Table S1: SNPs linked to CV disease states

Single nucleotide polymorphisms (SNPs) associated with CVD were used as indicators of predisposed genetic risk for cardiovascular disease. The reference SNP cluster identifier (rs cluster), associated gene, and human chromosome (Chr) location of each SNP used within the algorithm is detailed in the following table along with the ancestral allele and disease-linked variant alleles associated with the given disease states. Disease terms associated with the given rs clusters are Aneurysm (A), Aortic Aneurysm (AA), Arrhythmia (ARR), Arrhythmogenic Right Ventricular Dysplasia (ARVD), Arterial Occlusive Disease (AOC), Brugada Syndrome (BS), Cardiac Amyloidosis (CAM), Cardiac Arrest (CA), Cardiomyopathy (CM), Cardiovascular (CV), Dilated Cardiomyopathy (DCM), Dyslipidemia (DL), Elevated Triglycerides (ET), Familial Dilated Cardiomyopathy (FDCM), Familial Hypercholesterolemia (FHC), High-Density Lipoprotein (HDL), Heart Disease (HD), Heart Valve Disease (HVD), Hemorrhagic Stroke (HS), High Blood Pressure (HBP), Hypercholesterolemia (HC), Hypertension (H), Insulin Resistance (IR), Ischemic Stroke (IS), Long QT Syndrome (LQTS), Low-Density Lipoprotein (LDL), Marfan Syndrome (MS), Mitral (M), Mitral Valve Prolapse (MVP), Noncompaction Cardiomyopathy (NCM), Obesity (O), Prolapse (P), Pulmonary Hypertension (PH), Restrictive Cardiomyopathy (RCM), Short QT Syndrome (SQTS), Stroke (S), and Thrombosis (T).

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs1126742	CYP4A11	(C:C) and (C:T) -- higher risk for hypertension ; (T:T) -- normal	1	46,932,824	A	G				IS
rs11591147	PCSK9	(G:G) -- normal; (G:T) and (T:T) -- 2-3 fold lower risk of heart disease	1	55,039,974	G	A	T			LDL, PH, HDL
rs16847548		(C:C) -- 2.6x increased risk for sudden cardiac death in Caucasians; (C:T) -- 1.3x increased risk for sudden cardiac death in Caucasians; (T:T) -- normal	1	162065484	T	C				IS, PH
rs17465637	MIA3	(C:C) and (A:C) -- 1.3x higher risk for myocardial infarction; (A:A) -- normal	1	222,650,187	A	C	G	T		CV, IS
rs17672135	FMN2	(T:T) -- 1.3x risk of heart disease; (C:C) -- normal	1	240,282,296	T	C				HDL
rs2820037		(A:T) -- 1.5x higher risk for high blood pressure; (T:T) -- 1.1x higher risk for high blood pressure; (A:A) -- normal	1	239,273,242	A	T				CV
rs3093059	CRP	(C:C) -- associated with elevated C-reactive protein levels and hypertension	1	159,715,346	A	G				IS

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs376923877	TNNT2	(A:G) -- Familial hypertrophic cardiomyopathy (possible); (G:G) -- normal	1	201359637	G	A	T			IS, CV, HVD, M, LDL
rs3903239	PRRX1	(C:C) -- higher frequency of atrial fibrillation	1	170,600,176	A	G	T			CM
rs5174	LRP8	(A:G) and (A:A) -- 1.3x increased risk for heart disease; (G:G) -- normal	1	53247055	C	T				IS
rs5361	SELE	(C:C) -- 4x increased risk for recurrent venous thromboembolism; (A:A) and (A:C) -- normal	1	169,731,919	T	G				CV, IS
rs55883237	OBSCN	(C:G) -- Left ventricular noncompaction possible (likely?); (G:G) -- normal	1	228,374,584	G	A	C			A
rs599839	PSRC1	(A:A) and (A:G) -- 1.3x increased risk for heart disease; (G:G) -- normal	1	109,279,544	G	A	C			CV, IS, HD, A, AA
rs6025	F5	(A:A) -- 11.4x higher risk of thrombosis; (A:G) -- 3.5-4.4x risk of thrombosis; (G:G) -- normal	1	169,549,811	C	T				CV, HD, AA, IS
rs63750197	PSEN2	(C:T) -- dilated cardiomyopathy; (C:C) -- normal	1	226,885,570	C	T				A
rs646776	CELSR2	(A:A) -- 1.2x risk of coronary artery disease	1	109,275,908	C	T				AA, MS
rs699	AGT	(C:C) and (C:T) -- increased risk of hypertension; (T:T) -- normal	1	230,710,048	A	G				H, HBP
rs74315379	TNNT2	(A:G) -- Hypertrophic Cardiomyopathy; (C:T) -- Familial Hypertrophic Cardiomyopathy; (C:C) -- normal	1	201,364,336	G	A	T			CV, LQTS, ARR

