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Supplemental Data

Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans

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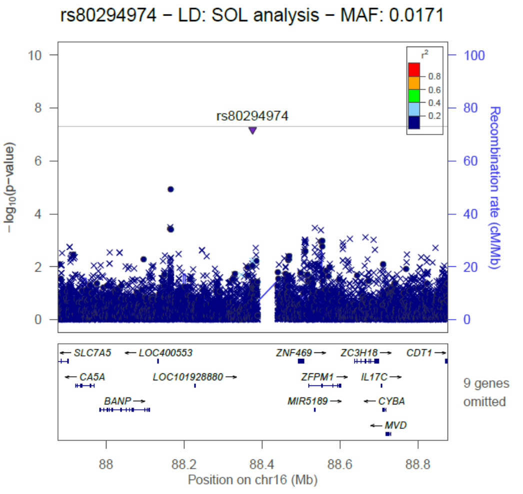
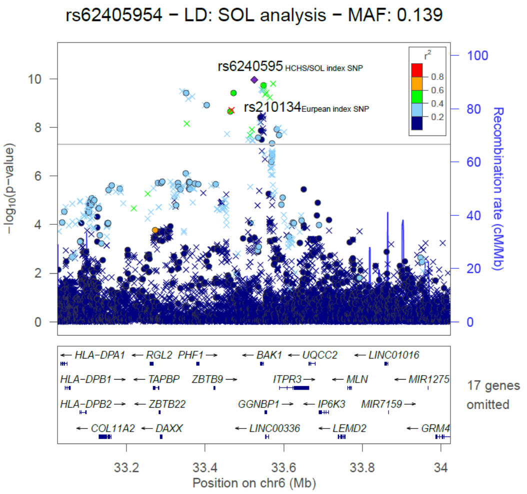
A.


rs80294974 − LD: SOL analysis − MAF: 0.0171
rs80294974
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
10
0
20
40
60
80
100
SLC7A5
LOC400553
ZNF469
ZC3H18
CDT1
CA5A
LOC101928880
ZFPM1
IL17C
BANP
MIR5189
CYBA
MVD
9 genes omitted
88
88.2
88.4
88.6
88.8
Position on chr16 (Mb)

B.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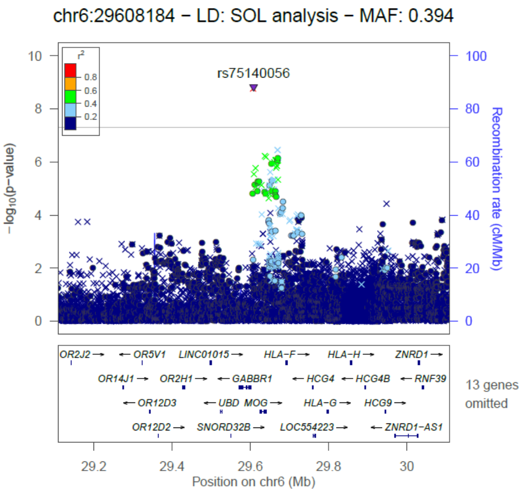
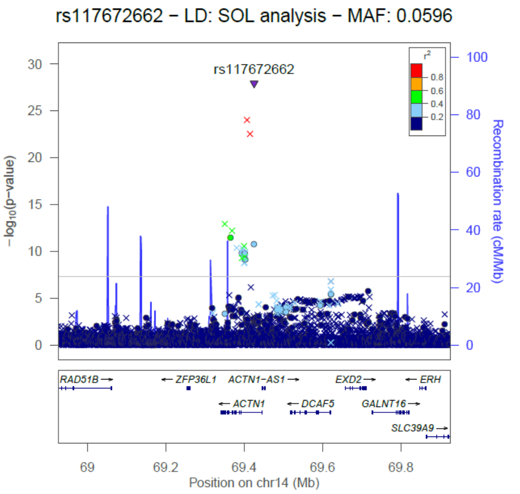
rs6240595 HCHS/SOL index SNP
rs210134 Eurpean index SNP
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
10
0
20
40
60
80
100
HLA−DPA1
RGL2
PHF1
BAK1
UQCC2
LINC01016
HLA−DPB1
TAPBP
ZBTB9
ITPR3
MLN
MIR1275
HLA−DPB2
ZBTB22
GGNBP1
IP6K3
MIR7159
COL11A2
DAXX
LINC00336
LEMD2
GRM4
17 genes omitted
33.2
33.4
33.6
33.8
34
Position on chr6 (Mb)

C.


chr6:29608184 − LD: SOL analysis − MAF: 0.394
rs75140056
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
10
0
20
40
60
80
100
OR2J2
OR5V1
LINC01015
HLA−F
HLA−H
ZNRD1
OR14J1
OR2H1
GABBR1
HCG4
HCG4B
RNF39
OR12D3
UBD
MOG
HLA−G
HCG9
OR12D2
SNORD32B
LOC554223
ZNRD1−AS1
13 genes omitted
29.2
29.4
29.6
29.8
30
Position on chr6 (Mb)

D.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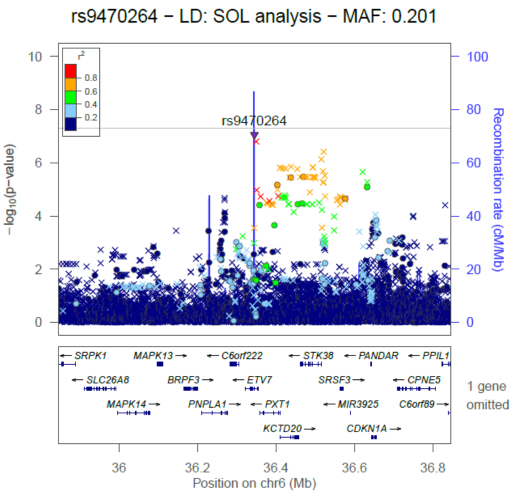
rs117672662
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
0
5
10
15
20
25
30
0
20
40
60
80
100
RAD51B
ZFP36L1
ACTN1−AS1
EXD2
ERH
ACTN1
DCAF5
GALNT16
SLC39A9
69
69.2
69.4
69.6
69.8
Position on chr14 (Mb)

E.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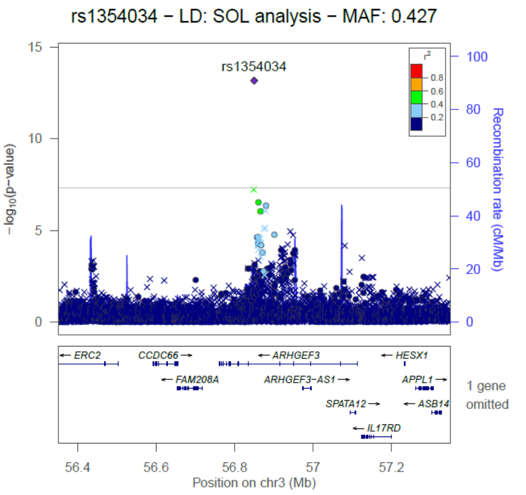
rs9470264
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
10
0
20
40
60
80
100
SRPK1
MAPK13
C6orf222
STK38
PANDAR
PPIL1
SLC26A8
BRPF3
ETV7
SRSF3
CPNE5
MAPK14
PNPLA1
PXT1
MIR3925
C6orf89
KCTD20
CDKN1A
1 gene omitted
36
36.2
36.4
36.6
36.8
Position on chr6 (Mb)

F.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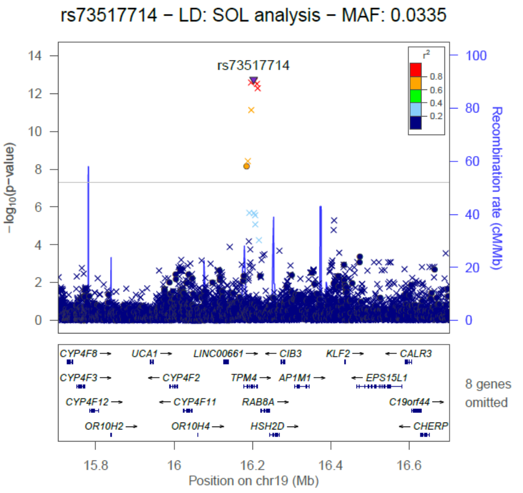
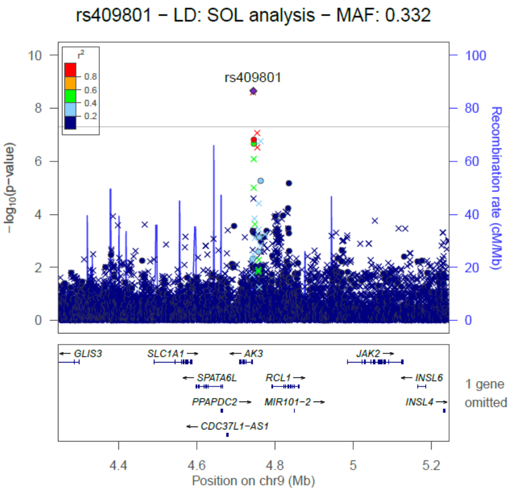
rs1354034
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
0
5
10
15
0
20
40
60
80
100
ERC2
CCDC66
ARHGEF3
HESX1
FAM208A
ARHGEF3−AS1
APPL1
SPATA12
ASB14
IL17RD
1 gene omitted
56.4
56.6
56.8
57
57.2
Position on chr3 (Mb)

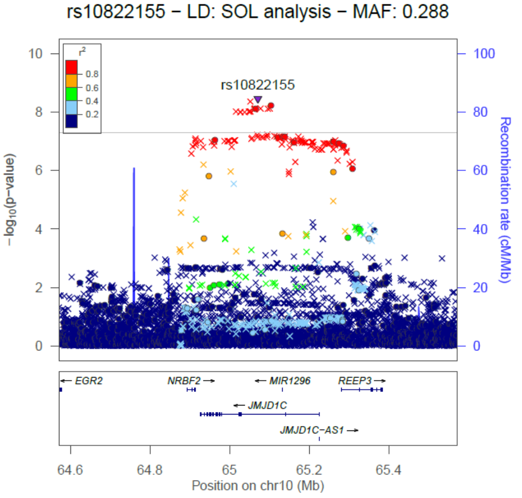
G.


rs73517714 – LD: SOL analysis – MAF: 0.0335
rs73517714
−log10(p−value)
Recombination rate (cM/Mb)
r²
0.8
0.6
0.4
0.2
CYP4F8
UCA1
LINC00661
CIB3
KLF2
CALR3
CYP4F3
CYP4F2
TPM4
AP1M1
EPS15L1
CYP4F12
CYP4F11
RAB8A
C19orf44
OR10H2
OR10H4
HSH2D
CHERP
8 genes omitted
Position on chr19 (Mb)

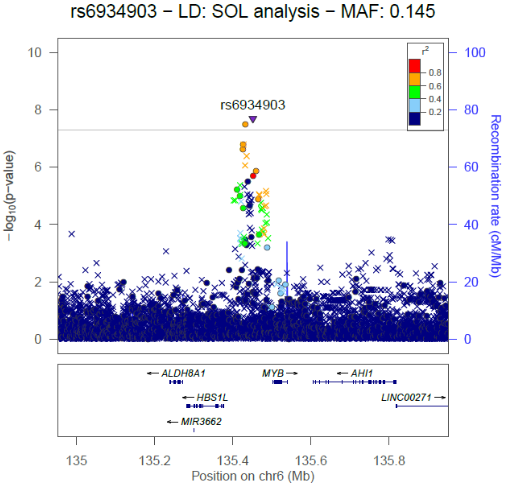
H.


rs409801 – LD: SOL analysis – MAF: 0.332
rs409801
−log10(p−value)
Recombination rate (cM/Mb)
r²
0.8
0.6
0.4
0.2
GLIS3
SLC1A1
AK3
JAK2
SPATA6L
RCL1
INSL6
PPAPDC2
MIR101−2
INSL4
CDC37L1−AS1
1 gene omitted
Position on chr9 (Mb)

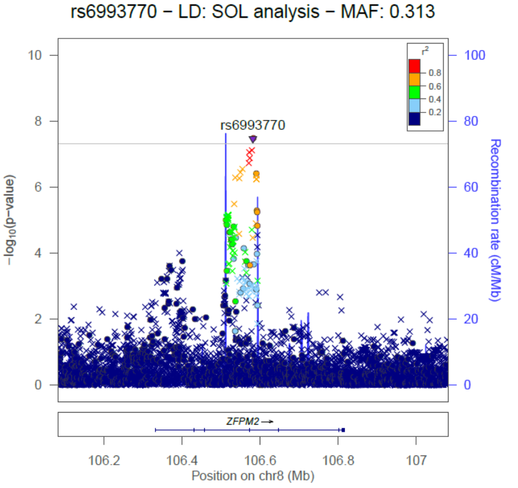
I. .


rs10822155 – LD: SOL analysis – MAF: 0.288
rs10822155
−log10(p−value)
Recombination rate (cM/Mb)
r²
0.8
0.6
0.4
0.2
EGR2
NRBF2
MIR1296
REEP3
JMJD1C
JMJD1C−AS1
Position on chr10 (Mb)

J.


rs6934903 – LD: SOL analysis – MAF: 0.145
rs6934903
−log10(p−value)
Recombination rate (cM/Mb)
r²
0.8
0.6
0.4
0.2
ALDH8A1
MYB
AHI1
HBS1L
LINC00271
MIR3662
Position on chr6 (Mb)

K.


rs6993770 – LD: SOL analysis – MAF: 0.313
rs6993770
−log10(p−value)
Recombination rate (cM/Mb)
r²
0.8
0.6
0.4
0.2
ZFPM2
Position on chr8 (Mb)

L.

