

Table S9. Genetic loci selected for the high-density DNA tiling array.

(A) Association loci									
#	Gene(s)	GWA index SNP(s)		Trait(s)	Reference(s)	Genomic position			Interval (kb)
		ID	Position			Chromosome	Start	End	
1	<i>PCSK9</i>	rs11206510	55,268,627	Early-onset MI	[1]	1p32.3	55,240,000	55,300,000	60.00
2	<i>VAV3^b</i>	rs17229705	107,940,484	PLS	[2]	1p13.3	107,890,000	108,055,000	165.00
3	<i>CELSR2, PSRC1, SORT1</i>	rs599839	109,623,689	CAD	[3,4]	1p13.3	109,489,481	109,739,481	250.00
		rs646776	109,620,053	Early-onset MI	[1]				
4	<i>PEAR1^b</i>	rs3737224	155,146,204	PLS	[2]	1q23.1	155,100,000	155,250,000	150.00
5	<i>FCER1G^{a,b}</i>	rs3557	159,455,517	PLS	[2]	1q23.3	159,441,711	159,465,662	23.95
6	<i>DNM3</i>	rs10914144	170,216,373	MPV	[5]	1q24.3	170,130,000	170,390,000	260.00
7	<i>TMCC2</i>	rs1668873	203,502,613	MPV	[5]	1q32.1	203,445,000	203,540,000	95.00
8	<i>MIA3</i>	rs17465637	220,890,152	CAD / early-onset MI	[1,3]	1q41	220,678,228	221,078,228	400.00
		rs3008621	220,870,669	CAD	[4]				
9	<i>EHD3</i>	rs647316	31,318,333	MPV	[5]	2p23.1	31,305,000	31,346,000	41.00
10	<i>STK39^b</i>	rs6749447	168,749,632	SBP / DBP	[6]	2q24.3	168,695,000	168,800,000	105.00
		rs3754777	168,724,160						
11	<i>WDR12^a</i>	rs6725887	203,454,130	Early-onset MI	[1]	2q33.1	203,443,575	203,494,639	51.06
12	<i>gene desert</i>	rs2943634	226,776,324	CAD	[3,4]	2q36.3	226,532,739	226,982,739	450.00
13	<i>ITPR1^b</i>	rs17786144	4,804,575	PLS	[2]	3p26.2	4,760,000	4,860,000	100.00
14	<i>RAF1^{a,b}</i>	rs3729931	12,601,516	PLS	[2]	3p25.1	12,590,108	12,690,678	100.57
15	<i>ULK4</i>	rs9815354	41,887,655	DBP	[7,8]	3p22.1	41,710,000	41,970,000	260.00
16	<i>ARHGEF3</i>	rs12485738	56,840,816	MPV	[5,9]	3p14.3	56,750,000	56,880,000	130.00
17	<i>MRAS</i>	rs9818870	139,604,812	CAD / MI	[10]	3q22.3	139,550,000	139,613,000	63.00
18	<i>P2RY12^b</i>	rs1472122	152,517,292	PLS	[2]	3q25.1	152,410,000	152,580,000	170.00
19	<i>ITGA2^b</i>	rs41305896	52,311,475	PLS	[2]	5q11.2	52,267,000	52,436,366	169.37
20	<i>PHACTR1</i>	rs12526453	13,035,530	Early-onset MI	[1]	6p24.1	12,985,000	13,060,000	75.00