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs1010	VAMP8	(A:G) and (G:G) -- 1.75x risk of MI; (A:A) -- normal	2	85581859	T	C	G			CV, FDCM, NCM, CM, DCM
rs12713559	APOB	(C:T) -- carrier of possible familial hypercholesterolemia mutation; (C:C) -- normal	2	21,006,196	G	A				CV, LDL, FHC, HDL
rs137852752	BMPR2	(C:G) -- Pulmonary arterial hypertension; (G:G) -- normal	2	202,556,361	G	A	C			DCM, CM
rs144467873	APOB	(A:G) -- carrier of familial hypercholesterolemia mutation; (A:A) -- Dominant mutation associated with Familial Hypercholesterolemia; (G:G) -- normal	2	21,006,289	G	A				FHC
rs200948870	BMPR2	(A:G) -- Pulmonary arterial hypertension; (G:G) -- normal	2	202,520,142	G	A				FHC
rs2229169	ADRA2B	(A:A) -- 1.5x increased risk of heart attack and stroke but better emotional memory and stop-go performance; (C:C) -- normal	2	96,114,968	T	A	G			FHC
rs2943634		(C:C) -- Slightly higher risk of ischemic stroke; (A:A) -- lower risk of ischemic stroke	2	226,203,364	A	C	G			IS,A
rs3754777	STK39	(A:G) and (A:A) -- slightly higher blood pressure if Caucasian; (G:G) -- normal	2	168,159,404	C	T				CV, AA, IS, HD
rs3755351	ADD2	(A:C) -- 1.3x higher risk for hypertension; (A:A) -- >1.3x higher risk for hypertension ; (C:C) -- normal	2	70,747,758	G	T				CV

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs4665058	BAZ2B	(A:A) -- ~4x increased risk among Europeans for sudden cardiac death; (A:C) -- 2x increased risk among Europeans for sudden cardiac death; (C:C) -- normal	2	159,333,698	A	C				CV
rs557172581	BMPR2	(A:G) -- Pulmonary arterial hypertension; (G:G) -- normal	2	202,555,352	G	A				PH
rs6749447	STK39	(G:G) and (G:T) -- slightly higher blood pressure if Caucasian; (T:T) -- normal	2	168,184,876	T	G				CV, FHC, LDL
rs700651	BOLL	(A:G) -- ~1.11x increased risk of intracranial aneurysm; (G:G) -- ~1.23x increased risk of intracranial aneurysm ; (A:A) -- normal	2	197766990	G	A				FHC
rs139794067	MYL3	(A:G) -- familial hypertrophic cardiomyopathy; (G:G) -- normal	3	46,860,813	G	A	C	T		CV, CM
rs17300539	ADIPOQ	(G:G) -- increased risk of insulin resistance; (A:G) -- normal	3	186841671	G	A				AA, IR
rs1801282	PPARG	(G:G) and (C:G) -- Unconfirmed higher risk of cardiovascular disease with high saturated fat diet; (C:C) -- normal fat metabolism	3	12,351,626	C	G				FHC
rs3900940	MYH15	(C:C) and (C:T) -- slightly increased risk of coronary heart disease; (T:T) -- normal	3	108,428,881	T	A	C			FHC
rs41261344	SCN5A	(C:T) and (T:T)-- Probably benign; previously, thought to confer possible susceptibility to long QT syndrome; (C:C) -- normal	3	38,575,385	C	T				FHC

