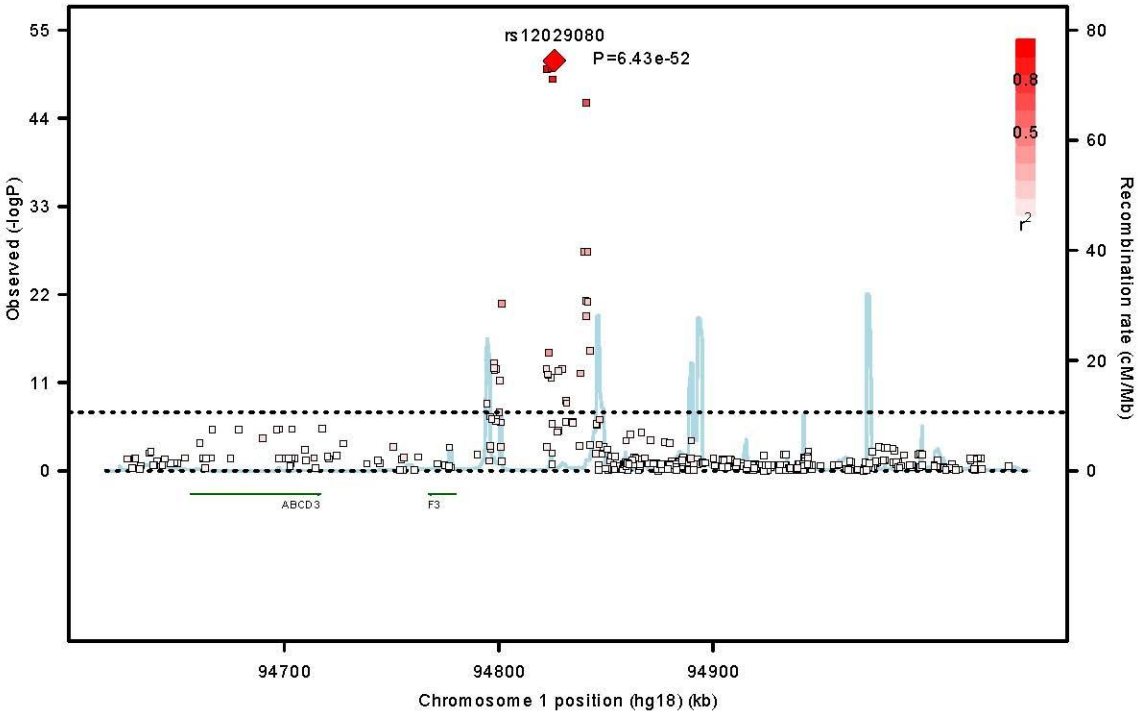
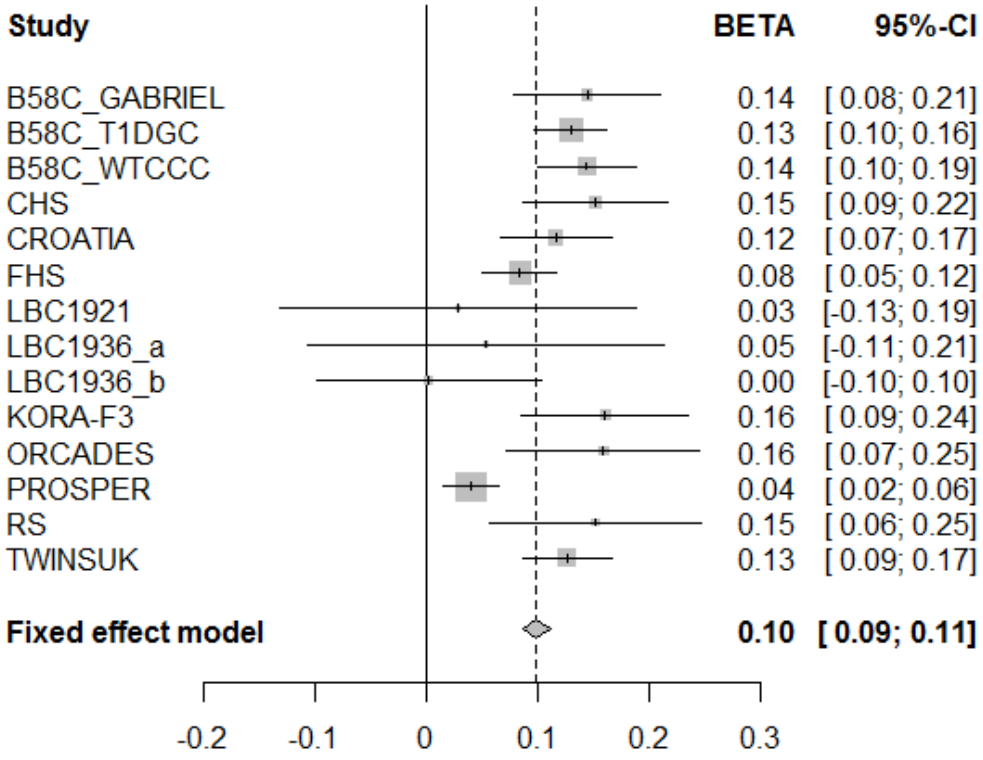
Supplemental Materials