21	<i>HFE</i>	rs1800562	26,201,120	MCV	[5]	6p22.1	26,190,000	26,260,000	70.00
22	<i>BAK1</i>	rs210135	33,648,670	PLT	[5]	6p21.31	33,644,000	33,665,000	21.00
23	<i>MAPK14^b</i>	rs851007	36,172,014	PLS	[2]	6p21.31	36,050,000	36,210,000	160.00
24	<i>BSYL, CCND3</i>	rs11970772	42,033,268	MCV	[5]	6p21.1	41,985,000	42,105,000	120.00
25	<i>HBS1L, MYB</i>	rs9402686	135,469,510	MCV	[5]	6q23.3	135,400,000	135,582,003	182.00
26	<i>MTHFD1L</i>	rs6922269	151,294,678	CAD	[3,4,11]	6q25.1	151,199,579	151,399,579	200.00
27	<i>SLC22A3, LPAL2, LPA</i>	rs2048327–rs3127599– rs7767084–rs10755578 haplotype		CAD	[12]	6q25.3–q26	160,780,000	161,055,000	275.00
28	<i>CD36^b</i>	rs1049654	80,113,391	PLS	[2]	7q21.11	80,045,000	80,137,000	92.00
29	<i>TFR2</i>	rs7385804	100,073,906	RBC	[5]	7q22.1	100,050,000	100,100,000	50.00
30	<i>FLJ36031, PIK3CG</i>	rs342293	106,159,455	MPV	[5,13]	7q22.3	106,085,000	106,190,000	105.00
31	<i>AK3, RCL1, JAK2^(b, for PLS)</i>	rs385893	4,753,176	PLT	[5]	9p24.1	4,730,000	5,050,000	320.00
		rs10429491	5,040,706	PLS	[2]				
32	<i>CDKN2A, CDKN2B</i>	rs1333049	22,115,503	CAD / MI	[1,3,4,11,14]	9p21.3	21,900,000	22,200,000	300.00
		rs4977574	22,088,574	Early-onset MI	[1]				
33	<i>CACNB2</i>	rs11014166	18,748,804	DBP	[7,8]	10p12.33	18,570,000	18,840,000	270.00
34	<i>CXCL12/SDF1</i>	rs501120	44,073,873	CAD	[3,4]	10q11.21	43,950,000	44,200,000	250.00
		rs1746048	44,095,830	Early-onset MI	[1]				
35	<i>JMJD1C^a</i>	rs2393967	64,803,162	MPV	[5]	10q21.2–q21.3	64,586,991	64,905,728	318.74
36	<i>CYP17A1, C10orf32</i>	rs1004467	104,584,497	SBP	[7,8]	10q24.32	104,520,000	104,690,000	170.00
37	<i>BET1L, SIRT3, PSMD13</i>	rs11602954	192,856	MPV	[5]	11p15.5	180,000	240,000	60.00
38	<i>PLEKHA7</i>	rs381815	16,858,844	SBP	[7,8]	11p15.1	16,795,000	16,960,000	165.00
39	<i>ATP2B1</i>	rs2681492	88,537,220	SBP	[7,8]	12q21.33	88,460,000	88,650,000	190.00
		rs2681472	88,533,090	HYP / DBP	[7,8]				
40	<i>SH2B3/LNK, ATXN2</i>	rs3184504	110,368,991	MI; SBP / DBP	[7,8,15]	12q24.12	110,310,000	110,570,000	260.00
		rs11065987	110,556,807	PLT; CAD / MI	[5]				
41	<i>PTPN11^a</i>	rs11066301	111,355,755	PLT; CAD / MI	[5]	12q24.13	111,330,919	111,442,100	111.18