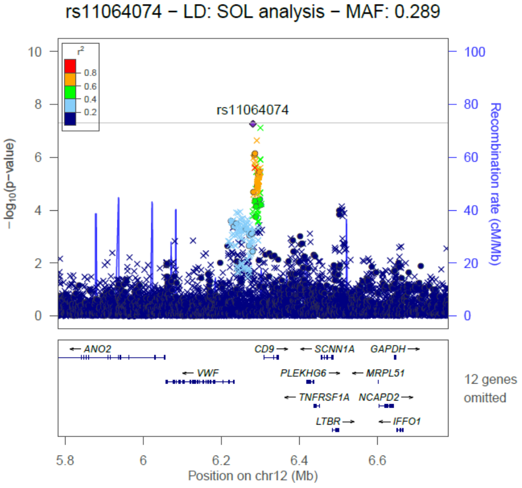
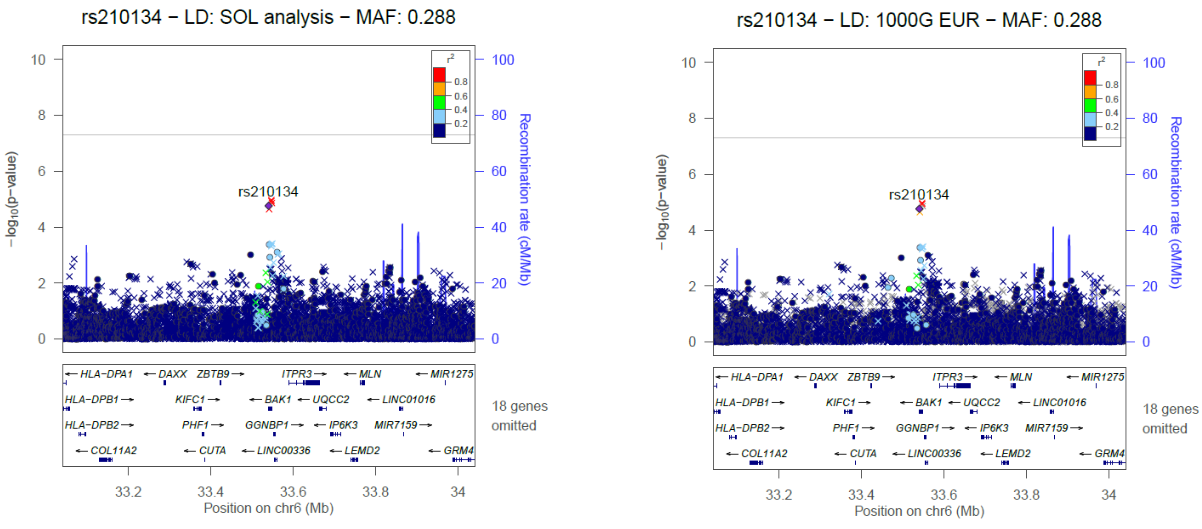

rs11064074 – LD: SOL analysis – MAF: 0.289
rs11064074
−log10(p−value)
Recombination rate (cM/Mb)
r²
0.8
0.6
0.4
0.2
ANO2
CD9
SCNN1A
GAPDH
VWF
PLEKHG6
MRPL51
TNFRSF1A
NCAPD2
LTBR
IFFO1
12 genes omitted
Position on chr12 (Mb)

Figure S1: LocusZoom plots of loci that have discovery p-values less than 1×10^{-7}. In each, the top panel reflects the main PLT GWAS analysis results. The LD estimates were calculated in the SOL discovery sample and are presented with respect to the lowest P-value SNP (reference). The genotyped reference SNP is denoted by a filled diamond, imputed reference SNP is denoted by a filled triangle, other imputed SNPs are denoted by a cross, and other genotyped SNPs are denoted by a filled circle. Recombination hotspots are indicated by the blue lines and scaled according to the y-axis on the right side of the plot. The dashed line indicates the nominal significance threshold p-value $\leq 5 \times 10^{-8}$. The bottom panel shows the genes and their orientation for each region. A. *BANP-ZFPM1* with rs80294974 as index variant, B. *ZBTB9-BAK1* with rs62405954 as index variant, C. *GABBR1-MOG* with rs75140056 as index variant, D. *ACTN1* with rs117672662 as index variant, E. *ETV7* with rs9470264 as index variant, F. *ARGHEF3* with rs1354034 as index variant, G. *TPM4* with rs73517714 as index variant, H. *AK3-RCL1* with rs409801 as index variant, I. *JMJD1C* with rs10822155 as index variant, J. *HBS1L-MYB* with rs6934903 as index variants, K. *ZFPM2* with rs6993770 as index variant, L. *VWF-CD9* with rs11064074 as index variant.

A.

i) ii)



B.

i) i)

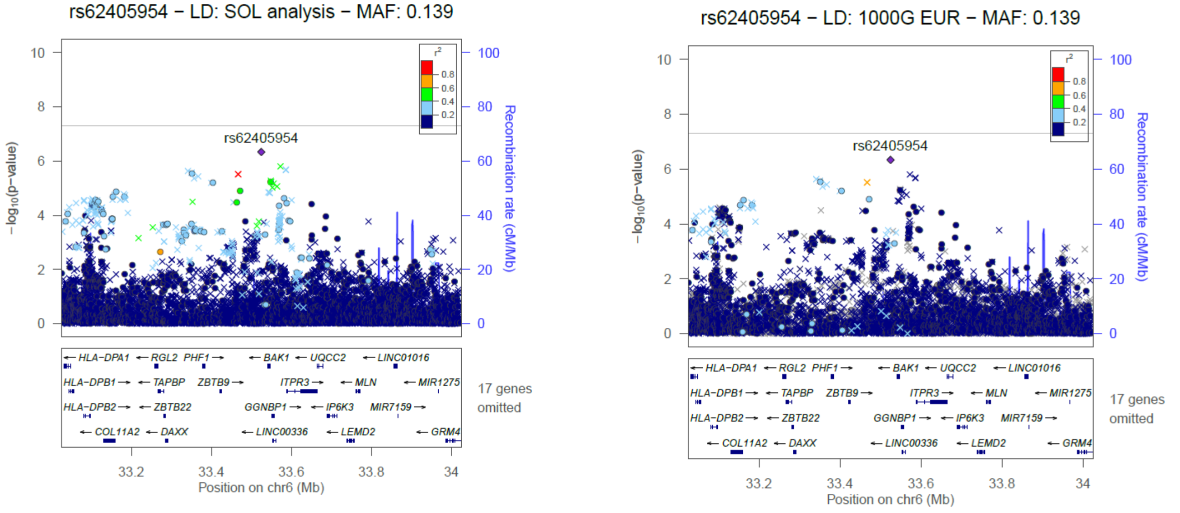


Figure S2. LocusZoom plots of conditional analysis at *ZBTB9-BAK1* locus. In each, the top panel reflects the conditional analysis results. The LD estimates with respect to the indicated reference SNP at each locus are color coded based on the scale indicated in each plot. As indicated, the LD estimates are either derived using HCHS/SOL population or the 1000 genomes EUR super-population. The genotyped reference SNP is denoted by a filled diamond, imputed reference SNP is denoted by a filled triangle, other imputed SNPs are denoted by a cross, and other genotyped SNPs are denoted by a filled circle. Recombination hotspots are indicated by the blue lines. The dashed line indicates the nominal significance threshold p-value $\leq 5 \text{ x } 10^{-8}$.The bottom panel shows the genes and their orientation for each region. **A. C**onditioned on HCHS/SOL index SNP rs62405954 and color coded by i) LD estimates from I HCHS/SOL population, and ii) LD estimates from 1000genomes EUR super-population. B) **B.** Conditioned on the European GWAS index SNP rs210134 and color coded by i) LD estimates from HCHS/SOL population, and ii) LD estimates from 1000genomes EUR super-population.

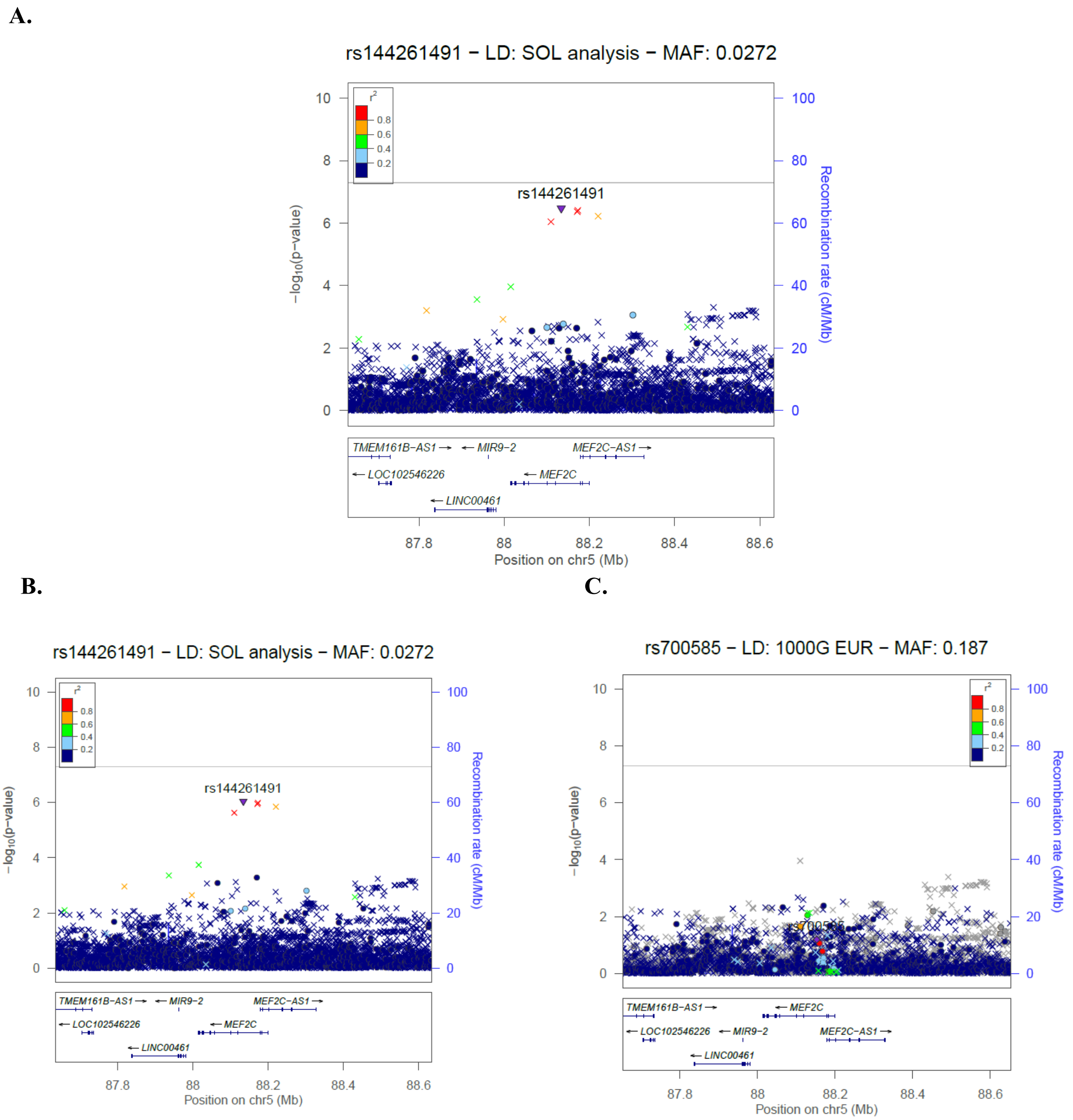


Figure S3. LocusZoom plots of main and conditional analysis at *MEF2C* locus. In each, the top panel reflects the main PLT GWAS or conditional analysis results, as indicated. The LD estimates with respect to the indicated reference SNP at each locus are color coded based on the scale indicated in each plot. As noted, the LD estimates are either derived using HCHS/SOL population or the 1000 genomes EUR super-population. The genotyped reference SNP is denoted by a filled diamond, imputed reference SNP is denoted by a filled triangle, other imputed SNPs are denoted by a cross and other genotyped SNPs are denoted by a filled circle. Recombination hotspots are indicated by the blue lines. The dashed line indicates the nominal significance threshold p-value $\leq 5 \times 10^{-8}$. The bottom panel shows the genes and their orientation for each region.**A.** MEF2C locus from the main PLT GWAS analysis color coded by LD estimates from HCHCS/SOL with reference to HCHS/SOL index SNP rs144261491. **B.** *MEF2C* locus conditioned on European GWAS index SNP rs700585 and color coded by LD estimates from HCHS/SOL population. **C**. *MEF2C* locus conditioned on HCHS/SOL index SNP rs144261491 and color coded LD estimates from 1000 genomes EUR super-population

