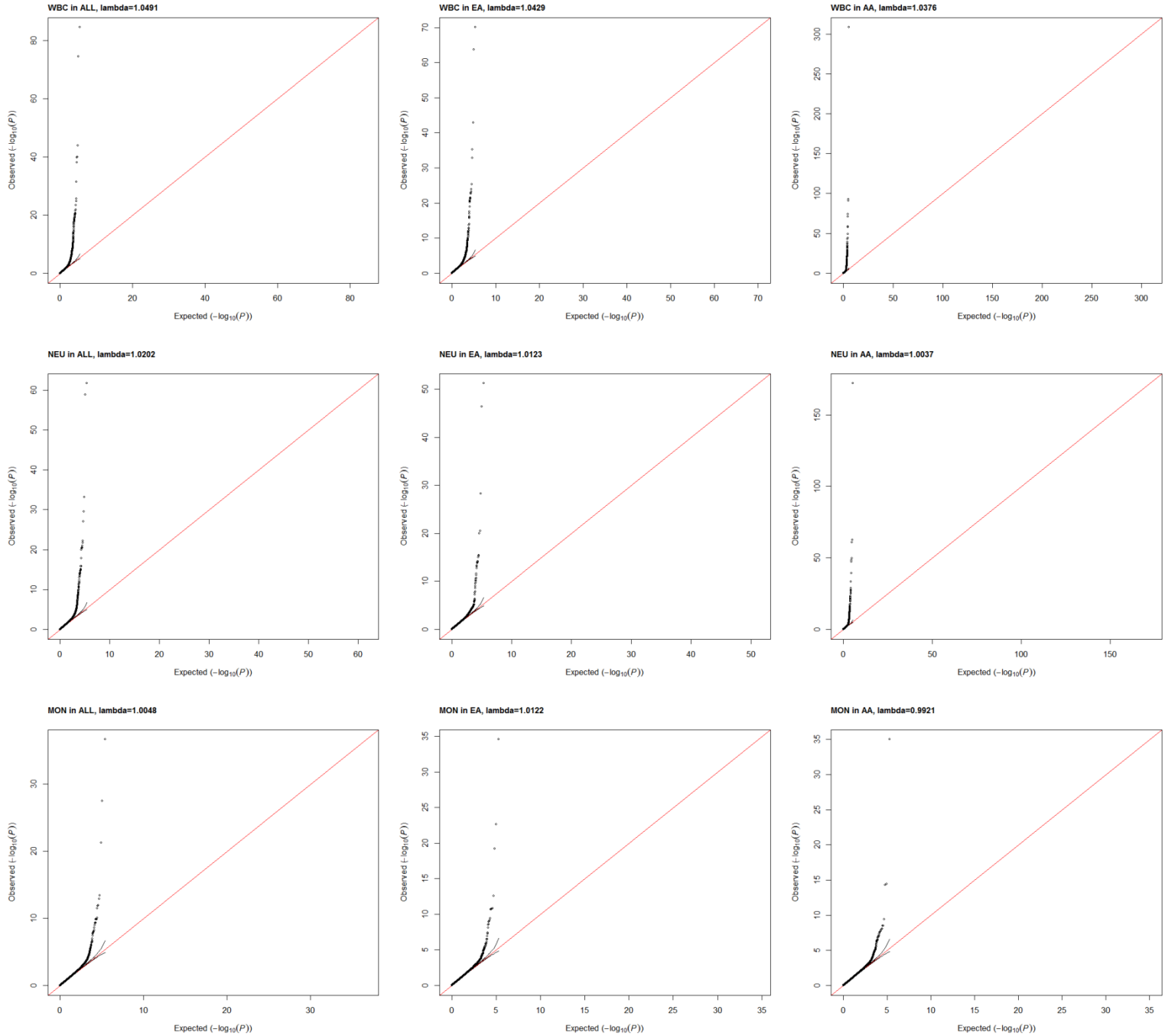
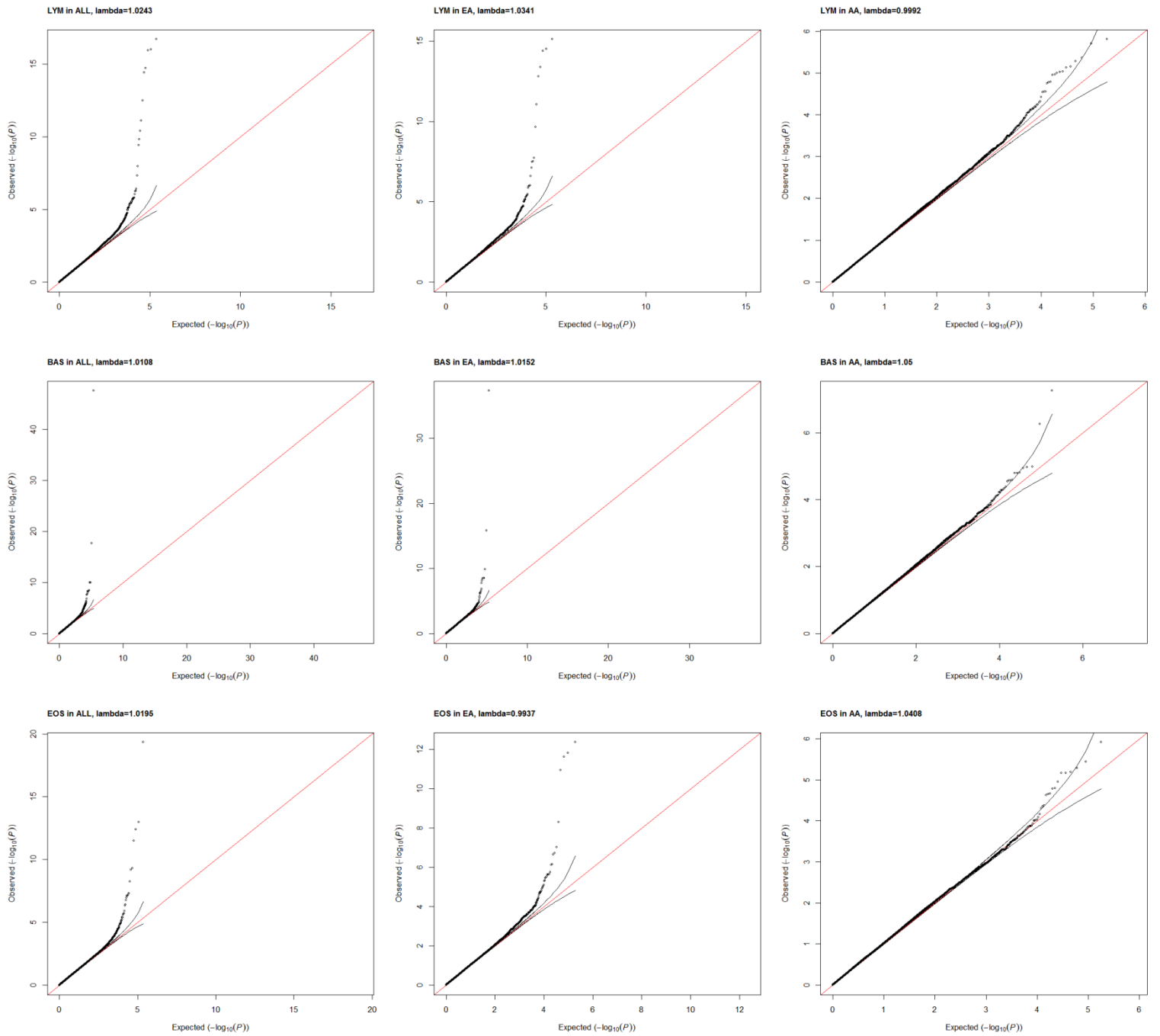


