Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Samani NJ, Erdmann J, Hall AS, et al. Genomewide association analysis of coronary artery disease. N Engl J Med 2007;357. DOI: 10.1056/NEJMoa072366.

Online Supplementary Materials

Genome-wide association analysis of coronary artery disease

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The supplementary materials have the following sections in order:

1. Recruitment of Subjects

WTCCC cases Cases were European Caucasians who had a validated history of either myocardial infarction (MI) or coronary revascularisation (coronary artery bypass surgery or percutaneous coronary angioplasty) before their 66th birthday. Recruitment was carried out on a national basis through (i) responses to a sustained UK-wide media campaign (ii) through responses to posters placed within hospitals and GP (family physician) surgeries throughout the UK and (iii) in a pilot-phase contacting patients listed on computer based coronary artery disease databases in the two lead centres (Leeds and Leicester). The recruitment period was from April 1998 to November 2003. The primary purpose was to recruit families with two or more available siblings with CAD for a linkage study called the BHF Family Heart Study (BHF-FHS). [1] During the course of the project we however also recruited subjects with CAD who had a family history of premature CAD (in parents or another sibling) but in whom a further affected sib was not available, for a related project called the GRACE Study. [2] In GRACE unaffected siblings were also recruited. In both studies affected subjects were only included if independent verification of history of CAD was obtained either via examination of hospital records or via the GP. For the WTCCC Study we selected individuals from the combined BHF-FHS and GRACE cohorts, to study 2,000 unrelated cases affected by premature CAD. From each family we selected first for the presence of MI and then on the age of onset of disease. 1,518 (76.4%) individuals come from families included in the BHF-FHS linkage analysis. [1] 470 (23.6%) individuals came from families included in the overlapping GRACE Project. [2]

WTCCC controls In the WTCCC Study, two independent European Caucasian control groups were studied. The British 1958 Birth Cohort (58BC, also known as the National Child Development Study), which includes all births in England, Wales and Scotland during one week in 1958, provided 1,504 samples. The second 1,500 (UK Blood Services [UKBS]) controls were selected from a sample of healthy blood donors recruited as part of the WTCCC project. More details about the control cohorts are provided in Ref 3. [3] Briefly, the subjects were about equally divided into males and females. Like the case collection, both control cohorts were geographically widely distributed across the UK. [3] The 58BC samples were by definition of the same age. The UKBS controls had a wide age range with the majority of subjects between 40-59 years. [3] Apart from gender and 10 year age-band other phenotypic information was not available on the control cohorts. There was no evidence of systematic or marked differences in overall allele frequencies between the two control groups. [3] Indeed,

significant associations were obtained for each of the strongly associated regions reported in this paper when control groups were analysed separately (data not shown).

German cases MI patients were ascertained by screening of >200,000 patient charts in 17 cardiac in-hospital rehabilitation centers. Index patients were selected from those who had suffered a MI prior to the age of 60 years. If at least one additional first-degree family member (preferentially a sibling) had suffered from MI or had severe coronary artery disease (percutaneous transluminal coronary angioplasty [PTCA] or bypass surgery [CABG]), the family (index patient, available parents and all siblings) was contacted and invited to participate in the study. [4, 5] Thus, as in the WTCCC Study, the phenotypic characterisation was based on familial clustering and premature onset of the phenotype (Table 1, main paper). All events in index patients and family members were validated through inspection of hospital charts. All index patients were Caucasians of German descent. The majority (>70%) was recruited in the vicinity of Augsburg and the Southern part of Germany (Clinics in Starnberg/Höhenried, Prien) in the years 1997-2002. Genotyping in German MI Family Study was performed on 875 patients. Like in the WTCCC study, only one subject from each family was selected for genotyping, either the youngest male MI patient, or preferentially, an affected female MI patient.

German controls All 1,644 controls subjects were Caucasians of German origin who participated in the population based MONICA/KORA Augsburg study in the years 1994/95 and a follow-up of this survey in the years 2004/05 that was conducted as part of the German National Genome Research Network (NGFN). [6] This survey represents a gender- and age-stratified random sample of all German residents of the Augsburg area and consists of individuals 25 to 74 years of age, with about 300 subjects for each 10-year increment. The population was studied by physical examination, blood testing, and a standardized interview including medical history, physical activity, medication, and personal habits. By questionnaire 22% of the probands reported a positive parental family history for MI.

The Peterborough and Fenland Research Ethic Committee and the University of Regensburg Ethics Committee approved the study protocols for the WTCCC Study and the German MI Family Study, respectively and all participants gave written informed consent.

2. Genotyping and quality control

Genotype calling was performed with the Chiamo++ algorithm in the WTCCC Study [3] and with the BRLMM analysis tool in the German MI Family Study, which agree well for SNPs with sufficient genotyping quality. [3] In the WTCCC Study [3], several filters were applied for exclusion of a subject based on the genotype data. These included a SNP call rate <97% (missingness), heterozygosity >30% or <23% across all SNPs, evidence of non-European ancestry, evidence that the sample was a duplicate or evidence that an individual was a relative of another subject in the study (> 86% IBS sharing). This resulted in the exclusion of 62 case subjects and 66 controls subjects (24 from the 58Bc cohort and 42 from the UKBS cohort) from the study **(Supplementary Table 7)**. Some of the filters were also applied to the German study resulting in the exclusion of 13 cases **(Supplementary Table 7)**.

Individual SNPs were excluded from a study if any of the following quality criteria was met: $p \leq 10^{-4}$ in test for deviation from Hardy-Weinberg equilibrium in the control groups (WTCCC 10,945 SNPs; German Study 39,907 SNPs); minor allele frequency (MAF) ≤1% in the cases and controls combined (WTCCC Study 70,365; German Study 62,303 SNPs); SNP call rate ≤98% per study group (WTCCC Study 109,139 SNPs; German Study 178,413 SNPs), trend-test $p \geq 10^{-3}$ between WTCCC control groups (1,933 SNPs); Some SNPs failed on more than one criterion. We also did not analyse X chromosome SNPs (see below). The combined effect was to reduce the number of evaluated SNPs in WTCCC to 377,857 and in the German Study to 272,602. The higher number in the WTCCC Study reflects the better performance of the Chiamo++ calling algorithm compared with the BRLMM algorithm which particularly reduced the number of SNPs that failed on the SNP call rate and the Hasrdy-Weinberg criterion.

In addition for all SNPs that came through the above filters and had an association test $p<10^{-3}$ the signal intensity plots were directly visually inspected by two independent reviewers in each study to exclude possible artefactual results due to miscalling. Assessment of signal intensity plots for a random 100 SNPs from the WTCCC Study and for 100 SNPs from German Study showed >95% agreement between independent assessors regarding suitability or non-suitability of a SNP based on visual discrimination of the genotypes.

The Affymetrix platform does not assay the Y chromosome. In addition, we excluded analysis of X chromosome SNPs for several reasons. First, the relative weight to be given to males and females in comparisons between cases and controls in the trend test statistic is unclear. In particular, because most loci on the X chromosome are subject to X inactivation, whether males should be treated as if they were homozygous females is unsettled. These issues have a different impact on the calculation and interpretation of the FPRP for X chromosome SNPs compared to the autosomal SNPs. Furthermore, under some of these assumptions the WTCCC had conducted an analysis of the X chromosome SNPs for their seven diseases. [3] No powerful signal emerged from CAD. Therefore in the analysis for this paper, we did not include the X chromosome SNPs.

To further ensure the quality of the genotyping on the Affymetrix 500K array we re-genotyped a total of 26 SNPs covering 6/9 regions including the lead SNPs for chromosome 9 and 6 using the Sequenom's iPLEX assay. Two multiplex reactions were designed and genotyped in 1,152 samples (UKBS controls and CAD cases from the WTCCC Study). The overall concordance rate between genotypes generated by the Affymetrix 500K array and the Sequenom iPLEX assay was 99.8% and did not differ between cases and controls. In addition, we validated the three most significant SNPs (rs1333049, rs6922269, and rs2943634) in 500 cases and 500 controls from the German Study using TaqMan based genotyping. The overall

concordance rate between genotypes generated by the Affymetrix 500K array and TaqMan was between 98.6-98.8% and did not differ between cases and controls.

3. Analysis for population sub-structure

In the WTCCC Study, geographic location was available for all cases (from the seven diseases) and both sets of controls. The WTCCC were therefore able to test for regional differences in allele frequencies and to compare P-values with and without adjustment for region. [3] Only 12 autosomal genetic loci were identified (plus one on the X chromosome) that showed marked geographic variation. [3] None of these regions featured in our analyses on CAD. Over-dispersion of tests for association in the trend tests, λ, was estimated by the method of Devlin & Roeder. [7] The estimate of λ for CAD was 1.06 and ranged from 1.03-1.11 for the other diseases. [3]. When we restricted the analysis to SNPs that passed our more stringent criteria (see Section 2), the estimate of λ was little changed at 1.07. In the German study the λ estimate was 1.02. In fact, in a prior study we extensively investigated population stratification in the entire German population. [8] The genetic differentiation is low between North and South Germany ($F_{st} = 1.7x10^{-4}$) and between East and South Germany ($F_{st} = 5.4x10^{-4}$). Such minor degree of population substructure cannot be detected from methods without using prior information of subpopulation membership. With respect to the present study, both cases and controls were ascertained to a large extent in the vicinity of Augsburg, Bavaria. Bavaria is genetically substantially more homogeneous than Germany: It is bounded by the Alps in the South, and it is geographically smaller as it is only one of 16 German federal states.

We thus consider that population sub-structure is negligible in both studies and unlikely to explain the associations observed. The Q-Q-plots for the two studies are shown in **Supplementary Figure 2**.

4. Additional information on statistical analysis

In the primary analysis all quality checked SNPs that displayed evidence for association with CAD in the WTCCC Study ($P<10^{-3}$ from the two-sided Cochran-Armitage trend test) were assessed for the false positive report probability (FPRP). [9] A small FPRP suggests that a SNP is unlikely to be a false positive. This approach employs the P-value, the assumed and estimated effect size, the estimated variability of the effect size and the expected proportion of true positive SNPs. [9] The main reason for preferring ordering by FPRP (rather than P-value alone) is that it can be interpreted without concern for multiple testing. [9] It is therefore easier to judge whether a SNP is worthy of further investigation. P-values are designed for hypothesis testing and not for screening. Having said this, as the P value contributes to the estimation of the FPRP, there is often similarity in the ordering of SNPs by the two methods, and indeed all the loci (on 1q43, 5q21.1, 6q25, 9p21, 16q23, 19q12, and 22q12) identified by the WTCCC in their analysis based on P values [3] were picked up by our approach with two additional loci (on chromosomes 2 and 16) **(Supplementary Table 1)**

The FPRP was calculated by modifying the method of Wacholder et al. [9] to use likelihood ratios in place of the ratio of tail areas. From a systematic literature search we estimate that one in 5,000 SNPs is a true positive. [10] Calculations were based on an alternative odds ratio of 1.25. The results were confirmed by a sensitivity analysis and a full Bayesian analysis of the noteworthy SNPs **(Supplementary Table 8)**. As suggested by Wacholder et al., [9] SNPs with a FPRP of less than 0.5 were further analysed. The first step in this attempt was to search for clustering of significant SNPs, i.e. the lead SNP(s) with the FPRP of less than 0.5 and all SNPs with a $p<10^{-3}$ within 100 kb of this lead SNP were considered to represent a single locus. The second step was to test for association of such chromosomal loci with MI in the

German Study. We used the global 5% test-level and the two-sided trend-test for the 9 distinct chromosomal loci harbouring one or multiple SNP(s) with a FPRP of <0.5 and adjustments for multiple testing between SNPs from different chromosomal regions were performed according to Šidak-Holm. [11] Power for validation in the German Study was estimated for each locus for an OR of 1.25 per allele and a significance level of 0.05 using the two-sided trend-test and allowing for multiple testing. Pooled ORs and CIs were calculated using a stratified fixed effects model.

Logistic regression analyses and population attributable fractions (PAF) estimates were determined in the German study using the lead SNP with lowest FPRP from the three replicated regions as described. [12] We performed this analysis in the German Study because the case and control subjects had been extensively phenotyped for cardiovascular risk factors in a comparable fashion [13] and also to reduce the chance of over-inflation of the estimates that would have arisen from carrying out the calculations in the screening (WTCCC) study.We determined the functional form of adjustments for age, gender, their interactions, the PROCAM score [14], and the Framingham risk score [15] using multivariate fractional polynomials. [16] We used both scores to maximise the adjustment for traditional risk factors and identify the independent risk related to the chromosomal loci. While taking into account standard cardiovascular risk factors, the difference in the fit to the data of models with and without SNP markers was measured using the deviance. [17] Sensitivity analyses using the Framingham risk score or the PROCAM score separately yielded consistent findings (results not shown).

5. Haplotype analysis

Haplotype association analysis was performed on the WTCCC data using the THESIAS software implementing the Stochastic-EM algorithm. [18] This allows one to simultaneously estimate haplotype frequencies and haplotype effects under the assumption of additive effects of haplotypes on phenotype. A global test of association between haplotypes and the phenotype was performed by a likelihood ratio test (LRT) (χ^2 with m-1 df in the case of m haplotypes). LRT statistic also allowed comparing the effects between subsets of haplotypes, in particular subsets of haplotypes carrying the same allele at a given locus.

Chromosome 9

In the chromosome 9 region, 19 SNPs were found associated with CAD in the WTCCC Study (**Supplementary Tables 1 and 3**). The 19 SNPs were in strong LD with each other, both in controls and in cases **(Figure 2 (main paper))**. However, two different blocks of LD could be distinguished, with very strong LD within each block (average |D'| > 0.90) and moderate LD (average |D'| ~ 0.60) between blocks. The first block (block 1) includes SNPs rs643319 to rs10965219 and the second block (block 2) includes SNPs rs9632884 to rs1333049 **(Figure 2 (main paper))**. The SNPs in block 1 generate 5 haplotypes with frequency greater than 2% that explained about 97% of the haplotype diversity of block 1. Only 3 tag SNPs (rs7044859, rs1292136 and rs7865618) were sufficient to characterize these 5 haplotypes. For block 2, two common haplotypes explained more than 90% (about 45% each) of all chromosomes, the estimated haplotype frequency of each of the other inferred haplotypes being less than 1%. Only one tag SNP was therefore required to characterize block 2. SNP rs1333049 was chosen as tagSNP as it was the strongest signal seen in single locus analysis **(Supplementary Table 1)**. As a consequence of this structure, haplotype association analysis in relation with the disease was performed using only 4 tag SNPs. The results of this analysis are shown in the

Table below. As expected, the haplotype frequency distribution was highly significantly different between cases and controls (χ^2 = 67.94 with 6 df, P=1x10^{-12}). It can be deduced from the table that the association was mainly due to two yin-yang (TTGG and ACAC) haplotypes whose frequencies were different between cases and controls, but in the opposite direction. By comparison to the TTGG haplotype, the OR for MI associated with the ACAC haplotype was 1.48 [1.34 – 1.64] (P=2.1x10^{-14}). Independent analysis of the German dataset identified the same risk haplotypes. The OR for MI associated with the ACAC haplotype compared with the TTGG haplotype was 1.34 (1.12, 1.59), P = 0.0012.

Chromosome 9. Association analysis between the main haplotypes derived from the rs7044859, rs12921396, rs7865618 and rs1333049 SNPs and risk of CAD in the WTCCC Study.

Polymorphisms				**Haplotype Frequency**	
rs7044859 (T/A)	**rs1292136 (C/T)**	**rs7865618 (A/G)**	**rs1333049 (C/G)**	**Controls**	**Cases**
T	C	G	G	0.042	0.037
T	T	A	C	0.055	0.059
T	T	A	G	0.042	0.037
T	T	G	C	0.074	0.078
T	T	G	G	0.333	0.271
A	C	A	C	0.324	0.386
A	C	A	G	0.107	0.098

Chromosome 6

To better clarify the association for chromosome 6, haplotype analysis was performed on the 8 SNPs located in the block of LD around rs6922269 **(Supplementary Figure 1A)**. This includes SNP rs4869954 to rs803446. These 8 SNPs generate 6 haplotypes with frequency greater that 2% in the WTCCC dataset that explained about 95% of the haplotype diversity. Only 4 tag SNPs (rs4869954, rs6922269, rs11155760 and rs803446) were sufficient to characterize these 6 haplotypes. Results of the haplotype analysis performed on these 4 tag SNPs are reported in the table below. As expected, the haplotype frequency distribution was highly significantly different between cases and controls (χ^2 = 20.45 with 5 df, P=0.001). In particular, the rs6922269-A allele was carried out by two haplotypes that tended to be more frequent in cases than in controls. These data were compatible with the hypothesis that these two haplotypes were homogeneously associated with increased risk of MI. The same two haplotypes were also identified as disease-associated in the German Study (data not shown).