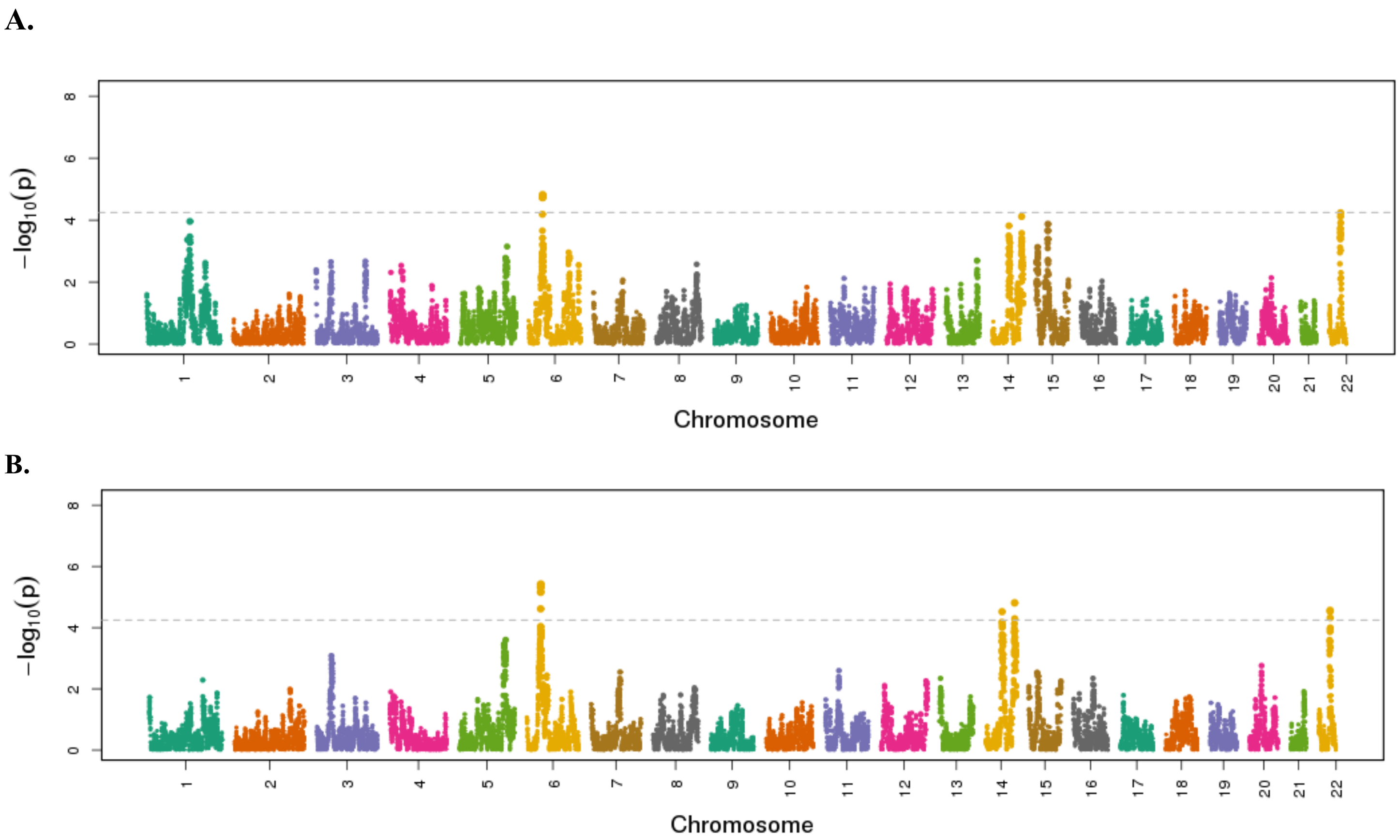


Figure S4: A. Genome-wide admixture scan with a joint test of all three local ancestry estimates (Amerindian, European, African) from RFMix with dashed line indicating the significance threshold p-value≤ -$\log_{10}(5.7 \text{ x } 10^{-5})$, B. Genome-wide admixture scan of Amerindian against any other ancestry from from RFMix with dashed line indicating the significance threshold p-value≤ -$\log_{10}(5.7 \text{ x } 10^{-5})$.

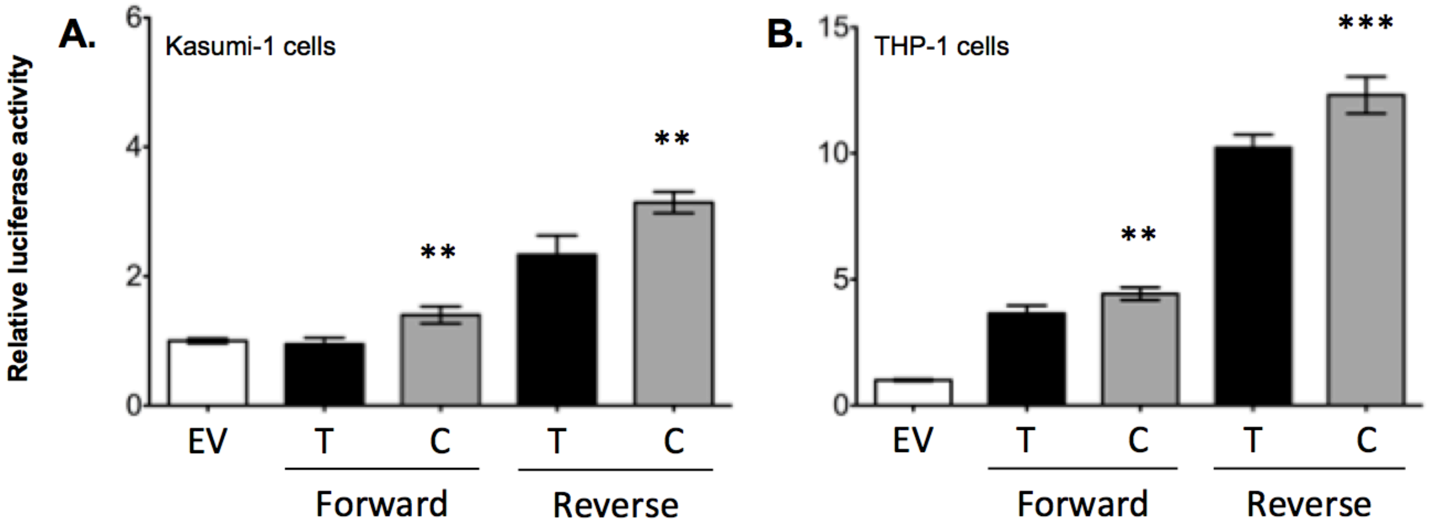


Figure S5: Allelic differences in transcriptional activity of variant rs117672662. A 186 bp PCR product approximately centered on rs117672662 was cloned in both orientations (Forward and Reverse) relative to a minimal promoter in a transcriptional reporter vector (pGL4.23). Clones were transfected into (A) Kasumi-1 cells: a myeloblast, cell line established from the peripheral blood of an acute myeloid leukemia patient and (B) THP-1 cells: a monocyte cell line, isolated from peripheral blood of an acute monocyte leukemia patient. The cells were incubated for 48 hrs, and luciferase and Renilla activity were measured in the cell lysate. Results are shown as relative luciferase/Renilla activity normalized to empty vector. Error bars represent the standard deviation of results for four clones. EV: Empty Vector

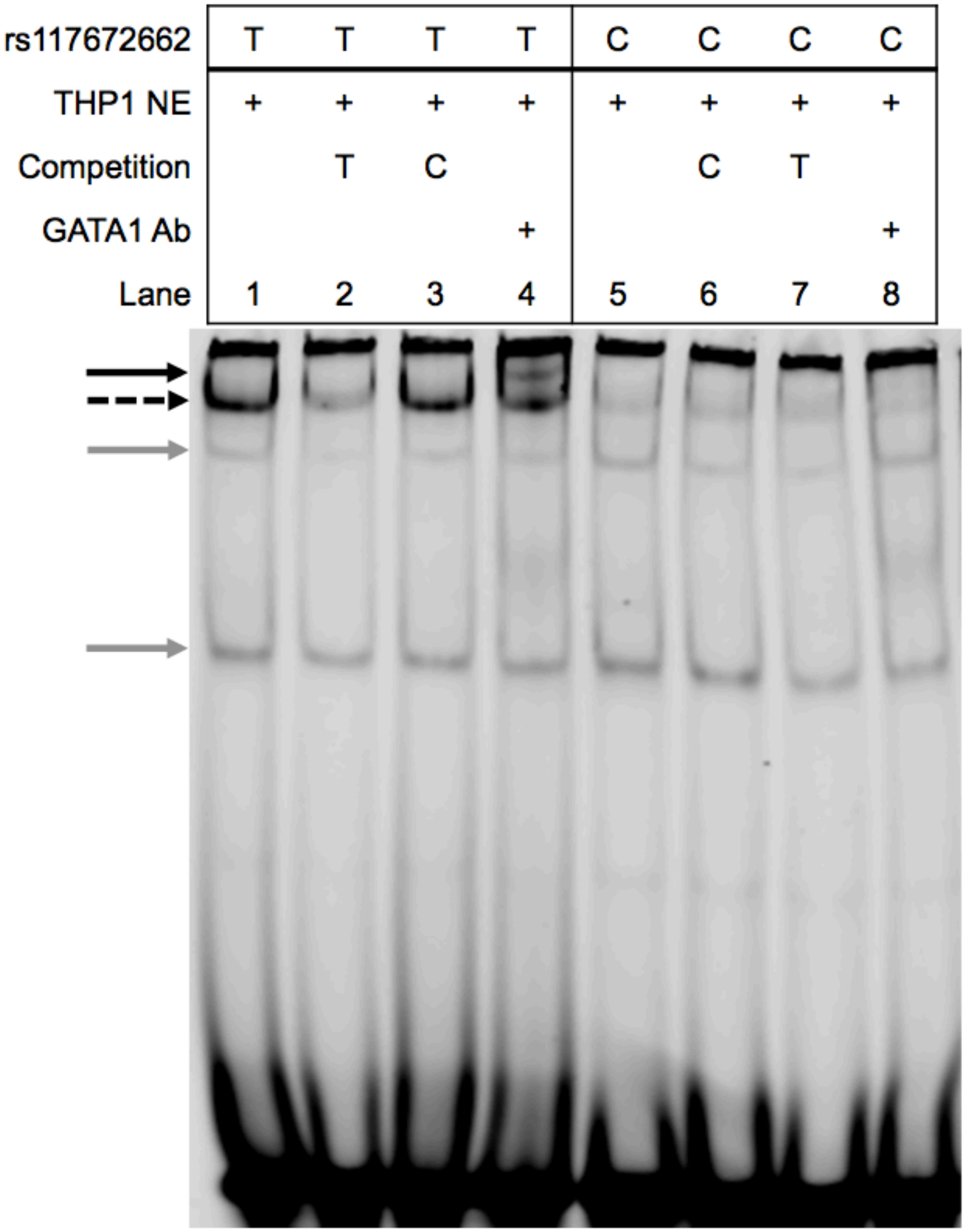


Figure S6: Further support of allelic differences in protein binding at rs117672662. EMSA using oligonucleotide probes containing different alleles at rs117672662 (T allele: lanes 1 to 4, C allele: lanes 5 to 8). Nuclear extracts from human monocyte THP-1 cells were incubated with IRDye-labeled double-stranded oligonucleotide probe alone (lanes 1, 5) or with 70-fold excess of unlabeled probe (lanes 2, 3, 6 and 7) or GATA1 antibodies (lanes 4 and 8). The dotted black arrow indicates probe-protein complexes, the solid black arrow indicates probe-protein-antibody complexes and the grey arrows indicate non-specific probe-protein binding complexes. The unlabeled T-allele probe shows stronger competition than the unlabeled C-allele probe. The faint band remaining in lane 2 may represent incomplete competition or another non-specific probe-protein complex.

