Additional Information

Large-scale association analyses identifies 13 new susceptibility loci for coronary artery disease

Additional Figures

Additional Figure 1: GWA studies ask for large numbers.

Additional Tables

Additional Table 1a: Description of the genotyping methods in participating GWA studies in the discovery phase.

Additional Table 1b: Description of the genotyping methods in participating studies for replication.

Additional Table 2: Association analysis of novel regions assuming different modes of inheritance and estimating the likely mode of inheritance.

Additional Table 3: Non-synonymous or splice-site variants in linkage disequilibrium (r2 > 0.8, D´>0.9) with lead SNPs (from HapMap CEU).

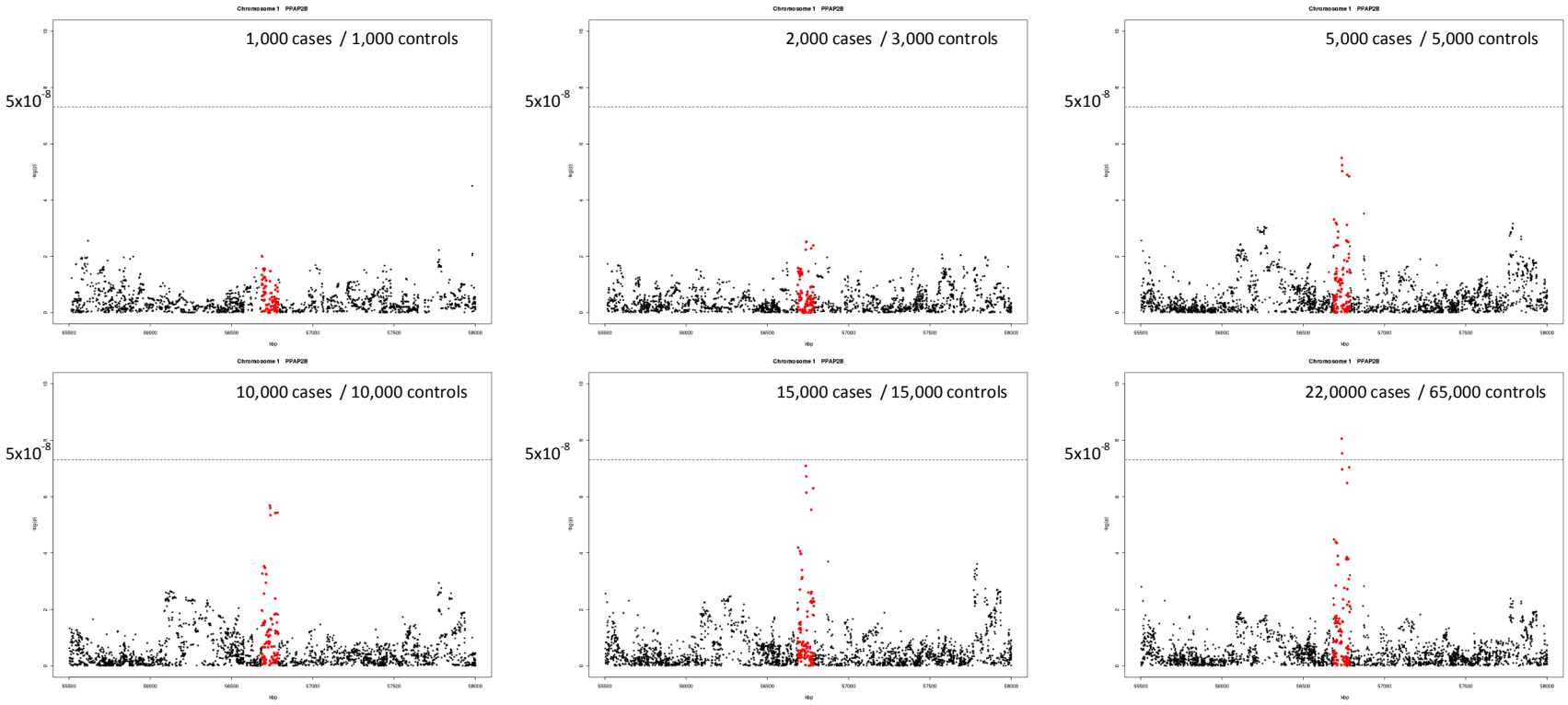
Additional Table 4: eQTL results for the known and novel coronary disease loci.

Additional Table 5: Evidence of cis effects through allelic expression (AE) imbalance using a first generation AE map.