Chromosome 6. Association between the main haplotype derived from rs4869954, rs6922269, rs11155760 and rs803446 and risk of CAD in the WTCCC Study

Polymorphisms				**Haplotype Frequency**	
rs4869954 (T/C)	**rs6922269 (G/A)**	**rs11155760 (A/T)**	**rs803446 (G/A)**	**Controls**	**Cases**
T	G	A	G	0.431	0.401
T	G	A	A	0.194	0.189
T	G	T	G	0.063	0.064
C	G	A	G	0.058	0.052
C	A	A	G	0.047	0.055
C	A	T	G	0.198	0.230

Chromosome 2

Haplotype analysis was also performed on all SNPs located in the LD block around rs2943634. This includes 22 SNPs from rs13395556 to rs10933137 (**Figure 1B, supplement material**). As a consequence of strong LD within this block, 8 haplotypes with frequency greater than 2.5% that explained more than 90% of the whole chromosomes were inferred in the WTCCC Study. These 8 haplotypes were tagged by 7 SNPs (rs13395556, rs2943634, rs2943640, SNP-A-2198190, rs950503, rs2673148 and rs10933137) among which the rs2943634 was the strongest signal seen in single locus analysis. The rs2943634-A allele was carried out by only two haplotypes that were both less frequent in cases than in controls. By symmetry, the 6 haplotypes carrying the rs2943634-G allele were on average more frequent in cases than in controls and detailed haplotype analysis showed that the other associations with MI observed within this block of LD were in fact due to LD with the rs2943634. Analysis of the German Study showed similar results (data not shown).

Association between haplotypes derived from rs13395556, rs2943634, rs2943640, SNP-A-2198190, rs950503, rs2673148 and rs10933137 and the risk of CAD in the WTCCC Study

Polymorphisms							**Haplotype Frequency**	
rs13395556 (C/G)	rs2943634 (C/A)	rs2943640 (C/A)	SNP-A-2198190 (T/C)	rs950503 (G/A)	rs2673148 (C/A)	rs10933137 (C/T)	Controls	Cases
C	C	C	T	G	C	C	0.045	0.056
C	C	C	T	G	C	T	0.274	0.301
C	C	C	T	A	A	C	0.139	0.133
C	C	A	T	G	A	C	0.025	0.029
C	A	A	T	G	A	C	0.294	0.260
C	A	A	T	G	A	T	0.026	0.021
G	C	C	T	G	C	T	0.034	0.035
G	C	C	C	G	C	C	0.076	0.071

6. Selection and analysis of candidate genes

We searched PubMed for original articles published before May, 2007 that reported statistically significant associations between specific genotypes and MI or CAD. Search terms included: *myocardial infarction, coronary artery disease, association study, polymorphism,* and *genetic association.* Reports were included if they fulfilled the following criteria: either i) positive association a single large study (n>500 cases), or ii) positive association in two smaller studies (each >250 cases), or iii) positive association in more than two studies (each >250 cases) if another published report was negative or iv) positive association in meta-analyses. [10] We identified a total of 126 genetic variants in 76 genes previously associated with CAD. In addition, we analysed 15 genes mentioned by Morgan et al. [19] that did not meet our selection criteria (16 SNPs).

7. Supplementary Tables 1-8

Supplementary Table 1. Details on SNPs meeting quality criteria* in the WTCCC study with $p < 10^{-3}$ from the trend test and a false positive report probability (FPRP)# of < 0.5

Chromosome	SNP	Position	Minor Allele	Risk Allele	MAF (controls)	Genotype Cases			Genotype Controls			Per risk allele OR	P-value	FPRP
						Min	Het	Maj	Min	Het	Maj			
1	rs2133189	219202837	C	T	0.29	136	702	1088	266	1192	1476	1.22 (1.12,1.34)	1.38E-05	0.473
1	rs17465637	219211924	A	C	0.29	133	702	1089	265	1191	1480	1.23 (1.12,1.34)	1.00E-05	0.399
2	rs2943634	226893585	A	C	0.34	177	799	936	354	1304	1262	1.22 (1.11,1.33)	1.19E-05	0.466
5	rs383830	99976881	A	T	0.22	56	588	1278	151	990	1793	1.27 (1.14,1.4)	5.72E-06	0.269
5	rs449650	99976917	T	G	0.22	57	587	1280	151	990	1796	1.27 (1.14,1.4)	6.74E-06	0.296
5	rs565928	99981589	T	C	0.22	61	581	1282	155	988	1794	1.27 (1.14,1.4)	5.71E-06	0.270
6	rs6922269	151345099	A	A	0.25	179	775	971	183	1118	1637	1.23 (1.13,1.35)	6.33E-06	0.291
9	rs643319	22007836	A	C	0.49	391	945	586	751	1464	711	1.26 (1.16,1.37)	3.13E-08	0.002
9	rs7044859	22008781	A	A	0.43	449	972	502	539	1447	950	1.26 (1.16,1.36)	4.82E-08	0.004
9	rs523096	22009129	G	A	0.46	314	960	649	637	1442	857	1.22 (1.13,1.33)	1.43E-06	0.094
9	rs518394	22009673	C	G	0.46	310	964	648	631	1445	856	1.23 (1.13,1.33)	1.41E-06	0.092
9	rs10757264	22009732	G	G	0.47	509	976	437	623	1485	828	1.24 (1.15,1.35)	1.89E-07	0.013
9	rs10965212	22013795	A	A	0.45	513	950	459	603	1428	895	1.29 (1.19,1.4)	9.54E-10	0.000
9	rs1292136	22014351	T	C	0.49	382	951	590	746	1482	708	1.28 (1.18,1.39)	4.93E-09	0.000
9	rs7049105	22018801	G	G	0.45	506	950	461	593	1439	897	1.29 (1.19,1.4)	1.05E-09	0.000
9	rs10965215	22019445	A	A	0.45	506	954	463	588	1447	902	1.29 (1.19,1.4)	5.15E-10	0.000
9	Rs564398	22019547	C	T	0.44	277	925	721	583	1428	921	1.27 (1.17,1.38)	1.79E-08	0.001
9	rs7865618	22021005	G	A	0.45	289	929	706	619	1429	888	1.29 (1.19,1.4)	1.33E-09	0.000
9	rs10965219	22043687	G	G	0.46	530	956	439	613	1444	876	1.31 (1.21,1.43)	4.99E-11	0.000
9	rs9632884	22062301	G	C	0.48	381	949	592	818	1422	693	1.35 (1.24,1.46)	3.80E-13	0.000
9	rs6475606	22071850	C	T	0.47	380	957	588	830	1425	683	1.37 (1.26,1.48)	4.39E-14	0.000
9	rs4977574	22088574	A	G	0.48	382	937	605	804	1435	698	1.35 (1.24,1.46)	4.28E-13	0.000
9	rs2891168	22088619	A	G	0.48	383	938	605	803	1435	698	1.35 (1.24,1.46)	5.90E-13	0.000
9	rs1333042	22093813	A	G	0.49	365	939	617	770	1426	724	1.34 (1.23,1.45)	2.45E-12	0.000
9	rs1333048	22115347	A	C	0.49	354	951	619	781	1423	730	1.36 (1.25,1.48)	1.28E-13	0.000
9	rs1333049	22115503	G	C	0.47	378	960	586	829	1431	676	1.37 (1.27,1.49)	1.80E-14	0.000
16	rs8055236	81769899	T	G	0.20	42	539	1342	133	895	1907	1.27 (1.14,1.41)	9.73E-06	0.382
16	Rs889595	85069581	T	A	0.30	142	709	1068	262	1233	1432	1.23 (1.12,1.34)	1.13E-05	0.421
19	rs7250581	34756236	A	G	0.22	75	551	1295	144	997	1779	1.26 (1.14,1.39)	9.12E-06	0.357
22	Rs688034	25014189	T	T	0.31	265	832	823	276	1266	1386	1.22 (1.12,1.33)	6.90E-06	0.334

Legend to Supplementary Table 1: *The quality criteria are described in Supplementary Materials section 2. # The calculation of the false positive report probability (FPRP) is described in Supplementary Materials section 4. MAF, minor allele frequency; OR, odds

ratio (95% CI);. Min (Maj), number of subjects being homozygous for the minor (major) allele. Het, number of heterozygous subjects. Bold horizontal lines mark distinct chromosomal regions.

Supplementary Table 2. Details on SNPs meeting quality criteria* which show association in the WTCCC Study but not in the German MI Family Study

				WTCCC									German MI Study								
Chromo-some	SNP	Position	Risk Allele	MAF Controls	Genotypes Cases			Genotypes Controls			Per Allele OR	P value	MAF Controls	Genotypes Cases			Genotype Controls			Per Allele OR	P-value	FPRP
					Min	Het	Maj	Min	Het	Maj				Min	Het	Maj	Min	Het	Maj			
1	rs17672135	236771637	T	0.13	28	357	1530	30	721	2163	1.29 (1.13,1.47)	1.04E-04	0.13	14	194	627	24	357	1228	0.94 (0.79,1.12)	0.48	0.999
5	rs383830	99976881	T	0.22	56	588	1278	151	990	1793	1.27 (1.14,1.4)	5.72E-06	0.20	29	261	460	73	511	1033	0.94 (0.81,1.1)	0.45	0.996
16	rs8055236	81769899	G	0.20	42	539	1342	133	895	1907	1.27 (1.14,1.41)	9.73E-06	0.19	28	261	559	69	470	1086	1.00 (0.86,1.16)	0.99	0.978
16	rs889595	85069581	A	0.30	142	709	1068	262	1233	1432	1.23 (1.12,1.34)	1.13E-05	0.30	63	374	411	124	707	766	1.02(0.89,1.17)	0.75	0.983
19	rs7250581	34756236	G	0.22	75	551	1295	144	997	1779	1.26(1.14,1.39)	9.12E-06	0.18	28	267	551	45	477	1085	0.91(0.78,1.06)	0.21	0.999
22	rs688034	25014189	T	0.31	265	832	823	276	1266	1386	1.22 (1.12,1.33)	6.90E-06	0.33	90	401	368	165	740	737	1.06 (0.93,1.2)	0.37	0.903

*The quality criteria are described in Supplementary Materials section 2. FPRP, false positive report probability calculated as described in Supplementary Materials Section 4. MAF, minor allele frequency; OR, odds ratio (95% CI). Min (Maj), number of subjects being homozygous for the minor (major) allele. Het, number of heterozygous subjects. Power to replicate the SNPs in the German study using the global significance level of 5%, the two-sided trend-test and assuming a true OR of 1.25 was: rs17672135 (43%), rs383830 (55%), rs8055236 (51%), rs889595 (73%), rs7250581 (55%) and rs688034 (80%).

Supplementary Table 3. Combined Analysis: Details on SNPs meeting quality criteria* with a false positive report probability (FPRP)# of < 20% from a combined analysis of SNPs with p $<10^{-3}$ in both the WTCCC and German MI Family Study

					WTCCC									German MI study									Pooled			
Chromosome	SNP	Position	Minor Allele	Risk Allele	MAF Controls	Genotypes Cases			Genotypes Controls			Per Risk Allele OR	P-value	MAF Controls	Genotypes Cases			Genotypes Controls			Per Risk Allele OR	P-value	Per Risk Allele OR	P-value	FPRP
						Min	Het	Maj	Min	Het	Mah				Min	Het	Maj	Min	Het	Maj					
1	rs599839	109534208	G	A	0.23	76	587	1260	144	1052	1740	1.24 (1.12,1.38)	2.19E-05	0.22	26	208	522	82	574	986	1.39 (1.19,1.63)	3.17E-05	1.29 (1.18,1.4)	4.05E-09	0.001
1	rs3008621	219192441	A	G	0.14	24	410	1488	68	712	2153	1.25 (1.1,1.41)	3.48E-04	0.15	7	174	645	30	405	1158	1.34 (1.12,1.61)	1.67E-03	1.28 (1.15,1.41)	1.92E-06	0.144
1	rs17465637	219211924	A	C	0.29	133	702	1089	265	1191	1480	1.23 (1.12,1.34)	1.00E-05	0.26	49	306	502	115	627	889	1.15 (1.01,1.32)	3.82E-02	1.20 (1.12,1.3)	1.27E-06	0.131
2	rs2943634	226893585	A	C	0.34	177	799	936	354	1304	1262	1.22 (1.11,1.33)	1.19E-05	0.36	96	362	397	221	755	664	1.20 (1.06,1.35)	4.33E-03	1.21 (1.13,1.3)	1.61E-07	0.019
6	rs6922269	151345099	A	A	0.25	179	775	971	183	1118	1637	1.23 (1.13,1.35)	6.33E-06	0.26	69	373	410	117	607	915	1.24 (1.09,1.41)	1.14E-03	1.23 (1.15,1.33)	2.90E-08	0.002
9	rs643319	22007836	A	C	0.51	391	945	586	751	1464	711	1.26 (1.16,1.37)	3.13E-08	0.49	144	376	236	363	863	407	1.22 (1.08,1.38)	1.84E-03	1.25 (1.16,1.34)	2.21E-10	0.000
9	rs7044859	22008781	A	A	0.43	449	972	502	539	1447	950	1.26 (1.16,1.36)	4.82E-08	0.45	194	343	187	295	853	471	1.28 (1.13,1.45)	1.42E-04	1.26 (1.18,1.35)	2.90E-11	0.000
9	rs523096	22009129	G	A	0.46	314	960	649	637	1442	857	1.22 (1.13,1.33)	1.43E-06	0.45	126	360	272	304	867	465	1.22 (1.08,1.39)	1.79E-03	1.22 (1.14,1.31)	8.64E-09	0.001
9	rs518394	22009673	C	G	0.46	310	964	648	631	1445	856	1.23 (1.13,1.33)	1.41E-06	0.45	115	354	274	293	823	459	1.26 (1.11,1.43)	3.86E-04	1.24 (1.15,1.32)	2.10E-09	0.000
9	rs10757264	22009732	G	G	0.47	509	976	437	623	1485	828	1.24 (1.15,1.35)	1.89E-07	0.48	208	384	170	351	881	411	1.20 (1.06,1.36)	4.20E-03	1.23 (1.15,1.32)	3.02E-09	0.000
9	rs10965212	22013795	A	A	0.45	513	950	459	603	1428	895	1.29 (1.19,1.4)	9.54E-10	0.47	228	417	205	344	846	440	1.19 (1.06,1.34)	3.70E-03	1.26 (1.18,1.34)	2.18E-11	0.000
9	rs1292136	22014351	T	C	0.51	382	951	590	746	1482	708	1.28 (1.18,1.39)	4.93E-09	0.49	143	380	234	361	865	410	1.21 (1.07,1.37)	2.93E-03	1.26 (1.17,1.35)	6.39E-11	0.000
9	rs7049105	22018801	G	G	0.45	506	950	461	593	1439	897	1.29 (1.19,1.4)	1.05E-09	0.47	201	365	171	346	836	437	1.22 (1.08,1.38)	1.83E-03	1.27 (1.18,1.36)	9.21E-12	0.000
9	rs10965215	22019445	A	A	0.45	506	954	463	588	1447	902	1.29 (1.19,1.4)	5.15E-10	0.47	211	375	176	343	854	447	1.25 (1.11,1.42)	3.63E-04	1.28 (1.2,1.37)	8.28E-13	0.000
9	rs564398	22019547	C	T	0.44	277	925	721	583	1428	921	1.27 (1.17,1.38)	1.79E-08	0.42	108	348	305	264	842	530	1.23 (1.08,1.4)	1.31E-03	1.26 (1.17,1.35)	8.58E-11	0.000
9	rs7865618	22021005	G	A	0.45	289	929	706	619	1429	888	1.29 (1.19,1.4)	1.33E-09	0.43	138	390	331	286	842	511	1.20 (1.07,1.36)	2.71E-03	1.26 (1.18,1.35)	1.90E-11	0.000
9	rs10965219	22043687	G	G	0.46	530	956	439	613	1444	876	1.31 (1.21,1.43)	4.99E-11	0.48	225	407	195	349	826	425	1.19 (1.05,1.34)	5.27E-03	1.27 (1.19,1.36)	2.33E-12	0.000
9	rs9632884	22062301	G	C	0.52	381	949	592	818	1422	693	1.35 (1.24,1.46)	3.80E-13	0.47	247	424	179	355	818	453	1.33 (1.18,1.49)	2.67E-06	1.34 (1.26,1.44)	4.68E-18	0.000