Table S1. Demographic Characteristics of Discovery and Replication Cohorts

Study	**Phase**	**N**	**Study Design**	**Mean Platelet Count[a] (Standard Deviation)**	**% Female**	**Age[b] Mean (Standard Deviation)**
HCHS/SOL	Discovery	12941	Population- and family-based	252 (65)	59	46 (14)
Bio*Me*	Replication	2854	Population-based, unrelated	233 (71)	62	59 (15)
WHI	Replication	3534	Population-based, unrelated	245 (56)	100	60 (7)
MESA	Replication	782	Population-based, unrelated	234 (66)	53	69 (9)

[a] Platelet count unit = 10^9/L, [b] Age = years.

Table S2. Variants reaching the genome-wide (P-value<$5x10^{-8}$) or suggestive (P-value< $1x10^{-7}$) significance in HCHS/SOL

Novel or Known	Nearest Gene(s) (genomic context)	Chromosome: position (GRCh37/hg19)	rsID	Coded / alternative allele on (+) strand	HCHS/SOL Coded Allele Frequency	N	Beta (Standard Error)	P-value
Novel	*ACTN1* (intronic)	chr14:69425467	rs117672662	T/C	0.94	12491	0.604(0.054)	$1.16x10^{-28}$
Novel	*ZBTB9-BAK1* (intergenic)	chr6:33524820	rs62405954	T/C	0.86	12491	-0.239(0.037)	$1.10x10^{-10}$
Novel	*GABBR1-MOG* (intergenic)	chr6:29608184	rs75140056	C/CAT	0.39	12491	-0.151(0.025)	$1.47x10^{-09}$
Novel	*BANP-ZFPM1* (intergenic)	chr16:88376014	rs80294974	G/A	0.98	12491	0.555(0.103)	$6.60x10^{-08}$
Novel	*ETV7* (intronic)	chr6:36344980	rs9470264	G/A	0.8	12491	-0.181(0.034)	$8.80x10^{-08}$
Known	*ARGHEF3* (intronic)	chr3:56849749	rs1354034	T/C	0.57	12491	-0.189(0.025)	$6.89x10^{-14}$
Known	*TPM4* (intronic)	chr19:16203304	rs73517714	C/A	0.97	12491	0.508(0.069)	$1.80x10^{-13}$
Known	*AK3-RCL1* (integenic)	chr9:4744743	rs409801	T/C	0.67	12491	-0.163(0.027)	$2.21x10^{-09}$
Known	*JMJD1C* (intronic)	chr10:65071215	rs10822155	C/A	0.71	12491	-0.168(0.028)	$3.50x10^{-09}$
Known	*HBS1L-MYB* (intergenic)	chr6:135451564	rs6934903	T/A	0.85	12491	-0.198(0.035)	$2.02x10^{-08}$
Known	*ZFPM2* (intronic)	chr8:106581528	rs6993770	A/T	0.69	12490	0.148(0.027)	$3.43x10^{-08}$
Known	*VWF-CD9* (intergenic)	chr12:6281039	rs11064074	C/T	0.71	12491	0.150(0.028)	$5.38x10^{-08}$

Table S3. Results from the generalization of European[1-4], African-American[5], and Japanese[6] GWAS PLT-associated variants to HCHS/SOL Hispanic/Latinos. The line separates the SNPs that generalized (top panel) from those that failed to generalize (bottom panel).

rsID	Nearest gene(s) (genomic context)	Chr:Position (build 37-hg19)	Coded / Alt. Allele	Discovery					HCHS/SOL					Meta-analysis		Ref.
				Ancestry	N	MAF[a]	Beta (SE)	p-value	MAF	CAF	Beta (SE)	2-sided p-value	r-value	Beta (SE)	p-value	
rs3811444	*TRIM58* (nonsynonymous)	1:248039450	C/T	European	27955	NA	3.35 (0.57)	5.6E-09	0.28	0.72	3.45 (0.89)	1.06E-04	5.58E-04	3.38 (0.48)	2.57E-12	[1]
rs1260326	*GCKR* (nonsynonymous)	2:27730939	T/C	European	54396	NA	2.33 (0.38)	9.12E-10	0.34	0.34	2.53 (0.86)	3.12E-03	9.35E-03	2.37 (0.35)	1.06E-11	[1]
rs625132	*EHD3* (intronic)	2:31482299	G/A	European	45217	NA	4.24 (0.57)	9.15E-14	0.11	0.89	3.93 (1.25)	1.67E-03	5.81E-03	4.18 (0.52)	5.97E-16	[1]
rs1354034	*ARHGEF3* (intronic)	3:56849749	T/C	European	6234	0.41	-9.44 (1.61)	4.35E-09	0.43	0.57	-5.87 (0.8)	2.44E-13	4.75E-04	-6.58 (0.72)	4.41E-20	[2]
rs1354034	*ARHGEF3* (intronic)	3:56849749	C/T	European	13582	0.39	7.97 (0.79)	6.00E-24	0.43	0.43	5.87 (0.8)	2.44E-13	7.32E-13	6.94 (0.56)	6.39E-35	[3]
rs6141	*THPO* (3' downstream)	3:184090266	T/C	Japanese	14806	0.45	0.08 (0.01)	5.38E-11	0.33	0.67	0.06 (0.01)	3.61E-05	3.61E-05	0.07 (0.01)	6.75E-14	[6]
rs700585	*MEF2C* (intronic)	5:88152116	C/T	European	55469	NA	2.7 (0.44)	9.86E-10	0.19	0.19	2.41 (1.01)	1.70E-02	3.76E-02	2.66 (0.4)	5.42E-11	[1]
rs12526480	*LRRC16A* (intronic)	6:25533534	G/T	African	16388	0.31	-4.39 (0.76)	9.15E-29	0.36	0.36	-2.6 (0.82)	1.53E-03	2.54E-03	-3.56 (0.56)	1.66E-10	[5]
rs210134	*BAK1* (3' downstream)	6:33540209	A/G	African	16388	0.29	-6.16 (0.78)	2.32E-15	0.29	0.29	-4.94 (0.86)	9.31E-09	9.31E-08	-5.61 (0.58)	2.79E-22	[5]
rs5745568	*BAK1* (5' upstream)	6:33548394	T/G	Japanese	14806	0.23	0.09 (0.01)	6.66E-11	0.24	0.24	0.10 (0.01)	1.89E-10	7.50E-06	0.09 (0.01)	1.48E-19	[6]
rs4895441	*HBS1L-MYB* (intergenic)	6:135426573	A/G	European	13582	0.27	-5.42 (0.88)	9.00E-10	0.18	0.82	-5.39 (1.02)	1.24E-07	4.29E-05	-5.41 (0.67)	5.84E-16	[3]
rs9494145	*HBS1L-MYB* (intergenic)	6:135432552	C/T	African	16388	0.07	8.19 (1.38)	2.79E-09	0.16	0.16	5.88 (1.07)	3.92E-08	9.81E-08	6.75 (0.85)	1.48E-15	[5]
rs342275	*AF086203* (intronic)	7:106359215	C/T	European	58571	NA	3.74 (0.36)	5.57E-25	0.33	0.67	3.6 (0.86)	2.82E-05	2.37E-04	3.72 (0.33)	9.42E-29	[1]
rs342293	*AF086203* (intronic)	7:106372219	G/C	African	16388	0.39	-4.05 (0.72)	1.58E-08	0.39	0.39	-3.41 (0.82)	2.92E-05	5.84E-05	-3.77 (0.54)	2.88E-12	[5]
rs6993770	*ZFPM2* (intronic)	8:106581527	A/T	European	54960	NA	3.67 (0.44)	4.30E-17	0.31	0.69	4.74 (0.85)	2.87E-08	1.21E-06	3.89 (0.39)	1.52E-23	[1]
rs6995402	*PLEC* (intronic)	8:145005560	C/T	European	57593	NA	2.30 (0.37)	5.09E-10	0.05	0.05	5.27 (2.24)	1.88E-02	3.96E-02	2.38 (0.37)	7.50E-11	[1]
rs385893	*AK3-RCL1* (intergenic)	9:4763176	T/C	Japanese	14806	0.25	-0.10 (0.01)	2.95E-13	0.40	0.60	-0.06 (0.01)	5.44E-06	1.09E-05	-0.08 (0.01)	2.87E-16	[6]
rs385893	*AK3-RCL1* (intergenic)	9:4763176	C/T	European	9316	0.44	6.26 (0.75)	8.50E-17	0.40	0.40	3.74 (0.83)	5.88E-06	1.18E-05	5.12 (0.56)	3.62E-20	[4]
rs423955	*AK3-RCL1* (intergenic)	9:4792339	A/G	European	13582	0.34	4.94 (0.81)	1.0E-9	0.40	0.60	1.85 (0.82)	2.33E-02	2.33E-02	3.41 (0.57)	2.89E-09	[3]
rs10761731	*RCL1* (5' upstream)	10:65027609	T/A	European	54344	NA	3.85 (0.38)	2.02E-24	0.31	0.31	4.81 (0.89)	6.44E-08	1.35E-06	4.00 (0.35)	1.56E-30	[1]
rs7896518	*JMJD1C* (intronic)	10:65104500	G/A	African	16388	0.32	5.18 (0.74)	2.26E-212	0.30	0.30	4.89 (0.89)	3.91E-08	9.81E-08	5.06 (0.57)	5.82E-19	[5]
rs505404	*PSMD13* (intronic)	11:243267	G/T	European	54642	NA	4.66 (0.45)	7.44E-25	0.26	0.26	2.53 (0.91)	5.68E-03	1.59E-02	4.24 (0.41)	1.48E-25	[1]
rs4938642	*CBL* (intronic)	11:119099905	C/G	European	56605	NA	4.73 (0.73)	7.66E-11	0.05	0.05	5.57 (1.75)	1.47E-03	5.62E-03	4.85 (0.67)	4.89E-13	[1]
rs7342306	*VWF-CD9* (intergenic)	12:6291092	G/A	European	55636	NA	2.53 (0.38)	4.29E-11	0.25	0.75	4.81 (0.92)	1.69E-07	7.75E-06	2.87 (0.35)	5.51E-16	[1]
rs4326844	*COPZ1* (intronic)	12:54736470	A/G	European	6234	0.45	-8.68 (1.59)	4.57E-08	0.27	0.27	-2.81 (0.93)	2.61E-03	2.61E-03	-4.31 (0.8)	7.95E-08	[2]
rs941207	*BAZ2A* (intronic)	12:57023283	G/C	European	55653	NA	2.75 (0.43)	1.74E-10	0.22	0.22	3.01 (0.96)	1.80E-03	5.81E-03	2.79 (0.39)	1.24E-12	[1]
rs3184504	*SH2B3* (nonsynonymous)	12:111884607	T/C	European	56354	NA	3.99 (0.37)	1.22E-26	0.27	0.27	3.75 (0.96)	8.61E-05	5.17E-04	3.96 (0.35)	6.19E-30	[1]
rs739496	*SH2B3* (3' UTR)	12:111887659	A/G	Japanese	14806	0.16	-0.14 (0.02)	4.75E-19	0.31	0.69	-0.06 (0.01)	2.94E-05	3.61E-05	-0.09 (0.01)	3.59E-19	[6]
rs11065987	*BRAP* (intergenic)	12:112072424	G/A	European	9316	0.34	5.07 (0.69)	2.20E-13	0.25	0.25	3.65 (0.97)	1.79E-04	1.79E-04	4.60 (0.56)	3.75E-16	[4]

