56235359	0.988854	T	C	-0.0108465	0.00794866	0.172387	543	0.437646
0.37309853	0.997157	T	C	-0.00481856	0.00791766	0.5428	543	0.37309853
0.88165838	0.970473	T	G	-0.00763968	0.0119609	0.523003	543	0.118342
0.44195101	0.975386	G	A	0.00842891	0.00805541	0.295392	543	0.44195101
0.11871315	0.97708	C	A	0.00795742	0.0119383	0.505061	543	0.11871315
0.45435912	0.996356	G	A	-0.0113565	0.00772852	0.141716	543	0.45435912
0.45435912	0.996356	T	A	-0.0113565	0.00772852	0.141716	543	0.45435912
0.48123757	0.991337	G	A	-0.00996079	0.00784058	0.203937	543	0.48123757
0.56348987	0.9926	T	C	-0.0108145	0.00794266	0.173334	543	0.43651
0.83353591	0.973577	G	A	-0.0090938	0.0099117	0.35889	543	0.166464
0.62696961	0.997072	T	C	0.00483154	0.0079174	0.5417	543	0.37303
0.52126703	0.996285	T	A	0.0114748	0.00787762	0.145219	543	0.478733
0.11921	0.988668	C	A	0.00837811	0.0119052	0.481597	543	0.11921
0.45436096	0.996379	G	C	-0.0113562	0.00772845	0.141723	543	0.45436096
0.55253775	0.929136	G	C	0.0137417	0.00802022	0.0866426	543	0.447462
0.56200921	0.993575	T	C	-0.010712	0.00795096	0.177897	543	0.437991
0.62678637	0.979427	G	A	0.004209	0.00797248	0.59754	543	0.373214
0.1309618	0.923353	G	A	0.0137601	0.0118015	0.243628	543	0.1309618
0.43715396	0.995151	G	C	0.0107899	0.00794355	0.174362	543	0.43715396
0.38537569	0.996956	G	A	-0.00981888	0.00795422	0.217045	543	0.38537569
0.38558287	0.993777	G	A	-0.0101803	0.00799874	0.203112	543	0.38558287
0.51660681	0.989133	G	A	0.00908687	0.00786849	0.248155	543	0.483393
0.51045764	0.961637	G	A	0.00965181	0.00809391	0.233074	543	0.489542
0.51874862	0.989337	T	C	0.0101464	0.00785672	0.196554	543	0.481251
0.52031676	0.997197	G	C	0.0112935	0.00788147	0.151882	543	0.479683
0.50969429	0.955598	G	A	0.00978531	0.00790963	0.216036	543	0.490306
0.2269663	0.90447	T	C	-0.00278971	0.00962386	0.771913	543	0.2269663
0.47800092	0.997753	G	A	-0.0110825	0.00785415	0.158234	543	0.47800092
0.42189669	0.978759	T	A	0.0152775	0.00798404	0.0556826	543	0.42189669
0.47768692	0.975452	G	A	-0.010603	0.00789852	0.179467	543	0.47768692
0.34436556	0.986964	T	C	0.00990849	0.00781596	0.204896	543	0.34436556
0.58027256	0.988324	G	A	-0.0130404	0.00791982	0.0996502	543	0.419727
0.42163112	0.995303	G	A	0.0130349	0.0078584	0.0971719	543	0.42163112
0.42154807	0.995632	G	A	0.0130904	0.00785495	0.0956099	543	0.42154807
0.42157735	0.99582	G	C	0.013064	0.00785565	0.09631	543	0.42157735
0.03104144	0.719309	G	C	-0.0221084	0.0273471	0.41884	543	0.03104144

0.42153039	0.995917	G	A	0.0130873	0.00785433	0.0956628	543	0.42153039
0.62990055	0.829774	G	C	-0.00885344	0.00871733	0.309813	543	0.370099
0.89743554	0.95325	T	C	-0.0012671	0.0128217	0.921277	543	0.102564
0.62997882	0.854452	T	C	0.002174	0.00848338	0.797746	543	0.370021