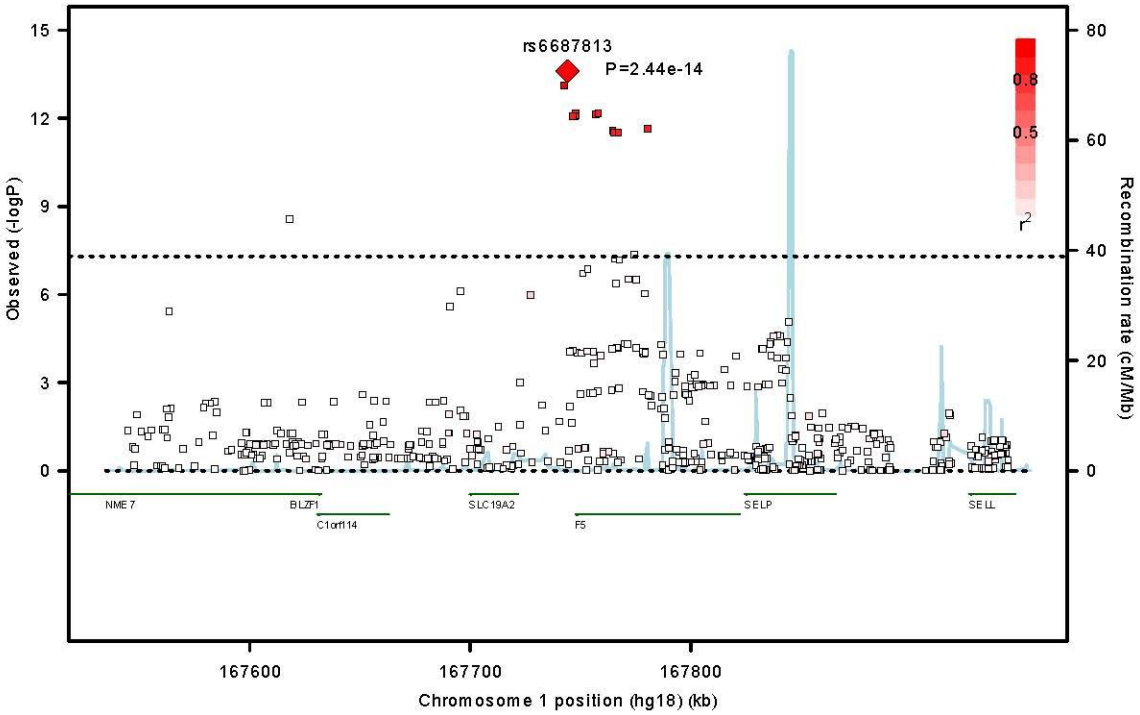
Supplemental Figure S1. Regional plot of *F3*



