SUPPLEMENTAL MATERIAL

Supplementary Table 1. SNPs included in the Genetic Risk Scores.

SNP	GRS	Risk allele	Trait	Reference	Genotype source	Alleles		Call Rate	HWE	MAF	O/E ratio	risk
						minor	major					
rs11206510	13 SNP	C	MI	Kathiresan et al (1)	Illumina	C	T	100	0.901391	0.187422		+
rs1122608	13 SNP	G	MI	MIgen (2)	Illumina	T	G	100	0.927459	0.257584		+
rs12526453	13 SNP	C	MI	MIgen	Illumina	G	C	100	0.490701	0.338967		+
rs1746048	13 SNP	C	MI	MIgen	Illumina	T	C	100	0.607481	0.144341		+
rs17465637	13 SNP	C	MI	MIgen	Illumina	A	C	100	0.976142	0.297548		+
rs2259816	13 SNP	T	MI	Erdmann et al.(3)	Illumina	A	C	100	0.906508	0.381355		+
rs3184504	13 SNP	T	MI	Gudbjartsson et al (4)	Illumina	T	C	100	0.920563	0.494598		+
rs3798220	13 SNP	C	MI	Clarke et al (5)	SHARe genotyped	C	T	99.82367	0.506117	0.016133		+
rs4977574	13 SNP	G	MI	MIgen	Illumina	A	G	100	1	0.476797		+
rs646776	13 SNP	T	MI	MIgen	Illumina	G	A	100	0.62563	0.216789		+
rs6725887	13 SNP	C	MI	MIgen	Illumina	C	T	99.9861	0.923596	0.122679		+
rs9818870	13 SNP	T	MI	MIgen	Illumina	T	C	99.9861		0.143876		+
rs9982601	13 SNP	T	MI	MIgen	Illumina	T	C	100	0.991943	0.136376		+
rs10838738	102 SNP	G	BMI	Willer et al. (6)	Illumina	G	A	100	0.992439	0.357252		+
rs10938397	102 SNP	G	BMI	Willer et al.	Illumina	G	A	99.9584	0.667494	0.428769		+
rs11084753	102 SNP	G	BMI	Willer et al	Illumina	A	G	99.9723	0.919315	0.335527		+
rs17782313	102 SNP	C	BMI	Willer et al.	Illumina	C	T	100	0.65171	0.216373		+
rs2568958	102 SNP	A	BMI	Thorleifsson et al. (7)	SHARe imputed	G	A			0.366943	1.018409	+
rs6265	102 SNP	G	BMI	Thorleifsson et al.	SHARe genotyped	T	C	99.98824	0.70728	0.188749		+
rs6499640	102 SNP	A	BMI	Thorleifsson et al.	SHARe imputed	G	A			0.401886	0.976767	+
rs6548238	102 SNP	C	BMI	Willer et al.	Illumina	T	C	100	0.989963	0.176063		+
rs7498665	102 SNP	G	BMI	Willer et al.	Illumina	G	A	100	0.880818	0.357044		+
rs7647305	102 SNP	C	BMI	Thorleifsson et al.	Illumina	T	C	100	0.782279	0.221776		+