Additional Table 6: Novel and known coronary disease loci associated with other traits and diseases.

Additional Figures

Additional Figure 1: GWA studies ask for large numbers. The figure represents the P for association with coronary disease at the chromosome 1p32.2 locus (denoted by red dots) depending on the number of cases and controls studied.



Additional Tables

Additional Table 1a: Description of the genotyping methods in participating GWA studies in the discovery phase.

Study	Platform	Calling	Genotyped SNPs	Imputation algorithms / NCBI build / HapMap	Total SNPs	QC at study center
ADVANCE	Illumina 550k v3	BeadStudio	561,466	BIMBAM / 36 / r22a	3,732,514	Sample call rate >0.985 SNP call rate >0.95 HWE p >0.001
CADomics	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed	602,459	IMPUTE / 36 / r22a	2,588,156	Sample call rate >0.97 SNP call rate >0.98 HWE p(controls) >10^{-4} MAF >0.01
CHARGE*	Illumina HCNV370 Duo BeadChip	BeadStudio	353,202	MACH/36/ r22	2,533,153	Sample call rate >0.97 SNP call rate >0.97 HWE p(controls) >10^{-6} MAF >0.01
CHARGE*	Affymetrix 6.0	Birdseed	589,253	MACH/35/r21	2,516,204	Sample call rate >0.95 SNP call rate >0.90 HWE p>10^{-6}
	Affymetrix 500K (Nsp 250K and Sty 250K) + MPS 50k	BRLMM	534,982	MACH/36/ r22,	2,543,887	Sample call rate >0.97 SNP call rate >0.97 Subject heterozygosity <5 SD from mean No excessive Mendelian errors
	Illumina Infinium HumanHap 550K	BeadStudio	530,683	MACH/36/ r22,	2,586,725	Subject call rate >0.975, heterozygosity <0.336, match on sex, no IBS outliers, SNP call rate >=0.98, HWE p >10^{-6}, MAF >0.01
deCODE CAD	Illumina HH300/HHCNV370	BeadStudio		Impute / 36		Sample call rate >0.98 SNP call rate >0.96
GerMIFS I	Affymetrix Mapping 500K Array Set	BRLMM	262,338(NSP)/ 238,378(STY)	MACH / 36 / r22a	2,543,887	Sample call rate >0.97 SNP call rate >0.98 HWE p(controls) >10^{-4} MAF >0.01

Study	Platform	Calling	Genotyped SNPs	Imputation algorithms / NCBI build / HapMap	Total SNPs	QC at study center
GerMIFS II	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed	909,622	MACH / 36 / r22a	2,543,887	Sample call rate >0.97 SNP call rate >0.98 HWE p(controls) >10^{-4} MAF >0.01
GerMIFS III (KORA)	Affymetrix Genome-Wide Human SNP Array 5.0 / 6.0	BRLMM-P	503,590(5.0)/ 904,954(6.0)	MACH / 36 / r22a	2,536,369	Sample call rate >0.97 SNP call rate >0.98 HWE p(controls) >10^{-4} MAF >0.01
LURIC/ AtheroRemo 1	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed	905,484	NA	905,484	SNP call rate >0.9†
LURIC/ AtheroRemo 2	Affymetrix Mapping 500K Array Set	DM-3	492,555	NA	492,555	SNP call rate >0.9†
MedStar	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed	869,223	MACH / 36 / r22a	2,749,197	Sample call rate >0.95 SNP call rate >0.95 HWE – NA MAF – NA
MIGen	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed	727,496	MACH / 35	2,557,744	Sample call rate >0.95 SNP call rate >0.95 HWE p(controls) >10^{-6} MAF >0.01
OHGS 1	Affymetrix Mapping 500K Array Set / Genome-Wide Human SNP Array 6.0	BRLMM/ Birdseed	325,040	Impute / 36 / r22	2,469,454	SNP call rate >0.95 HWE p(controls) >10^{-3} MAF >0.05
PennCATH	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed	869,223	MACH / 36 / r22a	2,749,197	Sample call rate >0.95 SNP call rate >0.95 HWE – NA MAF – NA
WTCCC	Affymetrix Mapping 500K Array Set	CHIAMO	477,459	IMPUTE / 36	2,614,446	Sample call rate >0.97 SNP call rate >0.98 HWE p(controls) >10^{-4} MAF - NA