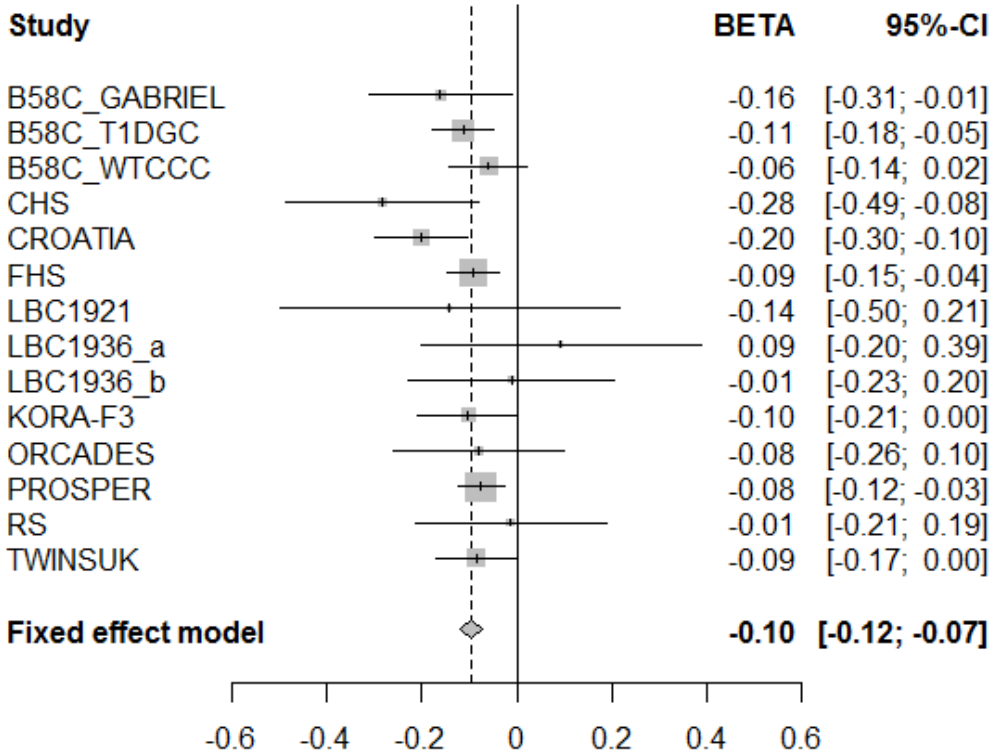
Supplemental Figure S2. Forest plot of rs12029080



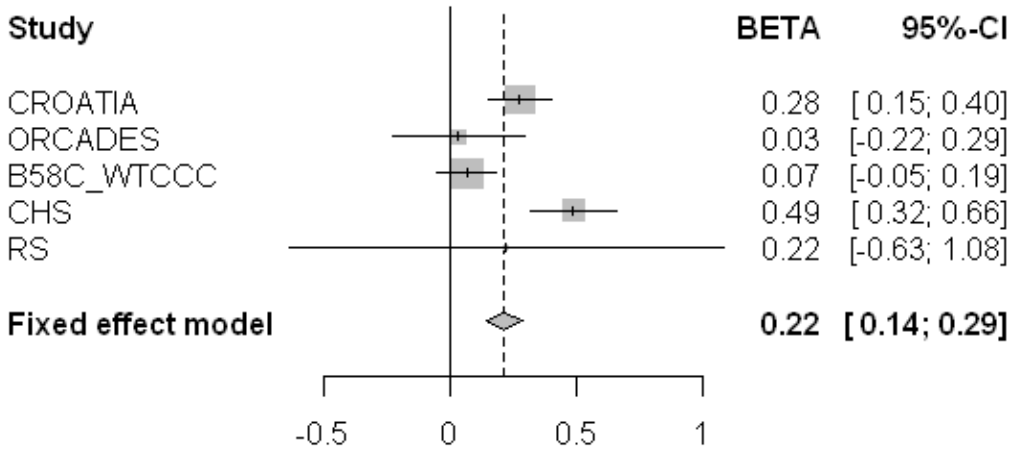
Supplemental Figure S3. Regional plot of *F5*