9	rs6475606	22071850	C	T	0.53	380	957	588	830	1425	683	1.37 (1.26,1.48)	4.39E-14	0.47	231	443	186	351	824	461	1.28 (1.13,1.44)	5.16E-05	1.34 (1.25,1.43)	1.45E-17	0.000
9	rs4977574	22088574	A	G	0.52	382	937	605	804	1435	698	1.35 (1.24,1.46)	4.28E-13	0.47	239	452	169	354	826	463	1.36 (1.2,1.53)	5.20E-07	1.35 (1.26,1.45)	1.03E-18	0.000
9	rs2891168	22088619	A	G	0.52	383	938	605	803	1435	698	1.35 (1.24,1.46)	5.90E-13	0.47	238	451	169	351	827	462	1.36 (1.2,1.53)	4.87E-07	1.35 (1.26,1.44)	1.34E-18	0.000
9	rs1333049	22115503	G	C	0.53	378	960	586	829	1431	676	1.37 (1.27,1.49)	1.80E-14	0.48	233	453	158	349	831	425	1.33 (1.18,1.51)	3.40E-06	1.36 (1.27,1.46)	2.91E-19	0.000
10	rs622472	44069217	C	A	0.14	30	394	1500	46	711	2181	1.19 (1.05,1.34)	7.00E-03	0.16	11	144	603	43	431	1168	1.51 (1.25,1.82)	1.20E-05	1.28 (1.16,1.42)	1.84E-06	0.179
10	rs687175	44071916	C	T	0.13	29	384	1513	41	708	2186	1.20 (1.06,1.36)	3.76E-03	0.16	11	141	608	43	427	1167	1.54 (1.27,1.85)	5.93E-06	1.30 (1.17,1.44)	4.77E-07	0.071
10	rs535949	44072336	T	G	0.13	27	380	1513	41	698	2185	1.21 (1.07,1.37)	2.85E-03	0.16	11	142	604	43	427	1163	1.52 (1.26,1.84)	8.56E-06	1.30 (1.18,1.45)	4.06E-07	0.062
10	rs671765	44072982	G	A	0.13	29	383	1512	42	706	2186	1.20 (1.06,1.37)	3.49E-03	0.16	11	142	606	42	430	1166	1.53 (1.27,1.84)	7.55E-06	1.30 (1.17,1.44)	5.10E-07	0.073
10	rs501120	44073873	C	T	0.13	21	375	1509	33	695	2176	1.24 (1.09,1.41)	1.31E-03	0.16	11	139	602	43	423	1154	1.54 (1.28,1.86)	5.28E-06	1.33 (1.2,1.48)	9.46E-08	0.023
10	rs1746048	44095830	T	C	0.13	29	381	1514	41	706	2184	1.21 (1.07,1.37)	2.96E-03	0.16	14	162	684	42	425	1169	1.47 (1.23,1.76)	1.61E-05	1.29 (1.17,1.43)	5.73E-07	0.069
10	rs1746049	44096316	T	C	0.13	28	373	1520	39	695	2201	1.21 (1.07,1.37)	3.17E-03	0.15	14	158	689	40	418	1186	1.46 (1.22,1.75)	2.64E-05	1.29 (1.16,1.43)	8.77E-07	0.097
15	rs17228212	65245693	C	C	0.30	211	856	856	250	1235	1451	1.19 (1.09,1.3)	1.18E-04	0.26	81	362	417	121	600	923	1.26 (1.11,1.44)	3.09E-04	1.21 (1.13,1.3)	1.98E-07	0.018

*The quality criteria are described in Supplementary Materials section 2. # The calculation of the false positive report probability (FPRP) is described in Supplementary Materials section 4. MAF, minor allele frequency. OR, odds ratio (with 95% CI). Min (Maj), number of subjects being homozygous for the minor (major) allele. Het, number of heterozygous subjects. The pooled OR and p value are from a stratified fixed effects model.

TABLE 4. Comparison of the effects of the seven associated loci separately in subjects with a history of myocardial infarction (MI, n = 1377) and with subjects with history of Coronary Artery Disease only (CAD, n = 549) in the WTCCC Study

CHR.	POSITION	SNP	MINOR ALLELE	RISK ALLELE	OR MI (95% CI)	P-VALUE MI	OR CAD (95% CI)	P-VALUE CAD	P-VALUE FOR HETEROGENEITY OF RISK
1	109534208	**rs599839**	G	A	1.24 (1.11,1.39)	$1.47x10^{-4}$	1.25 (1.06,1.48)	$6.21x10^{-3}$	0.95
1	219211924	**rs17465637**	A	C	1.24 (1.12,1.38)	$2.36x10-^{5}$	1.19 (1.03,1.37)	$1.81x10^{-2}$	0.58
2	226893585	**rs2943634**	A	C	1.21 (1.10,1.33)	$1.44x10-^{4}$	1.24 (1.08,1.42)	$2.60x10^{-3}$	0.74
6	151345099	**rs6922269**	A	A	1.24 (1.12,1.38)	$2.39x10-^{5}$	1.21 (1.05,1.39)	$1.06x10^{-2}$	0.69
9	22115503	**rs1333049**	C	C	1.35 (1.23,1.48)	$1.00x10-^{10}$	1.44 (1.27,1.64)	$2.47x10^{-14}$	0.32
10	44073873	**rs501120**	C	T	1.20 (1.04,1.39)	$1.17x10^{-2}$	1.34 (1.08,1.66)	$6.76x10^{-3}$	0.38
15	65245693	**rs17228212**	C	C	1.12 (1.01,1.23)	$2.94x10^{-2}$	1.39 (1.21,1.59)	$3.24x10^{-6}$	0.004

Legend to Table 4: See legends to Supplementary Tables 2 and 3 for explanation of terms. Odds ratios (OR) with 95% CI are per copy of the risk allele without adjustments for covariates. The P value for interaction is from a test of whether the effect in subjects with MI is different from that in subjects with CAD.

TABLE 5 Comparison of effects of the seven associated loci in men and women separately from combined analysis of the WTCCC Study and German Study

CHR.	POSITION	SNP	MINOR ALLELE	RISK ALLELE LLELE	OR MALE (95% CI)	P VALUE MALE	OR FEMALE (95% CI)	P VALUE FEMALE	P VALUE INTER-ACTION
1	109534208	**rs599839**	G	A	1.36 (1.16,1.59)	$1.33x10^{-4}$	1.27 (1.14,1.41)	$7.61x10^{-6}$	0.50
1	219211924	**rs17465637**	A	C	1.24 (1.12,1.36)	$1.15x10^{-5}$	1.19 (1.04,1.37)	$1.24x10^{-2}$	0.67
2	226893585	**rs2943634**	A	C	1.20 (1.10,1.32)	$4.48x10^{-5}$	1.22 (1.07,1.39)	$2.30x10^{-3}$	0.86
6	151345099	**rs6922269**	A	A	1.24 (1.13,1.37)	$4.56x10^{-6}$	1.23 (1.07,1.41)	$3.13x10^{-3}$	0.87
9	22115503	**rs1333049**	C	C	1.35 (1.24,1.47)	$7.03x10^{-12}$	1.35 (1.19,1.52)	$1.90x10^{-6}$	0.99
10	44073873	**rs501120**	C	T	1.30 (1.14,1.48)	$8.20x10^{-5}$	1.56 (1.27,1.91)	$1.30x10^{-5}$	0.14
15	65245693	**rs17228212**	C	C	1.24 (1.13,1.36)	$7.68x10^{-6}$	1.16 (1.02,1.33)	$2.56x10^{-2}$	0.47

Legend to Table 5: See legends to Supplementary Tables 2 and 3 for explanation of terms. There were 2,117 male cases and 2,259 male controls and 684 female cases and 2,323 female controls. The odds ratios (OR) with 95% CI are per copy of the risk allele without adjustments for covariates. The P value for interaction is from a test of whether the effect in men and women is different.

TABLE 6: Candidate gene analysis

GeneSymbol	Variant	AlternativeSNP	r^2	D´	Code#	WTCCCstudy				Germandata			
						QC	MAF	OR	P value	QC	MAF	OR	p value
ABCA1	Cys564Thr				3								
ABCA1	**Lys1587Arg**	**SNP_A-2072988**			**1**	N				**Y**	**0.26**	**0.76 [0.66,0.88]**	**0.0001**
ABCA1	**Arg219Lys**	**rs2472433**	**1.00**		**2**	Y	0.26	1.02[0.92,1.13]	0.85	**Y**	**0.28**	**0.79 [0.69,0.91]**	**0.001**
ADD1	Gly460Trp	rs2239728	0.95		2	Y	0.20	1.01[0.90,1.13]	0.50	Y	0.19	1.07 [0.92,1.24]	0.39
ADD1		rs4690001	0.87		2	Y	0.21	1.02[0.91,1.14]	0.53	Y	0.21	1.05 [0.91,1.22]	0.5
ADD1		rs1263345	0.91		2	Y	0.20	1.00[0.89,1.12]	0.37	Y	0.20	1.03 [0.88,1.20]	0.71
ADD1		rs17833250		1.00	2	Y	0.28	0.98[0.88,1.08]	0.67	Y	0.31	0.90 [0.78,1.02]	0.1
ADD1		rs10026792		1.00	2	Y	0.29	0.97[0.87,1.07]	0.49	Y	0.32	0.91 [0.79,1.04]	0.15
ADD1		rs6600769		1.00	2	Y	0.28	0.99[0.90,1.10]	0.92	Y	0.30	0.88 [0.77,1.01]	0.07
ADD1		rs422734		1.00	2	Y	0.29	1.06[0.96,1.17]	0.18	N			
ADD1		rs16843589		1.00	2	N				N			
ADD1		**rs1014947**		**1.00**	**2**	Y	0.28	0.99[0.89,1.09]	0.84	**Y**	**0.30**	**0.86 [0.75,0.98]**	**0.02**
ADH1C	Ile350Val/Phe350Val				3								
ACDC	+276G/T	rs3821799		1.00	2	Y	0.44	0.92[0.84,1.01]	0.54	Y	0.45	0.99 [0.88,1.13]	0.92
ACDC		rs3774261		1.00	2	Y	0.38	0.92[0.84,1.01]	0.25	Y	0.39	0.97 [0.86,1.11]	0.68
ACDC		rs6773957		1.00	2	Y	0.38	0.91[0.83,1.00]	0.20	Y	0.39	0.97 [0.85,1.10]	0.65
ACDC	Gly15Gly				3								
ADRB1	Arg389Gly				3								
ADRB2	Glu27Gln				3								
ADRB2	Thr164Ile				3								
ADRB2	Gly16Arg				3								
ADRB3	Arg64Trp				3								
AGER	-429C/T				3								
AGER	-374T/A	rs1035798	0.94		2	Y	0.21	0.96[0.86,1.07]	0.88	N			
AGER	Gly82Ser				3								
AGT	Thr174Met	rs11122577		1.00	2	Y	0.16	1.06[0.94,1.20]	0.59	Y	0.18	1.06 [0.90,1.25]	0.48
AGT	Thr235Met	rs11122577		1.00	2	Y	0.16	1.06[0.94,1.20]	0.59	Y	0.18	1.06 [0.90,1.25]	0.48
AGT		rs11122576		1.00	2	Y	0.09	1.03[0.87,1.21]	0.69	N			
AGT		rs2071406		1.00	2	Y	0.04	1.18[0.92,1.50]	0.14	Y	0.05	0.84 [0.62,1.11]	0.2
AGT		**rs2071404**		**1.00**	**2**	Y	0.11	1.02[0.88,1.18]	0.81	**Y**	**0.12**	**1.22 [1.01,1.47]**	**0.03**

AGT	-6C/T			3									
AGTR1	+1166A/C			3									
AGTR1	-825T/A	SNP_A-2079652		1	N				N				
AGTR1	-1106A/T			3									
AGTR1	+10208A/G			3									
AGTR1	Leu191Leu	rs13097326	1.00	2	Y	0.29	0.94[0.85,1.03]	0.35	Y	0.26	1.05 [0.91,1.21]	0.51
AGTR2	+1675G/A			3									
ALOX5AP	+16698A/G			3									
ALOX5AP	+2353A/T			3									
ALOX5AP	+22804A/C			3									
APOA1	-75G/A			3									
APOA4	Gln380His			3									
APOA5	-1131T/C			3									
APOA5	Ser19Trp			3									
APOE	Arg130Cys			3									
APOE	Arg176Cys			3									
CCL11	Ala23Thr			3									
CCL5	-403G/A	rs16971600	1.00	2	N				N				
CCL5		rs1065341	1.00	2	Y	0.05	1.05[0.85,1.30]	0.73	N				
CCL5		rs4796120	1.00	2	Y	0.10	0.98[0.84,1.13]	0.96	N				
CCL5		rs16963927	1.00	2	Y	0.05	0.95[0.77,1.17]	0.33	N				
CCL5		rs16971624	1.00	2	N				Y	0.05	0.93 [0.70,1.23]	0.63
CCL5		rs4796123	1.00	2	Y	0.12	1.03[0.89,1.18]	0.68	N				
CCR2	Val64Ile			3									
CD14	-260C/T			3									
CD36	-33137A/G			3									
CD36	-31118A/G			3									
CD36	+25443C/T	rs3211928	1.00	2	Y	0.43	1.01[0.92,1.11]	0.42	N				
CD36		rs3211931	1.00	2	Y	0.43	1.01[0.92,1.11]	0.44	Y	0.46	1.02 [0.91,1.16]	0.69
CD36		rs3211932	1.00	2	Y	0.43	1.01[0.92,1.11]	0.45	Y	0.45	0.97 [0.86,1.09]	0.63
CD36	27645del>ins			3									
CD36	30294G/C			3									
CETP	-629C/A	SNP_A-2182111		1	N				N				
CETP	ILe405Val	rs1800774	1.00	2	N				N				
MHC2TA	-168G/A			3									