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs45620037	SCN5A	(C:T) and (T:T) -- Now: Probably benign. Formerly: increased risk for dilated cardiomyopathy; (C:C) -- normal	3	38,613,787	G	A				FHC
rs5186	AGTR1	(C:C) -- 7.3x increased risk of hypertension; (A:C) -- ~1.4x increased risk of hypertension; (A:A) -- normal	3	148,742,201	A	C				ARR
rs6797312	SERPINI1	(A:A) and (A:T) -- 2x higher stroke risk in Caucasian women; (T:T) -- normal	3	167,769,515	A	T				BS
rs10033464	LPA	(T:T) -- 1.4x increased risk of Atrial Fibrillation and cardioembolic stroke; (G:T) -- 1.28x increased risk of Atrial Fibrillation and cardioembolic stroke; (G:G) -- normal	4	110,799,605	T	G				CV, HD, HDL
rs1799895	SOD3	(G:G) -- Lower risk for lung disease; Higher risk for ischemic heart disease ; (C:G) -- Slightly (~1.5x) higher relative risk for ischemic heart disease plus lower risk for lung disease; (C:C) -- normal	4	24,800,212	C	G				IR
rs2200733	LOC729065	(C:T) -- 1.4x increased risk of Atrial Fibrillation and ischemic stroke; (T:T) 1.5x increased risk of Atrial Fibrillation and ischemic stroke; (C:C) -- normal	4	110,789,013	C	T				CV, IS
rs2231137	ABCG2	(G:G) -- Most common genotype, with slightly higher stroke risk; (A:A) and (A:G) -- normal	4	88,139,962	C	T				CV, HD
rs4961	ADD1	(G:T) and (T:T) -- 1.8x increased risk for high blood pressure; (G:G) -- normal	4	2,904,980	G	A	T			CV, DL, HDL, ET

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs5335	EDNRA	(G:G) and (C:G) -- Pulmonary arterial hypertension; (C:C) -- normal	4	147,542,688	G	A	C			HD
rs7439293	PALLD	(A:A) and (A:G) -- increased risk of coronary heart disease; better response to statins; (G:G) -- normal	4	168,756,335	G	A				IR
rs8192678	PPARGC1A	(A:A) and (A:G) -- higher blood pressures if <50; (G:G) -- normal	4	23,814,039	C	T				PH
rs1800888	ADRB2	(T:T) and (C:T) -- increased risk of coronary artery disease; (C:C) -- normal	5	148,827,322	C	T				CV, T, IR, IS, PH, HS
rs1801020	F12, SLC34A1	(C:T) and (T:T) -- 1.31x increased risk of heart disease	5	177,409,531	A	G				PH, CV, IS, T, AOC
rs383830	F12, SLC34A1	(A:A) -- 1.9x risk; (T:T) - normal	5	100,613,278	A	T				IR
rs966221	PDE4D	(C:C) -- 1.5x increased stroke risk; (T:T) -- normal	5	60,206,693	A	G				CV
rs1041981	LOC100287329, LTA	(A:A) -- Higher myocardial infarction risk; (C:C) -- normal	6	31,573,007	C	A				CV
rs10455872	LPA	(G:G) -- 2,57x increased Coronary Heart disease risk; (A:G) -- 1,51x increased Coronary Heart disease risk; (A:A) -- normal	6	160,589,086	A	G				CV, FDCM, DCM
rs1799945	HFE	(C:G) -- One copy of H63D, carrier of hemochromatosis, likely unaffected unless also C282Y carrier.; (G:G) -- Two copies of H63D, likely affected by mild form of hemochromatosis; (C:C) -- normal	6	26,090,951	C	G				CV, AA, T, IS
rs1800629	TNF	(A:A) and (A:G) -- complex; generally higher risk for certain diseases; (G:G) -- normal	6	31,575,254	G	A				IS