ADVANCE = Atherosclerotic Disease, VAscular functioN, and genetiC Epidemiology; GerMIFS = German Myocardial Infarction Family Studies; WTCCC = Wellcome Trust Case Control Consortium; CHARGE = Cohorts for Heart and Aging Research in Genomic Epidemiology; LURIC = Ludwigshafen Risk and Cardiovascular Heath Study; OHGS = Ottawa Heart Genomics Study

QC = quality control; HWE = test for deviation from Hardy-Weinberg equilibrium; MAF = minor allele frequency

* Four entries for Charge refer to the studies AGES, ARIC, Fram HS, and RS

† Further criteria in LURIC/AtheroRemo: Removed samples based on relatedness, incorrect gender, outliers in the MDS map

Additional Table 1b: Description of the genotyping methods in participating studies for replication.

Study	Genotyping Platform
AMI/DHS	Sequenom
ADVANCE	TaqMan OpenArray
AMC-PAS	Sequenom
Angio-Lueb/GoKard	Sequenom
CHAOS	Sequenom
CC/OHGS2	Affymetrix 6.0
EPIC-CAD	Sequenom
GENDER	Sequenom
GraceGenetics	Sequenom
INTERHEART/EpiDREAM/OHGS3	Affymetrix 6.0
IHCS	Sequenom
IFS	Sequenom
IATVB	Affymetrix 6.0
LEEDS	Sequenom
MDCS	Sequenom
MAHI	Sequenom
PopGen	Sequenom
SAS	Sequenom
SMILE	Sequenom
SHEEP	Sequenom
The Emory Genebank Study	Centaurus (Nanogen)
The Johns Hopkins GeneSTAR Research Program	Illumina HumanHap 1M BeadArray
The New Zealand CAD Study	Centaurus (Nanogen)
THISEAS	Sequenom
UKMI	Sequenom
VHS	Sequenom

For explanation of study abbreviations, see Supplementary Table 1b.

Additional Table 2: Association analysis of novel regions assuming different modes of inheritance and estimating the likely mode of inheritance.

SNP	Band	Gene in region	Risk allele	P additive	P dominant	P recessive	MOI
rs17114036	1p32.2	*PPAP2B*	A	$1.43 \cdot 10^{-08}$	$9.87 \cdot 10^{-02}$	$7.63 \cdot 10^{-10}$	rec
rs17609940	6p21.31	*ANKS1A*	G	$2.21 \cdot 10^{-06}$	$4.30 \cdot 10^{-03}$	$1.57 \cdot 10^{-06}$	rec
rs12190287	6q23.2	*TCF21*	C	$4.64 \cdot 10^{-11}$	$1.00 \cdot 10^{-04}$	$1.12 \cdot 10^{-08}$	add
rs11556924	7q32.2	*ZC3HC1*	C	$2.22 \cdot 10^{-09}$	$6.88 \cdot 10^{-06}$	$1.70 \cdot 10^{-07}$	add
rs579459	9q34.2	*ABO*	C	$1.16 \cdot 10^{-07}$	$1.18 \cdot 10^{-08}$	$1.50 \cdot 10^{-02}$	dom
rs12413409	10q24.32	*CYP17A1, CNNM2, NT5C2*	G	$1.47 \cdot 10^{-06}$	$2.11 \cdot 10^{-02}$	$1.52 \cdot 10^{-05}$	rec
rs964184	11q23.3	*ZNF259, APOA5, APOA1*	G	$8.02 \cdot 10^{-10}$	$1.59 \cdot 10^{-09}$	$6.00 \cdot 10^{-04}$	add
rs4773144	13q34	*COL4A1, COL4A2*	G	$4.15 \cdot 10^{-07}$	$8.99 \cdot 10^{-06}$	$3.00 \cdot 10^{-04}$	add
rs2895811	14q32.2	*HHIPL1, CYP46A1*	C	$2.67 \cdot 10^{-07}$	$1.20 \cdot 10^{-03}$	$2.71 \cdot 10^{-06}$	rec
rs3825807	15q25.1	*ADAMTS7*	A	$9.63 \cdot 10^{-06}$	$1.60 \cdot 10^{-03}$	$1.35 \cdot 10^{-05}$	rec
rs12936587	17p11.2	*Rall, PEMT, RADS1*	G	$4.89 \cdot 10^{-07}$	$2.00 \cdot 10^{-04}$	$3.05 \cdot 10^{-06}$	add
rs216172	17p13.3	*SMG6, SRR*	C	$6.22 \cdot 10^{-07}$	$5.87 \cdot 10^{-08}$	$4.00 \cdot 10^{-04}$	dom
rs46522	17q21.32	*UBE2Z*	T	$3.57 \cdot 10^{-06}$	$1.55 \cdot 10^{-05}$	$6.17 \cdot 10^{-05}$	add

P additive, dominant and recessive = association p-values assuming an additive, dominant and recessive mode of inheritance. MOI = estimated mode of inheritance.