## Supplemental Figure

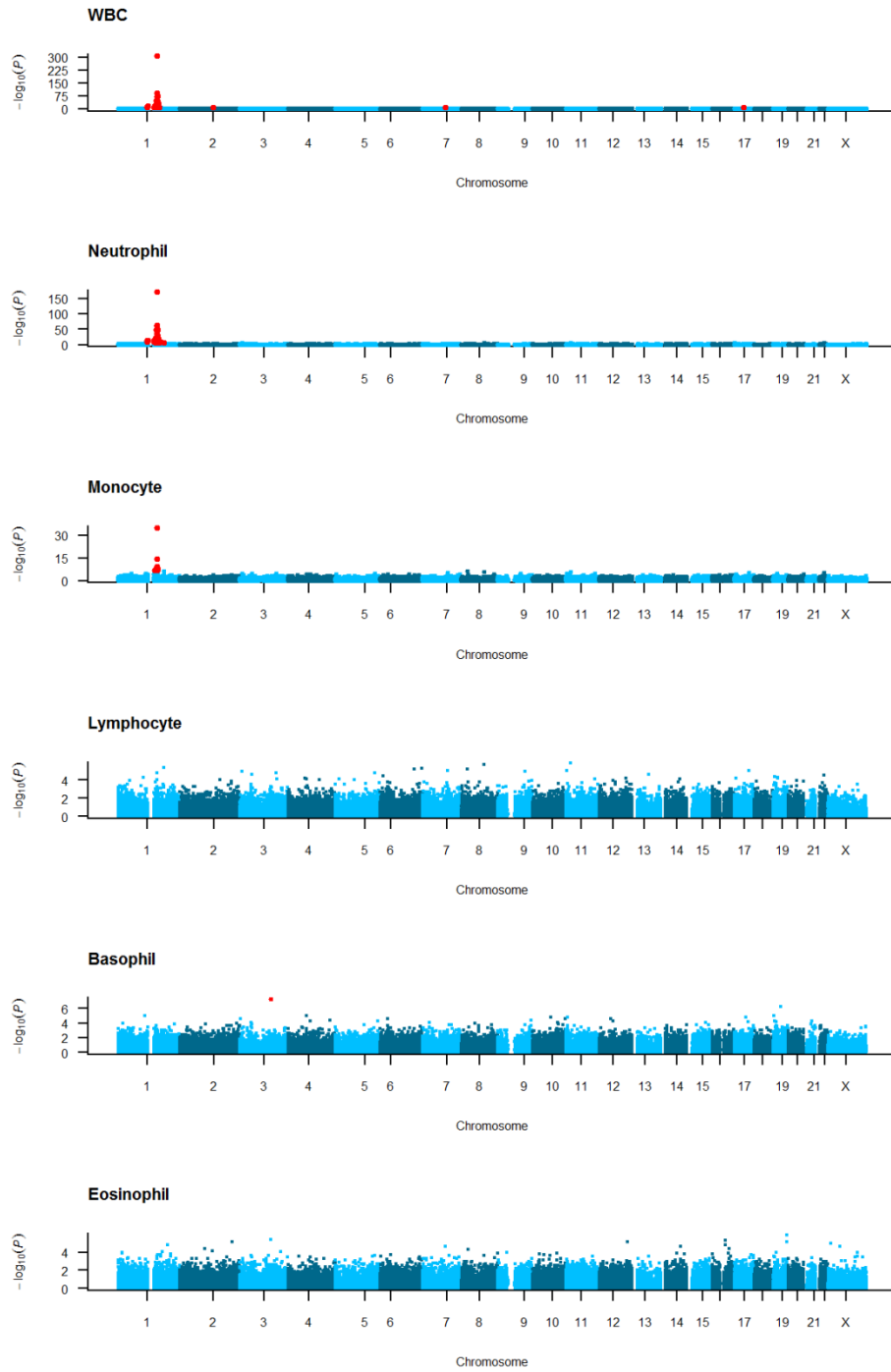
**Figure S1. Quantile-quantile plots of p-values of white blood cell traits.** Results of the three sets of discovery meta-analyses in combined all ancestries (ALL), European ancestry (EA), and African ancestry (AA) individuals are shown here. The combined all ancestry samples include Hispanic Americans, East Asians, and South Asians in addition to EAs and AAs.



**Figure S1. Continued**



**Figure S2. Manhattan plots of discovery p-values of white blood cell traits in African Americans**



## Supplemental Tables

See Table S1 and Table S2 in the accompanying Excel file.

Table S3. Sample size across ethnicities for white blood cell exome-wide association analysis

Study	Total WBC					Neutrophil					Monocyte			Lymphocyte			Basophil			Eosinophil					
	Ethnicity					Ethnicity					Ethnicity			Ethnicity			Ethnicity			Ethnicity					
	EA	AA	HA	EAS	SA	EA	AA	HA	EAS	SA	EA	AA	HA	EA	AA	HA	EA	AA	HA/HL	EA	AA	HA			
<b>Discovery</b>																									
AGES	2,955					2,954					2,954	368		2,954							2,954				
ARIC	10,345	2,821				6,792	368				6,792	368		6,792	368		6,792	368		6,792	368		6,792	368	
BIOME	1,043	2,328	3,319			636	1,981	2,688			10,209	1,981	2,688	636	1,981	2,688	636	1,981	2,688	636	1,981	2,688	636	1,981	2,688
BIOVU - I	21,276	1,921				10,208	909				636	910		10,218	911		14,903	1,357		14,903	1,357				
BIOVU - II		1,020					385					384			385										
CARDIA	2,110	1,946				2,110	1,942				2,095	1,928		2,110	1,942		1,637	1,350				1,955	1,762		
CHS	4,197	776																							
ECGUT	974					973					973			973			962					968			
FHS	5,610					2,314					2,314			2,314			2,314					2,314			
SOLID TIMI-52	8,025	198	874	254	116	8,026	198	874	251	116															
GSK-STABILITY	8,490	118	500	714	348	8,487	118	500	714	347															
HABC	1,251					1,251					1,251			1,251			1,251					1,251			
HANDLS		834					834					834			834			813					832		
JHS		2,039					2,027					2,026			2,028			1,898					1,989		
LBC1921	475					473					473			473											
LBC1936	963					963					963			963											
MESA	1,266	750	843			1,122	673	763			1,123	675	764	1,121	675	762	1,123	673	765	1,123	673	765	1,121	671	762
MHIBB	7,911					6,978					6,978			6,978			6,978					6,978			
REGARDS		5,030																							
RS	2,794													2,758											
SHIP	7,251					4,076					4,076			4,076			4,075					4,077			
WHI	21,660	3,469				3,488	684				3,488	684		3,488	684		3,467	676		3,467	676		3,471	679	
Total per ancestry	108,596	23,250	5,536	968	464	60,851	10,119	4,825	965	463	44,325	9,790	3,452	47,105	9,808	3,450	44,138	9,509	3,453	44,138	9,509	3,453	32,517	8,282	3,450
<b>Total per trait</b>					<b>138,814</b>																				
<b>Replication</b>																									
AIRWAVE	14,887					14,887					14,887			14,887			14,887					14,887			
BIOVU-Replication (EA)	1,987					888					888			888			905								
FINCAVAS	911					397					397			397			397					440			
GeneSTAR	1,023					894					894			937											
<b>Total per ancestry</b>	<b>18,808</b>					<b>17,066</b>					<b>17,066</b>			<b>17,109</b>			<b>16,189</b>					<b>15,327</b>			
Total per trait					18,808					17,066			17,066			17,109		16,189				15,327			
<b>Grand Total</b>					<b>157,622</b>					<b>94,289</b>			<b>74,633</b>			<b>77,472</b>		<b>73,289</b>				<b>59,576</b>			

Abbreviations: EA, European Ancestry; AA, African Ancestry; HA, Hispanic American; EAS, East Asian; SA, South Asian.