COMT	**Val158Met**	**rs4646312**		**1.00**	**2**	**Y**	**0.40**	**0.90[0.82,0.98]**	**0.01**	**Y**	**0.37**	**0.90 [0.79,1.01]**	**0.08**
COMT		**rs4633**	**0.97**		**2**	**Y**	**0.48**	**0.87[0.80,0.95]**	**0.001**	Y	0.46	0.96 [0.85,1.09]	0.53
CPB2	Ala169Thr	rs9526140	1.00		2	Y	0.33	1.01[0.92,1.11]	0.68	Y	0.33	0.93 [0.82,1.06]	0.29
CPB2		rs9534307	1.00		2	Y	0.33	1.01[0.92,1.12]	0.62	Y	0.33	0.94 [0.82,1.07]	0.33
CPB2		rs9316180	1.00		2	N				N			
CPB2		rs9316179	1.00		2	Y	0.33	1.01[0.92,1.11]	0.79	N			
CPB2		rs9567613	1.00		2	Y	0.33	1.02[0.92,1.12]	0.62	Y	0.33	0.95 [0.83,1.08]	0.4
CPB2		rs11618062	1.00		2	Y	0.33	1.01[0.92,1.11]	0.67	Y	0.33	0.94 [0.82,1.07]	0.31
CPB2		rs953412	1.00		2	Y	0.08	1.07[0.90,1.26]	0.58	N			
CPB2		rs7337140		1.00	2	Y	0.25	1.07[0.97,1.19]	0.13	N			
CPB2		rs1548325		1.00	2	Y	0.25	1.02[0.92,1.13]	0.52	N			
CPB2		rs1926446		1.00	2	Y	0.28	1.03[0.93,1.14]	0.49	Y	0.29	1.00 [0.88,1.14]	1
CPB2		rs1926447		1.00	2	Y	0.28	1.03[0.93,1.14]	0.46	N			
CPB2		rs1022952		1.00	2	N				N			
CPB2		rs9567621		1.00	2	Y	0.25	1.08[0.97,1.20]	0.09	N			
CPB2		rs1409432		1.00	2	Y	0.25	1.08[0.97,1.19]	0.10	Y	0.25	0.95 [0.83,1.09]	0.47
CX3CR1	Val249Ile	rs11713282	1.00		2	Y	0.27	1.03[0.93,1.14]	0.83	N			
CX3CR1	Thr280Met	rs11713282		1.00	2	Y	0.27	1.03[0.93,1.14]	0.83	N			
CYBA	His72Tyr				3								
CYBA	640A/G				3								
CYP11B2	-344C/T	rs7831617	1.00		2	Y	0.44	0.97[0.88,1.06]	0.30	Y	0.45	0.97 [0.85,1.10]	0.6
CYP1A1	-163A/C				3								
CYP1A2					3								
CYP2C9	Arg144Cys	SNP_A-2307767		1.00	1	N				N			
CYP2C9		rs2860975			2	Y	0.42	0.92[0.84,1.01]	0.20	Y	0.39	1.05 [0.93,1.19]	0.42
ENPP1	Lys121Gln	rs9375831		1.00	2	Y	0.24	0.92[0.83,1.03]	0.06	Y	0.24	1.02 [0.89,1.17]	0.74
ENPP1		rs7767502	1.00		2	Y	0.14	1.01[0.89,1.15]	0.53	N			
ESR1	-397T/C				3								
ESR1	-351A/G				3								
F12	Arg353Gln				3								
F13A1	Val34Leu	rs3024339		1.00	2	Y	0.07	0.98[0.82,1.18]	0.51	Y	0.06	1.00 [0.76,1.30]	0.98
F13A1		rs3024317		1.00	2	Y	0.39	1.03[0.94,1.13]	0.56	Y	0.37	1.04 [0.91,1.18]	0.55
F13A1		rs1781790		1.00	2	N				N			
F13A1		rs1674045		1.00	2	Y	0.28	1.04[0.94,1.15]	0.53	Y	0.28	0.95 [0.82,1.09]	0.42
F13A1		rs1674043		1.00	2	Y	0.28	1.04[0.94,1.15]	0.53	Y	0.28	0.97 [0.84,1.12]	0.67

F13A1		rs2755413		1.00	2	Y	0.28	1.05[0.95,1.16]	0.31	N			
F13A1		rs7758057		1.00	2	Y	0.34	0.96[0.87,1.05]	0.78	N			
F13A1		rs1267913		1.00	2	Y	0.22	0.96[0.86,1.07]	0.64	Y	0.23	0.95 [0.81,1.10]	0.48
F2	20210G/A				3								
F3	–603A/G				3								
F5	1691G/A				3								
F7	**Arg353Gln**	**rs1755685**	**0.85**		**2**	Y	0.11	1.03[0.89,1.18]	0.89	**Y**	**0.13**	**0.82 [0.69,0.99]**	**0.03**
F7	-402G/A				3								
F7	–32310-bpdel-ins				3								
F7	-670A/C				3								
FGB	-463A/G	rs2059503	0.86		2	Y	0.17	1.07[0.94,1.20]	0.55	N			
FGB		rs2227426	0.86		2	Y	0.17	1.06[0.94,1.19]	0.66	N			
FGB		**rs2227424**	**0.86**		**2**	Y	0.17	1.09[0.96,1.22]	0.38	**Y**	**0.21**	**0.83 [0.71,0.97]**	**0.01**
FGB		**rs4681**	**0.86**		**2**	Y	0.17	1.07[0.95,1.21]	0.47	**Y**	**0.21**	**0.83 [0.72,0.96]**	**0.01**
GCK	-30G/A	SNP_A-4276984			1	Y	0.18	0.98[0.87,1.11]	0.79	Y	0.19	0.98 [0.83,1.15]	0.79
GCK	-89C/T	rs2908282	1.00		2	Y	0.18	0.98[0.87,1.1]	0.79	Y	0.19	0.94 [0.80,1.09]	0.4
GCLM	-23A/C				3								
GJA4	Pro319Ser				3								
GJA4	C1019T				3								
GNB3	+4423C/T				3								
GP1BA	-5C/T	rs2243100			2	Y	0.12	1.00[0.87,1.15]	0.77	N			
GP1BA		rs2243102		1.00	2	Y	0.41	1.00[0.91,1.1]	1.00	Y	0.43	1.06 [0.94,1.19]	0.33
GP6	Ser219Pro	rs12981732		1.00	2	Y	0.22	1.02[0.91,1.13]	0.85	Y	0.21	1.07 [0.92,1.24]	0.36
GP6		rs1654416	0.84		2	Y	0.18	1.02[0.91,1.15]	0.25	Y	0.18	0.92 [0.78,1.09]	0.32
GP6		rs11671922	0.84		2	Y	0.19	1.01[0.90,1.13]	0.30	N			
GP6		rs11084382	0.72		2	Y	0.22	0.98[0.88,1.09]	0.62	Y	0.22	0.97 [0.84,1.13]	0.73
GP6		rs11668169	0.84		2	Y	0.19	1.01[0.90,1.13]	0.31	N			
GP6		rs11672026	0.84		2	Y	0.19	1.01[0.90,1.13]	0.29	Y	0.19	0.93 [0.79,1.10]	0.4
GP6		rs1654419	0.84		2	Y	0.19	1.01[0.90,1.13]	0.31	Y	0.18	0.89 [0.76,1.04]	0.12
GP6		rs1654420	0.84		2	Y	0.19	1.00[0.9,1.12]	0.31	Y	0.18	0.88 [0.75,1.03]	0.1
GP6		rs1654421	0.84		2	Y	0.19	1.01[0.90,1.13]	0.43	Y	0.18	0.88 [0.75,1.03]	0.1
GP6		rs17836542		1.00	2	Y	0.05	1.10[0.89,1.36]	0.42	N			
GP6		rs2569513	0.89		2	Y	0.17	1.02[0.91,1.15]	0.23	N			
GP6		rs1671214		1.00	2	Y	0.31	0.99[0.90,1.10]	0.87	Y	0.33	1.01 [0.89,1.15]	0.86
GP6		rs1654439	0.86		2	Y	0.17	1.05[0.93,1.19]	0.18	N			

GP6		rs8113032		1.00	2	Y	0.41	1.07[0.97,1.17]	0.23	N				
HMOX1	-496A/T	rs9306300		1.00	2	Y	0.05	1.04[0.85,1.27]	0.88	N				
HMOX1		rs2071749	0.82		2	Y	0.48	0.99[0.90,1.08]	0.88	Y	0.46	0.96 [0.85,1.09]	0.52
HTR2A	102C/T	SNP_A-2053884			1	N				N			
HTR2A		rs1360020		1.00	2	Y	0.47	1.03[0.94,1.13]	0.29	N			
HTR2A		rs1928040	0.84		2	N				N			
HTR2A		rs4941573	1.00		2	Y	0.41	0.99[0.90,1.08]	0.85	Y	0.42	0.93 [0.82,1.06]	0.25
ICAM1	**Glu469Lys**	**rs2569702**	**0.90**		**2**	Y	0.38	1.03[0.94,1.13]	0.75	**Y**	**0.39**	**1.19 [1.05,1.35]**	**0.01**
IL1B	-511G/T				3								
IL6	174G/C				3								
IL6	-596A/G	rs1800795	0.93		2	Y	0.42	1.00[0.91,1.09]	0.62	N			
ITGA2	Phe253Phe	rs1421933		1.00	2	Y	0.27	0.96[0.87,1.06]	0.49	Y	0.28	0.99 [0.86,1.14]	0.85
ITGA2		rs3212486		1.00	2	Y	0.29	1.04[0.95,1.15]	0.24	N			
ITGA2		rs1421937		1.00	2	Y	0.29	1.04[0.95,1.15]	0.25	N			
ITGA2		rs3212439		1.00	2	Y	0.29	1.04[0.95,1.15]	0.25	Y	0.28	1.03 [0.90,1.18]	0.67
ITGA2		rs989073		1.00	2	Y	0.32	1.06[0.96,1.17]	0.11	Y	0.32	1.03 [0.91,1.17]	0.64
ITGA2		rs7735277		1.00	2	Y	0.23	0.96[0.86,1.07]	0.52	N			
ITGA2		rs3212527		1.00	2	Y	0.49	1.01[0.92,1.11]	0.78	Y	0.49	0.94 [0.83,1.07]	0.36
ITGA2		rs12515434		1.00	2	Y	0.09	1.02[0.87,1.19]	0.34	N			
ITGA2		rs12521915		1.00	2	Y	0.37	1.03[0.94,1.13]	0.28	Y	0.38	0.97 [0.85,1.09]	0.57
ITGA2	G873A	rs1421933		1.00	2	Y	0.27	0.96[0.87,1.06]	0.49	Y	0.28	0.99 [0.86,1.14]	0.85
ITGA2		rs3212486		1.00	2	Y	0.29	1.04[0.95,1.15]	0.24	N			
ITGA2		rs1421937		1.00	2	Y	0.29	1.04[0.95,1.15]	0.25	N			
ITGA2		rs3212439		1.00	2	Y	0.29	1.04[0.95,1.15]	0.25	Y	0.28	1.03 [0.90,1.18]	0.67
ITGA2		rs989073		1.00	2	Y	0.32	1.06[0.96,1.17]	0.11	Y	0.32	1.03 [0.91,1.17]	0.64
ITGA2		rs7735277		1.00	2	Y	0.23	0.96[0.86,1.07]	0.52	N			
ITGA2		rs3212527		1.00	2	Y	0.49	1.01[0.92,1.11]	0.78	Y	0.49	0.94 [0.83,1.07]	0.36
ITGA2		rs12515434		1.00	2	Y	0.09	1.02[0.87,1.19]	0.34	N			
ITGA2		rs12521915	0.83		2	Y	0.37	1.03[0.94,1.13]	0.28	Y	0.38	0.97 [0.85,1.09]	0.57
ITGB2	Leu10Leu				3								
ITGB3	Leu59Pro	rs8069732	1.00		2	Y	0.15	0.97[0.85,1.09]	0.67	Y	0.15	1.04 [0.88,1.24]	0.62
ITGB3		rs8077375	0.93		2	Y	0.15	0.91[0.80,1.04]	0.25	Y	0.15	1.06 [0.90,1.24]	0.5
ITGB3		rs11657517		1.00	2	Y	0.24	0.97[0.88,1.08]	0.68	Y	0.25	1.09 [0.94,1.27]	0.22
ITGB3		rs4525555		1.00	2	Y	0.30	0.98[0.89,1.08]	0.93	Y	0.32	1.05 [0.92,1.19]	0.46
ITGB3		rs8080254		1.00	2	Y	0.27	0.96[0.87,1.06]	0.78	Y	0.28	1.09 [0.96,1.25]	0.19

ITGB3		rs4629024		1.00	2	Y	0.30	0.98[0.89,1.08]	0.99	N			
ITGB3		rs8066295		1.00	2	N				N			
LGALS2	3279C/T	rs5756736	1.00		2	Y	0.41	0.95[0.87,1.04]	0.27	N			
LIPC	**-514C/T**	**rs6494005**		**1.00**	**2**	**Y**	**0.47**	**1.13[1.03,1.24]**	**0.05**	**N**			
LIPC		rs11632618		1.00	2	Y	0.06	1.01[0.84,1.22]	0.70	N			
LIPC		rs261332	0.92		2	Y	0.20	1.08[0.97,1.21]	0.22	Y	0.20	1.05 [0.90,1.23]	0.52
LPA	115618T/C	rs10755578		1.00	2	Y	0.48	1.05[0.96,1.15]	0.29	Y	0.48	1.02 [0.91,1.15]	0.71
LPA		**rs6919346**		**1.00**	**2**	Y	0.17	0.89[0.79,1.01]	0.10	**Y**	**0.18**	**0.77 [0.65,0.91]**	**0.002**
LPA		rs3127595		1.00	2	Y	0.47	1.02[0.93,1.12]	0.39	Y	0.46	1.02 [0.90,1.15]	0.77
LPA		**rs9346818**		**1.00**	**2**	**Y**	**0.39**	**0.91[0.83,0.99]**	**0.04**	Y	0.41	1.10 [0.97,1.25]	0.13
LPA		rs7749836		1.00	2	Y	0.19	0.96[0.85,1.07]	0.26	N			
LPA		rs4708869		1.00	2	Y	0.18	0.89[0.79,1.00]	0.11	N			
LPA		rs9365166		1.00	2	Y	0.48	1.01[0.92,1.10]	0.89	Y	0.49	0.94 [0.83,1.06]	0.32
LPA		rs9347407		1.00	2	Y	0.50	1.01[0.92,1.10]	0.84	Y	0.49	1.05 [0.93,1.19]	0.4
LPA		rs3127599		1.00	2	Y	0.31	1.06[0.96,1.16]	0.19	Y	0.30	0.96 [0.83,1.10]	0.51
LPL	Ser447Ter	rs17482753	1.00		2	Y	0.10	0.94[0.80,1.09]	0.31	Y	0.10	0.86 [0.70,1.05]	0.13
LPL		SNP_A-2305697	0.93		2	Y	0.11	0.94[0.81,1.08]	0.46	Y	0.12	0.88 [0.73,1.05]	0.16
LPL		**rs17489268**		**1.00**	**2**	**Y**	**0.26**	**0.86[0.78,0.96]**	**0.004**	**Y**	**0.26**	**0.80 [0.69,0.92]**	**0.002**
LPL		rs17411024	0.93	1.00	2	Y	0.10	0.96[0.82,1.11]	0.53	N			
LPL		**rs17411031**		**1.00**	**2**	**Y**	**0.26**	**0.86[0.78,0.96]**	**0.004**	**Y**	**0.27**	**0.81 [0.70,0.94]**	**0.004**
LPL		**rs17411045**		**1.00**	**2**	**Y**	**0.26**	**0.89[0.80,0.98]**	**0.01**	**N**			
LPL		**rs17489282**		**1.00**	**2**	**Y**	**0.26**	**0.86[0.78,0.96]**	**0.005**	**N**			
LPL		rs4922117		1.00	2	N				N			
LPL		rs10503669	1.00		2	Y	0.10	0.93[0.79,1.08]	0.25	N			
LPL	Asp9Asn				3								
LPL	Asn291Se				3								
LRP1	355C/T				3								
LRP1	Ala217Val				3								
LRP1	45014C/T				3								
LTA	A252G	rs1799964		1.00	1	Y	0.20	1.04[0.931,1.161]	0.67	Y	0.21	1.03 [0.88,1.20]	0.71
LTA	Thr60Asn	rs1799964		1.00	1	Y	0.20	1.04[0.931,1.161]	0.67	Y	0.21	1.03 [0.88,1.20]	0.71
MGP	102T/A				3								
MGP	-63A/G				3								
MMP3	5A/6A				3								
MMP3	-439G/C				3								