Additional Table 3: Non-synonymous or splice-site variants in linkage disequilibrium (r^2 > 0.8, D´>0.9) with lead SNPs (from HapMap CEU).

Band	Lead SNP	Proxy SNP	Distance from lead SNP	r^2	D´	Gene	Coding change	Type
7q32.2	rs11556924		0	1	1	*ZC3HC1*	R363H	non-synonymous
14q32.2	rs2895811	rs7158073	7,747	0.82	0.95	*HHIPL1*	V691A	non-synonymous
15q25.1	rs3825807		0	1	1	*ADAMTS7*	S214P	non-synonymous
17q21.32	rs46522	rs2291725	50,535	1	1	*GIP*	S103G	non-synonymous
		rs2291726	50,657	0.94	1	*GIP*	c.258-73A>G	cryptic splice-site alteration

Additional Table 4: eQTL results for the known and novel coronary disease loci.

								SNP with strongest association with expression [c]		
Band	**SNP**	**Position**	**Gene (Transcript)**	**Tissue**	**E** [a]	**P**	**P_{adj}** [b]	**SNP (r^2)** [d]	**P**	**P_{adj}** [e]
Novel loci reported in this study										
6q23.2	rs12190287[C]	134256218	*TCF21* (NM_003206)	Omental	+	1.2×10^{-8}				
"	"	"	*TCF21* (NM_003206)	Liver	+	2.3×10^{-8}				
17p11.2	rs12936587[G]	17484447	*PEMT* (ILMN_1745806)[f]	Monocytes	-	3.1×10^{-9}				
"	"	"	*RASD1* (ILMN_1740426)[f]	Monocytes	+	2.0×10^{-14}				
"	"	"	*SMCR3* (HSS00330572)	Subq	+	9.9×10^{-12}	0.73	rs12945496 (0.85)	1.5×10^{-13}	0.48
17q21.32	rs46522[T]	44343596	*UBE2Z* (NM_023079)	Blood	+	1.7×10^{-12}	0.82	rs12453394 (0.93)	9.9×10^{-13}	0.33
Previously reported loci										
1p13.3	rs599839[A]	109623689	*PSRC1* (ILMN_1671843)[g]	Monocytes	-	7.7×10^{-21}				
"	"	"	*PSRC1* (ILMN_1671843)[g]	Macrophages	-	4.8×10^{-20}				
"	"	"	*PSRC1* (ILMN_2315964)[g]	Macrophages	-	9.8×10^{-7}				
"	"	"	*PSRC1* (NM_032636)	Subq	-	1.3×10^{-9}	0.66	rs4970834 (0.60)	2.7×10^{-11}	0.19
"	"	"	*CELSR2* (NM_001408)	Liver	-	2.8×10^{-70}	1	rs646776 (0.89)	5.0×10^{-73}	0.78
"	"	"	*PSRC1* (NM_032636)	Liver	-	1.2×10^{-182}	0.97	rs646776 (0.89)	1.4×10^{-193}	0.51
"	"	"	*SORT1* (AK000757)	Liver	-	4.7×10^{-213}	0.86	rs646776 (0.89)	3.8×10^{-227}	0.49
"	"	"	*SORT1* (NM_002959)	Liver	-	2.1×10^{-141}	0.94	rs646776 (0.89)	4.8×10^{-147}	0.75
"	"	"	*PSRC1* (NM_032636)	Blood	-	2.1×10^{-24}	0.14	rs660240 (0.85)	1.1×10^{-26}	0.00085
3q22.3	rs2306374[C]	139602642	(hCT1951505.1)	Subq	+	3.7×10^{-6}				
9p21.3	rs4977574[G]	22088574	*CDKN2B* (NM_078487)	Omental	-	5.0×10^{-6}	0.98	rs2383207 (0.90)	1.0×10^{-6}	0.82
19p13.2	rs1122608[G]	11024601	*SMARCA4* (NM_003072)	Omental	+	9.2×10^{-6}	0.69	rs7258189 (0.70)	4.6×10^{-6}	0.71
21q22.11	rs9982601[T]	34520998	*MRPS6* (NM_032476)	Blood	+	5.6×10^{-11}	0.55	rs7278204 (0.84)	2.7×10^{-11}	0.19