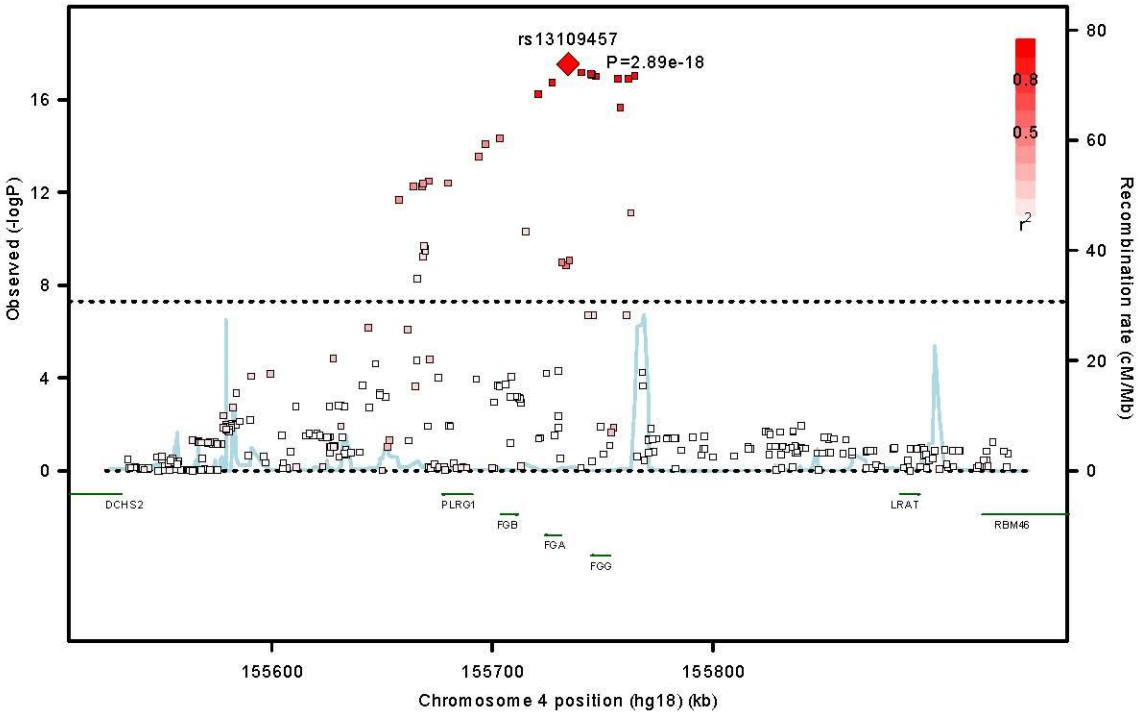
Supplemental Figure S4. Forest plot of rs6687813