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs2076295	DSP	(G:G) and (G:T) -- Slightly increased risk for pulmonary fibrosis; (T:T) -- normal	6	7,562,999	T	G				CV, IR, DCM, CM, SQTS
rs3798220	ApoA	(C:C) and (C:T) -- 2-3x higher risk for cardiovascular events; (T:T) -- Normal	6	160,540,105	T	C				CV, LDL
rs5370	EDN1	(T:T) and (G:T) -- possibly lower HDL cholesterol in women; (G:G) -- normal	6	12296022	G	T				CV, ARR, LQTS
rs6922269	MTHFD1L	(A:A) and (A:G) -- 1.2x risk of coronary artery disease; (G:G) -- normal	6	150,931,849	G	A				HDL
rs1137617	KCNH2	(A:T) -- potential cardiac arrhythmia; (C:C), (C:T), and (T:T) -- normal	7	150,951,110	A	C	G	T		FHC
rs1799999	PPP1R3A	(T:T) -- insulin resistance; (G:G) -- normal	7	113878379	C	A				IS
rs1800796	IL6	(C:C) and (C:G) -- Slightly increased risk for abdominal aortic aneurysm; (G:G) -- normal	7	22,726,627	G	C				CM
rs662	PON1	(A:A) -- 2x higher risk of CHD in some studies but lower in others; (A:G) -- elevated risk of CHD in some studies; (G:G) -- Conflicting results reported related to stroke and CAD	7	95,308,134	T	C				FHC
rs6971091	FAM71F1	(A:G) and (A:A) -- >2x increased risk for familial obesity; (G:G) -- normal	7	128723233	G	A				PH
rs854560	PON1	(A:A) and (A:T) -- higher risk for heart disease, diabetic retinopathy; (T:T) -- normal	7	95,316,772	A	C	G	N	T	FHC
rs10958409		(A:G) -- ~1.37x increased risk of aneurysm; (A:A) -- ~1.79x increased risk of aneurysm ; (G:G) -- normal	8	54414531	G	A				FHC

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs17482753		(G:T) and (T:T) -- elevated triglycerides; (G:G) -- normal	8	19,975,135	G	T				FHC
rs268	LPL	(A:G) and (G:G) -- 3X increased risk for venous thromboembolism; (A:A) -- normal	8	19,956,018	A	G				P, MVP, M
rs326	LPL	(A:A) and (A:G) -- lower HDL cholesterol; (G:G) -- normal	8	19961928	A	G				BS
rs4994	ADRB3	(C:C) and (C:T) -- 2x higher risk in certain women for cardiac events; (T:T) -- normal	8	37,966,280	A	G				ARVD
rs6997709		(G:T) -- 1.2x higher risk for hypertension; (G:G) -- 1.5x higher risk for hypertension ; (T:T) -- normal	8	139,167,781	G	T				AA
rs9298506	RP1	(A:G) -- ~1.21x increased risk of aneurysm; (A:A) -- ~1.46x increased risk of aneurysm ; (G:G) -- normal	8	54524964	A	G				IS, S
rs10306114	PTGS1	(A:G) and (G:G) -- Higher risk of bleeding during coronary angiography?; (A:A) -- normal	9	122,370,243	A	G				FHC, LDL, DL, HDL
rs10757272	CDKN2B-AS1	(T:T) -- 1.54x increased risk for Coronary artery disease; (C:T) -- 1.30x increased risk for Coronary artery disease; (C:C) -- normal	9	22088261	C	T				CV, IS
rs10757274	CDKN2B-AS1	(G:G) and (A:G) -- 1.2x increased risk for heart disease; (A:A) -- normal	9	22,096,056	A	G				CV, IS