rs6490294	*ACAD10* (intronic)	12:112190438	C/A	African	16388	0.34	-4.38 (0.75)	4.78E-09	0.37	0.63	-2.5 (0.86)	3.44E-03	4.91E-03	-3.56 (0.56)	2.62E-10	[5]
rs4148441	*ABCC4* (intronic)	13:95898206	G/A	European	64120	NA	4.12 (0.6)	6.76E-12	0.14	0.86	4.19 (1.14)	2.48E-04	1.16E-03	4.13 (0.53)	7.32E-15	[1]
rs11628318	*ANKRD9-RCOR1* (intergenic)	14:103040086	A/T	European	62438	NA	2.57 (0.41)	2.04E-10	0.38	0.62	2.07 (0.83)	1.27E-02	2.96E-02	2.48 (0.36)	1.04E-11	[1]
rs2297067	*EXOC3L4* (nonsynonymous)	14:103566784	T/C	European	41687	NA	3.54 (0.55)	1.58E-10	0.20	0.20	2.65 (0.98)	7.04E-03	1.83E-02	3.32 (0.48)	5.29E-12	[1]
rs10512472	*SLFN14* (nonsynonymous)	17:33884803	C/T	European	58692	NA	3.64 (0.48)	2.40E-14	0.23	0.23	3.08 (0.94)	1.10E-03	4.63E-03	3.52 (0.43)	1.29E-16	[1]
rs11082304	*CABLES1* (intronic)	18:20720972	G/T	European	58215	NA	2.48 (0.38)	5.27E-11	0.36	0.64	3.36 (0.83)	5.01E-05	3.50E-04	2.63 (0.34)	1.97E-14	[1]
rs8109288	*TPM4* (intronic)	19:16185558	G/A	European	29014	NA	11.95 (1.89)	2.75E-10	0.03	0.97	13.83 (2.46)	2.01E-08	3.73E-05	12.64 (1.5)	3.61E-17	[1]
rs8109288	*TPM4* (intronic)	19:16185559	A/G	African	16388	0.10	-8.72 (1.4)	5.02E-10	0.03	0.03	-13.83 (2.46)	2.01E-08	9.81E-08	-9.97 (1.22)	2.67E-16	[5]
rs17356664	*EXCOC3L2-MARK4* (intergenic)	19:45740770	C/T	European	55487	NA	2.60 (0.42)	3.60E-10	0.19	0.81	2.81 (1.05)	7.41E-03	1.83E-02	2.63 (0.39)	9.86E-12	[1]
rs2336384	*MFN2* (intronic)	1:12046062	G/T	European	57366	NA	2.17 (0.38)	1.25E-08	0.43	0.43	1.12 (0.81)	1.67E-01	2.42E-01	1.98 (0.35)	9.99E-09	[1]
rs10914144	*DNM3* (intronic)	1:171949749	T/C	European	54978	NA	3.42 (0.49)	2.22E-12	0.22	0.22	1.94 (0.99)	4.96E-02	8.68E-02	3.13 (0.44)	7.97E-13	[1]
rs1668871	*TMCC2* (intronic)	1:205237136	C/T	European	58108	NA	2.80 (0.37)	2.59E-14	0.23	0.23	-0.41 (0.94)	6.62E-01	1.00E+00	2.38 (0.34)	4.09E-12	[1]
rs7550918	*GCSAMLL* (intronic)	1:247675558	T/C	European	54171	NA	3.13 (0.47)	2.91E-11	0.27	0.73	0.97 (0.9)	2.78E-01	3.54E-01	2.67 (0.42)	1.62E-10	[1]
rs17030845	*THADA* (intronic)	2:43687878	C/T	European	65738	NA	3.58 (0.56)	1.27E-10	0.08	0.92	1.13 (1.49)	4.50E-01	4.97E-01	3.28 (0.52)	3.14E-10	[1]
rs7694379	*KLHL8-HSD17B13* (intergenic)	4:88186508	A/G	European	56430	NA	2.13 (0.37)	8.70E-09	0.32	0.32	0.02 (0.87)	9.83E-01	1.00E+00	1.80 (0.34)	1.16E-07	[1]
rs17568628	*F2R-F2RL1* (intergenic)	5:76046938	T/C	European	44759	NA	6.07 (0.99)	9.61E-10	0.02	0.98	6.13 (3.02)	4.24E-02	7.74E-02	6.08 (0.94)	1.16E-10	[1]
rs2070729	*IRF1* (intronic)	5:131819920	A/C	European	56469	NA	2.39 (0.37)	1.13E-10	0.45	0.55	0.58 (0.82)	4.76E-01	5.12E-01	2.08 (0.34)	6.85E-10	[1]
rs13236689	*CD36* (intronic)	7:80236014	G/T	African	16388	0.44	4.18 (0.7)	2.84E-09	0.36	0.36	1.64 (0.84)	5.00E-02	6.02E-02	3.14 (0.54)	5.26E-09	[5]
rs4731120	WASL-HYALP1 (intergenic)	7:123411222	C/A	European	66147	NA	4.14 (0.59)	2.77E-12	0.06	0.06	2.25 (1.63)	1.67E-01	2.42E-01	3.92 (0.56)	1.85E-12	[1]
rs4246215	*FEN1* (3' UTR)	11:61564298	T/G	European	56299	NA	2.45 (0.39)	3.31E-10	0.49	0.49	1.87 (0.9)	3.85E-02	7.35E-02	2.36 (0.36)	4.39E-11	[1]
rs477895	*BAD* (intronic)	11:64048912	C/T	African	16388	0.45	-4.19 (0.77)	4.91E-08	0.21	0.21	-1.94 (1.01)	5.42E-02	6.02E-02	-3.36 (0.61)	3.99E-08	[5]
rs17824620	*RPH3A* (intronic)	12:113100993	C/A	European	51530	NA	2.46 (0.43)	9.67E-09	0.32	0.68	1.09 (0.86)	2.10E-01	2.93E-01	2.19 (0.38)	1.19E-08	[1]
rs7961894	*WDR66* (intronic)	12:122365582	C/T	European	51897	NA	3.92 (0.61)	1.22E-10	0.07	0.93	1.97 (1.6)	2.18E-01	2.95E-01	3.68 (0.57)	1.06E-10	[1]
rs8022206	*RAD61B* (intronic)	14:68520905	G/A	European	52251	NA	3.20 (0.5)	1.55E-10	0.18	0.82	0.49 (1.03)	6.36E-01	6.67E-01	2.68 (0.45)	2.51E-09	[1]
rs8006385	*ITPK1* (intronic)	14:93501025	G/A	European	64929	NA	3.59 (0.56)	1.24E-10	0.11	0.11	1.12 (1.29)	3.85E-01	4.49E-01	3.2 (0.51)	4.26E-10	[1]
rs7149242	*BEGAIN-DLK1* (intergenic)	14:101159415	G/T	European	61247	NA	2.14 (0.39)	2.68E-08	0.32	0.68	0.73 (0.87)	4.02E-01	4.56E-01	1.91 (0.35)	5.77E-08	[1]
rs3809566	*TPM1* (5' upstream)	15:63333723	G/A	European	57113	NA	2.44 (0.39)	3.65E-10	0.27	0.73	1.08 (0.89)	2.26E-01	2.96E-01	2.22 (0.36)	4.84E-10	[1]
rs1719271	*PLEKHO2-ANKDD1A* (intergenic)	15:65183800	G/A	European	56782	NA	3.41 (0.5)	1.05E-11	0.27	0.27	0.94 (0.92)	3.04E-01	3.76E-01	2.85 (0.44)	1.05E-10	[1]
rs6065	*GP1BA* (nonsynonymous)	17:4836380	T/C	European	64987	NA	4.19 (0.63)	2.92E-11	0.14	0.14	2.13 (1.15)	6.34E-02	1.07E-01	3.71 (0.55)	1.77E-11	[1]
rs397969	*ULK2-AKAP10* (intergenic)	17:19804246	C/T	European	60944	NA	2.13 (0.36)	2.32E-09	0.43	0.43	0.71 (0.8)	3.78E-01	4.49E-01	1.89 (0.33)	6.23E-09	[1]
rs559972	*TAOK1* (intronic)	17:27814495	T/C	European	53460	NA	3.26 (0.38)	3.30E-18	0.39	0.39	1.19 (0.81)	1.43E-01	2.22E-01	2.9 (0.34)	1.64E-17	[1]
rs708382	*FAM171A2* (5' upstream)	17:42442343	T/C	European	50036	NA	2.44 (0.43)	1.51E-08	0.37	0.63	1.81 (0.81)	2.55E-02	5.10E-02	2.3 (0.38)	1.50E-09	[1]
rs151361	*SLMO2* (intronic)	20:57614002	G/A	African	16388	0.26	4.49 (0.78)	9.44E-09	0.21	0.21	1.51 (0.98)	1.22E-01	1.22E-01	3.33 (0.61)	4.73E-08	[5]
rs1034566	*ARVCF* (intronic)	22:19984276	T/C	European	61469	NA	2.13 (0.38)	3.06E-08	0.21	0.21	1.79 (0.98)	6.87E-02	1.11E-01	2.08 (0.36)	5.73E-09	[1]

SNPs previously reported as genome-wide significant in GWA studies of platelet count that met or exceeded the generalization p-value are included. [a]Allele frequencies reported for 1000G CEU, not study population, by Soranzo, et al, 2009.,MAF = Minor Allele Frequency; CAF = Coded Allele Frequency; SE= Standard Error. Study population allele frequency not reported (NA) by Gieger, et al, 2011.

Table S4. Count of European, African, and Native American ancestral alleles vs. genotype rs117672662 on chromosome 14

	Ancestral Allele Count	**rs117672662 Genotype**		
		0	**1**	**2**
European	**0**	64	743	2,325
	1	0	625	4,797
	2	0	16	4,223
African	**0**	64	1,246	8,450
	1	0	138	2,338
	2	0	0	557
Native American	**0**	0	19	6,625
	1	0	757	3,445
	2	64	608	1,275

Table S5. Association of novel PLT variants from the HCHS/SOL discovery analysis with mean platelet volume (MPV) in a subset of the replication samples (N=4041)

				WHI			**Bio*Me***			**Meta-analysis**		
Annotated Gene(s) (location)	**Chromosome: Position (build 37-hg19)**	**rsID**	**Coded/ Alt. Allele on (+) strand**	**N**	**Beta (SE)**	**p-value**	**N**	**Beta (SE)**	**p-value**	**N**	**Beta (SE)**	**p-value**
ACTN1 (intronic)	chr14:69425467	rs117672662	T/C	1,187	0.46 (0.09)	6.5E-08	2,854	0.63 (0.09)	6.7E-12	4,041	0.54 (0.06)	3.9E-18
ZBTB9-BAK1 (intergenic)	chr6:33524820	rs62405954	T/C	1,187	-0.11 (0.08)	0.156	2,854	-0.10 (0.06)	0.112	4,041	-0.10 (0.05)	0.032
GABBR1-MOG (intergenic)	chr6:29608184	rs75140056	C/CAT	1,187	0.15 (0.06)	0.011	2,854	0.06 (0.03)	0.049	4,041	0.08 (0.03)	0.003
ETV7 (intronic)	chr6:36344980	rs9470264	G/A	1,187	-0.16 (0.03)	0.009	2,854	-0.24 (0.05)	4.5E-07	4,041	-0.18 (0.02)	1.9E-15
MEF2C (intronic)	chr5:88133921	rs144261491	C/T	1,187	0.12 (0.15)	0.415	NA	NA	NA	4,041	0.12 (0.15)	0.42

SE= Standard Error

Table S6. Datasets used for functional annotation and their sources.

Dataset[a]	**Project/Study**	**Download/Access resource**
All datasets of CD34-negative, CD41-positive, CD42-positive megakaryocyte cells	BLUEPRINT[7]	UCSC browser, BLUEPRINT trackhub
All K562 datasets	ENCODE[8]	UCSC browser, ENCODE Analysis trackhub and Integrated Regulation from ENCODE Tracks
GSM607949(GATA1 in megakaryocytes)	Tjissen et al, 2011[9]	CODEX,http://codex.stemcells.cam.ac.uk/
GSM607950(GATA2 in megakaryocytes)	Tjissen et al, 2011[9]	CODEX,http://codex.stemcells.cam.ac.uk/
GSM607951(RUNX1 in megakaryocytes)	Tjissen et al, 2011[9]	CODEX,http://codex.stemcells.cam.ac.uk/
GSM607952(FLI1 in megakaryocytes)	Tjissen et al, 2011[9]	CODEX,http://codex.stemcells.cam.ac.uk/
GSM607953(TAL1 in megakaryocytes)	Tjissen et al, 2011[9]	CODEX,http://codex.stemcells.cam.ac.uk/
GSE23730(SKNO-1_ERG)	Martens et al,2012[10]	BLOODCHIP, http://149.171.101.136/python/BloodChIP/
GSE23730(SKNO-1_FLI1)	Martens et al,2012[10]	BLOODCHIP, http://149.171.101.136/python/BloodChIP/
GSE23730(SKNO-1_RUNX1)	Martens et al,2012[10]	BLOODCHIP, http://149.171.101.136/python/BloodChIP/

[a] All datasets were mapped against Human Genome Build 37/hg19

Table S7. Significant Blood Browser[11] cis-eQTL for Results for PLT-associated SNPs and their LD partners (r^2 ≥0.4)