Table S4. Mean and standard deviations of white blood cell traits in participating cohorts of the Blood-Cell Consortium

Study	Age	% Female	Total WBC	Neutrophil	Monocyte	Lymphocyte	Basophil	Eosinophil
AIRWAVE	40.87 (9.03)	37.3	6.52 (1.71)	3.94 (1.34)	0.4 (0.18)	1.8 (0.53)	0.06 (0.04)	0.2 (0.12)
n	14887	5550	14887	14886	14887	14886	14865	14866
AGES	76.4 (5.5)	57.9	6.05 (1.81)	3.55 (1.30)	0.541 (0.0178)	1.74 (0.972)	0.0286 (0.0256)	0.207 (0.145)
n	2953	1711	2955	2954	2954	2954	2954	2954
ARIC-AA	56.5 (5.8)	62.8	5.6 (1.9)	3.1 (1.4)	0.3 (0.1)	2.0 (0.6)	0.1 (0.0)	0.1 (0.1)
n	2832	1779	2832	369	369	369	160	355
ARIC-EA	57.3 (5.7)	53	6.2 (2.0)	3.8 (1.4)	0.4 (0.2)	1.8 (0.7)	0.1 (0.0)	0.2 (0.1)
n	10347	5489	10346	6792	6792	6792	2351	3893
BioME-AA	57 (14)	38.6	6.6 (2.2)	3.8 (1.8)	0.5 (0.2)	2.0 (0.8)	0.0 (0.0)	0.2 (0.1)
n	2653	1024	2329	1966	1966	1966	1966	1966
BioME-EA	68 (11)	38.9	7.2 (2.9)	4.7 (2.4)	0.6 (0.2)	1.7 (1.6)	0.0 (0.0)	0.2 (0.1)
n	1090	424	1046	634	634	634	634	634
BioME-HA	61 (15)	62	7.4 (2.3)	4.6 (1.9)	0.6 (0.2)	2.0 (0.8)	0.0 (0.0)	0.2 (0.2)
n	3640	2258	3319	2660	2660	2660	2660	2660
BioVU-I-EA	56.42 (16.82)	54.8	7.87 (5.34)	5.03 (3.16)	0.64 (0.54)	1.88 (2.76)	0.0456 (0.0433)	NA
N	21276	11654	21276	10208	10209	10218	14903	NA
BioVU-I-AA	49.58 (18.37)	61.1	7.30 (3.45)	4.56 (0.04)	0.59 (0.32)	2.06 (3.44)	0.0337 (0.0341)	NA
n	1921	1174	1921	909	910	911	1357	NA
BioVU-II-EA	50.93 (15.22)	100	7.75 (2.58)	4.93 (2.58)	0.58 (0.27)	1.9 (0.81)	0.036 (0.026)	NA
n	2298	2298	1987	888	888	888	928	NA
BioVU-II-AA	39.40 (13.60)	100	7.63 (3.17)	4.58 (3.14)	0.56 (0.33)	2.53 (5.91)	0.0346 (0.0497)	NA
n	1375	1375	1020	385	384	385	393	NA
CARDIA-EA	25.41 (3.36)	52.7	6.25 (1.78)	3.50 (1.40)	0.32 (0.18)	2.13 (0.65)	0.04 (0.05)	0.17 (0.14)
n	2110	1113	2110	2110	2095	2110	1637	1955
CARDIA-AA	24.23 (3.77)	56.3	5.90 (1.95)	3.12 (1.49)	0.31 (0.17)	2.24 (0.83)	0.05 (0.04)	0.16 (0.13)
n	1946	1095	1946	1942	1928	1942	1348	1760
CHS-EA	72.8 (5.6)	56.3	6.4 (2.0)	NA	NA	NA	NA	NA
n	4197	2361	4197	NA	NA	NA	NA	NA
CHS-AA	72.8 (5.6)	62.2	5.9 (1.9)	NA	NA	NA	NA	NA
n	776	483	776	NA	NA	NA	NA	NA
EGCUT	47.08 (16.72)	46.9	6.36 (1.7842)	3.70 (1.4080)	0.51 (0.1773)	1.96 (0.6362)	0.0299 (0.0194)	0.154 (0.1217)
n	974	457	974	973	973	973	974	973
FHS	42.6 (13.9)	53.1	6.1 (1.6)	3.6 (1.2)	0.5 (0.1)	1.7 (0.5)	0.0 (0.0)	0.2 (0.1)
n	5790	3077	5610	2315	2315	2315	2315	2315
FINCAVAS	53.3 (13.9)	41.9	7.3 (2.5)	4.1 (2.2)	0.5 (0.2)	2.2 (1.1)	0.04 (0.03)	0.23 (0.2)
n	913	383	912	396	396	396	396	436
GeneSTAR-EA	42.47 (12.67)	52.20	6.64 (2.00)	4.21 (1.55)	0.38 (0.18)	2.09 (0.63)	NA	NA
n	1023	534	1023	894	894	937	NA	NA
GeneSTAR-AA	42.40 (12.34)	61.99	6.01 (1.87)	3.47 (1.47)	0.3 (0.16)	2.23 (0.7)	NA	NA
n	613	380	613	543	543	562	NA	NA
HABC-EA	75.72 (2.83)	52.5	6.593 (3.69)	3.837 (1.44)	0.564 (0.20)	1.93 (3.20)	0.0636 (0.04)	0.19 (0.17)
n	1251	657	1251	1251	1251	1251	1251	1251
HANDLS	48.13 (8.90)	54.7	6.23 (2.06)	3.55 (1.66)	0.40 (0.16)	2.08 (0.72)	0.03 (0.02)	0.16 (0.13)
n	870	476	834	834	834	834	813	832
JHS	53.0 (13.0)	37.5	5.59 (1.87)	3.09 (1.48)	0.39 (0.14)	1.93 (0.66)	0.03 (0.02)	0.14 (0.13)
n	2258	846	2044	2032	2030	2032	1903	2000
LBC1936	69.6 (0.8)	49.6	7.0 (1.9)	4.4 (1.5)	0.5 (0.2)	1.8 (0.8)	NA	NA
n	964	478	963	963	963	963	NA	NA
LBC1921	79.1 (0.6)	58.3	7.1 (1.9)	4.6 (1.4)	0.5 (0.2)	1.7 (1.1)	NA	NA
n	475	277	475	473	473	473	NA	NA
MESA-EA	69.49 (9.55)	50.1	6.139 (1.706)	3.79 (1.299)	0.483 (0.1842)	1.666 (0.5854)	0.028 (0.0445)	0.171 (0.1275)
n	1267	635	1266	1193	1194	1193	1179	1186
MESA-AA	69.54 (9.10)	53.9	5.779 (1.93)	3.205 (1.4436)	0.428 (0.166)	1.883 (0.6357)	0.018 (0.0341)	0.162 (0.1284)
n	750	404	750	669	670	670	653	667
MESA-HA	68.93 (9.43)	52	6.185 (1.6204)	3.68647 (1.3285)	0.433 (0.1618)	1.789 (0.5582)	0.020 (0.0385)	0.1721 (0.1322)