All expression associations with $P < 10^{-5}$ where the coronary artery disease SNP is the strongest expression SNP (eSNP) in the region for the given genes or is in high correlation ($r^2 \geq 0.60$) with the strongest eSNP. [a]Direction of effect. [b]P for correlation tested conditional on the SNP that shows most significant correlation with expression. [c]The SNP in the 1 Mb window that shows the strongest correlation with expression. [d]Correlation r^2 between the coronary artery disease-associated SNP and the SNP that shows strongest correlation with expression. [e]P for correlation tested conditioned on the coronary artery disease-associated SNP. [f]A proxy, rs2955359, with $r^2 = 0.85$ with rs12936587 was tested. [g]A proxy, rs646776, with $r^2 = 0.89$ with rs599839 was tested. A more detailed explanation of the table contents and analyses is provided in Supplementary Methods.

Additional Table 5: Evidence of cis effects through allelic expression (AE) imbalance using a first generation AE map (Ge B, Pokholok DK, Kwan T, et al. Global patterns of cis variation in human cells revealed by high-density allelic expression analysis. Nat Genet 2009;41:1216-22). Only CARDIoGRAM lead SNPs located within one or more of the 7785 significant measure AE windows reported by Ge et al. are included. Entries with high LD (r2 > 0.5) are shaded in grey.

CARDIOGRAM lead SNP			Measured AE window			Allelic expression association						Transcript overlapping AE window			
rs	chr	position	Start position	End position	No. of Measured SNPs	Start position	End position	Tag-SNP	Nominal P	Significance level*	r^2 between Tag & lead SNPs	Start position	End position	GENE SYMBOL	locuslink ID
Novel Loci															
Window based AE association															
rs17114036	1	56735409	56748430	56770370	6	56684634	56741065	rs7525717	3.14E-05	0.005	0.0495	56732526	56817845	PPAP2B	8613
rs11556924	7	129450732	129403173	129445118	9	129416799	129485998	rs2242488	2.80E-05	0.005	0.235	129445361	129478469	ZC3HC1	51530
rs579459	9	135143989	135141266	135182445	13	135122575	135149361	rs579459	4.48E-06	0.001	1	135115608	135454453	ABO	28
rs12413409	10	104709086	104747699	104804152	12	104618863	104859028	rs3897401	1.18E-07	0.001	0.0323	104668061	104828334	CNNM2	54805
rs12413409	10	104709086	104839458	104842638	3	104618863	104921574	rs12764154	1.37E-07	0.001	0.0187	104837903	104943041	NT5C2	22978
rs12413409	10	104709086	104859028	104867025	4	104695402	104991787	rs1926030	1.19E-12	Genome-wide	0.081	104837903	104943041	NT5C2	22978
rs3825807	15	76876166	76845627	76886593	4	76869486	76912484	rs12438008	4.76E-08	0.001	0.3049	76838600	76890830	ADAMTS7	11173
rs216172	17	2073254	2142838	2150203	6	2045089	2163008	rs216219	5.68E-12	Genome-wide	0.7454	1909882	2153819	SMG6	23293
rs46522	17	44343596	44329733	44333352	3	44305495	44408827	rs2291726	9.89E-10	Genome-wide	0.9334	44325127	44328229	ATP5G1	516
rs46522	17	44343596	44359722	44360508	3	44305495	44408827	rs318095	1.73E-09	Genome-wide	1	44340828	44362724	UBE2Z	65264
rs46522	17	44343596	44362496	44369126	5	44305495	44408827	rs2291726	5.37E-10	Genome-wide	0.9334	44340828	44362724	UBE2Z	65264
rs46522	17	44343596	44362496	44369126	5	44305495	44408827	rs2291726	5.37E-10	Genome-wide	0.9334	44362459	44377171	SNF8	11267
rs46522	17	44343596	44329733	44333352	3	44305495	44408827	rs2291726	9.89E-10	Genome-wide	0.9334	44390916	44400954	GIP	2695
High confidence full transcript AE association															
none															