Gene	Index rsID	Proxy rsID	Chr: Position (build 37/hg19)	r^2	type[a]	p-value	Probe Center Position	Alleles on (+) strand	Allele Assessed	Overall Z-Score	HUGO Gene Name	FDR
ETV7	rs9470264	rs7758498	6:36344213	0.53	0	3.80E-18	6:36686912	G/A	A	-8.69	-	0
ETV7	rs9470264	rs7758498	6:36344213	0.53	0	6.50E-07	6:36570090	G/A	A	4.98	*STK38*	0
ETV7	rs9470264	rs7758498	6:36344213	0.53	0	1.10E-06	6:36565873	G/A	A	-4.87	*KCTD20*	0
ETV7	rs9470264	rs7758498	6:36344213	0.53	0	2.10E-06	6:36678715	G/A	A	-4.75	*SFRS3*	0.001
ETV7	rs9470264	rs1998266	6:36358289	0.58	2	3.10E-28	6:36686912	C/T	T	-11.02	-	0
ETV7	rs9470264	rs1998266	6:36358289	0.58	2	2.70E-08	6:36678715	C/T	T	-5.56	*SFRS3*	0
ETV7	rs9470264	rs1998266	6:36358289	0.58	2	1.70E-07	6:36570090	C/T	T	5.23	*STK38*	0
ETV7	rs9470264	rs4713971	6:36369786	0.40	0	2.60E-23	6:36686912	G/C	G	-9.95	-	0
ETV7	rs9470264	rs4713971	6:36369786	0.40	0	3.30E-08	6:36678715	G/C	G	-5.53	*SFRS3*	0
ETV7	rs9470264	rs4713971	6:36369786	0.40	0	3.10E-07	6:36570090	G/C	G	5.12	*STK38*	0
ETV7	rs9470264	rs941816	6:36375304	0.40	2	9.60E-24	6:36686912	G/A	G	-10.05	-	0
ETV7	rs9470264	rs941816	6:36375304	0.40	2	4.00E-08	6:36678715	G/A	G	-5.49	*SFRS3*	0
ETV7	rs9470264	rs941816	6:36375304	0.40	2	3.00E-07	6:36570090	G/A	G	5.12	*STK38*	0
ETV7	rs9470264	rs6457915	6:36380644	0.40	0	3.30E-08	6:36678715	T/C	C	-5.52	*SFRS3*	0
ETV7	rs9470264	rs6457915	6:36380644	0.40	0	2.10E-23	6:36686912	T/C	C	-9.97	-	0
ETV7	rs9470264	rs6457915	6:36380644	0.40	0	2.50E-07	6:36570090	T/C	C	5.16	*STK38*	0
ETV7	rs9470264	rs4713975	6:36395761	0.59	2	2.10E-34	6:36686912	G/A	A	-12.23	-	0
ETV7	rs9470264	rs4713975	6:36395761	0.59	2	1.50E-08	6:36565873	G/A	A	-5.67	*KCTD20*	0
ETV7	rs9470264	rs4713975	6:36395761	0.59	2	1.10E-08	6:36570090	G/A	A	5.72	*STK38*	0
ETV7	rs9470264	rs4713975	6:36395761	0.59	2	4.60E-08	6:36678715	G/A	A	-5.47	*SFRS3*	0
ETV7	rs9470264	rs1744653	6:36397688	0.46	0	6.50E-11	6:36678715	G/A	A	-6.53	*SFRS3*	0
ETV7	rs9470264	rs1744653	6:36397688	0.46	0	8.00E-24	6:36686912	G/A	A	-10.06	-	0
ETV7	rs9470264	rs1744653	6:36397688	0.46	0	2.40E-05	6:36570090	G/A	A	4.23	*STK38*	0.011
ETV7	rs9470264	rs7741260	6:36399120	0.46	2	6.90E-24	6:36686912	C/T	T	-10.08	-	0
ETV7	rs9470264	rs7741260	6:36399120	0.46	2	5.40E-11	6:36678715	C/T	T	-6.56	*SFRS3*	0
ETV7	rs9470264	rs7741260	6:36399120	0.46	2	2.40E-05	6:36570090	C/T	T	4.23	*STK38*	0.011
ETV7	rs9470264	rs16888605	6:36433408	0.57	0	3.50E-09	6:36565873	A/G	G	-5.9	*KCTD20*	0
ETV7	rs9470264	rs16888605	6:36433408	0.57	0	1.40E-35	6:36686912	A/G	G	-12.45	-	0
ETV7	rs9470264	rs16888605	6:36433408	0.57	0	9.40E-09	6:36678715	A/G	G	-5.74	*SFRS3*	0
ETV7	rs9470264	rs16888605	6:36433408	0.57	0	2.80E-09	6:36570090	A/G	G	5.94	*STK38*	0
ETV7	rs9470264	rs4713978	6:36466787	0.56	2	1.20E-08	6:36678715	C/A	A	-5.7	*SFRS3*	0
ETV7	rs9470264	rs4713978	6:36466787	0.56	2	1.40E-09	6:36570090	C/A	A	6.06	*STK38*	0
ETV7	rs9470264	rs4713978	6:36466787	0.56	2	1.60E-36	6:36686912	C/A	A	-12.62	-	0
ETV7	rs9470264	rs4713978	6:36466787	0.56	2	7.40E-10	6:36565873	C/A	A	-6.16	*KCTD20*	0
GABBR1-MOG	rs75140056	rs29273	6:29610989	0.45	2	2.10E-09	6:29811988	G/C	C	5.99	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs29273	6:29610989	0.45	2	3.40E-21	6:29906646	G/C	C	9.45	*HLA-G*	0
GABBR1-MOG	rs75140056	rs29273	6:29610989	0.45	2	1.10E-48	6:29800135	G/C	C	-14.66	*HLA-F*	0
GABBR1-MOG	rs75140056	rs9257928	6:29613218	0.42	0	3.20E-35	6:29800135	C/T	T	-12.38	*HLA-F*	0
GABBR1-MOG	rs75140056	rs9257928	6:29613218	0.42	0	4.60E-10	6:29811988	C/T	T	6.23	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs9257928	6:29613218	0.42	0	1.40E-09	6:29906646	C/T	T	6.06	*HLA-G*	0
GABBR1-MOG	rs75140056	rs29269	6:29617747	0.45	2	1.10E-48	6:29800135	C/T	T	-14.67	*HLA-F*	0
GABBR1-MOG	rs75140056	rs29269	6:29617747	0.45	2	1.60E-09	6:29811988	C/T	T	6.04	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs29269	6:29617747	0.45	2	3.70E-21	6:29906646	C/T	T	9.44	*HLA-G*	0
GABBR1-MOG	rs75140056	rs29231	6:29618525	0.44	2	2.40E-09	6:29811988	C/T	T	5.97	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs29231	6:29618525	0.44	2	1.10E-46	6:29800135	C/T	T	-14.35	*HLA-F*	0
GABBR1-MOG	rs75140056	rs29231	6:29618525	0.44	2	1.80E-20	6:29906646	C/T	T	9.28	*HLA-G*	0
GABBR1-MOG	rs75140056	rs2535246	6:29636409	0.42	2	3.40E-10	6:29811988	T/G	G	6.28	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs2535246	6:29636409	0.42	2	1.20E-20	6:29906646	T/G	G	9.32	*HLA-G*	0

GABBR1-MOG	rs75140056	rs2535246	6:29636409	0.42	2	3.40E-47	6:29800135	T/G	G	-14.43	*HLA-F*	0
GABBR1-MOG	rs75140056	rs2535246	6:29636409	0.42	2	3.60E-05	6:29783657	T/G	G	4.13	-	0.016
GABBR1-MOG	rs75140056	rs1122947	6:29638434	0.42	2	2.70E-47	6:29800135	A/G	G	-14.44	*HLA-F*	0
GABBR1-MOG	rs75140056	rs1122947	6:29638434	0.42	2	3.40E-10	6:29811988	A/G	G	6.28	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs1122947	6:29638434	0.42	2	1.00E-20	6:29906646	A/G	G	9.33	*HLA-G*	0
GABBR1-MOG	rs75140056	rs1122947	6:29638434	0.42	2	3.60E-05	6:29783657	A/G	G	4.13	-	0.016
GABBR1-MOG	rs75140056	rs2747453	6:29654943	0.44	2	1.40E-49	6:29800135	T/C	C	-14.8	*HLA-F*	0
GABBR1-MOG	rs75140056	rs2747453	6:29654943	0.44	2	1.40E-22	6:29906646	T/C	C	9.78	*HLA-G*	0
GABBR1-MOG	rs75140056	rs2747453	6:29654943	0.44	2	1.20E-08	6:29811988	T/C	C	5.7	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs3129090	6:29664131	0.44	2	7.60E-44	6:29800135	C/T	T	-13.89	*HLA-F*	0
GABBR1-MOG	rs75140056	rs3129090	6:29664131	0.44	2	2.90E-09	6:29811988	C/T	T	5.94	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs3129090	6:29664131	0.44	2	8.50E-22	6:29906646	C/T	T	9.59	*HLA-G*	0
GABBR1-MOG	rs75140056	rs3131879	6:29665458	0.43	0	2.40E-09	6:29811988	A/C	C	5.97	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs3131879	6:29665458	0.43	0	1.30E-22	6:29906646	A/C	C	9.78	*HLA-G*	0
GABBR1-MOG	rs75140056	rs3131879	6:29665458	0.43	0	1.00E-41	6:29800135	A/C	C	-13.53	*HLA-F*	0
GABBR1-MOG	rs75140056	rs9258102	6:29668913	0.43	2	5.40E-22	6:29906646	T/C	C	9.64	*HLA-G*	0
GABBR1-MOG	rs75140056	rs9258102	6:29668913	0.43	2	4.70E-44	6:29800135	T/C	C	-13.92	*HLA-F*	0
GABBR1-MOG	rs75140056	rs9258102	6:29668913	0.43	2	2.80E-09	6:29811988	T/C	C	5.94	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs9258114	6:29669640	0.43	2	7.10E-09	6:29811988	C/A	A	5.79	*AL645939.6-3*	0
GABBR1-MOG	rs75140056	rs9258114	6:29669640	0.43	2	1.10E-62	6:29800135	C/A	A	-16.71	*HLA-F*	0
GABBR1-MOG	rs75140056	rs9258114	6:29669640	0.43	2	8.60E-19	6:29906646	C/A	A	8.85	*HLA-G*	0
GABBR1-MOG	rs75140056	rs6456993	6:29670536	0.43	0	1.70E-21	6:29906646	G/A	A	9.52	*HLA-G*	0
GABBR1-MOG	rs75140056	rs6456993	6:29670536	0.43	0	7.20E-45	6:29800135	G/A	A	-14.05	*HLA-F*	0
GABBR1-MOG	rs75140056	rs6456993	6:29670536	0.43	0	8.60E-10	6:29811988	G/A	A	6.13	*AL645939.6-3*	0
BAK1	rs62405954	rs12206050	6:33564296	0.46	0	3.18E-05	6:33493262	A/T	T	4.16	*CUTA*	0.014
BAK1	rs62405954	rs12206050	6:33564296	0.46	0	3.88E-12	6:33492459	A/T	T	6.94	*CUTA*	0
BAK1	rs62405954	rs12664430	6:33272677	0.62	2	4.59E-09	6:33162754	C/T	T	-5.86	*HLA-DPB1*	0
BAK1	rs62405954	rs12664430	6:33272677	0.62	2	2.19E-04	6:33533115	C/T	T	3.7	*SYNGAP1,ZBTB9*	0.078
BAK1	rs62405954	rs12664430	6:33272677	0.62	2	3.88E-08	6:33354286	C/T	T	-5.5	*B3GALT4*	0
BAK1	rs62405954	rs12664430	6:33272677	0.62	2	1.02E-06	6:33375735	C/T	T	4.89	*TAPBP*	3.02E-04
BAK1	rs62405954	rs12664430	6:33272677	0.62	2	3.67E-04	6:33379629	C/T	T	3.56	*TAPBP*	0.117
BAK1	rs62405954	rs12664430	6:33272677	0.62	2	3.47E-03	6:33492459	C/T	T	2.92	*CUTA*	0.496
BAK1	rs62405954	rs3846855	6:33555877	0.47	0	1.48E-10	6:33492459	G/A	A	6.41	*CUTA*	0
BAK1	rs62405954	rs3846855	6:33555877	0.47	0	1.61E-05	6:33493262	G/A	A	4.31	*CUTA*	0.007
BAK1	rs62405954	rs5745568	6:33548394	0.46	2	1.89E-08	6:33492459	G/T	T	5.62	*CUTA*	0
BAK1	rs62405954	rs5745568	6:33548394	0.46	2	5.95E-05	6:33493262	G/T	T	4.01	*CUTA*	0.025
BAK1	rs62405954	rs9380365	6:33472317	0.42	2	5.06E-10	6:33354286	T/A	A	-6.22	*B3GALT4*	0
BAK1	rs62405954	rs9380365	6:33472317	0.42	2	1.95E-07	6:33491946	T/A	A	5.2	*PHF1*	6.31E-05
BAK1	rs62405954	rs9380365	6:33472317	0.42	2	7.90E-06	6:33533115	T/A	A	4.47	*SYNGAP1,ZBTB9*	0.004
BAK1	rs62405954	rs9380365	6:33472317	0.42	2	7.41E-04	6:33493262	T/A	A	3.37	*CUTA*	0.198
BAK1	rs62405954	rs9380365	6:33472317	0.42	2	5.22E-17	6:33375735	T/A	A	8.38	*TAPBP*	0
BAK1	rs62405954	rs9380365	6:33472317	0.42	2	1.95E-07	6:33491946	T/A	A	5.2	*PHF1*	6.31E-05
BAK1	rs62405954	rs9380365	6:33472317	0.42	2	7.90E-06	6:33533115	T/A	A	4.47	*SYNGAP1,ZBTB9*	0.004
BAK1	rs62405954	rs9380365	6:33472317	0.42	2	7.41E-04	6:33493262	T/A	A	3.37	*CUTA*	0.198
BAK1	rs62405954	rs9380365	6:33472317	0.42	2	5.22E-17	6:33375735	T/A	A	8.38	*TAPBP*	0