MMP3	Lys45Glu	rs655403		1.00	2	Y	0.12	1.17[1.01,1.34]	0.11	N			
MMP3		rs650108		1.00	2	N				N			
MMP9	-1562C/T				3								
MMP9	Arg279Gln				3								
MMP9	7476C/T				3								
MTCO2	-738C/G				3								
MTHFR	Ala222Val	rs9651118		1.00	2	Y	0.22	0.97[0.87,1.08]	0.91	N			
MTHFR		rs17367504		1.00	2	Y	0.16	0.93[0.82,1.05]	0.18	N			
MTHFR		rs4845882		1.00	2	Y	0.39	0.97[0.88,1.06]	0.68	Y	0.39	0.98 [0.86,1.10]	0.7
MTR		SNP_A-1989628			1	N				Y	0.18	0.99 [0.88,1.12]	0.88
MTR	Asp919Gly	rs10733117		1.00	2	Y	0.40	0.98[0.90,1.08]	0.68	Y	0.41	0.99 [0.88,1.12]	0.88
MTR		rs10733118		1.00	2	Y	0.38	0.98[0.89,1.07]	0.69	Y	0.38	1.01 [0.90,1.14]	0.83
MTR		rs2185208		1.00	2	Y	0.37	0.97[0.88,1.07]	0.54	N			
MTR		rs2385504	0.88		2	Y	0.17	0.94[0.83,1.06]	0.33	Y	0.16	0.99 [0.84,1.18]	0.95
MTR		rs2385509		1.00	2	Y	0.42	1.07[0.98,1.17]	0.11	Y	0.42	1.03 [0.90,1.16]	0.7
MTR		rs2385500		1.00	2	Y	0.42	1.06[0.97,1.16]	0.15	Y	0.42	1.00 [0.88,1.13]	0.96
MTR		rs17599657	1.00		2	Y	0.18	0.91[0.81,1.02]	0.14	Y	0.17	0.96 [0.81,1.14]	0.66
MTR		rs3768139		1.00	2	Y	0.37	0.96[0.88,1.06]	0.48	Y	0.37	1.01 [0.90,1.14]	0.86
MTR		rs4659736	1.00		2	Y	0.18	0.90[0.80,1.02]	0.12	N			
MTR		rs4659738		1.00	2	Y	0.37	0.97[0.88,1.06]	0.50	Y	0.37	0.99 [0.87,1.12]	0.82
MTR		rs4659739		1.00	2	Y	0.37	0.95[0.87,1.05]	0.35	Y	0.38	0.97 [0.85,1.10]	0.63
MTR		rs2275565	0.89		2	Y	0.21	0.96[0.86,1.07]	0.48	Y	0.21	1.00 [0.86,1.17]	0.99
MTR		rs10158822	1.00		2	Y	0.19	0.92[0.82,1.03]	0.19	N			
MTR		rs1266164		1.00	2	Y	0.37	0.97[0.88,1.06]	0.49	N			
MTR		rs16834516		1.00		N				N			
MTR		rs2282369		1.00	2	Y	0.38	0.99[0.90,1.09]	0.92	Y	0.40	0.99 [0.88,1.12]	0.88
MTR		rs1252252		1.00	2	Y	0.37	0.97[0.88,1.06]	0.36	N			
MTR		rs10737812		1.00	2	Y	0.42	1.02[0.93,1.12]	0.81	Y	0.43	0.98 [0.87,1.11]	0.77
MTR		rs4659743		1.00	2	Y	0.38	0.97[0.88,1.06]	0.44	Y	0.38	1.00 [0.89,1.13]	0.98
MTR		rs2853523		1.00	2	Y	0.37	0.97[0.88,1.06]	0.51	N			
MTR		rs10925273	0.88		2	Y	0.17	0.90[0.80,1.01]	0.19	Y	0.17	1.06 [0.89,1.25]	0.5
MTR		rs1252101		1.00	2	Y	0.33	0.94[0.85,1.03]	0.24	Y	0.33	0.94 [0.83,1.06]	0.3
MTR		rs7553232		1.00	2	Y	0.06	0.97[0.80,1.18]	0.76	N			
MTR		rs1270972		1.00	2	Y	0.26	1.05[0.95,1.16]	0.35	Y	0.28	1.09 [0.96,1.25]	0.18
MTR		rs10925261	1.00		2	Y	0.19	0.92[0.82,1.03]	0.19	N			

MTTP	–493G/T				3									
NOS3	Glu298Asp	rs3918188		0.90	2	Y	0.36	0.97[0.89,1.07]	0.95	Y	0.36	0.94 [0.82,1.06]	0.3
NOS3	-786T/C				3									
NPPA	T2238C	SNP_A-4245831			1	N				Y	0.14	0.89 [0.74,1.07]	0.21
NR3C1	Asn362Ser				3									
OLR1	**Lys167Asn**	**rs4495966**		**1.00**	**2**	**Y**	**0.49**	**1.10[1.01,1.21]**	**0.04**	Y	0.48	1.01 [0.89,1.14]	0.88
OLR1		rs2742115		1.00	2	Y	0.26	0.96[0.87,1.07]	0.94	Y	0.25	0.95 [0.83,1.09]	0.49
OLR1		rs7300650		1.00	2	Y	0.41	0.93[0.85,1.02]	0.45	N			
PCSK9	Arg45Lys				3								
PECAM1		SNP_A-1856272			1	N				N			
PECAM1		SNP_A-1834715			1	N				N			
PECAM1	**Val125Leu**	**rs11653087**	**0.82**		**2**	Y	0.49	1.02[0.93,1.11]	0.64	**Y**	**0.50**	**1.13 [1.00,1.28]**	**0.04**
PECAM1		**rs6416939**	**0.97**		**2**	Y	0.48	1.00[0.91,1.09]	1.00	**Y**	**0.48**	**0.88 [0.78,1.00]**	**0.04**
PECAM1		**rs12944077**	**0.84**		**2**	Y	0.50	1.01[0.92,1.10]	0.77	**Y**	**0.50**	**0.89 [0.79,0.99]**	**0.04**
PECAM1	**Ser563Asn**	**rs12944077**	**1.00**		**2**	Y	0.50	1.01[0.92,1.10]	0.77	**Y**	**0.50**	**0.89 [0.79,0.99]**	**0.04**
PECAM1	**Arg55Gly**	**rs6416939**	**0.87**		**2**	Y	0.48	1.00[0.91,1.09]	1.00	**Y**	**0.48**	**0.88 [0.78,1.00]**	**0.04**
PECAM1		**rs6416939**	**0.87**		**2**	Y	0.48	1.00[0.91,1.09]	1.00	**Y**	**0.48**	**0.88 [0.78,1.00]**	**0.04**
PECAM1		**rs12944077**	**1.00**		**2**	Y	0.50	1.01[0.92,1.10]	0.77	**Y**	**0.50**	**0.89 [0.79,0.99]**	**0.04**
PECAM1	Ser7Ser				3								
PLA2G7	Leu65Val	rs12528857		1.00	2	Y	0.22	1.00[0.90,1.12]	0.33	N			
PLA2G7		rs1421372	1.00		2	N				N			
PLA2G7		rs1421378		1.00	2	Y	0.38	0.99[0.90,1.09]	0.70	Y	0.37	0.94 [0.83,1.07]	0.35
PON1	Gln192Arg	rs17773605		1.00	2	Y	0.06	1.12[0.92,1.35]	0.66	Y	0.05	0.84 [0.64,1.09]	0.18
PON1		**rs3917551**	**0.10**	**1.00**	**2**	Y	0.06	0.94[0.77,1.14]	0.67	**Y**	**0.05**	**1.35 [1.03,1.77]**	**0.02**
PON1		rs3917550		1.00	2	Y	0.13	0.99[0.86,1.13]	0.83	Y	0.13	1.10 [0.93,1.31]	0.25
PON1		rs3917541		1.00	2	N				N			
PON1		rs3917538	0.80		2	Y	0.23	0.98[0.88,1.09]	0.43	Y	0.23	0.99 [0.86,1.14]	0.93
PON1		rs2158155		1.00	2	Y	0.06	0.93[0.77,1.14]	0.59	N			
PON1		rs2057681	1.00		2	Y	0.29	0.97[0.88,1.07]	0.37	Y	0.28	1.06 [0.93,1.21]	0.36
PON1		rs3917527		1.00	2	Y	0.06	0.95[0.79,1.16]	0.73	N			
PON1		rs2299257		1.00	2	Y	0.39	0.98[0.90,1.08]	0.39	N			
PON1	Leu55Met	rs3917550		1.00	2	Y	0.13	0.99[0.86,1.13]	0.83	Y	0.13	1.10 [0.93,1.31]	0.25
PON1		rs2272365		1.00	2	Y	0.15	1.03[0.91,1.17]	0.90	N			
PON1	**C907G**	**SNP_A-2012725**			**1**	N				**Y**	**0.51**	**1.20 [1.07,1.35]**	**0.002**
PON1		rs705382		1.00	2	Y	0.38	1.01[0.92,1.11]	0.96	N			

PON2		SNP_A-2179271			1	N				Y	0.23	1.08 [0.94,1.24]	0.29
PON2		rs11764079	0.87		2	Y	0.27	0.98[0.89,1.09]	0.86	Y	0.25	1.01 [0.87,1.16]	0.91
PON2		rs2299263	1.00		2	Y	0.24	0.94[0.84,1.04]	0.52	Y	0.23	1.08 [0.94,1.24]	0.27
PON2		rs1639		1.00	2	Y	0.21	1.05[0.94,1.17]	0.40	N			
PON2		rs7785039		1.00	2	Y	0.21	0.98[0.88,1.10]	0.61	N			
PON2		rs7778623		1.00	2	Y	0.34	0.98[0.89,1.08]	0.95	Y	0.33	1.09 [0.96,1.24]	0.18
PON2		rs3757707		1.00	2	Y	0.31	1.00[0.90,1.10]	0.53	Y	0.27	1.09 [0.95,1.25]	0.22
PPARA	Leu162Val	rs4253754		1.00	2	Y	0.21	0.95[0.85,1.06]	0.89	Y	0.20	1.04 [0.90,1.21]	0.6
PPARG	His476His	rs17036188		1.00	2	Y	0.03	0.94[0.71,1.24]	0.28	N			
PPARG		rs4135283		1.00	2	Y	0.03	0.90[0.69,1.17]	0.13	N			
PPARG		rs4684859		1.00	2	Y	0.43	0.98[0.90,1.08]	0.88	Y	0.43	1.06 [0.94,1.21]	0.31
PPARG	Pro12Ala	SNP_A-1971790		1.00	1	N				Y	0.14	0.93 [0.78,1.10]	0.39
PPARG		rs11709077	1.00		2	Y	0.12	0.94[0.82,1.08]	0.43	Y	0.14	0.93 [0.78,1.11]	0.44
PPARG		rs17036328	1.00		2	Y	0.12	0.94[0.82,1.08]	0.45	Y	0.14	0.92 [0.77,1.11]	0.38
SELE	Ser128Arg	rs3917410	1.00		2	Y	0.10	0.88[0.76,1.02]	0.07	Y	0.11	0.98 [0.81,1.18]	0.8
SELE		**rs3917392**	**1.00**		**2**	**Y**	**0.10**	**0.86[0.74,1.00]**	**0.04**	Y	0.11	1.04 [0.86,1.25]	0.67
SELE		rs3917411	1.00		2	Y	0.10	0.88[0.76,1.02]	0.09	Y	0.11	1.04 [0.86,1.25]	0.68
SELE		rs1534904		1.00	2	Y	0.34	0.90[0.82,0.99]	0.14	Y	0.31	0.92 [0.81,1.05]	0.2
SELE		**rs3917425**	**1.00**		**2**	**Y**	**0.10**	**0.87[0.75,1.01]**	**0.05**	Y	0.11	1.04 [0.86,1.26]	0.67
SELE		rs12133642	1.00		2	Y	0.10	0.87[0.75,1.01]	0.06	Y	0.11	1.05 [0.87,1.26]	0.62
SELE		rs4656701		1.00	2	Y	0.25	1.08[0.97,1.20]	0.26	Y	0.26	1.02 [0.89,1.18]	0.73
SELE	G98T	rs3917410	1.00		2	Y	0.10	0.88[0.76,1.02]	0.07	Y	0.11	0.98 [0.81,1.18]	0.8
SELE		**rs3917392**	**1.00**		**2**	**Y**	**0.10**	**0.86[0.74,1.00]**	**0.04**	Y	0.11	1.04 [0.86,1.25]	0.67
SELE		rs3917411	1.00		2	Y	0.10	0.88[0.76,1.02]	0.09	Y	0.11	1.04 [0.86,1.25]	0.68
SELE		rs1534904		1.00	2	Y	0.34	0.90[0.82,0.99]	0.14	Y	0.31	0.92 [0.81,1.05]	0.2
SELE		**rs3917425**	**1.00**		**2**	**Y**	**0.10**	**0.87[0.75,1.01]**	**0.05**	Y	0.11	1.04 [0.86,1.26]	0.67
SELE		rs12133642	1.00		2	Y	0.10	0.87[0.75,1.01]	0.06	Y	0.11	1.05 [0.87,1.26]	0.62
SELE		rs4656701		1.00	2	Y	0.25	1.08[0.97,1.20]	0.26	Y	0.26	1.02 [0.89,1.18]	0.73
SELP	Thr719Pro	rs3753305		1.00	2	Y	0.45	0.97[0.89,1.06]	0.65	Y	0.45	1.02 [0.90,1.15]	0.76
SELP		rs10489185		1.00	2	Y	0.40	0.99[0.90,1.08]	0.36	N			
SELP		rs6662176		1.00	2	Y	0.31	1.01[0.92,1.11]	0.94	Y	0.30	0.98 [0.86,1.12]	0.76
SELP		rs2213873		1.00	2	Y	0.32	0.99[0.90,1.09]	0.77	N			
SELP		rs12406092		1.00	2	Y	0.31	1.00[0.91,1.10]	0.92	N			
SELP		rs6691048		1.00	2	Y	0.32	0.99[0.90,1.09]	0.82	N			
SELP		**rs6663533**		**1.00**	**2**	**Y**	**0.06**	**1.23[1.01,1.48]**	**0.02**	Y	0.05	1.09 [0.84,1.41]	0.5

SELP		rs9332542		1.00	2	Y	0.31	1.00[0.91,1.10]	0.88	Y	0.30	0.97 [0.86,1.11]	0.69
SELP		rs2298905		1.00	2	Y	0.32	1.00[0.91,1.10]	0.91	N			
SELP		rs3917786		1.00	2	Y	0.44	0.98[0.89,1.07]	0.60	Y	0.44	1.01 [0.89,1.14]	0.91
SELP		rs2420378		1.00	2	Y	0.35	1.02[0.93,1.12]	0.96	Y	0.37	0.95 [0.84,1.08]	0.45
SELP		rs2205895		1.00	2	Y	0.36	1.02[0.93,1.12]	0.93	Y	0.37	1.00 [0.89,1.13]	0.99
SELP		rs3917768		1.00	2	Y	0.44	0.99[0.91,1.09]	0.32	Y	0.45	1.00 [0.88,1.12]	0.94
SELP	-1696A/G	rs3917731		1.00	2	Y	0.29	0.99[0.89,1.09]	0.75	Y	0.28	1.05 [0.91,1.20]	0.5
SELPLG	Ser236Pro				3								
SELPLG	Val264Met				3								
TFPI					3								
TGFB1	Arg25Pro				3								
TGFB1	Ala1969Gly				3								
THBD	Pro246Ser				3								
THBD	Val264Met				3								
THBS1	Val292Met	rs2618162		1.00	2	Y	0.30	1.04[0.95,1.15]	0.44	Y	0.30	1.01 [0.88,1.15]	0.93
THBS1		rs1051442		1.00	2	Y	0.18	1.09[0.96,1.22]	0.35	Y	0.18	1.11 [0.94,1.30]	0.2
THBS4	Leu10Pro	SNP_A-1889351			1	Y	0.21	1.05[0.86,1.17]	0.70	Y	0.20	1.03 [0.89,1.19]	0.7
THBS4		rs4703797		1.00	2	Y	0.33	1.05[0.96,1.16]	0.23	Y	0.30	1.08 [0.94,1.23]	0.28
THBS4		rs12332694		1.00	2	Y	0.33	1.04[0.94,1.14]	0.34	Y	0.30	1.00 [0.88,1.14]	1
TLR4		**rs7864330**	**1.00**		**2**	**Y**	**0.06**	**1.13[0.93,1.36]**	**0.05**	N			
TLR4	**Ala387Pro**	**rs7864330**	**1.00**		**2**	**Y**	**0.06**	**1.13[0.93,1.36]**	**0.05**	N			
TNF	-308G/A				3								
TNFRSF11B	T950C	rs10505346		1.00	2	Y	0.18	1.04[0.93,1.17]	0.28	Y	0.19	0.91 [0.78,1.07]	0.25
TNFRSF11B		rs11573870		1.00	2	Y	0.02	1.28[0.92,1.78]	0.30	N			
TNFRSF11B		rs11573871		1.00	2	Y	0.07	0.90[0.761.07]	0.18	Y	0.06	1.26 [0.99,1.59]	0.06
TNFRSF11B		rs11573884		1.00	2	Y	0.09	1.06[0.91,1.24]	0.48	N			
TNFRSF11B		rs11573896		1.00	2	Y	0.16	1.06[0.94,1.20]	0.29	Y	0.15	0.93 [0.78,1.10]	0.39
TNFRSF11B		rs11573897		1.00	2	Y	0.02	1.27[0.92,1.75]	0.30	N			
TNFRSF11B		rs3102724		1.00	2	Y	0.34	1.04[0.94,1.14]	0.45	Y	0.33	1.11 [0.98,1.26]	0.09
TNFRSF11B		rs11573901		1.00	2	Y	0.04	1.05[0.82,1.33]	0.58	Y	0.04	0.82 [0.60,1.10]	0.17
TNFRSF11B		rs10505348		1.00	2	Y	0.46	0.91[0.83,1.00]	0.11	Y	0.47	1.01 [0.90,1.13]	0.89
TNFRSF11B		rs10505349		1.00	2	Y	0.18	1.04[0.93,1.17]	0.28	Y	0.19	0.90 [0.77,1.04]	0.15
TNFRSF11B		rs7014574		1.00	2	N				N			
TNFRSF11B	Lys3Asn	rs10505346		1.00	2	Y	0.18	1.04[0.93,1.17]	0.28	Y	0.19	0.91 [0.78,1.07]	0.25
TNFRSF11B		rs11573870		1.00	2	Y	0.02	1.28[0.92,1.78]	0.30	N			