Known Loci

Window based AE association

rs6725887	2	203454130	203727576	203742096	5	203440515	203809573	rs10188105	4.57E-06	0.001	0.059	203587846	203659747	ALS2CR16	130029
rs6725887	2	203454130	203727576	203742096	5	203440515	203809573	rs10188105	4.57E-06	0.001	0.059	203484415	203557439	ALS2CR8	79800
rs6725887	2	203454130	203727576	203742096	5	203440515	203809573	rs10188105	4.57E-06	0.001	0.059	203346117	203444953	ICA1L	130026
rs6725887	2	203454130	203727576	203742096	5	203440515	203809573	rs10188105	4.57E-06	0.001	0.059	203708717	203799345	NBEAL1	65065
rs6725887	2	203454130	203727576	203742096	5	203440515	203809573	rs10188105	4.57E-06	0.001	0.059	203453574	203485194	WDR12	55759
rs3184504	12	110368991	110436550	110446964	3	110317972	110614582	rs593226	5.23E-07	0.001	0.314	110608254	110679289	ACAD10	80724
rs3184504	12	110368991	110436550	110446964	3	110317972	110614582	rs593226	5.23E-07	0.001	0.314	110374401	110521863	ATXN2	6311
rs3184504	12	110368991	110436550	110446964	3	110317972	110614582	rs593226	5.23E-07	0.001	0.314	110565880	110608173	BRAP	8315
rs3184504	12	110368991	110436550	110446964	3	110317972	110614582	rs593226	5.23E-07	0.001	0.314	110328134	110373809	SH2B3	10019
rs3184504	12	110368991	110610448	110625616	4	110365692	110713097	rs3809276	2.09E-09	Genome-wide	0.154	110608254	110679289	ACAD10	80724
rs3184504	12	110368991	110610448	110625616	4	110365692	110713097	rs3809276	2.09E-09	Genome-wide	0.154	110688728	110732165	ALDH2	217
rs3184504	12	110368991	110610448	110625616	4	110365692	110713097	rs3809276	2.09E-09	Genome-wide	0.154	110374401	110521863	ATXN2	6311
rs3184504	12	110368991	110610448	110625616	4	110365692	110713097	rs3809276	2.09E-09	Genome-wide	0.154	110565880	110608173	BRAP	8315
rs3184504	12	110368991	110610448	110625616	4	110365692	110713097	rs3809276	2.09E-09	Genome-wide	0.154	110328134	110373809	SH2B3	10019

High confidence full transcript AE association

rs17464857**	1	220829332	NA	NA	NA	220804104	221023703	rs17532708	1.09E-08	0.001	0.253	220977180	220990625	FAM177B	400823

*Significance level is based on permutation analysis and is compartamentalized into three categories: 0.001< P < 0.005, 7.6x10–9 (genomewide) < P <0.001, P < 7.6x10–9 (genomewide)

**This AE imbalance was missed by window based approach either because of low-magnitude AE or due to window partitions excluding informative sections of the transcript

Additional Table 6: Novel and known coronary artery disease loci associated with other traits and diseases.