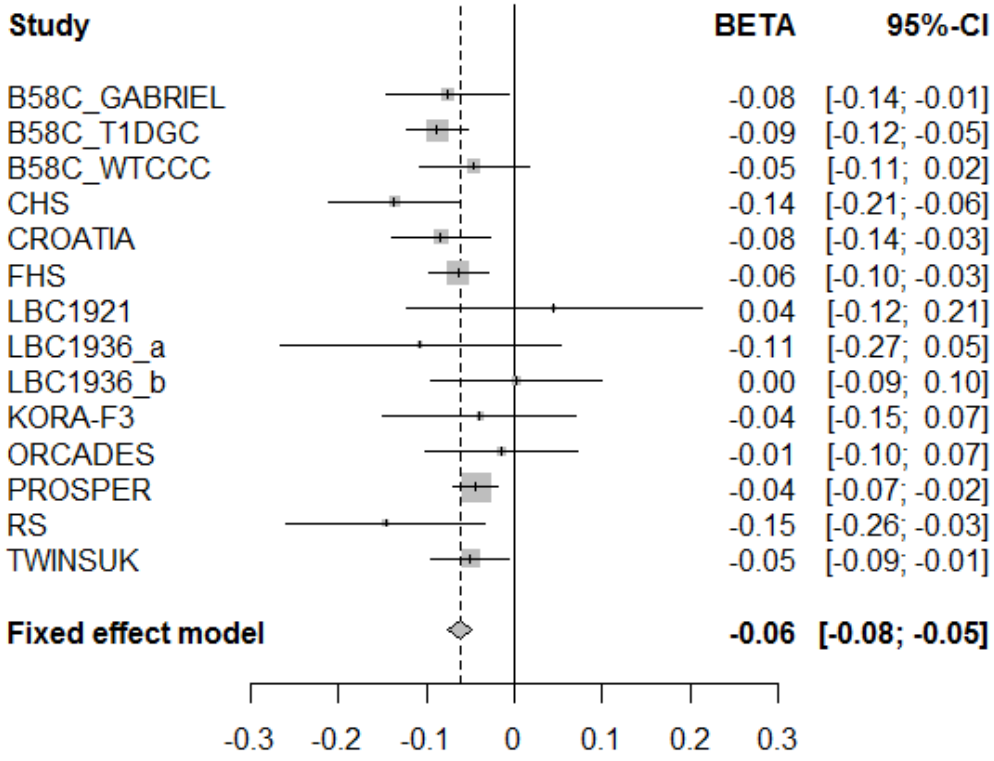
Supplemental Figure S5. Forest plot of rs6025



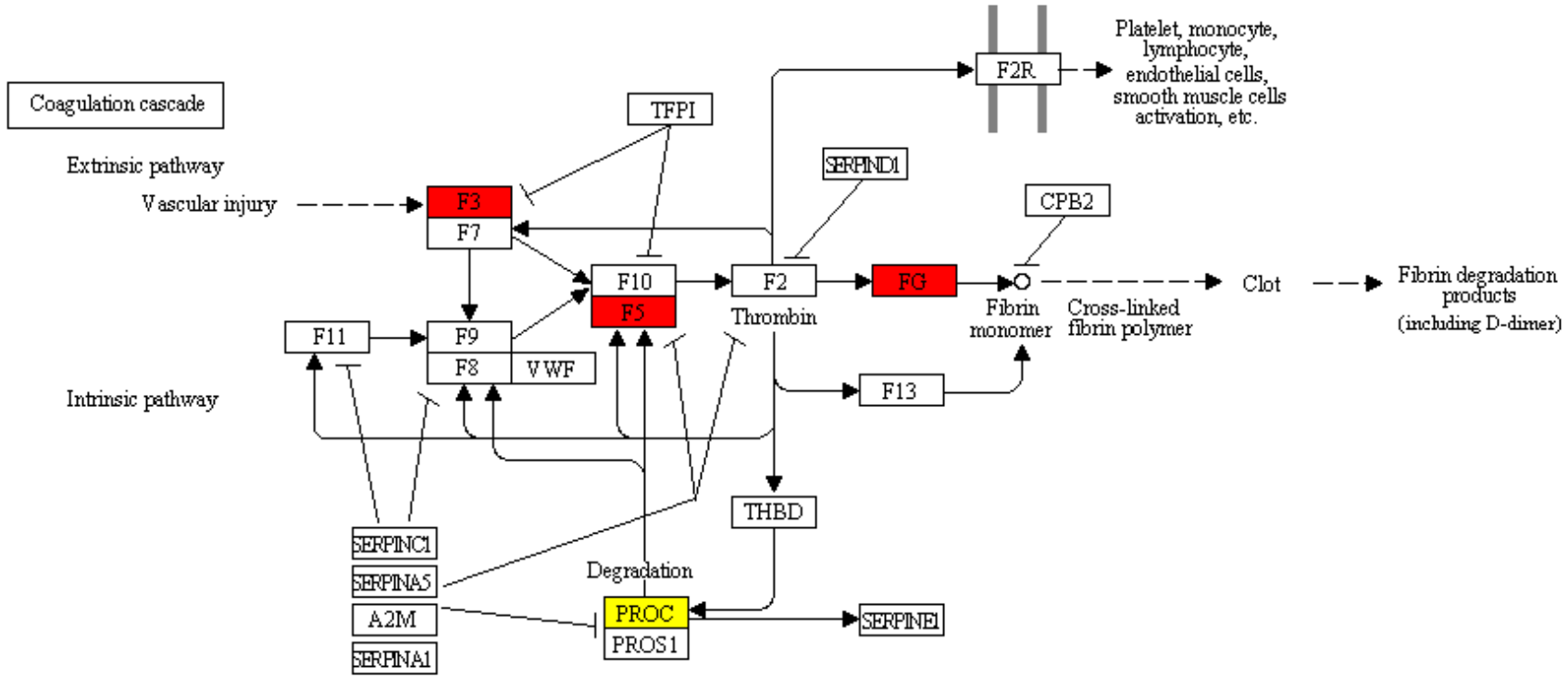
Supplemental Figure S6. Regional plot of *FGA*