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs10757278		(G:G) -- 1.6x increased risk for heart attack, 1.3x increased risk for abdominal aortic aneurysm and brain aneurysm; (A:G) -- 1.3x increased risk of heart attack, normal risk of aneurysm; (A:A) -- 0.78x reduced risk for CHD, 0.77x reduced for aneurysm	9	22,124,478	A	G				CV, HD, IS
rs1333040	CDKN2B-AS1	(C:T) -- 1.24x increased myocardial infarction risk, ~1.24x increased intracranial aneurysm risk; (T:T) -- 1.52x increased myocardial infarction risk, ~1.54x increased intracranial aneurysm risk; (C:C) -- normal	9	22,083,405	C	G	T			CV, A, AA, IS
rs1333048		(A:C) -- 1.3x increased coronary artery disease risk; (C:C) -- 1.5x increased coronary artery disease risk; 2x increased; (A:A) -- normal	9	22,125,348	A	C				IS, HDL
rs1333049		(C:C) and (C:G) -- 1.5x increased risk for coronary artery disease; (G:G) -- normal	9	22,125,504	G	C				H, HBP
rs2383206	CDKN2B-AS1	(G:G) and (A:G) -- 1.4x increased risk for heart disease; (A:A) -- normal	9	22,115,027	A	G				CV, HD, HDL, IR, IS
rs2383207	CDKN2B-AS1	(G:G) and (A:G) -- increased risk for heart disease; (A:A) -- normal	9	22,115,960	A	G				CV, HS, IS
rs3217992	CDKN2B, CDKN2B-AS1	(A:A) and (A:G) -- 1.24x increased myocardial infarction risk; (G:G) -- normal	9	22,003,224	C	T				IS
rs3842787	PTGS1	(T:T) and (C:T) -- Higher risk of bleeding during coronary angiography; (C:C) -- normal	9	122,371,228	C	T				HDL, DL

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs4977574	CDKN2B-AS1	(G:G) -- Most studies show a somewhat elevated risk for myocardial infarction; (A:G) -- Some studies, but not others, report slightly increased risk for MI; (A:A) -- normal	9	22,098,575	A	G	T			IS
rs4986790	TLR4	(G:G) -- complex; numerous associations reported; (A:A) and (A:G) -- normal	9	117,713,024	A	G	T			FHC
rs7025486	DAB2IP	(A:G) -- slight (1.2x) increase in risk for abdominal aortic aneurysm and some vascular disorders; (A:A) -- slight (1.4x) increase in risk for abdominal aortic aneurysm and other vascular disorders ; (G:G) -- normal	9	121660124	G	A				H, HBP, CV
rs1746048		(C:C) -- 1.03 increased risk for coronary heart disease; (C:T) and (T:T) -- normal	10	44,280,376	C	T				H, HBP
rs4244285	CYP2C19	(A:G) and (A:A) -- poor metabolizer of several popular medicines; patients prescribed Plavix get less benefit, and have higher risk for adverse cardiovascular events; (G:G) -- normal	10	94781859	G	A	C			FHC
rs45487699	LDB3	(C:T) -- left ventricular noncompaction; (C:C) -- normal	10	86,681,680	C	T				CM
rs501120		(A:A) and (A:G) -- 1.3x increased risk for heart disease; (C:C) and (G:G) normal	10	44,258,419	T	C				H, HBP
rs7080536	HABP2	(A:G) -- ~2x higher risk for carotid stenosis, venous thromboembolism; (A:A) -- significant increase (2 - 6x?) in risk possible for carotid stenosis, stroke and venous thromboembolism; (G:G) -- normal	10	113588287	G	A				S