Region	Lead SNP for CAD	Other trait mapped to the region	Lead SNP for other trait	r^2	D´	P for CAD of lead SNP for other trait	Reported genes in region	Ref
1p13.3	rs646776	LDL cholesterol	rs12740374	1.00	1.00	1.64E-09	CELSR2, PSRC1, SORT1	[1]
1p13.3	rs646776	Lp-PLA2 activity and mass	rs599839	1.00	1.00	2.89E-10	PSRC1	[2]
9p21.3	rs4977574	Glioma	rs4977756	0.47	0.95	4.05E-15	CDKN2A, CDKN2B	[3]
9p21.3	rs4977574	Intracranial aneurysm	rs1333040	0.67	1.00	6.99E-09	CDKN2A,CDKN2B	[4]
9q34.2	**rs579459**	**Angiotensin-converting enzyme activity**	**rs495828**	**1.00**	**1.00**	**1.63E-07**	**ABO**	[5]
9q34.2	**rs579459**	**Hematological and biochemical traits**	**rs495828**	**1.00**	**1.00**	**1.63E-07**	**ABO**	[6]
9q34.2	**rs579459**	**Pancreatic cancer**	**rs505922**	**0.38**	**0.88**	**7.14E-06**	**ABO**	[7]
9q34.2	**rs579459**	**Plasma E-selectin levels**	**rs651007**	**0.95**	**1.00**	**5.53E-07**	**ABO**	[8]
9q34.2	**rs579459**	**Protein quantitative trait loci**	**rs505922**	**0.38**	**0.88**	**7.14E-06**	**ABO**	[9]
9q34.2	**rs579459**	**Serum soluble E-selectin**	**rs579459**	**0.38**	**0.88**	**1.16E-07**	**ABO**	[10]
9q34.2	**rs579459**	**Soluble levels of adhesion molecules**	**rs649129**	**1.00**	**1.00**	**1.09E-07**	**ABO**	[11]
9q34.2	**rs579459**	**Venous thromboembolism**	**rs505922**	**0.38**	**0.88**	**7.14E-06**	**ABO**	[12]
10q24.32	**rs12413409**	**Intracranial aneurysm**	**rs12413409**	**1.00**	**1.00**	**1.47E-06**	**CNNM2**	[4]
10q24.32	**rs12413409**	**Systolic blood pressure**	**rs11191548**	**1.00**	**1.00**	**1.31E-05**	**CYP17A1, AS3MT, CNNM2, NT5C2**	[13]
11q23.3	**rs964184**	**HDL cholesterol**	**rs964184**	**1.00**	**1.00**	**8.02E-10**	**APOA1, APOC3, APOA4, APOA5**	[14]
11q23.3	**rs964184**	**Hematological and biochemical traits**	**rs7350481**	**0.28**	**0.81**	**8.50E-06**	**APO-A cluster**	[6]
11q23.3	**rs964184**	**LDL cholesterol**	**rs12272004**	**0.51**	**1.00**	**2.19E-02**	**APOA1, APOA4, APOA5, APOC3**	[14]
11q23.3	**rs964184**	**LDL cholesterol**	**rs6589566**	**0.31**	**1.00**	**2.15E-06**	**APOA1,APOC3,APOA5**	[15]
11q23.3	**rs964184**	**Lp-PLA2 activity and mass**	**rs12286037**	**0.59**	**1.00**	**4.98E-04**	**ZNF259**	[2]
11q23.3	**rs964184**	**Plasma carotenoid and tocopherol levels**	**rs12272004**	**0.51**	**1.00**	**1.29E-02**	**APOA5**	[16]
11q23.3	**rs964184**	**Triglycerides**	**rs964184**	**1.00**	**1.00**	**8.02E-10**	**APOA1, APOC3, APOA4, APOA5**	[1]
15q25.1	**rs3825807**	**Lung adenocarcinoma**	**rs1051730**	**0.21**	**0.51**	**7.00E-01**	**CHRNA3, CHRNA5**	[17]
15q25.1	**rs3825807**	**Smoking behavior**	**rs1051730**	**0.21**	**0.51**	**7.00E-01**	**NR**	[18]

Region	Lead SNP for CAD	Other trait mapped to the region	Lead SNP for other trait	r^2	D´	P for CAD of lead SNP for other trait	Reported genes in region	Ref
12q24.12	rs3184504	Celiac disease	rs653178	1.00	1.00	2.20E-06	SH2B3	[19]
12q24.12	rs3184504	Chronic kidney disease	rs653178	1.00	1.00	2.20E-06	ATXN2	[20]
12q24.12	rs3184504	Diastolic blood pressure	rs3184504	1.00	1.00	6.35E-06	SH2B3	[21]
12q24.12	rs3184504	Diastolic blood pressure	rs653178	1.00	1.00	2.20E-06	ATXN2, SH2B3	[13]
12q24.12	rs3184504	Hematocrit	rs11065987	0.69	0.96	5.62E-07	SH2B3, ATXN2	[22]
12q24.12	rs3184504	Hemoglobin	rs11065987	0.69	0.96	5.62E-07	TRAFD1	[22]
12q24.12	rs3184504	Plasma eosinophil count	rs3184504	1.00	1.00	6.35E-06	SH2B3	[23]
12q24.12	rs3184504	Systolic blood pressure	rs3184504	1.00	1.00	6.35E-06	SH2B3	[21]
12q24.12	rs3184504	Type 1 diabetes	rs3184504	1.00	1.00	6.35E-06	SH2B3	[24]
17p13.3	**rs216172**	**Aortic root size**	**rs10852932**	**0.73**	**0.90**	**5.23E-05**	**SMG6, SRR, TSR1, SGSM2**	[25]

Selection is based on the report in the NHGRI catalogue of published GWAS with genomewide level of significance ($P<5x10^{-8}$), based on a 1 mega base maximum distance and linkage disequilibrium ($r^2>0.2$) between the SNPs. Novel loci are in bold. Date of access June 28th 2010.
Lead SNP for other trait: SNP has documented $P < 5x10^{-8}$ for association with other trait listed (reference in superscript)
r^2, D': Linkage disequilibrium between lead SNP for coronary artery disease and lead SNP for other trait (HapMap)
P for CAD of lead SNP for other trait: P for association of the lead SNP from other trait with coronary artery disease in the CARDIoGRAM meta-analysis discovery phase