TNFRSF11B		rs11573871		1.00	2	Y	0.07	0.90[0.76,1.07]	0.18	Y	0.06	1.26 [0.99,1.59]	0.06
TNFRSF11B		rs11573896		1.00	2	Y	0.16	1.06[0.94,1.20]	0.29	Y	0.15	0.93 [0.78,1.10]	0.39
TNFRSF11B		rs11573897		1.00	2	Y	0.02	1.27[0.92,1.75]	0.30	N			
TNFRSF11B		rs3102724		1.00	2	Y	0.34	1.04[0.94,1.14]	0.45	Y	0.33	1.11 [0.98,1.26]	0.09
TNFRSF11B		rs11573901		1.00	2	Y	0.04	1.05[0.82,1.33]	0.58	Y	0.04	0.82 [0.60,1.10]	0.17
TNFRSF11B		rs10505348		1.00	2	Y	0.46	0.91[0.83,1.00]	0.11	Y	0.47	1.01 [0.90,1.13]	0.89
TNFRSF11B		rs10505349		1.00	2	Y	0.18	1.04[0.93,1.17]	0.28	Y	0.19	0.90 [0.77,1.04]	0.15
TNFRSF11B		rs7014574		1.00	2	Y	0.47	0.92[0.84,1.01]	0.15	N			
TNFRSF11B		**rs3134061**		**1.00**	**2**	Y	0.05	1.12[0.90,1.38]	0.63	**Y**	**0.05**	**0.75 [0.55,1.00]**	**0.05**
TNFRSF11B		**rs3134060**		**1.00**	**2**	Y	0.05	1.14[0.92,1.40]	0.46	**Y**	**0.05**	**0.74 [0.55,0.99]**	**0.04**
TNFRSF11B		rs3102725		1.00	2	Y	0.05	1.11[0.90,1.36]	0.62	N			
TNFRSF11B		rs17758011		1.00	2	Y	0.05	1.10[0.89,1.36]	0.80	N			
TNFRSF1A	Arg92Gln				3								
WRN		rs2737339		1.00	2	Y	0.39	1.04[0.95,1.14]	0.31	Y	0.35	0.91 [0.81,1.03]	0.14
WRN		rs7014045	0.95		2	Y	0.26	1.02[0.92,1.13]	0.55	Y	0.27	1.04 [0.91,1.19]	0.56
WRN		rs2725361		1.00	2	Y	0.38	1.03[0.94,1.13]	0.40	Y	0.35	0.91 [0.81,1.04]	0.15
WRN		rs2737334		1.00	2	Y	0.39	1.02[0.93,1.12]	0.63	Y	0.35	0.92 [0.81,1.04]	0.19
WRN		rs2737333		1.00	2	Y	0.40	1.02[0.93,1.12]	0.58	N			
WRN		rs2737365		1.00	2	Y	0.06	1.12[0.93,1.35]	0.34	Y	0.05	1.21 [0.93,1.58]	0.15
WRN		rs2737367		1.00	2	Y	0.06	1.13[0.94,1.37]	0.28	Y	0.05	1.21 [0.93,1.58]	0.14
WRN		rs2737368		1.00	2	Y	0.06	1.09[0.90,1.31]	0.51	N			

Legend to Table 6. Gene Symbol (Gene symbol and Gene full name are given on the next page in alphabetical order); variant, previously associated SNP; alternative SNP, rs-number of a SNP in complete or almost complete LD; r^2, LD measure, D′, LD measure (a SNP was choosen as an alternative SNP if $r^2 \geq 0.8$ or $D' \geq 0.9$); code, 1-original SNP, 2-proxy SNP, 3-no tagging SNP; QC, quality check based on intensity plots, deviation from HWE in controls $p \leq 0.001$, MAF ≤ 0.01, or missing frequency ≥ 0.02 (results are only shown for those SNPs with good cluster plots (y)); MAF, Minor Allele Frequency in controls (frequency is given for the WTCCC and German Controls, respectively); OR, P-values (Cochran-Armitage trend-test) for WTCCC and German data. SNPs with positive association in either the WTCCC or German study are in bold. Genotype distributions for cases and controls in either the WTCCC or German MI Studies are available on request. Odds ratios and P values for risk associated with the minor allele were computed for each SNP using the Cochran-Armitage trend test.

Table 6: Alphabetical list of gene symbols and gene full names

ABCA1, ATP-BINDING CASSETTE 1; **ADD1**, ADDUCIN 1; **ADH1C**, ALCOHOL DEHYDROGENASE 1C; **ACDC**, ADIPONECTIN; **ADRB1**, BETA-1-ADRENERGIC RECEPTOR; **ADRB2,** BETA-2-ADRENERGIC RECEPTOR; **ADRB3,** BETA-3-ADRENERGIC RECEPTOR; **AGER**, ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR; **AGT**, ANGIOTENSINOGEN; **AGTR1**, ANGIOTENSIN RECEPTOR 1; **AGTR2**, ANGIOTENSIN RECEPTOR 2; **ALOX5AP**, ARACHIDONATE 5-LIPOXYGENASE-ACTIVATING PROTEIN; **APOA1,** APOLIPOPROTEIN A-I; **APOA4**, APOLIPOPROTEIN A-IV, **APOA5,** APOLIPOPROTEIN A-V; **APOE**, APOLIPOPROTEIN E; **CCL11**, SMALL INDUCIBLE CYTOKINE A11; **CCL5**, SMALL INDUCIBLE CYTOKINE A5; **CCR2**, MONOCYTE CHEMOTACTIC PROTEIN 1 RECEPTOR; **CD14**, MONOCYTE DIFFERENTIATION ANTIGEN; **CD36**, GLYCOPROTEIN IIIb; **CETP**, CHOLESTERYL ESTER TRANSFER PROTEIN; **MHC2TA**, MHC CLASS II TRANSACTIVATOR; **COMT**, CATECHOL-O-METHYLTRANSFERASE; **CPB2**, CARBOXYPEPTIDASE B2; **CX3CR1**, G PROTEIN-COUPLED RECEPTOR 13; **CYBA**, p22-PHOX; **CYP11B2**, ALDOSTERONE SYNTHASE; **CYP1A1**, CYTOCHROME P450, SUBFAMILY I, POLYPEPTIDE 1; **CYP1A2**, CYTOCHROME P450, SUBFAMILY I, POLYPEPTIDE 2; **CYP2C9**, CYTOCHROME P450, SUBFAMILY IIC, POLYPEPTIDE 9; **ENPP1**, ECTONUCLEOTIDE PYROPHOSPHATASE/PHOSPHODIESTERASE 1; **ESR1**, ESTROGEN RECEPTOR 1; **F12**, COAGULATION FACTOR XII; **F13A1**, FACTOR XIII, A1 SUBUNIT; **F2**, COAGULATION FACTOR II; **F3**, COAGULATION FACTOR III; **F5**, COAGULATION FACTOR V; **F7**, COAGULATION FACTOR VII; **FGB**, FIBRINOGEN; **GCK**, GLUCOKINASE; **GCLM**, GLUTAMATE-CYSTEINE LIGASE; **GJA4**, CONNEXIN 37; **GNB3**, GUANINE NUCLEOTIDE-BINDING PROTEIN, BETA-3; **GP1BA**, GLYCOPROTEIN Ib; **GP6**, GLYCOPROTEIN VI; **HMOX1**, HEMOXYGENASE 1; **HTR2A**, SEROTONIN 5-HT-2A RECEPTOR; **ICAM1**, INTERCELLULAR ADHESION MOLECULE 1; **IL1B**, INTERLEUKIN 1-BETA; **IL6**, INTERLEUKIN 6; **ITGA2**, PLATELET GLYCOPROTEIN Ia/IIa; **ITGB2**, INTEGRIN, BETA-2; **ITGB3**, PLATELET GLYCOPROTEIN IIIa; **LGALS2**, GALECTIN 2; **LIPC**, HEPATIC LIPASE; **LPA**, LIPOPROTEIN(a); **LPL**, LIPOPROTEIN LIPASE; **LRP1**, LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1; **LTA**, LYMPHOTOXIN-ALPHA; **MGP**, MATRIX GAMMA-CARBOXYGLUTAMIC ACID; **MMP3**, MATRIX METALLOPROTEINASE 3; **MMP9**, MATRIX METALLOPROTEINASE 9; **MTCO2**, CYTOCHROME C OXIDASE II; **MTHFR**, METHYLENETETRAHYDROFOLATE REDUCTASE; **MTR**, METHIONINE SYNTHASE; **MTTP**, tRNA-PRO, MITOCHONDRIAL; **NOS3**, NITRIC OXIDE SYNTHASE 3; **NPPA**, NATRIURETIC PEPTIDE PRECURSOR A; **NR3C1**, GLUCOCORTICOID RECEPTOR; **OLR1**, OXIDIZED LOW DENSITY LIPOPROTEIN RECEPTOR 1; **PCSK9**, NEURAL APOPTOSIS-REGULATED CONVERTASE 1; **PECAM1**, PLATELET-ENDOTHELIAL CELL ADHESION MOLECULE 1; **PLA2G7**, PHOSPHOLIPASE A2; **PON1**, PARAOXONASE 1; **PON2**, PARAOXONASE 2; **PPARA**, PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR-ALPHA; **PPARG**, PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR-GAMMA; **SELE**, SELECTIN E; **SELP**, SELECTIN P; **SELPLG**, SELECTIN P LIGAND; **TFPI**, TISSUE FACTOR PATHWAY INHIBITOR; **TGFB1**, TRANSFORMING GROWTH FACTOR; **THBD**, THROMBOMODULIN; **THBS1**, THROMBOSPONDIN I; **THBS4**, THROMBOSPONDIN IV; **TLR4**, TOLL-LIKE RECEPTOR 4; **TNF**, TUMOR NECROSIS FACTOR; **TNFRSF11B**, OSTEOPROTEGERIN; **TNFRSF1A**, TUMOR NECROSIS FACTOR RECEPTOR 1; **WRN**, DNA HELICASE

Supplementary Table 7. Reasons for exclusion of subjects in WTCCC and German MI Family Study

	WTCCC Study				German MI Family Study		
Collection	**CAD cases**	**58BC controls**	**UKBS controls**	**Total**	**MI cases**	**MI controls**	**Total**
Missingness (per individual) >3%	41	9	8	58	7	-	7
Low heterozygosity	1	0	0	1	6	-	6
External discordance	0	4	5	9	-	-	-
Non-European ancestry	13	6	14	33	-	-	-
Duplicate	2	4	0	1	-	-	-
Cryptic relatedness	5	1	15	21	-	-	-
Total	**62**	**24**	**42**	**128**	**13**	**-**	**13**

CAD, coronary artery disease. 58BC, 1958 birth cohort. UKBS, blood donors recruited by United Kingdom Blood Service. Several filters were applied by the WTCCC Consortium to the WTCCC Study for sample exclusion [3] 1. SNP call rate < 97% (missingness). 2. Heterozygosity > 30% or < 23% across all SNPs. 3. External discordance with genotype or phenotype data. 4. Individuals identified as having non-European ancestry by PCA analysis. 5. Duplicates (the copy with more missing data was removed) 6. Individuals with too much IBS sharing (>86%); likely relatives. Some of the filters were also applied to the German Study as shown.

Supplementary Table 8. Sensitivity analysis for the False Positive Report Probability (FPRP) for the SNPs shown in Supplementary Table 2. Analysis presented in the paper are based on an alternative odds ratio of 1.25 and a prior probability of a true association of 1/5000.

		OR=1.20			OR=1.25			OR=1.30					
Chromosome	SNP	1/2500	1/5000	1/10000	1/2500	1/5000	1/10000	1/2500	1/5000	1/10000	Minimum FPRP	Maximum FPRP	Full Bayesian
1	rs2133189	0.303	0.465	0.635	0.309	0.473	0.642	0.490	0.658	0.794	0.303	0.794	0.475
1	rs17465637	0.256	0.408	0.580	0.249	0.399	0.570	0.398	0.569	0.725	0.249	0.725	0.402
2	rs2943634	0.271	0.426	0.597	0.303	0.466	0.635	0.528	0.691	0.817	0.271	0.817	0.466
5	rs383830	0.235	0.381	0.551	0.155	0.269	0.424	0.166	0.285	0.444	0.155	0.551	0.269
5	rs449650	0.254	0.405	0.577	0.174	0.296	0.457	0.190	0.319	0.484	0.174	0.577	0.295
5	rs565928	0.233	0.378	0.549	0.156	0.270	0.425	0.170	0.291	0.450	0.156	0.549	0.271
6	rs6922269	0.187	0.315	0.479	0.170	0.291	0.451	0.277	0.434	0.605	0.170	0.605	0.290
9	rs643319	0.002	0.005	0.009	0.001	0.002	0.005	0.002	0.003	0.006	0.001	0.009	0.003
9	rs7044859	0.003	0.007	0.013	0.002	0.004	0.007	0.003	0.005	0.010	0.002	0.013	0.005
9	rs523096	0.049	0.094	0.172	0.049	0.094	0.172	0.112	0.202	0.336	0.049	0.336	0.098
9	rs518394	0.049	0.094	0.171	0.048	0.092	0.169	0.108	0.195	0.327	0.048	0.327	0.095
9	rs10757264	0.010	0.019	0.037	0.007	0.013	0.026	0.011	0.022	0.044	0.007	0.044	0.015
9	rs10965212	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000
9	rs1292136	0.001	0.001	0.002	0.000	0.000	0.001	0.000	0.000	0.001	0.000	0.002	0.001
9	rs7049105	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000
9	rs10965215	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
9	rs564398	0.002	0.003	0.007	0.001	0.001	0.003	0.001	0.002	0.003	0.001	0.007	0.002
9	rs7865618	0.000	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000
9	rs10965219	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
9	rs9632884	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
9	rs6475606	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
9	rs4977574	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
9	rs2891168	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
9	rs1333042	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
9	rs1333048	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
9	rs1333049	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
16	rs8055236	0.341	0.509	0.674	0.236	0.382	0.553	0.242	0.390	0.561	0.236	0.674	0.376
16	rs889595	0.270	0.425	0.596	0.267	0.421	0.593	0.427	0.598	0.748	0.267	0.748	0.425
22	rs688034	0.179	0.304	0.466	0.200	0.334	0.501	0.394	0.566	0.723	0.179	0.723	0.327

The sensitivity analysis ranges the probability of a true association between 1/2500 and 1/10000 and the true odds ratio (OR) between 1.2 and 1.3. The Full Bayesian analysis used independent normal prior distributions for the log odds ratio and logit of the probability of a true association that were centred on an odds ratio of 1.25 and a probability of 1/5000 with standard deviations that allowed 95% of the distribution to be between 1.2 and 1.3 and between 1/2500 and 1/10,000 respectively. The full Bayesian results are very similar to those obtained from the modification of the Wacholder method [9] assuming 1.25 and 1/5000.

8. Supplementary Figures

Supplementary Figures 1A-1F. Overview of the associations observed on chromosomes 6q25.1 (Figure 1A) , 2q36.3 (Figure 1B). 1p13.3 (Figure 1C), 1q41 (Figure 1D), 10q11.21 (Figure 1E) and 15q22.33 (Figure 1F).