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs11570112	MYBPC3	(C:G) -- interpretation problematic vis-a-vis cardiomyopathy for several reasons; (C:C) -- normal	11	47,333,924	G	A	C			H, HBP
rs1799963	F2	(A:A) and (A:G) -- Pulmonary arterial hypertension; (G:G) -- normal	11	46,739,505	G	A				CV, DL, LDL, HDL, HVD
rs1800497	ANKK1	(C:T) -- A1/A2: Bad at avoidance of errors. 0.5x lower OCD risk, 0.87x lower Tardive Diskinesia risk, higher ADHD risk. More Alcohol Dependence. Lower risk of Postoperative Nausea. Increased obesity. Bupropion is not effective for smoking cessation.; (T:T) -- A1/A1: Bad at avoidance of errors. 0.25x lower OCD; 0.56x lower Tardive Diskinesia; higher ADHD; 1.4x Alcohol Dependence; lower Postoperative Nausea; Increased obesity; less pleasure response; Bupropion ineffective for smoking cessation.; 2.4x risk for adenoma recurrence.; (C:C) -- normal	11	113,400,106	G	A				CV, HD, T
rs187238	IL18	(G:G) -- hypertension increases risk 3.75x for sudden cardiac death; (C:C) and (C:G) -- normal	11	112,164,265	C	A	G			CV, IS
rs190228518	MYBPC3	(T:G) -- Familial hypertrophic cardiomyopathy (possible); (G:G) -- normal	11	47343070	G	A	T			HDL
rs201457110	DCHS1	(C:T) -- Mitral valve prolapse;(C:C) -- normal	11	6624138	C	T				CV, IS

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs3781719	CALCA	(C:C) and (C:T) -- 2x increased hypertension risk; (T:T) -- normal	11	14,972,978	A	G				PH
rs662799	APOA5	(G:G) -- 2x higher early heart attack risk; less weight gain on high fat diets; (A:G) -- 1.4x higher early heart attack risk; less weight gain on high fat diets; (A:A) -- normal	11	116,792,991	G	A				CV, BS, CM
rs964184	ZPR1	(G:G) -- increased risk of hypertriglyceridemia; (C:C) -- normal	11	116,778,201	G	C				T, CV
rs104894368	MYL2	(A:G) -- Familial hypertrophic cardiomyopathy (possible); (G:G) -- normal	12	110919133	C	A	G	T		CV, AOC, DL, LDL, AA
rs3794260	WSCD2	(A:G) -- 1.26x higher risk for hypertension; (A:A) -- >1.26x higher risk for hypertension ; (G:G) -- normal	12	108,204,497	G	A				CV, AA, DL, LDL, HDL
rs7961152	BCAT1	(A:C) -- 1.2x higher risk for hypertension; (A:A) -- 1.5x higher risk for hypertension ; (C:C) -- normal	12	248,286,77	A	C				DCM, FDCM, CM, NCM
rs9739493	WSCD2	(C:C) and (C:T) -- higher risk for hypertension ; (T:T) -- normal	12	108,250,412	T	C	G			CV, FDCM, BS, DCM, CM
rs10507391	ALOX5AP	(A:T) and (T:T) -- 1.24x increased stroke risk for males	13	30,737,959	A	T				HD
rs9315204	STARD13	(T:T) -- higher risk of aneurysm; (C:C) -- normal	13	33119700	C	T				CV, LDL, HS, H, HBP
rs1048990	PSMA6	(C:C) -- > 1.48x risk; (C:G) -- 1.48x risk;	14	35,292,469	C	G	T			IR
rs121917809	PSEN1	(A:G) -- Primary dilated cardiomyopathy; (A:A) -- normal	14	73,211,811	A	G	T			CV