n	845	439	843	623	622	622	609	613
MESA-EAS	65.12 (10.01)	47.1	5.314 (1.3629)	3.0834 (1.0671)	0.290 (0.108)	1.640 (0.5039)	0.030 (0.0311)	0.122 (0.1224)
n	119	56	119	94	94	94	82	86
MHIBB	63.9 (10.9)	36.6	7.3 (2.5)	4.6 (2.2)	0.6 (0.2)	1.8 (1.0)	0.0 (0.1)	0.2 (0.1)
n	7911	2899	7911	7911	7911	7911	7911	7911
REGARDS	63.5 (9.2)	68.0	5.6 (2.0)	NA	NA	NA	NA	NA
n	5039	3427	5030	NA	NA	NA	NA	NA
RS	69.8 (0.7)	53.6	7(2)	NA	NA	3 (1)	NA	NA
n	3016	1618	2794	NA	NA	2758	NA	NA
SHIP	49.19 (16.09)	51	6.74 (2.02)	NA	NA	NA	NA	NA
n	3164	1613	3159	NA	NA	NA	NA	NA
SHIP-Trend	52.00 (15.40)	51.3	6.15 (1.94)	3.64 (1.41)	0.53 (0.18)	1.75 (0.59)	0.03 (0.02)	0.16 (0.12)
n	4245	2179	4238	4222	4222	4222	4221	4223
SOLID-TIMI 52-AA	60.50 (10.13)	33.8	6.909 (2.137)	4.3402 (1.773)	NA	NA	NA	NA
n	201	68	200	200	NA	NA	NA	NA
SOLID-TIMI 52-EA	64.55 (9.25)	25.8	7.5738 (2.22)	5.0038 (1.81)	NA	NA	NA	NA
n	8111	2092	8035	8036	NA	NA	NA	NA
SOLID-TIMI 52-EAS	63.59 (10.4)	19.6	6.8109 (2.005)	4.2585 (1.65)	NA	NA	NA	NA
n	255	50	255	252	NA	NA	NA	NA
SOLID-TIMI 52-SA	58.28 (9.67)	15.4	8.1573 (2.396)	5.6544 (2.074)	NA	NA	NA	NA
n	117	18	116	116	NA	NA	NA	NA
SOLID-TIMI 52-HA	63.29 (9.74)	28.3	7.4106 (2.171)	4.8 (1.792)	NA	NA	NA	NA
n	893	253	875	875	NA	NA	NA	NA
GSK-STABILITY-AA	62.86 (10.22)	25.4	5.6873 (1.67)	3.3362 (1.379)	NA	NA	NA	NA
n	118	30	118	118	NA	NA	NA	NA
GSK-STABILITY-EA	65.91 (8.98)	17.6	6.8245 (1.839)	4.3007 (1.427)	NA	NA	NA	NA
n	8499	1499	8490	8487	NA	NA	NA	NA
GSK-STABILITY-EAS	64.25 (8.72)	22.3	6.7628 (1.87)	4.1576 (1.466)	NA	NA	NA	NA
n	714	159	714	714	NA	NA	NA	NA
GSK-STABILITY-SA	58.35 (10.84)	13	7.5481 (1.977)	4.8583 (1.697)	NA	NA	NA	NA
n	354	46	348	347	NA	NA	NA	NA
GSK-STABILITY-HL	66.34 (8.41)	17.2	6.6986 (1.768)	4.2348 (1.444)	NA	NA	NA	NA
n	500	86	500	500	NA	NA	NA	NA
WHI-EA	66.2 (6.7)	100	6.1 (1.7)	3.9 (1.4)	0.6 (0.2)	1.8 (1.0)	0.0 (0.0)	0.2 (0.1)
n	21867	21867	21841	3669	3669	3669	3669	3669
WHI-AA	65.0 (6.6)	100	5.6 (1.7)	3.2 (1.5)	0.5 (0.2)	1.9 (1.0)	0.0 (0.0)	0.2 (0.2)
n	3501	3501	3497	712	712	712	713	712
Total	134,770		133,273	78,123	58,450	61,248	56,263	42,615

Abbreviations: EA, European Ancestry; AA, African Ancestry; HA, Hispanic American; EAS, East Asian; SA, South Asian.

Table S5. Blood cell specific expression quantitative trait loci (eQTL) datasets used for lookups of white blood cell trait variants identified in the present study

Datasets	Reference [PMID]
Blood cell related eQTL studies included fresh lymphocytes	17873875
Fresh leukocytes	19966804
Leukocyte samples in individuals with Celiac disease	19128478
Whole blood samples	18344981, 21829388, 22692066, 23818875, 23359819, 23880221, 24013639, 23157493, 23715323, 24092820, 24314549, 24956270, 24592274, 24728292, 24740359, 25609184, 22563384, 25474530, 25816334, 25578447
Lymphoblastoid cell lines derived from asthmatic children	17873877, 23345460
Lymphoblastoid cell lines derived from 3 HapMap populations	17873874
Lymphoblastoid cell lines derived from HapMap CEU populations	18193047
Lymphoblastoid cell lines from population samples	19644074, 22286170, 22941192, 23755361, 23995691, 25010687, 25951796
Neutrophils	26151758, 26259071
CD19+ B cells	22446964
Primary phytohaemagglutinin (PHA)-stimulated T cells	19644074, 23755361
CD4+ T cells	20833654
Peripheral blood monocytes	19222302, 20502693, 22446964, 23300628, 25951796, 26019233
CD14+ monocytes before and after stimulation with lipopolysaccharide (LPS) or interferon-gamma	24604202
CD11+ dendritic cells before and after Mycobacterium tuberculosis infection	22233810
Dendritic cells before or after stimulation with lipopolysaccharide (LPS), influenza or interferon-beta	24604203
Micro-RNA QTLs	21691150, 26020509
DNase-I QTLs	22307276
Histone acetylation QTLs	25799442
Ribosomal occupancy QTLs	25657249
Splicing QTLs	25685889
Micro-RNA QTLs	25791433
Splicing QTLs	25685889
ScanDB eQTL data <sup>a</sup>	<a href="http://www.scandb.org/newinterface/about.html">http://www.scandb.org/newinterface/about.html</a>
Genotype-Tissue Expression (GTEx) whole blood eQTL <sup>b</sup>	23715323, <a href="http://www.gtexportal.org">www.gtexportal.org</a>
eQTL databases at University of Chicago	<a href="http://eqtl.uchicago.edu/Home.html">http://eqtl.uchicago.edu/Home.html</a>
Long non-coding RNAs in monocytes	25025429

<sup>a</sup>ScanDB cis-eQTLs were limited to those with  $P < 1.0E-6$  and trans-eQTLs with  $P < 5.0E-8$ .

<sup>b</sup>GTEx Analysis V4 for 13 tissues were downloaded from the GTEx Portal ([www.gtexportal.org](http://www.gtexportal.org)) and results were filtered using the following criteria: Splicing QTL (sQTL) results generated with sQTLseeker with false discovery rate  $P \leq 0.05$  were retained. For all gene-level eQTLs, if at least 1 SNP passed the tissue-specific empirical threshold in GTEx, the best SNP for that eQTL was always retained. All gene-level eQTL SNPs with  $P < 1.67E-11$  were also retained, reflecting a global threshold correction of  $P = 0.05 / (30,000 \text{ genes} \times 1,000,000 \text{ tests})$ .



See Table S6 in the accompanying Excel file.

Table S7. Independent single nucleotide variants (N=28) associated with white blood cell traits in European only and combined All ancestries meta-analysis