References

1. Kathiresan, S. *et al.* Common variants at 30 loci contribute to polygenic dyslipidemia. *Nat Genet* **41**, 56-65 (2009).
2. Suchindran, S. *et al.* Genome-wide association study of Lp-PLA(2) activity and mass in the Framingham Heart Study. *PLoS Genet* **6**, e1000928 (2010).
3. Shete, S. *et al.* Genome-wide association study identifies five susceptibility loci for glioma. *Nat Genet* **41**, 899-904 (2009).
4. Yasuno, K. *et al.* Genome-wide association study of intracranial aneurysm identifies three new risk loci. *Nat Genet* **42**, 420-5 (2010).
5. Chung, C.M. *et al.* A genome-wide association study identifies new loci for ACE activity: potential implications for response to ACE inhibitor. *Pharmacogenomics J* (2010).
6. Kamatani, Y. *et al.* Genome-wide association study of hematological and biochemical traits in a Japanese population. *Nat Genet* **42**, 210-5 (2010).
7. Amundadottir, L. *et al.* Genome-wide association study identifies variants in the ABO locus associated with susceptibility to pancreatic cancer. *Nat Genet* **41**, 986-90 (2009).
8. Qi, L. *et al.* Genetic variants in ABO blood group region, plasma soluble E-selectin levels and risk of type 2 diabetes. *Hum Mol Genet* **19**, 1856-62 (2010).
9. Melzer, D. *et al.* A genome-wide association study identifies protein quantitative trait loci (pQTLs). *PLoS Genet* **4**, e1000072 (2008).
10. Paterson, A.D. *et al.* Genome-wide association identifies the ABO blood group as a major locus associated with serum levels of soluble E-selectin. *Arterioscler Thromb Vasc Biol* **29**, 1958-67 (2009).
11. Barbalic, M. *et al.* Large-scale genomic studies reveal central role of ABO in sP-selectin and sICAM-1 levels. *Hum Mol Genet* **19**, 1863-72 (2010).
12. Tregouet, D.A. *et al.* Common susceptibility alleles are unlikely to contribute as strongly as the FV and ABO loci to VTE risk: results from a GWAS approach. *Blood* **113**, 5298-303 (2009).
13. Newton-Cheh, C. *et al.* Genome-wide association study identifies eight loci associated with blood pressure. *Nat Genet* (2009).
14. Aulchenko, Y.S. *et al.* Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. *Nat Genet* **41**, 47-55 (2009).
15. Wallace, C. *et al.* Genome-wide association study identifies genes for biomarkers of cardiovascular disease: serum urate and dyslipidemia. *Am J Hum Genet* **82**, 139-49 (2008).
16. Ferrucci, L. *et al.* Common variation in the beta-carotene 15,15'-monooxygenase 1 gene affects circulating levels of carotenoids: a genome-wide association study. *Am J Hum Genet* **84**, 123-33 (2009).
17. Landi, M.T. *et al.* A genome-wide association study of lung cancer identifies a region of chromosome 5p15 associated with risk for adenocarcinoma. *Am J Hum Genet* **85**, 679-91 (2009).
18. Thorgeirsson, T.E. *et al.* Sequence variants at CHRNB3-CHRNA6 and CYP2A6 affect smoking behavior. *Nat Genet* **42**, 448-53 (2010).
19. Dubois, P.C. *et al.* Multiple common variants for celiac disease influencing immune gene expression. *Nat Genet* **42**, 295-302 (2010).
20. Kottgen, A. *et al.* New loci associated with kidney function and chronic kidney disease. *Nat Genet* **42**, 376-84 (2010).
21. Levy, D. *et al.* Genome-wide association study of blood pressure and hypertension. *Nat Genet* (2009).
22. Ganesh, S.K. *et al.* Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. *Nat Genet* **41**, 1191-8 (2009).

23. Gudbjartsson, D.F. *et al.* Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. *Nat Genet* **41**, 342-7 (2009).
24. Barrett, J.C. *et al.* Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes. *Nat Genet* (2009).
25. Vasan, R.S. *et al.* Genetic variants associated with cardiac structure and function: a meta-analysis and replication of genome-wide association data. *JAMA* **302**, 168-78 (2009).