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs3783799	PRKCH	(A:A) and (A:G) -- 1.4x increased risk for stroke; (G:G) -- normal	14	614,524,988	C	T				CV, IR, HDL, IS, DCM, PH, IS
rs841	GCH1	(T:T) -- decreased baroreflex sensitivity, heart rate variability, and in women, hypertension; (C:C) -- normal	14	54,843,774	G	A				CV, IS
rs111671429	FBN1	(C:G) -- Marfan syndrome mutation;(C:C) -- normal	15	48596311	G	A	C			CV, IS, HD
rs17228212	SMAD3	(C:C) and (C:T) -- ~1.3x increased risk for heart disease; (T:T) -- normal	15	67,166,301	T	C				LDL
rs2118181	FBN1	(C:T) -- X1.32 higher risk of thoracic aortic dissection; (C:C) -- X1.8 higher risk of Thoracic aortic dissection; (T:T) -- normal	15	48623687	T	C				IS, CM, H, HBP, CA
rs13333226	UMOD	(A:A) -- common but slightly higher risk for hypertension; (A:G) and (G:G) -- normal	16	20,354,332	A	G				PH
rs1421085	FTO	(C:T) -- ~1.3x increased obesity risk ; (C:C) -- ~1.7x increased obesity risk; (T:T) -- normal	16	53767042	T	C				IS, AOC, T
rs17817449	FTO	(G:T) -- ~1.3x increased obesity risk; (G:G) -- ~1.7x increased obesity risk; (T:T) -- normal	16	53779455	T	A	G			HDL
rs183130	CETP	(C:C) and (C:T) -- lower HDL cholesterol; (T:T) -- normal	16	56,957,451	C	T				FHC
rs8055236	CDH13	(G:G) -- common, but 2.2x higher risk for heart disease; (G:T) -- 1.9x risk for heart disease; (T:T) -- normal	16	83,178,793	G	A	C	T		FHC, CM

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs9934438	VKORC1	(A:A) -- coumadin resistance; (G:G) -- normal	16	31,093,557	G	A	C			FHC
rs1024611	CCL2	(C:C) and (C:T) -- increased risk of exercise induced ischemia, (T:T) -- normal	17	34,252,769	A	G				FHC
rs34210653	ALOX15	(C:T) -- 1.6x increased risk for heart disease; (C:C) -- normal	17	4,632,019	G	A				PH
rs4969168	SOCS3	(A:A) -- Obesity and/or Insulin resistance associations	17	78357712	A	G				NCM, CM
rs5918	ITGB3	(C:C) and (C:T) -- MI risk; (T:T) -- normal	17	47,283,364	T	C				FHC
rs76992529	TTR	(A:A) and (A:G) -- TTR-related cardiac amyloidosi; (G:G) -- normal	18	31,598,655	G	A				FHC
rs10413089		(C:C) -- susceptibility to low HDL-cholesterol	19	44,952,331	T	C				FHC
rs13306512	LDLR	(A:C) and (C:G) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,107,513	C	A	G	T		FHC
rs13306515	LDLR	(A:C) and (C:G) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,110,767	C	A	G	T		IS, AOC, T
rs137853964	LDLR	(G:T) -- Familial hypercholesterolemia; (G:G) -- normal	19	11,129,602	G	A	T			FHC, CM
rs139361635	LDLR	(A:G) and (G:T) -- Familial Hypercholesterolemia; (G:G) -- normal	19	11,110,735	G	A	C	T		CV, DL, HD, LDL, AA
rs146651743	LDLR	(A:C) and (C:G) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,107,402	C	A	G	T		CV, AOC, T, PH, IS, S
rs146675823	LDLR	(A:G) -- Dominant mutation associated with Familial Hypercholesterolemia; (G:G) -- normal	19	11,102,706	G	A	T			DCM, CM