[a] Type: Imputed=0, genotyped=2

Table S8. Summary of findings from the functional annotation of the 5 novel SNPs and LD partners ($r^2 \geq 0.5$) identified in HCHS/SOL

Index SNP rsID	**fSNP[*] rsID**	**r^2**	**fSNP p-value**	**fSNP Beta (SE)**	**Nearest Genes to fSNP**	**coded/ alternate fSNP allele on (+) strand**	**fSNP CAF**	**fSNP oevar[a]**	**1000 genomes phase III coded allele frequency**						**Description of Findings**
									African	**European**	**Ad Mixed American**	**South Asian**	**East Asian**	**All**	
rs75140056	rs29269	0.5	1.23E-06	0.131 (0.029)	*GABBR1*	C/T	0.77	1.0	0.86	0.81	0.8	0.86	0.95	0.86	rs29269 lies in a putative active *GABBR1* promoter in megakaryocytes, also overlaps several transcription factor ChIP-Seq peaks including TBP and ETS1 in K562 cells. Also overlaps RNA PolI ChIP-Seq Peak
rs62405954	rs1002011	0.6	7.92E-06	-0.186 (0.044)	*VPS52*	G/A	0.89	1.0	1.00	1.00	0.88	1.00	1.00	0.98	Proxy SNP rs1002011 lies within a putative enhancer overlapping the 5' UTR of the *VPS52* gene. It also lies within a DNase1 hypersensitive peak and CFOS ChIP-Seq peak in HUVEC cells.
rs9470264	rs80331350	0.8	2.66E-05	-0.144 (0.034)	*PXT1*	T/C	0.81	1.1	0.87	0.99	0.78	0.99	0.87	0.9	rs80331350 lies in a putative megakaryocyte enhancer in *PXT1* intron. The putative enhancer element overlaps GATA1 ChIP-Seq peak in peripheral blood-derived erythroblasts (PBDE) cells
rs9470264	rs2273883	0.8	2.18E-05	-0.170 (0.035)	*KCTD20*	C/A	0.82	1.1	0.99	0.99	0.79	0.99	0.87	0.94	rs227883 (r2=0.8) lies within RUNX1 bound putative active *KCTD20* promoter in megakaryocytes. The putative promoter element overlaps ChIP-Seq peaks of promoter binding proteins RNA polymerase II, TBP, P300 and key megakaryocyte regulators including GATA1, GATA2, ETS1 and GABPA in K562 cells
rs9470264	rs113553570	0.8	1.05E-06	-0.168 (0.035)	*STK38*	G/A	0.82	1.1	0.89	0.99	0.78	0.99	0.87	0.91	proxy SNP rs113553570 lies in a putative enhancer in STK38 intron
rs9470264	rs2239541	0.8	1.11E-06	-0.168 (0.035)	*STK38*	G/A	0.82	1.1	0.89	0.99	0.78	0.99	0.87	0.91	proxy SNP rs2239541 (r2=0.8), which lies in a putative megakaryocyte enhancer in STK38 intron
rs9470264	rs201891379	0.8	1.11E-06	-0.172 (0.034)	*STK38*	ACAATACAATTAACTAAAC/A	0.81	1.1	0.87	0.99	0.8	0.99	0.87	0.91	proxy indel rs201891379 (r2=0.8), which lies in a putative promoter element upstream of STK38 gene. The putative enhancer element overlaps ChIP-Seq peaks of GABP and IRF1 in K562 cells
rs117672662	rs117672662	1.0	4.88E-07	0.609 (0.055)	*ACTN1*	T/C	0.94	1.0	1.00	1.00	0.93	1.00	1.00	0.99	rs117672662 lies in a megakaryocyte-specific putative enhancer containing a RUNX1 consensus sequence and overlaps ChIP-Seq peaks of key megakaryocyte regulators ERG, FLI1 and RUNX1 in SKNO-1 cells (an acute myeloid leukemia cell line)
rs144261491	rs200572016	0.8	8.65E-29	0.393 (0.081)	*MEF2C-AS1*	TGA/T	0.97	0.9	1.00	1.00	0.96	1.00	1.00	0.99	indel rs200572016 lies in a putative megakaryocyte-specific enhancer in *MEF2C-AS1* intron; this enhancer element is DNAse accessible in K562 cells and overlaps ChIP-Seq peaks of GATA2, TAL1 and P300 in these cells

Abbreviations: fSNP = Predicted functional single nucleotide polymorphism; [a] = ratio of the variances of the observed and the estimated allele counts; CAF= Coded Allele Frequency

Table S9. Summary of *in silico* functional prediction algorithm results for significant variants and their LD partners

Locus	**rsID**	**Chr:Position**	**r^2 with HCHS/SOL lead SNP**	**CADD[12] C-Score**	**GWAVA [13] Score**	**RegulomeDB [14] Score**	**deltaSVM[15] Score for K562 cell line**	**Prioritized functional variant**
ACTN1	rs117672662	14:69425467	Lead	0.56	0.32	4	9.84	fSNP
ACTN1	rs140754108	14:69407222	0.84	6.53	0.26	2b	0.69	-
ACTN1	rs12431622	14:69415032	0.81	2.93	0.32	5	-1.45	-
GABBR1-MOG	rs75140056 (indel)	6:29608184	Lead	7.06	NA	NA	NA	-
GABBR1-MOG	rs3131857	6:29606794	> 0.99	1.38	0.2	6	-0.46	-
GABBR1-MOG	rs4713235	6:29670478	0.60	4.29	0.34	2a	1.13	-
GABBR1-MOG	rs3131875	6:29666111	0.50	16.75	0.09	5	-2.03	-
GABBR1-MOG	NA (indel)	6:29608870	0.50	NA	NA	NA	NA	-
GABBR1-MOG	rs29269	6:29617747	0.50	7.00	0.71	4	-4.58	fSNP
ETV7	rs9470264	6:36344980	Lead	0.13	0.14	6	2.04	-
ETV7	rs3778028	6:36349666	0.94	5.87	0.37	3a	-1.62	-
ETV7	rs1885206	6:36351095	0.93	3.35	0.42	2b	-0.37	-
ETV7	rs76676074	6:36361063	0.90	8.84	0.21	5	0.35	-
ETV7	rs111654791	6:36376021	0.91	0.51	NA	No Data	-0.15	-
ETV7	rs80047437	6:36376369	0.91	4.63	0.11	6	0.23	-
ETV7	rs112394821	6:36379855	0.91	0.03	0.02	No Data	-1.88	-
ETV7	rs113849189	6:36383209	0.91	2.27	0.03	No Data	-0.56	-
ETV7	rs79235676	6:36388019	0.91	8.38	0.1	6	-1.55	-
ETV7	rs74555455	6:36389418	0.91	3.58	0.1	6	-2.95	-
ETV7	rs80331350	6:36391236	0.91	13.53	0.07	2b	1.07	fSNP
ETV7	rs150014990	6:36392403	0.90	0.72	0.31	No Data	1.29	-
ETV7	rs200860324	6:36403871	0.87	3.22	NA	6	-3.31	-
ETV7	rs12526415	6:36403874	0.84	0.33	0.11	6	1.75	-
ETV7	rs113585688	6:36405876	0.88	0.67	0.29	No Data	-2.42	-
ETV7	rs4711451	6:36410308	0.84	2.71	0.82	4	4.43	-
ETV7	rs4713976	6:36417410	0.84	11.93	0.05	5	0.64	-
ETV7	rs4713977	6:36424664	0.81	2.54	0.08	5	2.39	-
ETV7	rs79927326	6:36434643	0.81	0.81	0.09	5	0.07	-
ETV7	rs2273882	6:36437713	0.81	0.96	0.16	No Data	3.11	-
ETV7	rs941974	6:36438385	0.81	0.96	0.03	6	-5.21	-
ETV7	rs79328581	6:36454464	0.81	5.45	0.23	5	-1.02	-
ETV7	rs75297867	6:36461335	0.81	0.01	0.19	5	1.58	-
ETV7	rs4236051	6:36469821	0.81	0.97	0.09	5	-0.88	-
ETV7	rs2267930	6:36472788	0.81	4.91	0.05	5	-0.76	-
ETV7	rs75144098	6:36475146	0.81	9.50	0.15	5	3.97	-
ETV7	rs111800900	6:36480859	0.81	7.86	0.1	No Data	2.51	-
ETV7	rs112845031	6:36486403	0.80	0.14	0.08	No Data	1.94	-
ETV7	rs75112107	6:36492839	0.80	4.25	0.1	5	0.45	-
ETV7	rs113553570	6:36493878	0.80	0.17	0.19	6	0.12	fSNP
ETV7	rs223954	6:36494053	0.80	15.13	0.5	5	-1.94	fSNP
ETV7	rs2273883	6:88133921	0.76	10.32	0.94	1f	-0.14	fSNP
MEF2C	rs144261491	5:88133921	Lead	2.37	0.18	NA	0.71	-
MEF2C	rs151169192	5:88109756	> 0.99	5.25	0.28	4	-7.26	-
MEF2C	rs185717407	5:88171283	0.99	9.77	0.4	3a	-0.18	-
MEF2C	rs187320873	5:88172872	0.99	13.47	0.61	4	3.84	-
MEF2C	rs184480102	5:87997100	0.75	3.49	0.22	6	0.22	-
MEF2C	rs200572016	5:88220439	0.6	15.59	NA	3a	-0.38	fSNP
BAK1	rs141400340	6:33577487	Lead	4.07	0.6	2b	-0.84	fSNP
BAK1	rs62405954	6:33524820	Lead	9.19	0.30	4	-3.11	-
BAK1	rs186384986	6:33467086	0.91	3.80	0.01	6	0.19	-
BAK1	rs12526020	6:33467084	0.91	0.53	0.01	6	-0.28	-
BAK1	rs12664430	6:33272677	0.62	12.65	0.45	No Data	1.66	-
BAK1	rs186246149	6:33253646	0.59	4.12	0.03	No Data	-1.62	-
BAK1	rs1002011	6:33218237	0.56	3.33	0.94	4	0.055	fSNP
BAK1	rs144043427	6:33353011	0.53	NA	NA	6	NA	-
BAK1	rs5745564	6:33548696	0.50	NA	NA	5	NA	-
BAK1	rs75080135	6:33552707	0.48	0.79	0.65	5	-3.05	-

BAK1	rs3846855	6:33555877	0.47	2.28	0.13	6	-1.88	-
BAK1	rs5745568	6:33548394	0.46	NA	0.86	1b	-0.63	-
BAK1	rs9357161	6:33549403	0.46	3.66	0.36	No Data	0.74	-
BAK1	rs12206050	6:33564296	0.46	8.33	0.17	6	-0.27	-
BAK1	rs72882008	6:33572840	0.45	1.92	0.06	4	2.37	-
BAK1	rs12214883	6:33513968	0.45	0.074	0.10	6	-2.15	-
BAK1	rs11968218	6:33518845	0.45	4.17	0.05	5	-1.46	-
BAK1	rs9380365	6:33472317	0.42	5.31	0.08	5	0	-
BAK1	rs35144104	6:33463961	0.41	3.33	0.01	6	-2.87	-

Abbreviation: fSNP=predicted functional single nucleotide polymorphism

Table S10. Results from cis-eQTL analysis of *ACTN1* rs117672662 in 1,457 Native Americans