In each figure the following legends apply:

A. Plot of –log10 P values (Cochran-Armitage trend test) for association against chromosome position (bases). Blue triangles represent the WTCCC study and red circles represent the German study. For both studies the P values are from the two-sided Cochran-Armitage trend-test. The arrows mark the lead SNP in each region (see Main paper) for both studies.

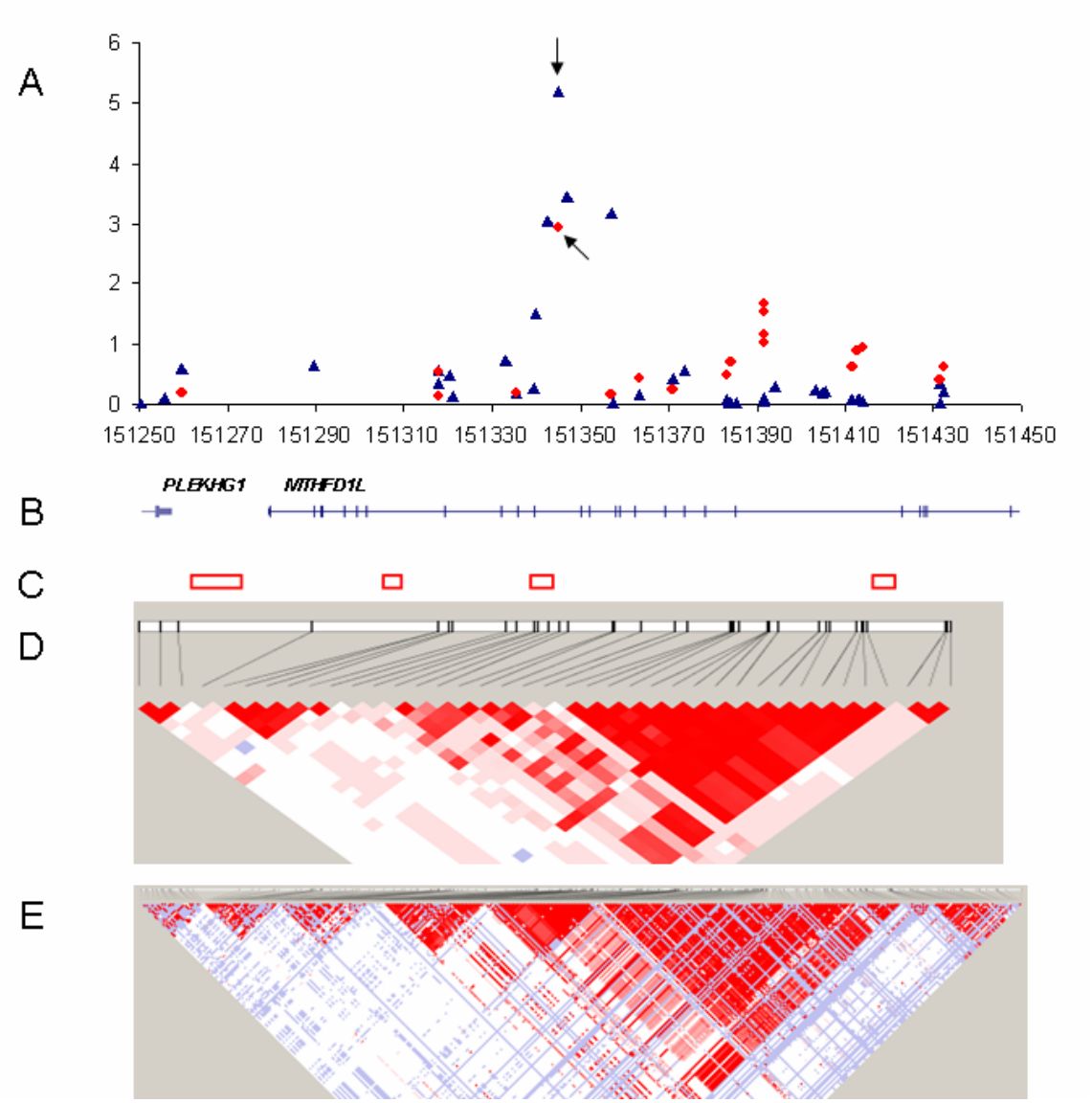
B. Genomic locations of RefSeq genes or mRNAs showing intron and exon structure. Spliced ESTs shown are the genomic locations of alignments (except those overlapping known genes in region where spliced ESTs are not shown) between human ESTs in GenBank and the genome, that show signs of splicing when aligned against the genome. All data obtained from the UCSC genome browser (NCBI Build 35). [20]

C. Red boxes represent recombination hotspots as estimated from Phase II HapMap data (release 21) using the methods described in McVean et al. (2004) and Winckler et al. (2005). [21, 22]

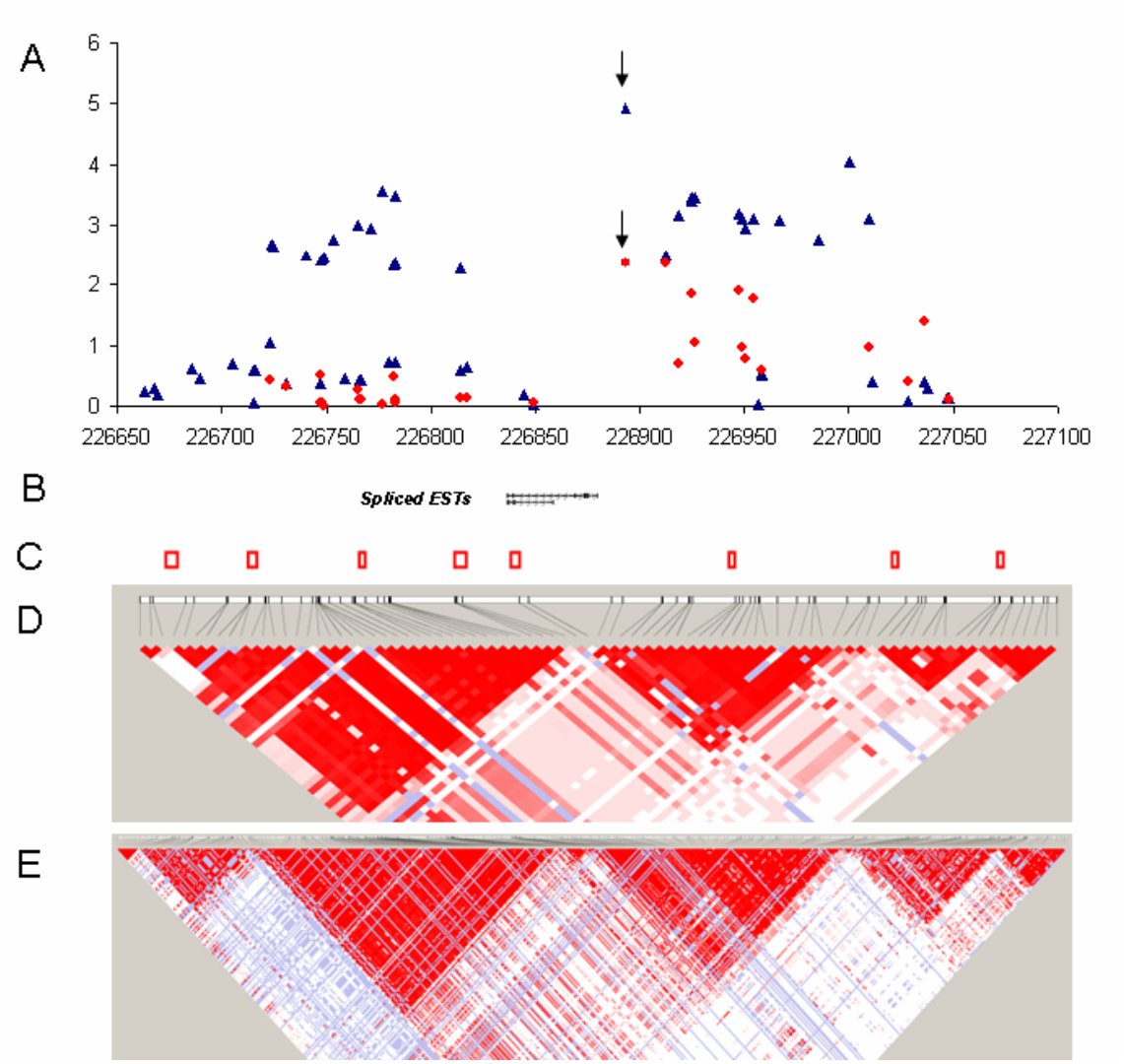
D. Haploview plot of linkage disequilibrium (D′) for SNPs genotyped in WTCCC CAD cases constructed as described by [23]. Colour scheme: D′<1 and LOD<2 = white, D′ =1 and LOD<2 = blue, D′ <1 and LOD≥2 = shades of pink/red, D′ =1 and LOD≥2 = bright red.

E. Haploview plot of linkage disequilibrium (|D'|) for all HapMap SNPs across the region (HapMap CEU data). Colour scheme as for **D.**