Trait (population)	dbSNPID	Chr	Pos	Alt	Ref	EAF	Gene	Annotation	AA Substitution	CADD Score	Discovery				Replication				
											N	Beta	SE	P	N	EAF	Beta	SE	P
WBC (EA)	rs4925663	1	247,614,617	T	C	0.39	<i>OR2B11</i>	Missense	p.Gly223Asp	24.10	107,345	0.0251	0.0046	4.55E-08	17,897	0.4	0.01693	0.0112	0.132
WBC (All)	rs4925663	1	247,614,617	T	C	0.37	<i>OR2B11</i>	Missense	p.Gly223Asp	24.10	131,513	0.026	0.0042	5.85E-10	17,897	0.4	0.01693	0.0112	0.132
WBC (All)	rs1260326	2	27,730,940	C	T	0.62	<i>GCKR</i>	Missense	p.Leu446Pro	0.11	132,764	-0.0299	0.0044	1.44E-11	17,897	0.6	-0.0437	0.012	0.00027
WBC (EA)	rs1260326	2	27,730,940	C	T	0.58	<i>GCKR</i>	Missense	p.Leu446Pro	0.11	108,596	-0.0298	0.0048	4.01E-10	17,897	0.6	-0.0437	0.012	0.00027
WBC (All)	rs2276853	3	47,282,303	A	G	0.58	<i>KIF9</i>	Missense	p.Arg573Trp	32.00	132,764	0.023	0.0042	3.65E-08	17,897	0.6	0.02516	0.0116	0.03
WBC (All)	rs9374080	6	109,616,420	C	T	0.43	<i>CCDC162P</i>	Intronic		3.79	132,764	0.0227	0.0041	4.01E-08	17,897	0.46	0.02512	0.0113	0.0255
Lym (All)	rs2229094	6	31,540,556	C	T	0.26	<i>LTA</i>	Missense	p.Cys13Arg	0.03	59,978	0.0451	0.0071	1.55E-10	16,711	0.25	0.07796	0.0175	8.54E-06
Lym (EA)	rs2229094	6	31,540,556	C	T	0.26	<i>LTA</i>	Missense	p.Cys13Arg	0.03	47,105	0.0456	0.0081	1.89E-08	16,711	0.25	0.07796	0.0175	8.54E-06
Neu (All)	rs185819 <sup>a</sup>	6	32,050,067	C	T	0.52	<i>TNXB</i>	Missense	p.His1161Arg	0.00	76,838	0.0308	0.0058	9.65E-08	16,669	0.47	0.02635	0.0158	0.0948
WBC (All)	rs185819	6	32,050,067	C	T	0.51	<i>TNXB</i>	Missense	p.His1161Arg	0.00	132,764	0.0307	0.0049	4.02E-10	17,897	0.47	0.03395	0.0149	0.0224
WBC (All)	rs1050331	7	44,808,091	G	T	0.48	<i>ZMIZ2</i>	3'UTR		5.30	123,297	0.0235	0.0041	1.25E-08	15,910	0.48	0.01149	0.0117	0.325
Mon (All)	rs4917014	7	50,305,863	G	T	0.28	<i>C7orf72-1KZF1</i>	Intergenic		1.91	57,183	-0.038	0.0068	1.97E-08	16,669	0.32	-0.0478	0.0122	8.92E-05
Mon (EA)	rs10107630	8	130,603,635	T	C	0.57	<i>CCDC26</i>	Intronic		5.39	44,325	-0.0683	0.0069	2.45E-23	15,781	0.57	-0.1069	0.0118	1.06E-19
Mon (All)	rs10107630	8	130,603,635	T	C	0.56	<i>CCDC26</i>	Intronic		5.39	57,183	-0.0663	0.006	3.11E-28	15,781	0.57	-0.1069	0.0118	1.06E-19
WBC (All)	rs1982151	9	86,617,265	G	A	0.71	<i>RM11</i>	Missense	p.Asn455Ser	0.00	132,764	0.0255	0.0044	6.97E-09	17,897	0.74	0.02095	0.0123	0.0896
WBC (EA)	rs4409764	10	101,284,237	G	T	0.51	<i>GOT1-LINC01475</i>	Intergenic		7.60	108,596	-0.0255	0.0046	3.34E-08	17,897	0.53	-4.00E-04	0.0115	0.974
Mon (All)	rs6584283	10	101,291,593	C	T	0.55	<i>LINC01475</i>	Intronic ncRNA		-	57,183	-0.035	0.0061	9.55E-09	16,669	0.53	-0.0121	0.0121	0.319
WBC (EA)	rs1935	10	64,927,823	G	C	0.49	<i>JMJD1C</i>	Missense	p.Glu2353Asp	16.64	108,596	-0.0261	0.0047	2.46E-08	17,897	0.46	-0.0271	0.0117	0.0206
Neu (All)	rs3747869	10	73,520,632	C	A	0.9	<i>C10orf54 (DD1a)</i>	Missense	p.Asp187Glu	10.88	76,838	0.0494	0.0087	1.58E-08	16,669	0.9	0.07326	0.019	0.00012
WBC (EA)	rs3747869	10	73,520,632	C	A	0.9	<i>C10orf54 (DD1a)</i>	Missense	p.Asp187Glu	10.88	108,596	0.0398	0.0073	4.26E-08	17,897	0.9	0.08289	0.0184	6.40E-06
Neu (EA)	rs3747869	10	73,520,632	C	A	0.9	<i>C10orf54 (DD1a)</i>	Missense	p.Asp187Glu	10.88	60,851	0.0533	0.0095	2.11E-08	16,669	0.9	0.07326	0.019	0.00012
WBC (All)	rs3747869	10	73,520,632	C	A	0.91	<i>C10orf54 (DD1a)</i>	Missense	p.Asp187Glu	10.88	132,764	0.0381	0.0068	2.31E-08	17,897	0.9	0.08289	0.0184	6.40E-06
Neu (EA)	rs144349650	11	55,432,976	G	C	0.00069	<i>OR4C6</i>	Missense	p.Leu112Val	13.09	60,851	0.7176	0.1096	5.95E-11	16,669	Monomorphic	NA	NA	NA
Neu (All)	rs144349650	11	55,432,976	G	C	0.00071	<i>OR4C6</i>	Missense	p.Leu112Val	13.09	76,838	0.6648	0.0962	4.92E-12	16,669	Monomorphic	NA	NA	NA
WBC (EA)	rs144349650	11	55,432,976	G	C	0.00042	<i>OR4C6</i>	Missense	p.Leu112Val	13.09	108,596	0.7207	0.1073	1.87E-11	17,897	2.81E-05	-0.6178	0.9965	0.535
WBC (All)	rs144349650	11	55,432,976	G	C	0.00044	<i>OR4C6</i>	Missense	p.Leu112Val	13.09	132,764	0.6379	0.0942	1.26E-11	17,897	2.81E-05	-0.6178	0.9965	0.535
Lym (EA)	rs199694284	11	5,632,403	C	T	5.3E-05	<i>TRIM6</i>	Missense	p.Val258Ala	25.20	40,313	-2.3971	0.4458	7.56E-08	16,711	5.98E-05	-0.9067	0.6995	0.195
Bas (EA)	rs4430553	12	66,698,895	C	T	0.54	<i>HELB</i>	Missense	p.Leu191Pro	5.73	44,138	0.0404	0.0068	3.02E-09	15,770	0.53	0.02111	0.0116	0.0681
Bas (All)	rs4430553	12	66,698,895	C	T	0.56	<i>HELB</i>	Missense	p.Leu191Pro	5.73	56,707	0.0391	0.006	9.73E-11	15,770	0.53	0.02111	0.0116	0.0681
Lym (All)	rs4763879	12	9,910,164	A	G	0.32	<i>CD69</i>	Intronic		3.03	59,978	-0.0366	0.0064	1.08E-08	16,711	0.36	-0.0381	0.0119	0.00136
Lym (EA)	rs4763879	12	9,910,164	A	G	0.36	<i>CD69</i>	Intronic		3.03	47,105	-0.0379	0.0069	3.08E-08	16,711	0.36	-0.0381	0.0119	0.00136
Mon (EA)	rs11625112	14	23,596,740	G	A	0.46	<i>SLCTA8</i>	Intronic		6.34	44,325	-0.0376	0.0068	3.82E-08	16,669	0.45	-0.031	0.0115	0.00704
WBC (EA)	rs2306331	15	51,217,361	C	T	0.46	<i>AP4E1</i>	Missense	p.Cys88Arg	6.49	100,571	-0.0249	0.0046	6.15E-08	15,910	0.47	-0.0174	0.0116	0.134
Mon (EA)	rs11642873 <sup>a</sup>	16	85,991,705	C	A	0.2	<i>IRF8-LINC01082</i>	Intergenic		0.75	44,325	0.0573	0.0085	1.41E-11	16,669	0.2	0.11251	0.0144	6.17E-15