rs925946	102 SNP	T	BMI	Thorleifsson et al.	SHARe imputed	T	G			0.2865	0.997901	+
rs1004467	102 SNP	A	BP	Levy et al. (8)	Illumina	C	T	100	0.979605	0.102646		+
rs11014166	102 SNP	A	BP	Levy et al.	Illumina	T	A	100	0.849542	0.35462		+
rs12946454	102 SNP	T	BP	Newton-Cheh et al.(9)	SHARe imputed	T	A			0.261302	0.915865	+
rs1530440	102 SNP	T	BP	Newton-Cheh et al.	SHARe imputed	T	C			0.176648	0.949084	-
rs16948048	102 SNP	G	BP	Newton-Cheh et al.	SHARe genotyped	G	A	99.90596	0.537301	0.363337		+
rs16998073	102 SNP	T	BP	Newton-Cheh et al.	SHARe imputed	T	A			0.226478	0.691973	+
rs17367504	102 SNP	G	BP	Newton-Cheh et al.	SHARe genotyped	G	A	99.07135	0.582622	0.14612		-
rs1918974	102 SNP	T	BP	Newton-Cheh et al.	SHARe genotyped	C	T	99.94122	0.039117	0.472595		-
rs2384550	102 SNP	A	BP	Levy et al.	SHARe genotyped	A	G	99.98824	0.935303	0.37068		-
rs2681472	102 SNP	A	BP	Levy et al.	Illumina	C	T	100	0.848595	0.190747		+
rs381815	102 SNP	T	BP	Levy et al.	Illumina	T	C	99.9861	0.423616	0.272721		+
rs6495122	102 SNP	A	BP	Levy et al.	Illumina	A	C	100	0.928355	0.432955		+
rs9815354	102 SNP	A	BP	Levy et al.	Illumina	A	G	99.626	0.304112	0.178184		+
rs4537545	102 SNP	T	CRP	Elliott et al.(10)	SHARe genotyped	T	C	98.5894	0.937062	0.417313		-
rs6700896	102 SNP	T	CRP	Elliott et al.	SHARe imputed	T	C			0.353084	0.960002	-
rs7553007	102 SNP	A	CRP	Elliott et al.	SHARe genotyped	A	G	99.8942	0.481445	0.3269		-
rs10811661	102 SNP	T	DIABGLUC	Scott et al. (11)	Illumina	C	T	100	0.736653	0.173639		+
rs10830963	102 SNP	G	DIABGLUC	Dupuis et al. (12)	Illumina	G	C	100	0.959713	0.262571		+
rs10885122	102 SNP	G	DIABGLUC	Dupuis et al.	SHARe imputed	T	G			0.110118	0.948183	+
rs10923931	102 SNP	T	DIABGLUC	Zeggini et al.(13)	Illumina	T	G	100	0.768142	0.096274		+
rs10946398	102 SNP	C	DIABGLUC	Zeggini et al.	Illumina	C	A	99.9861	0.988127	0.321973		+
rs11071657	102 SNP	A	DIABGLUC	Dupuis et al.	SHARe imputed	G	A			0.367333	0.674072	+
rs1111875	102 SNP	C	DIABGLUC	Saxena et al. (14)	Illumina	A	G	100	0.999957	0.395484		+
rs11605924	102 SNP	A	DIABGLUC	Dupuis et al.	SHARe imputed	C	A			0.537347	0.998308	+
rs11708067	102 SNP	A	DIABGLUC	Dupuis et al.	SHARe imputed	G	A			0.208443	0.936832	+
rs11920090	102 SNP	T	DIABGLUC	Dupuis et al.	SHARe imputed	A	T			0.132244	0.995684	+
rs12779790	102 SNP	G	DIABGLUC	Zeggini et al	Illumina	G	A	99.9446	0.947797	0.177339		+
rs13266634	102 SNP	C	DIABGLUC	Saxena et al.	Illumina	C	T	99.9584	0.997859	0.295316		+
rs2191349	102 SNP	T	DIABGLUC	Dupuis et al	SHARe imputed	T	G			0.555056	0.973185	+