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs150673992	LDLR	(C:T) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,106,627	C	T				CV, DL, LDL
rs172149856	TRPM4	(A:G) -- May - or may not - lead to progressive familial heart block type 1B; (G:G) -- normal	19	49188641	G	A				CV, M, DL, IR, HDL, IS
rs1800437	GIPR	(C:G) -- 0.72x risk for heart disease; (C:C) and (G:G) -- normal	19	45,678,134	G	C				CV, DL ,HDL, IS, O, HD
rs185098634	LDLR	(C:T) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,116,873	C	T				CV, HBP, H
rs200533979	LDLR	(A:C) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,111,541	C	A	T			IS, S, HDL
rs201016593	LDLR	(A:G) -- Familial Hypercholesterolemia; (G:G) -- normal	19	11,089,559	G	A				HD
rs201102461	LDLR	(A:G) -- Familial Hypercholesterolemia; (G:G) -- normal	19	11,105,250	G	A				CV, HD
rs201102492	LDLR	(A:G) and (G:T) -- Familial Hypercholesterolemia; (G:G) -- normal	19	11,116,937	G	A	T			O
rs201907325	TRPM4	(A:G) -- Progressive familial heart block type 1B (Brugada syndrome); (G:G) -- normal	19	49182608	G	A	T			IS, PH, CM
rs2228671	LDLR	(A:C) and (C:G) -- Familial Hypercholesterolemia; (C:C) and (C:T) -- normal	19	11,100,236	C	A	G	T		H, HBP
rs369943481	LDLR	(A:C) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,120,454	C	A	T			A
rs376207800	LDLR	(C:G) and (C:T) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,100,340	C	G	T			AA, A, PH, IS

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs429358	APOE	(C:C) -- one of 2 snps relevant to classifying APOE genotype; (C:T) -- 1.4x increased risk for heart disease; (T:T) -- Normal	19	44,908,684	T	C				T
rs4420638	APOC1	(G:G) and (A:G) -- 1.4x increased risk of heart disease; (A:A) -- Normal	19	44,919,689	A	G				HD
rs540073140	LDLR	(C:T) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,110,780	C	T				FHC
rs544453230	LDLR	(A:G) -- Familial Hypercholesterolemia; (G:G) -- normal	19	11,110,714	G	A	C			DCM, FDCM, CM, NCM
rs551747280	LDLR	(A:G) and (G:T) -- Familial Hypercholesterolemia; (G:G) -- normal	19	11,100,237	G	A	T			CV, IS
rs552422789	LDLR	(A:C) and (C:G) -- Familial Hypercholesterolemia; (G:G) -- normal	19	11,113,308	G	A	C			CV, CM, CAM
rs563382937	LDLR	(A:T) -- Familial Hypercholesterolemia; (A:A) -- normal	19	11,120,198	A	G	T			CV, FDCM, RCM
rs563390335	LDLR	(C:T) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,102,777	C	A	T			H, HBP
rs570942190	LDLR	(C:T) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,113,337	C	T				HD
rs577934998	LDLR	(G:T) and (C:T) -- Familial Hypercholesterolemia; (T:T) -- normal	19	11,105,570	T	C	G			CV, IR, CM
rs5933	LDLR	(C:G) -- Familial Hypercholesterolemia; (C:C) -- normal	19	11,113,414	C	G	T			IS
rs7250581	SEZ6L	(G:G) -- 1.4x risk; (A:A) and (A:G) -- normal	19	29,573,489	A	G				CV, IR, HDL, IS, HC

Reference SNP Cluster ID	Gene	Genomic State	Chr	Location	Ancestral Allele	Variant Allele	Variant Allele	Variant Allele	Variant Allele	Disease
rs72658860	LDLR	(A:G) -- Familial Hypercholesterolemia; (G:G) -- normal	19	11,110,681	G	A				A
rs77615401	TNNI3	(A:A) and (A:G) -- Familial hypertrophic cardiomyopathy, type 7 (possibly); (G:G) -- normal	19	55,156,239	G	A				A
rs3843763	PLTP	(T:T) and (C:T) -- Slightly lower HDL ("Good") Cholesterol; (C:C) -- normal	20	45,919,554	C	T				IS, HS, DL, HDL
rs1041740	SOD1	(T:T) -- Slight increase in cardiovascular risk; (C:C) -- normal	21	31,667,849	C	T				IS
rs1805127	KCNE1	(A:G) -- slight increase in risk for atrial fibrilation; (A:A) -- normal	21	34,449,523	T	C				H, HBP
rs688034	SEZ6L	(T:T) -- 1.6x risk; (C:T) -- 1.1x risk higher risk for coronary artery disease; (C:C) -- normal	22	26,293,669	C	T				CV