Mon (All)	rs11642873	16	85,991,705	C	A	0.17	<i>IRF8-LINC01082</i>	Intergenic		0.75	57,183	0.0561	0.0081	3.24E-12	16,669	0.2	0.11251	0.0144	6.17E-15
Mon (All)	rs1292053	17	57,963,537	G	A	0.45	<i>TUBD1</i>	Missense	p.Met76Thr	5.53	57,183	-0.0359	0.006	2.55E-09	16,669	0.44	-0.0398	0.0116	0.00061
WBC (All)	rs1292053	17	57,963,537	G	A	0.45	<i>TUBD1</i>	Missense	p.Met76Thr	5.53	132,764	-0.0287	0.004	1.06E-12	17,897	0.44	-0.027	0.0111	0.0151
WBC (EA)	rs1292053	17	57,963,537	G	A	0.45	<i>TUBD1</i>	Missense	p.Met76Thr	5.53	108,596	-0.0304	0.0045	1.28E-11	17,897	0.44	-0.027	0.0111	0.0151
Bas (All)	rs736289	19	33,757,062	C	T	0.43	<i>SLC7A10-CEBPA</i>	Intergenic		0.41	56,707	0.0343	0.0061	2.34E-08	15,770	0.4	0.01229	0.0116	0.291
Bas (EA)	rs736289	19	33,757,062	C	T	0.39	<i>SLC7A10-CEBPA</i>	Intergenic		0.41	44,138	0.0402	0.0069	7.02E-09	15,770	0.4	0.01229	0.0116	0.291
Neu (All)	rs4760	19	44,153,100	G	A	0.14	<i>CD87 (PLAUR)</i>	Missense	p.Lue272Pro	24.20	71,415	-0.0471	0.0079	2.33E-09	16,669	0.15	-0.044	0.0159	0.00555
WBC (EA)	rs4760	19	44,153,100	G	A	0.16	<i>CD87 (PLAUR)</i>	Missense	p.Lue272Pro	24.20	85,685	-0.043	0.0068	2.51E-10	17,897	0.15	-0.0518	0.0153	0.00071
WBC (All)	rs4760	19	44,153,100	G	A	0.14	<i>CD87 (PLAUR)</i>	Missense	p.Lue272Pro	24.20	106,384	-0.0424	0.0065	8.63E-11	17,897	0.15	-0.0518	0.0153	0.00071
Neu (EA)	rs4760	19	44,153,100	G	A	0.16	<i>CD87 (PLAUR)</i>	Missense	p.Lue272Pro	24.20	56,112	-0.0467	0.0083	1.54E-08	16,669	0.15	-0.044	0.0159	0.00555
WBC (All)	rs3865444	19	51,727,962	A	C	0.28	<i>CD33</i>	Upstream		3.79	107,635	-0.034	0.005	6.25E-12	17,897	0.32	-0.0329	0.0118	0.00514
WBC (EA)	rs3865444	19	51,727,962	A	C	0.31	<i>CD33</i>	Upstream		3.79	86,936	-0.0367	0.0053	3.51E-12	17,897	0.32	-0.0329	0.0118	0.00514
Lym (All)	rs6136489	20	1,923,734	G	T	0.4	<i>SIRPA-PDYN</i>	Intergenic		2.52	59,978	-0.0406	0.0061	3.99E-11	16,711	0.33	-0.0096	0.0121	0.428
WBC (All)	rs6136489	20	1,923,734	G	T	0.39	<i>SIRPA-PDYN</i>	Intergenic		2.52	132,764	-0.0246	0.0042	4.03E-09	17,897	0.33	-0.0179	0.0116	0.122
Lym (EA)	rs6136489	20	1,923,734	G	T	0.34	<i>SIRPA-PDYN</i>	Intergenic		2.52	47,105	-0.0384	0.007	3.33E-08	16,711	0.33	-0.0096	0.0121	0.428
Bas (EA)	rs2295764	20	31,025,163	G	A	0.36	<i>ASXL1</i>	3'UTR		0.10	44,138	-0.0419	0.0071	3.28E-09	15,770	0.36	-0.031	0.012	0.00978
Bas (All)	rs2295764	20	31,025,163	G	A	0.33	<i>ASXL1</i>	3'UTR		0.10	56,707	-0.0367	0.0064 1	1.07E-08	15,770	0.36	-0.031	0.012	0.00978
WBC (All)	rs2836878	21	40,465,534	A	G	0.26	<i>ETS2-PSMG1</i>	Intergenic		1.82	132,764	-0.0246	0.0046	8.36E-08	17,897	0.26	-0.0264	0.0125	0.0344

Abbreviations: Chr, chromosome; Pos, basepair position; Alt, effect allele; Ref, reference allele; EAF, effect allele frequency; AA, amino acid; CADD, Combined annotation dependent depletion; EA, European ancestry, All, combined European, African, Hispanic American, East Asian and South Asian ancestries; WBC, white blood cell; Neu, neutrophil; Mon, monocyte; Lym, lymphocyte; Bas, basophil.

\*Secondary signal identified through conditional analysis.

Table S8. Association between 16 replicated loci and white blood cell subtypes in the discovery meta-analysis. Primary associations are shown in bold.

dbSNPID	Chr	Pos	Gene	Alt/Ref	Trait (population)	N	EAF	Beta	SE	P
rs1260326	2	27,730,940	<i>GCKR</i>	C/T	<b>WBC (EA)</b>	<b>108,596</b>	<b>0.58</b>	<b>-0.030</b>	<b>0.005</b>	<b>4.01E-10</b>
					WBC (All)	132,764	0.62	-0.030	0.004	1.44E-11
					WBC (AA)	17,200	0.85	-0.039	0.016	1.44E-02
					NEU (EA)	60,851	0.58	-0.020	0.006	9.81E-04
					NEU (All)	76,838	0.62	-0.019	0.006	6.46E-04
					LYM (EA)	47,105	0.59	-0.016	0.007	2.15E-02
					LYM (All)	59,978	0.64	-0.013	0.006	3.91E-02
					BAS (EA)	44,138	0.59	-0.022	0.007	2.17E-03
					BAS (All)	56,707	0.64	-0.021	0.006	1.04E-03
rs2276853	3	47,282,303	<i>KIF9</i>	A/G	<b>WBC (All)</b>	<b>132,764</b>	<b>0.58</b>	<b>0.023</b>	<b>0.004</b>	<b>3.65E-08</b>
					WBC (EA)	108,596	0.60	0.022	0.005	1.39E-06
					NEU (EA)	60,851	0.60	0.017	0.006	4.56E-03
					NEU (All)	76,838	0.59	0.018	0.005	8.24E-04
					LYM (EA)	47,105	0.60	0.015	0.007	2.70E-02
					LYM (All)	59,978	0.58	0.018	0.006	2.52E-03
					LYM (AA)	9,423	0.53	0.039	0.015	7.86E-03
rs2229094	6	31,540,556	<i>LTA</i>	C/T	<b>LYM (EA)</b>	<b>47,105</b>	<b>0.26</b>	<b>0.046</b>	<b>0.008</b>	<b>1.89E-08</b>
					LYM (All)	59,978	0.26	0.045	0.007	1.55E-10
					LYM (AA)	9,423	0.28	0.044	0.017	7.30E-03
					WBC (EA)	108,596	0.26	0.035	0.006	2.73E-09
					WBC (All)	132,764	0.26	0.031	0.005	5.40E-09
					NEU (All)	76,838	0.26	0.015	0.006	1.74E-02
					BAS (EA)	44,138	0.26	0.026	0.008	1.37E-03
					BAS (All)	56,707	0.27	0.020	0.007	5.59E-03
rs185819	6	32,050,067	<i>TNXB</i>	C/T	<b>WBC (All)</b>	<b>132,764</b>	<b>0.51</b>	<b>0.031</b>	<b>0.005</b>	<b>4.02E-10</b>
					WBC (EA)	108,596	0.52	0.029	0.006	2.62E-07
					WBC (AA)	17,200	0.47	0.035	0.012	4.38E-03
					NEU (EA)	60,851	0.52	0.025	0.007	1.33E-04
					NEU (All)	76,838	0.52	0.031	0.006	9.65E-08
					NEU (AA)	9,734	0.47	0.058	0.016	1.80E-04
					MON (EA)	44,325	0.51	0.020	0.008	1.14E-02
					MON (All)	57,183	0.51	0.021	0.007	1.89E-03
					LYM (EA)	47,105	0.51	0.015	0.007	3.93E-02
					LYM (All)	59,978	0.50	0.019	0.006	3.23E-03
					LYM (AA)	9,423	0.47	0.041	0.015	5.79E-03
					EOS (EA)	32,517	0.48	0.019	0.009	4.39E-02
					EOS (All)	44,249	0.48	0.016	0.008	3.58E-02
					BAS (EA)	44,138	0.51	0.020	0.007	6.87E-03
BAS (All)	56,707	0.51	0.020	0.006	1.90E-03					
rs9374080	6	109,616,420	<i>CCDC162P</i>	C/T	<b>WBC (All)</b>	<b>132,764</b>	<b>0.43</b>	<b>0.023</b>	<b>0.004</b>	<b>4.01E-08</b>
					WBC (EA)	108,596	0.44	0.021	0.005	2.67E-06
					WBC (AA)	17,200	0.36	0.024	0.011	3.74E-02
					NEU (EA)	60,851	0.44	0.015	0.006	1.08E-02
					NEU (All)	76,838	0.42	0.018	0.005	5.69E-04
					MON (All)	57,183	0.43	0.014	0.006	2.71E-02
					BAS (EA)	44,138	0.45	0.026	0.007	1.34E-04
					BAS (All)	56,707	0.43	0.024	0.006	9.85E-05