42	<i>TBX3, TBX5</i>	rs2384550	113,837,114	DBP	[7,8]	12q24.21	113,810,000	113,930,000	120.00
43	<i>HNF1A/TCF1, C12orf43</i>	rs2259816	119,919,970	CAD / MI	[10]	12q24.31	119,850,000	119,980,000	130.00
44	<i>WDR66</i>	rs7961894	120,849,966	MPV	[5,9]	12q24.31	120,760,000	120,970,000	210.00
45	<i>TPM1</i>	rs11071720	61,129,049	MPV	[5]	15q22.2	61,080,000	61,160,000	80.00
46	<i>SMAD3^b</i>	rs17228212	65,245,693	CAD	[3]	15q22.33–q23	65,150,000	65,350,000	200.00
47	<i>CSK, ULK3</i>	rs6495122	72,912,698	DBP	[7,8]	15q24.1	72,810,000	73,030,000	220.00
48	<i>CDH13</i>	rs11646213	81,200,152	HYP / SBP / DBP	[16]	16q23.3	81,190,000	81,240,000	50.00
49	<i>MAP2K4^{a,b}</i>	rs41307923	11,968,409	PLS	[2]	17p12	11,854,860	11,997,776	142.92
50	<i>TAOK1</i>	rs2138852	24,727,475	MPV	[5,9]	17q11.2	24,680,000	24,930,000	250.00
51	<i>GSDMA, ORMDL3</i>	rs17609240	35,364,215	WBC	[5]	17q12	35,314,374	35,387,545	73.17
52	<i>CD226</i>	rs893001	65,667,825	MPV	[5]	18q22.2	65,620,000	65,730,000	110.00
53	<i>MAP2K2^b</i>	rs350916	4,045,775	PLS	[2]	19p13.3	4,025,000	4,095,000	70.00
54	<i>LDLR</i>	rs1122608	11,024,601	Early-onset MI	[1]	19p13.2	11,010,000	11,120,000	110.00
55	<i>AKT2^b</i>	rs41275750	45,429,935	PLS	[2]	19q13.2	45,380,000	45,520,000	140.00
56	<i>APOC1, APOC4, APOE^b</i>	rs4420638	50,114,786	CAD	[11]	19q13.32	50,000,000	50,230,000	230.00
57	<i>GP6^{a,b}</i>	rs1613662	60,228,407	PLS	[2]	19q13.42	60,206,885	60,251,444	44.56
58	<i>SIRPA</i>	rs6136489	1,871,734	MPV	[5]	20p13	1,820,000	1,950,000	130.00
59	<i>SLC5A3, MRPS6, KCNE2</i>	rs9982601	34,520,998	Early-onset MI	[1]	21q22.11	34,340,000	34,530,000	190.00
60	<i>GNAZ^b</i>	rs3788337	21,742,017	PLS	[2]	22q11.22	21,720,000	21,840,000	120.00
61	<i>FBXO7</i>	rs9609565	31,197,528	MCV	[5]	22q12.3	31,186,000	31,250,000	64.00
62	<i>TMPRSS6</i>	rs5756506	35,797,338	MCH	[5]	22q12.3	35,730,000	35,830,000	100.00

(B) Lineage-specific reference genes					
Lineage	Gene	Genomic position			Interval (kb)
		Chromosome	Start	End	
monocytic	<i>ASGR2</i>	17p13.1	6,943,365	6,960,852	17.49
	<i>CD163</i>	12p13.31	7,512,676	7,549,681	37.01
	<i>FER1L3</i>	10q23.33	95,054,176	95,234,029	179.85
	<i>KLF4</i>	9q31.2	109,284,956	109,293,576	8.62
	<i>PID1</i>	2q36.3	229,594,933	229,846,301	251.37
	<i>RIN2</i>	20p11.23	19,816,210	19,933,100	116.89
	<i>SLC46A2</i>	9q32	114,679,021	114,694,866	15.85
	<i>TMEM176A</i>	7q36.1	150,126,787	150,135,141	8.35
erythroblastoid	<i>CA1</i>	8q21.2	86,425,709	86,479,594	53.89
	<i>CALB2</i>	16q22.3	69,948,127	69,983,842	35.72
	<i>EPB42</i>	15q15.2	41,274,720	41,302,773	28.05
	<i>ERAF</i>	16p11.2	31,444,704	31,449,625	4.92
	<i>FAM83A</i>	8q24.13	124,261,933	124,293,499	31.57
	<i>GDF15</i>	19p13.11	18,355,968	18,362,986	7.02
	<i>HBZ</i>	16p13.3	140,854	146,504	5.65
	<i>LOC51252</i>	2q11.2	96,903,349	96,929,558	26.21
megakaryocytic	<i>ADCY6</i>	12q13.12	47,444,248	47,471,087	26.84
	<i>CMTM5</i>	14q11.2	22,913,857	22,920,821	6.96
	<i>DDEF2</i>	2p25.1	9,262,345	9,465,257	202.91
	<i>LY6G6D</i>	6p21.33	31,789,112	31,795,560	6.45
	<i>MEIS1</i>	2p14	66,514,036	66,655,395	141.36
	<i>MYLK</i>	3q21.1	124,811,833	125,087,839	276.01
	<i>NFIB</i>	9p23–p22.3	14,069,847	14,305,945	236.10
	<i>SELP</i>	1q24.2	167,822,711	167,868,001	45.29