Supplemental Figure S7. Forest plot of rs13109457



Supplement Figure S7. Depiction of major components of the coagulation cascade.



From Kyoto Encyclopedia of Genes and Genomes (http://www.genome.jp/kegg-bin/show_pathway?map04610)
A2M = alpha-2-macroglobulin; *CPB2* = plasma carboxypeptidase B2 (thrombin-activatable fibrinolysis inhibitor); *F2* = coagulation factor II (prothrombin); *F2R* = coagulation factor 2 receptor; *F3* = coagulation factor III (tissue factor); *F5* = coagulation factor V; *F7* = coagulation factor VII; *F8* = coagulation factor VIII; *F9* = coagulation factor IX; *F10* = coagulation factor X; *F11* = coagulation factor XI; *F13* = coagulation factor XIII; *FG* (includes *FGA*, *FGB*, *FGG*) = alpha, beta, and gama fibrinogen; *PROC* = protein C; *PROS1* = protein S; *SERPINA1* = alpha-1-antitrypsin; *SERPINA5* = protein C inhibitor; *SERPINC1* = antithrombin; *SERPIND1* = heparin cofactor II; *SERPINE1* = plasminogen activator inhibitor-1; *TFPI* = tissue-factor pathway inhibitor; *THBD* = thrombomodulin; *VWF* = von Willebrand factor.

Supplemental Table S1: Genotyping and imputation methods for autosomal chromosomes by study

Methods	B58C-WTCCC	B58C-T1DGC	B58C-GABRIEL	CHS	Croatia-Vis	FHS
Platform	Affymetrix	Illumina	Illumina	Illumina	Illumina	Affymetrix
Chip	500K	550K	610K	370 CNV	300v1	500K + 50K
SNPs investigated	490,032	539,438	582,892	306,655	317,500	490,700 (500K) 48,195 (50K)
SNP exclusion criteria*	Sample-wise	Call rates <0.98	excluded			
Call rate	none	none	none	Ò0.97	Ò0.98	Ò0.97
HWE p-value	None	None	None	$<1.0x10^{-5}$	$<1.0x10^{-6}$	<1 x 10E-6
Variants included for imputation	490,032	539,438	582,892	291,322	299,829	343,361 (500K) 34,841 (50K)
Percent of variants included	100%	100%	100%	95%	94.5%	70% (500k) 72% (50K)
Imputation software	IMPUTE	MACH	MACH	BIMBAM	MACH	MACH
Imputation software version	0.1.3	1.0.13	1.0.16	0.99	1.0.16	1.0.15
Genome build	35	35	36	36	36	36.2
Total number of SNPs	2,236,936	2,557,252	2,543,887	2,543,887	2,453,887	2,543,887