rs2237897	102 SNP	C	DIABGLUC	Unoki et al. (15)	SHARe imputed	T	C			0.064321	0.650195	+
rs2943641	102 SNP	C	DIABGLUC	Rung et al. (16)	SHARe imputed	T	C			0.365702	0.990504	+
rs340874	102 SNP	C	DIABGLUC	Dupuis et al.	SHARe imputed	T	C			0.472598	0.711865	+
rs4402960	102 SNP	T	DIABGLUC	Zeggini et al.	Illumina	T	G	100	0.225574	0.325807		+
rs4607103	102 SNP	C	DIABGLUC	Zeggini et al.	Illumina	T	C	100	0.982455	0.263956		+
rs4607517	102 SNP	A	DIABGLUC	Dupuis et al.	Illumina	A	G	99.9861	0.91579	0.179205		+
rs4689388	102 SNP	T	DIABGLUC	Rung et al	SHARe imputed	G	A			0.390698	0.765166	+
rs5219	102 SNP	T	DIABGLUC	Scott et al.	Illumina	T	C	100	0.403681	0.363277		+
rs560887	102 SNP	C	DIABGLUC	Dupuis et al	Illumina	A	G	100	0.970398	0.294431		+
rs7034200	102 SNP	A	DIABGLUC	Dupuis et al	SHARe imputed	C	A			0.509832	0.986822	+
rs7578597	102 SNP	T	DIABGLUC	Zeggini et al	SHARe genotyped	C	T	97.7783	0.666328	0.100625		+
rs7756992	102 SNP	G	DIABGLUC	Steithorsdottir et al (17)	Illumina	G	A	100	0.946147	0.282172		+
rs780094	102 SNP	C	DIABGLUC	Dupuis et al.	Illumina	A	G	99.9584	0.301372	0.44138		+
rs7901695	102 SNP	C	DIABGLUC	Zeggini et al.	Illumina	C	T	99.9861	0.870641	0.328692		+
rs7944584	102 SNP	A	DIABGLUC	Dupuis et al.	SHARe genotyped	T	A	99.90596	0.785999	0.296211		+
rs7961581	102 SNP	C	DIABGLUC	Zeggini et al.	Illumina	C	T	99.9307	0.992047	0.297477		+
rs8050136	102 SNP	A	DIABGLUC	Zeggini et al.	Illumina	A	C	100	0.984615	0.403796		+
rs864745	102 SNP	T	DIABGLUC	Zeggini et al.	Illumina	G	A	100	0.794844	0.497714		+
rs9300039	102 SNP	C	DIABGLUC	Scott et al.	Illumina	A	C	100	0.991408	0.091841		+
rs10468017	102 SNP	T	HDL	Kathiresan et al (1)	Illumina	T	C	99.9723	0.735977	0.29091		-
rs173539	102 SNP	T	HDL	Kathiresan et al.	Illumina	T	C	100	0.984585	0.326984		-
rs1800588	102 SNP	T	HDL	Kathiresan et al (18)	SHARe genotyped	T	C	99.95298	0.647233	0.216159		-
rs1800961	102 SNP	T	HDL	Kathiresan et al (1)	Illumina	T	C	100	0.999355	0.031168		+
rs1883025	102 SNP	T	HDL	Kathiresan et al (1)	Illumina	A	G	100	0.788467	0.267004		-
rs2156552	102 SNP	T	HDL	Willer et al. (19)	SHARe genotyped	A	T	99.96473	0.156618	0.162041		+
rs2271293	102 SNP	A	HDL	Kathiresan et al (1)	Illumina	A	G	100	0.326955	0.106109		-
rs2338104	102 SNP	C	HDL	Kathiresan et al (1)	Illumina	C	G	100	0.784938	0.45401		+
rs2967605	102 SNP	T	HDL	Kathiresan et al (1)	Illumina	A	G	100	0.824427	0.168791		+
rs471364	102 SNP	C	HDL	Kathiresan et al (1)	Illumina	G	A	100	0.81402	0.118437		+
rs4846914	102 SNP	G	HDL	Kathiresan et al (18)	Illumina	G	A	100	0.963632	0.396246		+