Genomic coordinates are based on the human reference genome, build hg18 (NCBI build 36). **Abbreviations:** CAD: coronary artery disease; MI: myocardial infarction; MPV: mean platelet volume; PLT: platelet counts; PLS: platelet signaling; WBC: white blood cell counts; RBC: red blood cell counts; MCV: mean corpuscular volume of erythrocytes; MCH: mean corpuscular hemoglobin; SBP: systolic blood pressure; DBP: diastolic blood pressure; HYP: hypertension. **Key:** ^atarget gene \pm 10 kb; ^bbiological evidence for association.

References:

1. Myocardial Infarction Genetics Consortium (2009) Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. *Nat Genet* 41: 334-340.

2. Jones CI, Bray S, Garner SF, Stephens J, de Bono B, et al. (2009) A functional genomics approach reveals novel quantitative trait loci associated with platelet signalling pathways. *Blood* 114: 1405-1416.
3. Samani NJ, Erdmann J, Hall AS, Hengstenberg C, Mangino M, et al. (2007) Genome-wide association analysis of coronary artery disease. *New Engl J Med* 357: 443-453.
4. Coronary Artery Disease Consortium (2009) Large scale association analysis of novel genetic loci for coronary artery disease. *Arterioscl Throm Vas Biol* 29: 774-780.
5. Soranzo N, Spector TD, Mangino M, Kühnel B, Rendon A, et al. (2009) A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. *Nat Genet* 41: 1182-1190.
6. Wang Y, O'Connell JR, McArdle PF, Wade JB, Dorff SE, et al. (2009) Whole-genome association study identifies STK39 as a hypertension susceptibility gene. *Proc Natl Acad Sci USA* 106: 226-231.
7. Newton-Cheh C, Johnson T, Gateva V, Tobin MD, Bochud M, et al. (2009) Genome-wide association study identifies eight loci associated with blood pressure. *Nat Genet* 41: 666-676.
8. Levy D, Ehret GB, Rice K, Verwoert GC, Launer LJ, et al. (2009) Genome-wide association study of blood pressure and hypertension. *Nat Genet* 41: 677-687.
9. Meisinger C, Prokisch H, Gieger C, Soranzo N, Mehta D, et al. (2009) A genome-wide association study identifies three loci associated with mean platelet volume. *Am J Hum Genet* 84: 66-71.
10. Erdmann J, Grohennig A, Braund PS, König IR, Hengstenberg C, et al. (2009) New susceptibility locus for coronary artery disease on chromosome 3q22.3. *Nat Genet* 41: 280-282.
11. The Wellcome Trust Case Control Consortium (2007) Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature* 447: 661-678.
12. Trégouët D-A, König IR, Erdmann J, Munteanu A, Braund PS, et al. (2009) Genome-wide haplotype association study identifies the SLC22A3-LPAL2-LPA gene cluster as a risk locus for coronary artery disease. *Nat Genet* 41: 283-285.
13. Soranzo N, Rendon A, Gieger C, Jones CI, Watkins NA, et al. (2009) A novel variant on chromosome 7q22.3 associated with mean platelet volume, counts and function. *Blood* 113: 3831-3837.
14. Schunkert H, Götz A, Braund P, McGinnis R, Trégouët D-A, et al. (2008) Repeated replication and a prospective meta-analysis of the association between chromosome 9p21.3 and coronary artery disease. *Circulation* 117: 1675-1684.
15. Gudbjartsson DF, Bjornsdottir US, Halapi E, Helgadottir A, Sulem P, et al. (2009) Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. *Nat Genet* 41: 342-347.
16. Org E, Eyheramendy S, Juhanson P, Gieger C, Lichtner P, et al. (2009) Genome-wide scan identifies CDH13 as a novel susceptibility locus contributing to blood pressure determination in two European populations. *Hum Mol Genet* 18: 2288-2296.