rs4917014	7	50,305,863	<i>C7orf72-IKZF1</i>	G/T	<b>MON (All)</b>	<b>57,183</b>	<b>0.28458</b>	<b>-0.038</b>	<b>0.00677</b>	<b>1.97E-08</b>
					MON (EA)	44,325	0.32243	-0.0336	0.00726	3.84E-06
					MON (AA)	9,406	0.08266	-0.0606	0.02683	2.40E-02
rs3747869	10	73,520,632	<i>C10orf54 (DD1a)</i>	C/A	<b>WBC (EA)</b>	<b>108,596</b>	<b>0.90</b>	<b>0.040</b>	<b>0.007</b>	<b>4.26E-08</b>
					WBC (All)	132,764	0.91	0.038	0.007	2.31E-08
					<b>NEU (EA)</b>	<b>60,851</b>	<b>0.90</b>	<b>0.053</b>	<b>0.010</b>	<b>2.11E-08</b>
					NEU (All)	76,838	0.90	0.049	0.009	1.58E-08
					MON (EA)	44,325	0.90	0.041	0.011	2.44E-04
					MON (All)	57,183	0.91	0.037	0.010	3.77E-04
					EOS (EA)	32,517	0.82	0.033	0.014	1.58E-02
EOS (All)	44,249	0.85	0.025	0.012	4.23E-02					
rs1935	10	64,927,823	<i>JMJD1C</i>	G/C	<b>WBC (EA)</b>	<b>108,596</b>	<b>0.49</b>	<b>-0.026</b>	<b>0.005</b>	<b>2.46E-08</b>
					WBC (All)	132,764	0.46	-0.025	0.004	6.57E-09
					NEU (EA)	60,851	0.49	-0.024	0.006	4.00E-05
					NEU (All)	76,838	0.46	-0.022	0.005	4.99E-05
					LYM (All)	59,978	0.45	-0.013	0.006	2.86E-02
					EOS (All)	44,249	0.41	-0.020	0.007	6.33E-03
rs4763879	12	9,910,164	<i>CD69</i>	A/G	<b>LYM (EA)</b>	<b>47,105</b>	<b>0.36</b>	<b>-0.038</b>	<b>0.007</b>	<b>3.08E-08</b>
					LYM (All)	59,978	0.32	-0.037	0.006	1.08E-08
					WBC (EA)	108,596	0.36	-0.014	0.005	2.63E-03
					WBC (All)	132,764	0.33	-0.013	0.004	2.94E-03
rs11625112	14	23,596,740	<i>SLC7A8</i>	G/A	<b>MON (EA)</b>	<b>44,325</b>	<b>0.46</b>	<b>-0.038</b>	<b>0.007</b>	<b>3.82E-08</b>
					MON (All)	57,183	0.46	-0.030	0.006	4.20E-07
					EOS (EA)	32,517	0.42	-0.021	0.008	1.17E-02
					EOS (All)	44,249	0.43	-0.021	0.007	2.77E-03
					BAS (EA)	44,138	0.46	-0.031	0.007	7.76E-06
					BAS (All)	56,707	0.46	-0.026	0.006	1.07E-05
rs11642873	16	85,991,705	<i>IRF8-LINC01082</i>	C/A	<b>MON (EA)</b>	<b>44,325</b>	<b>0.20</b>	<b>0.057</b>	<b>0.008</b>	<b>1.41E-11</b>
					MON (All)	57,183	0.17	0.056	0.008	3.24E-12
					EOS (EA)	32,517	0.18	0.036	0.010	5.94E-04
					EOS (All)	44,249	0.15	0.033	0.010	8.18E-04
					BAS (EA)	44,138	0.20	0.021	0.009	1.53E-02
					BAS (All)	56,707	0.17	0.016	0.008	4.73E-02
rs1292053	17	57,963,537	<i>TUBD1</i>	G/A	<b>WBC (EA)</b>	<b>108,596</b>	<b>0.45</b>	<b>-0.030</b>	<b>0.004</b>	<b>1.28E-11</b>
					WBC (All)	132,764	0.45	-0.029	0.004	1.06E-12
					WBC (AA)	17,200	0.48	-0.029	0.011	8.31E-03
					NEU (EA)	60,851	0.45	-0.023	0.006	1.04E-04
					NEU (All)	76,838	0.45	-0.020	0.005	1.28E-04
					MON (EA)	44,325	0.45	-0.032	0.007	2.25E-06
					<b>MON (All)</b>	<b>57,183</b>	<b>0.45</b>	<b>-0.036</b>	<b>0.006</b>	<b>2.55E-09</b>
					MON (AA)	9,406	0.48	-0.035	0.015	1.80E-02
					LYM (EA)	47,105	0.44	-0.016	0.007	1.46E-02
					LYM (All)	59,978	0.45	-0.013	0.006	3.05E-02
rs4760	19	44,153,100	<i>CD87 (PLAUR)</i>	G/A	<b>NEU (EA)</b>	<b>56,112</b>	<b>0.16</b>	<b>-0.047</b>	<b>0.008</b>	<b>1.54E-08</b>
					NEU (All)	71,415	0.14	-0.047	0.008	2.33E-09
					<b>WBC (EA)</b>	<b>85,685</b>	<b>0.16</b>	<b>-0.043</b>	<b>0.007</b>	<b>2.51E-10</b>
					WBC (All)	106,384	0.14	-0.042	0.007	8.63E-11
rs3865444	19	51,727,962	<i>CD33</i>	A/C	<b>WBC (EA)</b>	<b>86,936</b>	<b>0.31</b>	<b>-0.037</b>	<b>0.005</b>	<b>3.51E-12</b>
					WBC (All)	107,635	0.28	-0.034	0.005	6.25E-12

					NEU (EA)	57,363	0.31	-0.025	0.006	1.15E-04
					NEU (All)	72,666	0.28	-0.021	0.006	3.26E-04
					MON (EA)	40,837	0.31	-0.020	0.008	9.46E-03
					MON (All)	53,011	0.28	-0.016	0.007	2.51E-02
					EOS (EA)	29,046	0.28	-0.029	0.010	2.16E-03
					EOS (All)	40,099	0.25	-0.025	0.009	3.09E-03
rs2295764	20	31,025,163	<i>ASXLI</i>	G/A	<b>BAS (EA)</b>	<b>44,138</b>	<b>0.36</b>	<b>-0.042</b>	<b>0.007</b>	<b>3.28E-09</b>
					BAS (All)	56,707	0.33	-0.037	0.006	1.07E-08
					WBC (AA)	17,200	0.20	-0.029	0.013	3.23E-02
					MON (EA)	44,325	0.36	-0.032	0.007	5.64E-06
					MON (All)	57,183	0.33	-0.026	0.006	3.95E-05
					EOS (EA)	32,517	0.32	-0.027	0.009	2.14E-03
					EOS (All)	44,249	0.30	-0.025	0.008	9.81E-04
rs2836878	21	40,465,534	<i>ETS2-PSMGI</i>	A/G	<b>WBC (All)</b>	<b>132,764</b>	<b>0.26</b>	<b>-0.025</b>	<b>0.005</b>	<b>8.36E-08</b>
					WBC (EA)	108,596	0.27	-0.024	0.005	7.49E-07
					NEU (EA)	60,851	0.28	-0.025	0.006	1.08E-04
					NEU (All)	76,838	0.26	-0.025	0.006	3.38E-05
					MON (EA)	44,325	0.28	-0.026	0.008	7.28E-04
					MON (All)	57,183	0.25	-0.022	0.007	1.69E-03
					BAS (EA)	44,138	0.28	-0.019	0.008	1.29E-02
					BAS (All)	56,707	0.25	-0.018	0.007	9.80E-03

Abbreviations: Chr, chromosome; Pos, basepair position; Alt, effect allele; Ref, reference allele; EAF, effect allele frequency; EA, European ancestry; AA, African ancestry; All, combined European, African, Hispanic American, East Asian and South Asian ancestries; WBC, white blood cell; Neu, neutrophil; Mon, monocyte; Lym, lymphocyte; Eos, eosinophils; Bas, basophils.