rs7679	102 SNP	C	HDL	Kathiresan et al (1)	Illumina	C	T	100	0.963093	0.181812	+
rs9989419	102 SNP	G	HDL	Willer et al (19)	SHARe genotyped	A	G	99.84718	0.132589	0.394455	-
rs10401969	102 SNP	C	LDL	Kathiresan et al (1)	Illumina	C	T	100	0.698997	0.070647	-
rs11591147	102 SNP	T	LDL	Kathiresan et al (18)	Illumina	T	G	100	0.874035	0.016138	-
rs1501908	102 SNP	G	LDL	Kathiresan et al (1)	SHARe genotyped	G	C	99.88245	0.626716	0.373779	-
rs3846663	102 SNP	T	LDL	Kathiresan et al (18)	Illumina	T	C	100	0.939244	0.375814	+
rs4420638	102 SNP	G	LDL	Kathiresan et al. (1)	Illumina	G	A	99.9307	0.508047	0.1626	+
rs515135	102 SNP	T	LDL	Kathiresan et al (1)	Illumina	A	G	100	0.154704	0.208824	+
rs6102059	102 SNP	T	LDL	Kathiresan et al (1)	Illumina	T	C	100	0.954961	0.313686	-
rs693	102 SNP	A	LDL	Kathiresan et al (1)	Illumina	T	C	100	0.0028	0.497437	+
rs10503669	102 SNP	C	TG	Willer et al (19)	Illumina	A	C	100	0.988998	0.091218	+
rs10892151	102 SNP	A	TG	Pollin et al (20)	SHARe genotyped	T	C	99.97649	1	0.029336	-
rs12130333	102 SNP	T	TG	Kathiresan et al (18)	Illumina	T	C	100	0.972053	0.198296	-
rs174547	102 SNP	C	TG	Kathiresan et al (1)	Illumina	C	T	100	0.920265	0.324976	+
rs2954029	102 SNP	T	TG	Kathiresan et al (1)	Illumina	T	A	100	0.901494	0.438634	-
rs3812316	102 SNP	C	TG	Kooner et al. (21)	Illumina	G	C	100	0.251248	0.118992	+
rs7557067	102 SNP	G	TG	Kathiresan et al (1)	Illumina	G	A	100	0.77048	0.221568	-
rs7819412	102 SNP	G	TG	Kathiresan et al (1)	Illumina	G	A	99.9861	0.993425	0.482613	-
rs964184	102 SNP	G	TG	Kathiresan et al (1)	Illumina	G	C	100	0.858193	0.142679	+

The 13 SNP MI/CHD GRS consists of the first 13 SNPs (for "MI" trait) in the Supplementary Table.
HWE – Hardy-weinberg equilibrium p-value; MAF – mean allele frequency; O/E ratio – observed to expected ratio for imputed SNPs; Risk – direction of risk for CVD/MI (+ denotes increased risk whereas negative denotes decreased risk); MI – myocardial infarction or coronary heart disease; BMI – body mass index; BP – blood pressure; CRP – C-reactive protein; DIABGLUC – diabetes or high fasting glucose; LDL – low density lipoprotein; HDL – high density lipoprotein; TG - triglycerides

Supplementary Table 2. Additional MI/CHD SNPs included in the Genetic Risk Score

SNP	Reference	Risk Allele	Genotype Source	minor	major	Call Rate	HWE.p	MAF	O/E ratio
rs10953541	C4D (22)	C	SHARe imputed	T	C			0.252	0.982
rs11556924	Cardiogram (23)	C	SHARe genotyped	T	C	98.88	0.095	0.378	
rs12190287	Cardiogram	G	SHARe imputed	G	C			0.373	0.792
rs12413409	Cardiogram	C	SHARe genotyped	A	G	99.48	0.009	0.088	
rs12936587	Cardiogram	C	SHARe imputed	G	A			0.539	0.822
rs1412444	C4D	T	SHARe genotyped	T	C	99.93	0.610	0.333	
rs17114036	Cardiogram	A	SHARe imputed	G	A			0.110	0.859
rs17609940	Cardiogram	G	SHARe genotyped	C	G	99.48	0.269	0.196	
rs216172	Cardiogram	C	SHARe imputed	C	G			0.364	0.979
rs2505083	C4D	C	SHARe imputed	C	T			0.404	0.874
rs2895811	Cardiogram	C	SHARe imputed	C	T			0.389	0.761
rs3825807	Cardiogram	A	SHARe imputed	G	A			0.432	0.989
rs46522	Cardiogram	T	SHARe genotyped	C	T	99.60	0.399	0.469	
rs4773144 - excluded	Cardiogram	G	SHARe genotyped	A	G	90.20	2.29E-25	0.463	
rs579459	Cardiogram	C	SHARe imputed	C	T			0.218	0.934
rs964184	Cardiogram	G	Illumina	G	C	100	0.858	0.143	
rs974819	C4D	T	SHARe imputed	T	C			0.304	0.966

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