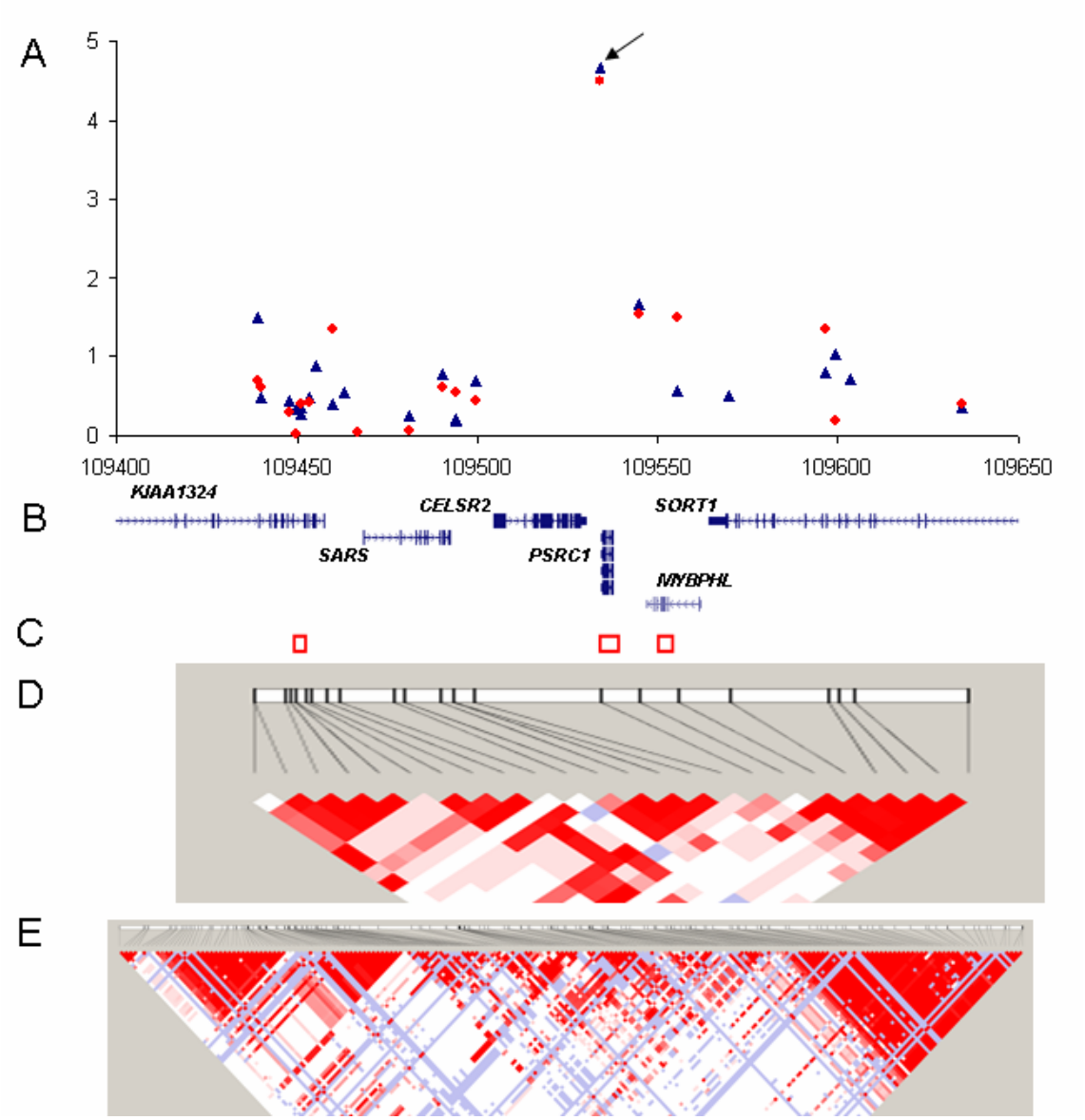
SUPPLEMENTARY FIGURE 1A



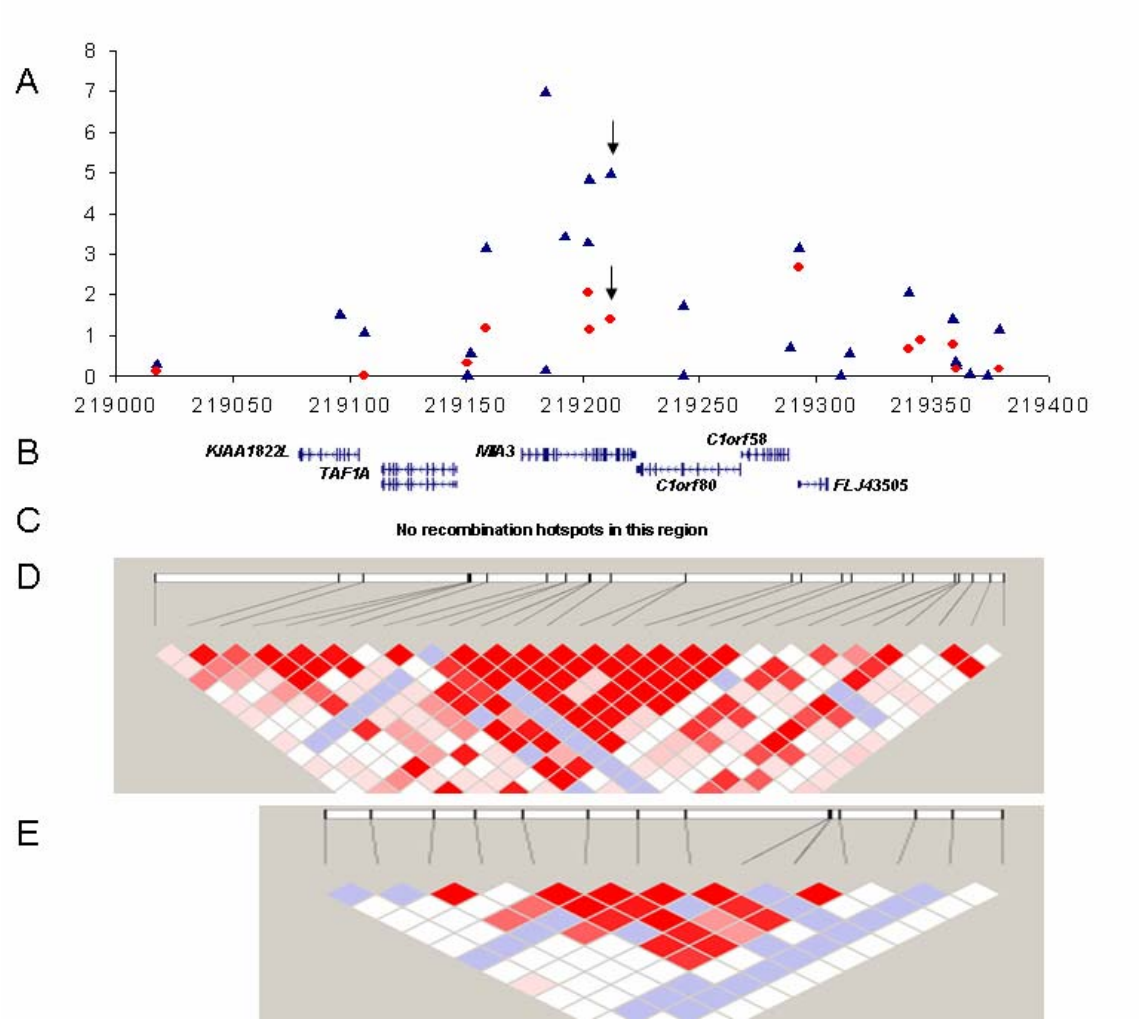
SUPLLEMENTARY FIGURE 1B



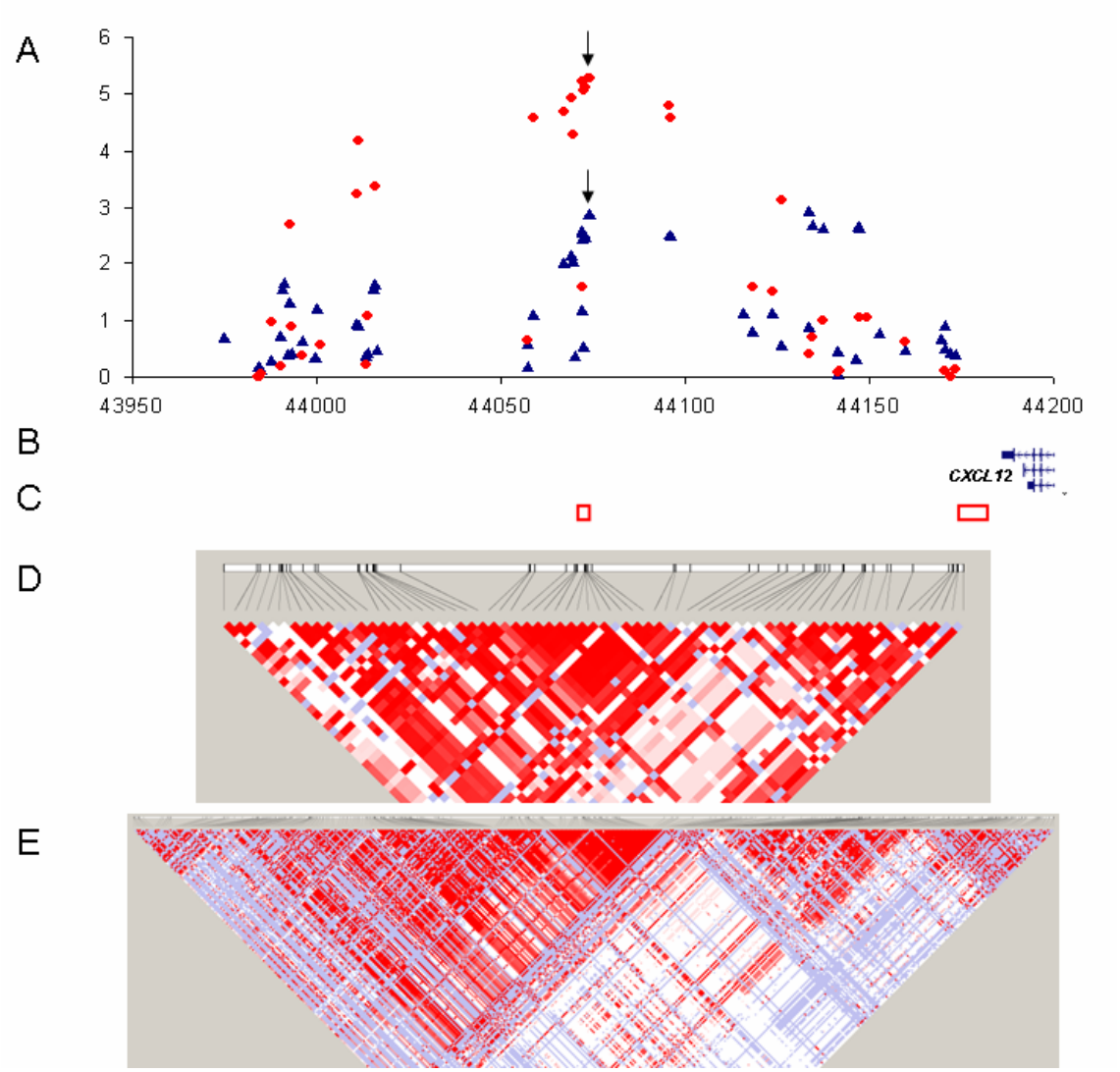
SUPPLEMENTARY FIGURE 1C



SUPPLEMENTARY FIGURE 1D



SUPPLEMENTARY FIGURE 1E



SUPPLEMENTARY FIGURE 1F

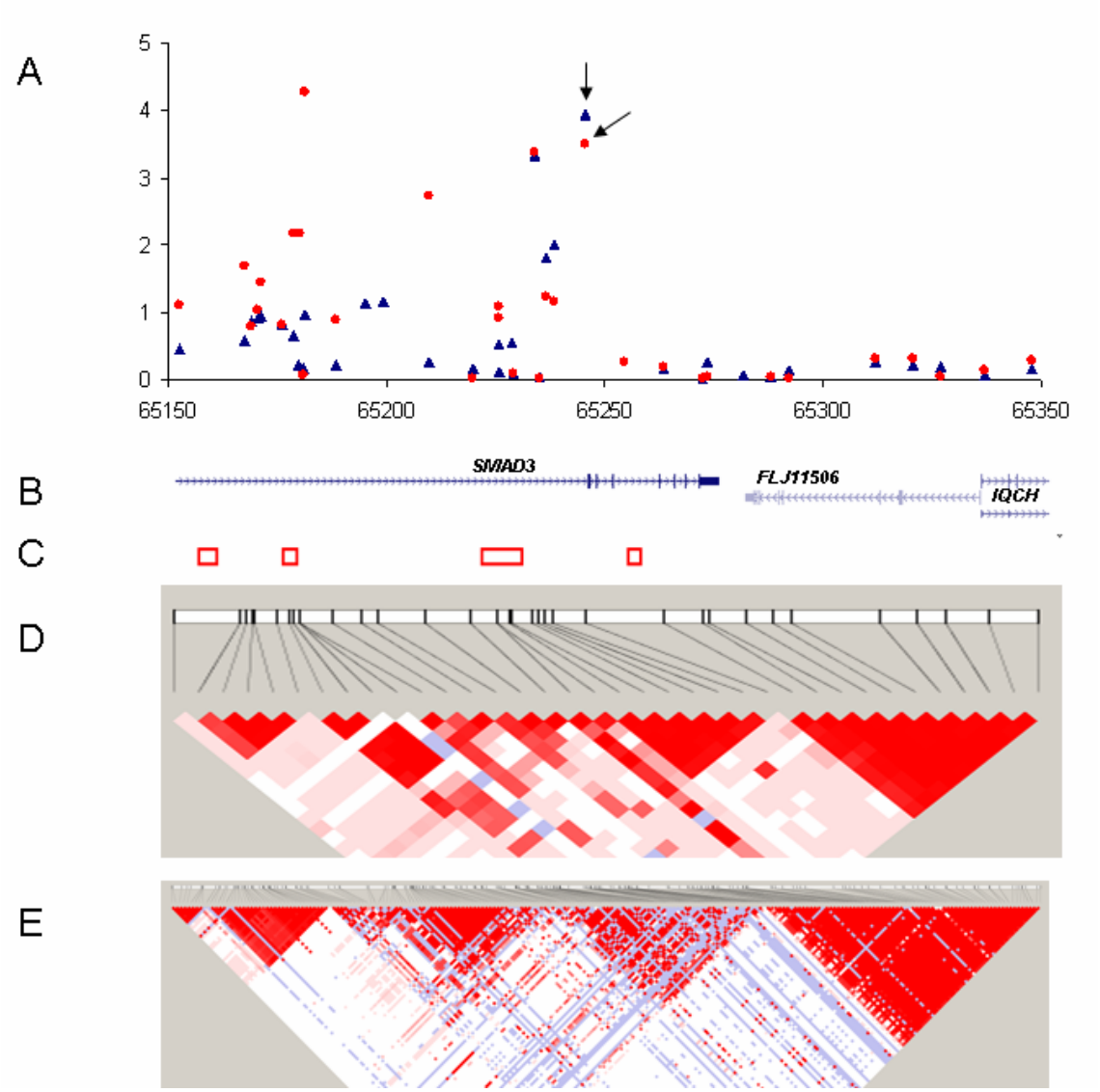


Figure 2. QQ-Plot of the WTCCC Study and German Study data

The QQ-plot includes all SNPs that passed the inclusion criteria (see Supplementary Materials section 2).

Figure 2A. WTCCC Study

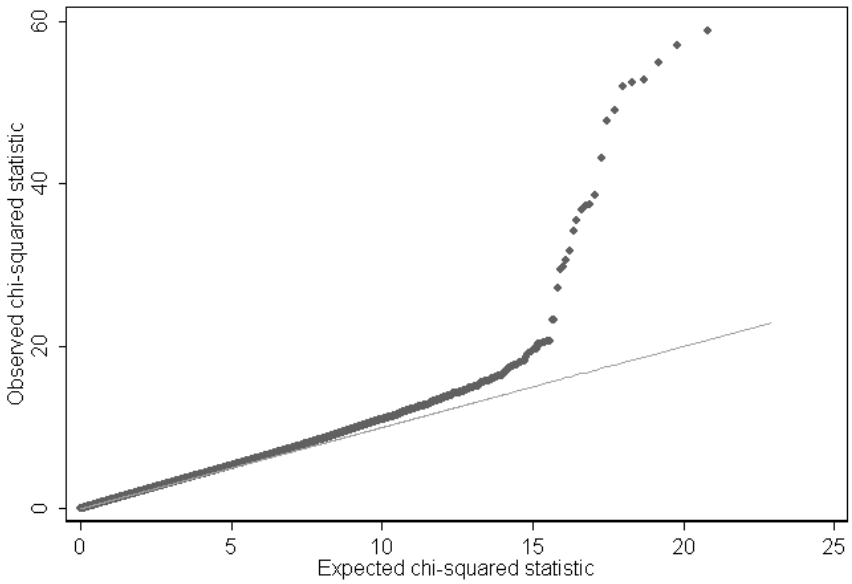
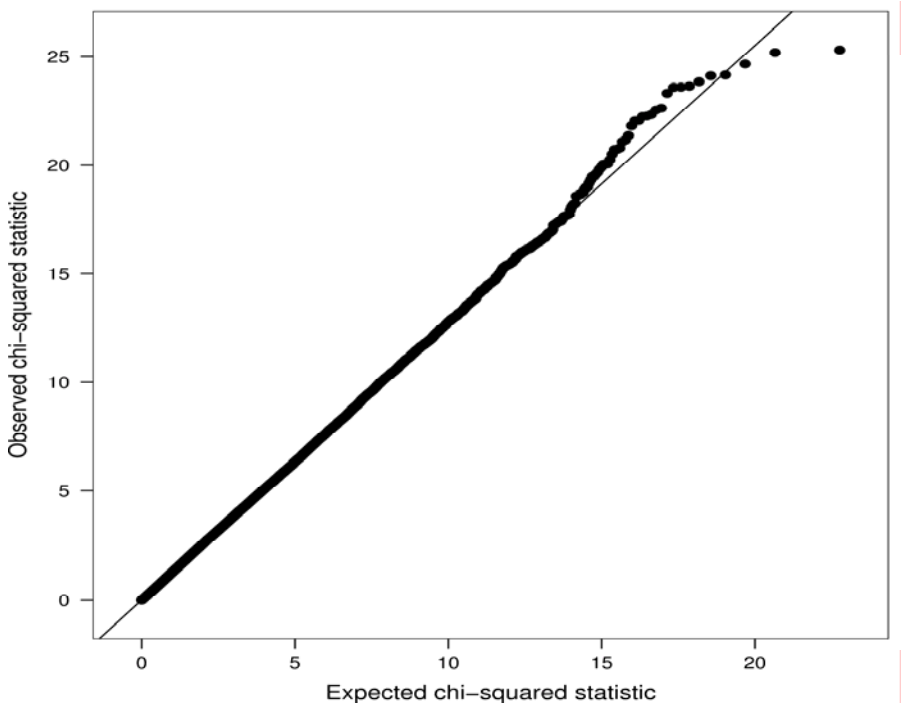


Figure 2B. German Study



9. Supplementary References

1. Samani NJ, Burton P, Mangino M, et al. A genomewide linkage study of 1,933 families affected by premature coronary artery disease: The British Heart Foundation (BHF) Family Heart Study. Am J Hum Genet 2005; 77(6):1011-20.

2. Alfakih K, Brown B, Lawrance RA, et al. Effect of a common X-linked angiotensin II type 2-receptor gene polymorphism (-1332 G/A) on the occurrence of premature myocardial infarction and stenotic atherosclerosis requiring revascularization. Atherosclerosis 2007 [Epub ahead of print].

3. The Wellcome Trust Case Control Consortium. Genomewide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature 2007 (in press).

4. Broeckel U, Hengstenberg C, Mayer B, et al. A comprehensive linkage analysis for myocardial infarction and its related risk factors. Nat Genet 2002; 30(2):210-4.

5. Fischer M, Broeckel U, Holmer S, et al. Distinct heritable patterns of angiographic coronary artery disease in families with myocardial infarction. Circulation 2005; 111(7):855-62.

6. Wichmann HE, Gieger C, Illig T. KORA-gen--resource for population genetics, controls and a broad spectrum of disease phenotypes. Gesundheitswesen 2005; 67 Suppl 1:S26-S30.

7. Devlin B, Roeder K. Genomic control for association studies. Biometrics 1999; 55(4):997-1004.

8. Steffens M, Lamina C, Illig T, et al. SNP-based analysis of genetic substructure in the German population. Human Heredity 2006; 62(1):20-9.

9. Wacholder S, Chanock S, Garcia-Closas M, El GL, Rothman N. Assessing the probability that a positive report is false: an approach for molecular epidemiology studies. J Natl Cancer Inst 2004; 96(6):434-42.

10. Mayer B, Erdmann J, Schunkert H. Genetics and heritability of coronary artery disease and myocardial infarction. Clin Res Cardiol 2007; 96(1):1-7.

11. Glantz SA. Primer of biostatistics. New York: 4th ed. McGraw Hill; 2005.

12. Brady AR. Adjusted population attributable fractions from logistic regression. Stat Tech Bull 1998 (42):8-12.

13. Mayer B, Lieb W, Gotz A, et al. Association of the T8590C polymorphism of CYP4A11 with hypertension in the MONICA Augsburg echocardiographic substudy. Hypertension 2005; 46(4):766-71.

14. Assmann G, Cullen P, Schulte H. Simple scoring scheme for calculating the risk of acute coronary events based on the 10-year follow-up of the prospective cardiovascular Munster (PROCAM) study. Circulation 2002; 105(3):310-5.

15. Wilson PW, D'Agostino RB, Levy D, Belanger AM, Silbershatz H, Kannel WB. Prediction of coronary heart disease using risk factor categories. Circulation 1998; 97(18):1837-47.

16. Royston P, Ambler G, Sauerbrei W. The use of fractional polynomials to model continuous risk variables in epidemiology. Int J Epidemiol 1999; 28(5):964-74.

17. McCullagh P, Nelder JA. Generalized Linear Models. 2nd Edition ed. London: Chapman & Hall 1989.

18. Tregouet D, Garelle V. A new JAVA interface implementation of THESIAS: Testing Haplotype EffectS In Association Studies. Bioinformatics 2007 [Epub ahead of print].

19. Morgan TM, Krumholz HM, Lifton RP, Spertus JA. Nonvalidation of reported genetic risk factors for acute coronary syndrome in a large-scale replication study. JAMA 2007; 297(14):1551-61.

20. Karolchik D, Baertsch R, Diekhans M, et al. The UCSC Genome Browser Database. Nucleic Acids Res 2003; 31(1):51-4.

21. McVean GA, Myers SR, Hunt S, Deloukas P, Bentley DR, Donnelly P. The fine-scale structure of recombination rate variation in the human genome. Science 2004; 304(5670):581-4.

22. Winckler W, Myers SR, Richter DJ, et al. Comparison of fine-scale recombination rates in humans and chimpanzees. Science 2005; 308(5718):107-11.

23. Barrett JC, Fry B, Maller J, Daly MJ. Haploview: analysis and visualization of LD and haplotype maps. Bioinformatics 2005; 21(2):263-5.

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