Methods	KORA-F3	LBC (all)	ORCADES	PROSPER	RS	Twins UK
Platform	Affymetrix	Illumina	Illumina	Illumina	Illumina	Illumina
Chip	500K	610-Quad v1	300 v2	660K	550 v3	300, 610Q, 1M, 1M-Duo, 1.2MDuo
SNPs I	490,032	542,050	373397	561.490	561,466	307,739 (300) 598,207 (610Q) 892,943 (1M)
SNP E						
Call	1.00	Ò0.98	Ò0.98	Ò0.95	Ò0.98	Ò0.97 (MAFÓ0.05) Ò0.99 (0.01ÒMAFÒ0.05)
HWE	-	<0.001	$<1.0x10^{-6}$	$<1.0x10^{-6}$	$<1.0x10^{-6}$	$<1.0x10^{-6}$
Variants	490,032	535,709	293,700	557,192	512,349	889,685 (Merged)
Percent	100%	99%	92%	99.2%	91.3%	99.6% (1M)
Software	MACH	MACH	MACH	MACH	MACH	Impute
Version	1.0.9	1.0.16	1.0.16	1.0.15	1.0.15	2
Build	35.21	36	36	36	36	36
Total SNPs	2,557,252	2,543,887	2,453,887	2,543,887	2,543,887	2,657,661

Supplemental Table S2. Description of subthreshold single-nucleotide-polymorphism marker associations with p-values less than $1.0x10^{-5}$ but more than $5.0x10^{-8}$

Chromosome	SNP		Position	Variant	MAF	P-value	Parameter coefficient*	Closest Gene (location/distance)
	Number of SNPs	Most significant						
1	4	rs2774920	94383888	G	0.085	$1.1x10^{-6}$	0.0513	*ABCA4* (25kb 5ð; *ARHGAP29* (23kb 3ð
1	2	rs16861990	167401751	C	0.061	$1.9x10^{-6}$	0.0614	*NME7* (intronic)
5	1	rs16871023	73250993	G	0.046	$1.4x10^{-6}$	-0.0761	*RGNEF* (intronic)
9	6	rs4246856	24082072	C	0.201	$6.2x10^{-6}$	0.0333	**
9	6	rs687621	135126886	G	0.317	$7.0x10^{-6}$	0.0284	*ABO* (intronic)
11	1	rs2306029	46849684	C	0.448	$7.8x10^{-6}$	-0.0269	*LRP4* (exonic: Ser1554Gly)
11	1	rs7117404	47083729	G	0.153	$8.5x10^{-6}$	-0.0398	*C11orf49* (intronic)
11	1	rs11039571	48163835	G	0.131	$9.4x10^{-6}$	-0.0390	*PTPRJ* (15kb 3ð
11	5	rs1351696	48339047	G	0.135	$7.9x10^{-6}$	-0.0382	*OR4C45* (9kb 5ð
12	1	rs7314285	110006409	G	0.065	$9.5x10^{-6}$	0.0542	*CUX2* (intronic)
16	4	rs1991867	81076729	C	0.111	$3.5x10^{-6}$	-0.0440	*CDH13* (141kb 5ð
18	34	rs8083346	61149755	G	0.346	$6.2x10^{-6}$	-0.0278	**
20	6	rs867186	33228215	G	0.091	$3.7x10^{-6}$	0.0484	*PROCR* (exonic: Ser219Gly)

CI = confidence interval based on a 2-sided Ŭ = 0.00000005; MAF = weighted minor allele frequency; SNP = single nucleotide polymorphism.
*Parameter coefficient represents change (% of activity or antigen) associated with 1-unit change in allele dosage. ** No genes within 200kb on either side of SNP.