Chr:Position	**Illumina ID**	**Transcript**	**Beta[a] (Standard Error)**	**P-value**	**SNP Number[b]**
14:66460685	ILMN_1723607	GPHN	-0.02 (0.08)	8.4E-01	1
14:66871825	ILMN_1750689	MPP5	-0.04 (0.07)	6.0-01	0
14:66874720	ILMN_1797310	ATP6V1D	0.04 (0.09)	6.2E-01	0
14:66922877	ILMN_1739821	EIF2S1	0.12 (0.08)	1.4E-01	0
14:66923813	ILMN_1811470	PLEK2	-0.01 (0.07)	8.8E-01	1
14:67126397	ILMN_1798395	PIGH	0.10 (0.07)	1.8E-01	0
14:67192886	ILMN_1693136	VTI1B	-0.08 (0.07)	2.7E-01	1
14:67213499	ILMN_2128741	RDH11	-0.07 (0.08)	3.6E-01	0
14:67213871	ILMN_1768719	RDH11	-0.07 (0.07)	3.1E-01	0
14:67283267	ILMN_1798061	ZFYVE26	0.13 (0.07)	6.9E-02	0
14:68324290	ILMN_1675448	ZFP36L1	-0.01 (0.07)	8.8E-01	0
14:68411163	ILMN_2232177	ACTN1	-0.05 (0.09)	5.6E-01	1
14:68587437	ILMN_1735402	WDR22	-0.04 (0.07)	5.7E-01	0
14:68778515	ILMN_1771689	EXD2	0.05 (0.07)	5.2E-01	0
14:68884396	ILMN_1799903	GALNTL1	-0.07 (0.07)	3.0E-01	1
14:68916937	ILMN_1781795	ERH	0.09 (0.07)	2.0E-01	0
14:68996734	ILMN_1756878	SLC39A9	0.01 (0.08)	9.2E-01	0
14:69251274	ILMN_2226917	KIAA0247	0.11 (0.07)	1.2E-01	1
14:69307877	ILMN_1761996	SFRS5	0.16 (0.07)	1.8E-02	0
14:69308064	ILMN_2378868	SFRS5	0.11 (0.07)	9.4E-02	1
14:69862844	ILMN_1706305	COX16	0.02 (0.07)	7.7E-01	0
14:69908650	ILMN_1697793	SYNJ2BP	-0.03 (0.08)	6.9E-01	0
14:70120755	ILMN_1654543	MED6	0.06 (0.09)	5.2E-01	0
14:70360380	ILMN_1900513	AW449499	-0.06 (0.07)	4.3E-01	0
14:70443342	ILMN_1882112	BX101252	-0.14 (0.07)	4.4E-02	1
14:70646545	ILMN_1740010	PCNX	-0.07 (0.07)	3.4E-01	0
14:70934827	ILMN_1715396	SNORD56B	-0.13 (0.07)	6.1E-02	0

[a] = Standard Deviation per copy of the C allele

[b]= Number of SNPs in probe

Table S12. Imputation scores for lead discovery variants and variants in high linkage disequilibrium (r^2>0.5)

Locus_name	rsID	chromosome	position	Type[a]	r^2 with the lead	oevar	Info[b]
ZBTB9-BAK1	rs62405954	6	33524820	2	1	1.06	1.00
ZBTB9-BAK1	rs186384986	6	33467086	0	0.9	1.03	0.97
ZBTB9-BAK1	rs12526020	6	33467084	0	0.9	1.03	0.97
ZBTB9-BAK1	rs12664430	6	33272677	2	0.6	1.04	1.00
ZBTB9-BAK1	rs186246149	6	33253646	0	0.6	1.07	0.99
ZBTB9-BAK1	rs147668544	6	33218237	0	0.6	0.98	0.90
ZBTB9-BAK1	rs144043427	6	33353011	0	0.5	0.99	0.97
ZBTB9-BAK1	rs5745564	6	33548696	0	0.5	1.05	1.00
ZBTB9-BAK1	rs75080135	6	33552707	0	0.5	1.04	0.99
ZBTB9-BAK1	rs3846855	6	33555877	0	0.5	1.04	0.99
ZBTB9-BAK1	rs5745568	6	33548394	2	0.5	1.04	1.00
ZBTB9-BAK1	rs9357161	6	33549403	0	0.5	1.03	1.00
ZBTB9-BAK1	rs12206050	6	33564296	0	0.5	1.04	1.00
ZBTB9-BAK1	rs72882008	6	33572840	0	0.5	1.01	0.98
MEF2C-AS1	rs144261491	5	88133921	0	1	0.87	0.84
MEF2C-AS1	rs151169192	5	88109756	0	1	0.87	0.83
MEF2C-AS1	rs185717407	5	88171283	0	1	0.87	0.84
MEF2C-AS1	rs187320873	5	88172872	0	1	0.87	0.84
MEF2C-AS1	rs184480102	5	87997100	0	0.7	0.71	0.68
MEF2C-AS1	rs200572016	5	88220439	0	0.7	0.89	0.86
MEF2C-AS1	rs184944447	5	87817728	0	0.7	0.84	0.80
MEF2C-AS1	rs188832904	5	87658662	0	0.5	0.82	0.79
MEF2C-AS1	rs142862331	5	88015336	0	0.5	0.53	0.52
GABBR1-MOG	rs75140056	6	29608184	0	1	1.03	1.00
GABBR1-MOG	rs114178179	6	29606794	0	1	1.02	0.99
GABBR1-MOG	rs115621016	6	29670478	0	0.6	1.03	1.00
GABBR1-MOG	rs3131875	6	29666111	2	0.5	1.03	1.00
GABBR1-MOG	rs71946391	6	29608870	0	0.5	0.91	0.90
GABBR1-MOG	rs29269	6	29617747	2	0.5	1.01	1.00
ETV7	rs9470264	6	36344980	0	1	1.06	0.96
ETV7	rs3778028	6	36349666	0	1	1.09	0.99
ETV7	rs1885206	6	36351095	0	0.9	1.09	0.99
ETV7	rs113585688	6	36405876	0	0.8	1.12	1.00
ETV7	rs76676074	6	36361063	0	0.8	1.12	0.99
ETV7	rs113849189	6	36383209	0	0.8	1.12	1.00
ETV7	rs16888788	6	36521517	0	0.8	1.13	0.99
ETV7	rs4711451	6	36410308	0	0.8	1.12	1.00
ETV7	rs2273883	6	36410801	0	0.8	1.12	1.00
ETV7	rs111654791	6	36376021	0	0.8	1.12	1.00
ETV7	rs80047437	6	36376369	0	0.8	1.12	1.00
ETV7	rs4713977	6	36424664	0	0.8	1.12	1.00
ETV7	rs4713976	6	36417410	0	0.8	1.12	1.00
ETV7	rs112394821	6	36379855	0	0.8	1.12	1.00
ETV7	rs79328581	6	36454464	0	0.8	1.12	1.00
ETV7	rs79235676	6	36388019	0	0.8	1.12	1.00
ETV7	chr6:36388436:I	6	36388436	0	0.8	1.12	1.00
ETV7	rs74555455	6	36389418	0	0.8	1.12	1.00
ETV7	rs80331350	6	36391236	0	0.8	1.12	1.00
ETV7	rs150014990	6	36392403	0	0.8	1.12	1.00
ETV7	rs113005836	6	36519616	0	0.8	1.12	1.00
ETV7	rs79927326	6	36434643	0	0.8	1.12	1.00
ETV7	rs2273882	6	36437713	2	0.8	1.12	1.00
ETV7	rs941974	6	36438385	0	0.8	1.12	1.00
ETV7	rs75297867	6	36461335	0	0.8	1.12	1.00
ETV7	rs4236051	6	36469821	2	0.8	1.12	1.00
ETV7	rs2267930	6	36472788	0	0.8	1.12	1.00
ETV7	rs75144098	6	36475146	0	0.8	1.12	1.00
ETV7	rs113412960	6	36500799	0	0.8	1.12	1.00
ETV7	rs111800900	6	36480859	0	0.8	1.12	1.00
ETV7	rs3819759	6	36496277	0	0.8	1.12	1.00
ETV7	rs111666164	6	36498423	0	0.8	1.12	1.00

ETV7	rs112740031	6	36498559	0	0.8	1.12	1.00
ETV7	rs75112107	6	36492839	0	0.8	1.12	1.00
ETV7	rs113553570	6	36493878	0	0.8	1.12	1.00
ETV7	rs2239541	6	36494053	0	0.8	1.12	1.00
ETV7	rs201891379	6	36515576	0	0.8	1.11	0.99
ETV7	rs12526415	6	36403874	2	0.8	1.11	1.00
ETV7	rs200860324	6	36403871	0	0.8	1.10	0.99
ETV7	rs116957783	6	36524594	0	0.8	1.11	0.99
ETV7	rs112845031	6	36486403	0	0.8	1.12	1.00
ETV7	rs78413663	6	36520101	0	0.7	1.11	1.00
ETV7	rs76976387	6	36521363	0	0.7	1.11	1.00
ETV7	rs202237535	6	36438384	0	0.7	1.01	0.90
ETV7	rs4140594	6	36564240	0	0.7	1.09	0.99
ETV7	rs3756907	6	36563129	0	0.7	1.09	0.99
ETV7	rs149171383	6	36517137	0	0.7	0.96	0.87
ETV7	rs7747978	6	36525321	0	0.7	1.06	0.97
ETV7	rs7740345	6	36344329	0	0.6	0.92	0.84
ETV7	rs4711454	6	36555422	0	0.6	1.08	1.00
ETV7	rs3756906	6	36563812	0	0.6	1.08	1.00
ETV7	rs76964964	6	36559290	0	0.6	1.08	1.00
ETV7	chr6:36576246:D	6	36576246	0	0.6	1.08	1.00
ETV7	rs59108254	6	36576153	0	0.6	1.08	1.00
ETV7	rs60633269	6	36576414	2	0.6	1.08	1.00
ETV7	rs4713975	6	36395761	2	0.6	1.09	1.00
ETV7	rs7382195	6	36621000	0	0.6	1.12	0.99
ETV7	rs1998266	6	36358289	2	0.6	1.05	1.00
ETV7	rs111624705	6	36413945	0	0.6	1.09	1.00
ETV7	rs78373049	6	36421695	0	0.6	1.09	1.00
ETV7	rs76019396	6	36425227	0	0.6	1.09	1.00
ETV7	rs112542373	6	36416790	0	0.6	1.09	1.00
ETV7	rs4711455	6	36632458	0	0.6	1.13	1.00
ETV7	rs140429491	6	36422215	0	0.6	1.09	1.00
ETV7	rs4713998	6	36632610	2	0.6	1.13	1.00
ETV7	rs16888605	6	36433408	0	0.6	1.09	1.00
ETV7	rs77660021	6	36431499	0	0.6	1.09	1.00
ETV7	rs75776623	6	36477822	0	0.6	1.09	1.00
ETV7	rs41272166	6	36455838	2	0.6	1.09	1.00
ETV7	rs116413447	6	36479537	0	0.6	1.09	1.00
ETV7	rs4713978	6	36466787	2	0.6	1.09	1.00
ETV7	rs80032245	6	36492550	0	0.6	1.09	1.00
ETV7	rs77693176	6	36548128	0	0.6	1.07	0.99
ETV7	rs111747725	6	36509866	0	0.6	1.09	1.00
ETV7	rs12525802	6	36445288	0	0.6	1.08	1.00
ETV7	rs144398714	6	36346581	2	0.5	1.09	1.00
ETV7	rs138977532	6	36349802	2	0.5	1.09	1.00
ETV7	rs183032639	6	36517164	0	0.5	0.88	0.81
ETV7	rs7758498	6	36344213	0	0.5	0.87	0.81
ETV7	rs7776298	6	36548225	0	0.5	1.06	0.99
ETV7	rs78502475	6	36315211	0	0.5	1.07	0.93
ETV7	rs1744653	6	36397688	0	0.5	1.07	1.00
ETV7	rs7741260	6	36399120	2	0.5	1.07	1.00
ETV7	rs74693071	6	36298059	0	0.5	0.98	0.86
ACTN1	rs117672662	14	69425467	0	1	1.01	0.98
ACTN1	rs140754108	14	69407222	0	0.8	1.02	0.99
ACTN1	rs12431622	14	69415032	0	0.8	1.01	0.98
ACTN1	rs143493318	14	69369122	0	0.6	1.04	0.98
ACTN1	rs3784133	14	69364953	2	0.5	1.06	1.00
ACTN1	rs190190833	14	69350614	0	0.5	0.82	0.80
ACTN1	rs76041256	14	69401213	0	0.5	1.01	1.00

[1]0=SNP was imputed,2= SNP was genotyped; [b]a statistical information metric from IMPUTE2

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