See Table S9 in the accompanying Excel file

Table S10. Genes associated with white blood cell and differential counts identified using gene-based association meta-analysis

Trait	Population	Gene	Test	Chr	Number of variants	Discovery						Replication				
						N	P	Beta	S.D.	MAF cutoff	cMAC	Test	N	P	Beta	S.D.
WBC	EA	<i>CXCR2</i>	SKAT	2	9	108,596	1.241E-14	-0.223	0.029	1	3,725	SKAT	2,898	0.0173	-0.406	0.169
WBC	All	<i>CXCR2</i>	SKAT	2	8	138,814	9.48E-15	-0.193	0.027	1	10,438					
WBC	EA	<i>CXCR2</i>	VT	2	9	108,596	7.239E-14	-0.223	0.029	0.012	3,725	VT	2,898	0.053	-0.406	0.169
WBC	All	<i>CXCR2</i>	VT	2	5	138,814	3.56E-13	-0.21	0.028	0.0023	10,438					
WBC	All	<i>JAK2</i>	VT	9	6	138,814	2.682E-06	0.334	0.066	0.00036	8,045	VT	2,898	0.0091	-0.505	0.163
<b>WBC</b>	<b>EA</b>	<b><i>TAF3</i></b>	<b>VT</b>	<b>10</b>	<b>6</b>	<b>108,596</b>	<b>1.583E-06</b>	<b>0.328</b>	<b>0.064</b>	<b>0.00037</b>	<b>6,848</b>	<b>VT</b>	2,898	<b>NA</b>	<b>NA</b>	<b>NA</b>
NEU	EA	<i>CXCR2</i>	SKAT	2	8	60,851	6.853E-09	-0.221	0.038	1	2,950	SKAT	1,285	0.190	-0.017	0.236
NEU	All	<i>CXCR2</i>	SKAT	2	7	77,223	5.062E-09	-0.203	0.035	1	9,252					
NEU	EA	<i>CXCR2</i>	VT	2	8	60,851	2.495E-08	-0.221	0.038	0.0185	2,950	VT	1,285	0.580	-0.392	0.335
NEU	All	<i>CXCR2</i>	VT	2	4	77,223	2.128E-08	-0.218	0.037	0.0023	9,252					
NEU	All	<i>JAK2</i>	VT	9	6	77,223	1.553E-07	0.431	0.077	0.00054	6,388	VT	1,285	NA	NA	NA
<b>NEU</b>	<b>EA</b>	<b><i>OR4C6</i></b>	<b>SKAT</b>	<b>11</b>	<b>15</b>	<b>60,851</b>	<b>2.561E-08</b>	<b>0.109</b>	<b>0.044</b>	<b>1</b>	<b>512</b>	<b>SKAT</b>	<b>1,285</b>	<b>0.4844</b>	<b>-0.1455</b>	<b>0.198</b>
NEU	EA	<i>IL17RA</i>	SKAT	22	18	44,325	1.004E-16	-0.128	0.026	1	10,016	SKAT	1,285	0.949	-0.018	0.176
<b>NEU</b>	<b>AA</b>	<b><i>ZNF439</i></b>	<b>VT</b>	<b>19</b>	<b>4</b>	<b>10,119</b>	<b>9.566E-07</b>	<b>-1.099</b>	<b>0.221</b>	<b>0.083</b>	<b>1,688</b>	<b>VT</b>	1,285	<b>NA</b>	<b>NA</b>	<b>NA</b>
MON	All	<i>IL17RA</i>	SKAT	22	19	57,567	1.174E-18	-0.104	0.023	1	23,595	SKAT	1,285	0.972	-0.004	0.176
<b>LYM</b>	<b>All</b>	<b><i>TBX3</i></b>	<b>VT</b>	<b>12</b>	<b>4</b>	<b>60,363</b>	<b>1.959E-06</b>	<b>0.419</b>	<b>0.083</b>	<b>0.00060</b>	<b>144</b>	<b>VT</b>	<b>1,285</b>	<b>NA</b>	<b>NA</b>	<b>NA</b>

Potentially novel genes are shown in bold.

Abbreviations: Chr, Chromosome; MAF, minor allele frequency; cMAC, cumulative minor allele count; WBC, white blood cell; Neu, neutrophil; Mon, monocytes; Lym, lymphocytes; SKAT, sequence kernel association test; VT, variable-threshold test; EA, European ancestry; AA, African ancestry; All, combined European, African, Hispanic American, East Asian and South Asian ancestries.



Table S11. Association between white blood cell trait associated variants and immunologically relevant quantitative traits in previous genome-wide association studies ( $P < 1.64E-04$ ).

Trait (population)	dbSNPID	Chr	Pos	Alt/Ref	Gene	Quantitative traits	Sample size	P <sup>a</sup>	PMID
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	C-reactive protein	70,410	3.80E-43	23263486, 21300955, 23505291, 22939635, 18439548
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	Plasma protein-C levels	9,424	2.00E-17	20802025
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	Serum urate	50,337	5.90E-17	20884846, 23263486, 21768215, 19503597, 21943158
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	Platelet count	37,438	9.10E-10	22139419
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	2-hour glucose tolerance test	133,010	9.00E-15	22885924, 20081857, 23263486
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	Fasting blood glucose	133,010	2.20E-41	22885924, 20081857, 20081858, 23263486
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	Fasting insulin	133,010	2.70E-22	22885924, 20081857, 20081858, 23263486
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	Factor VII activity in plasma	31,212	6.20E-24	21676895, 20231535, 21676895
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	Total cholesterol	140,059	4.40E-28	20686565, 23063622, 20339536, 20339536, 19060906
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	Triglycerides	140,059	1.30E-139	20686565, 22629316, 23063622, 19936222, 18193043, 20657596, 19060911, 19802338, 20339536, 23505323, 20139978, 19060910, 23236364, 21943158, 18454146, 19913121, 21862451, 19060906, 22171074
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	HDL cholesterol	26,768	6.30E-36	19936222
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	Height	183,727	9.40E-05	20881960
WBC(EA)	rs1260326	2	27,730,940	C/T	<i>GCKR</i>	HOMA-IR	122,744	9.20E-07	20081858, 20081857, 23263486
WBC(All)	rs185819	6	32,050,067	C/T	<i>TNXB</i>	Height	183,727	1.70E-06	20881960, 18391951
WBC(All)	rs9374080	6	109,616,420	C/T	<i>CCDC162P</i>	Mean corpuscular hemoglobin concentration	135,367	3.00E-21	23222517
WBC(All)	rs9374080	6	109,616,420	C/T	<i>CCDC162P</i>	Mean corpuscular volume	135,367	2.30E-18	23222517, 19862010, 20139978
WBC(All)	rs9374080	6	109,616,420	C/T	<i>CCDC162P</i>	Red blood cell count	135,367	1.60E-15	23222517
Mon(All)	rs4917014	7	50,305,863	G/T	<i>C7orf72-<i>IKZF1</i></i>	HDL cholesterol	140,059	2.40E-05	20686565
WBC(EA)	rs1935	10	64,927,823	G/C	<i>JMJD1C</i>	Platelet count	16,388	2.70E-08	22423221
WBC(EA)	rs1935	10	64,927,823	G/C	<i>JMJD1C</i>	Triglycerides	140,059	1.50E-07	20686565, 19060906
Mon(EA)	rs11625112 <sup>b</sup>	14	23,596,740	G/A	<i>SLC7A8</i>	Triglycerides	140,059	4.90E-05	20686565, 19060906
WBC(All)	rs2836878	21	40,465,534	A/G	<i>ETS2-<i>PSMG1</i></i>	C-reactive protein	82,725	4.00E-08	21300955, 22939635

<sup>a</sup>Lookup of 16 single nucleotide variants was performed and results with multiple testing corrected p-value  $< 1.64E-04$  (16 variants and 19 quantitative traits) are shown here. When multiple studies report the same variant-trait associations, results from the largest sample size are presented here.

<sup>b</sup>LD  $r^2$  between rs11625112 and rs2239633 in *SLC7A8* is 0.63.

Table S12. White blood cell trait variants associated with platelet and red blood cell related traits in the European and combined All ancestries of the Blood-Cell Consortium.

dbSNPID	Chr	Pos	Gene	Alt/Ref	EAF	Trait	Beta	SE	P
<b>European ancestry</b>									
rs1260326	2	27,730,940	<i>GCKR</i>	C/T	0.58	WBC	-0.03	0.005	4.01E-10
						PLT	-0.037	0.005	7.15E-14
						RBC	0.022	0.006	5.73E-04
						HCT	0.023	0.005	7.53E-06
						HGB	0.022	0.005	3.74E-06
rs2229094	6	31,540,556	<i>LTA</i>	C/T	0.26	LYM	0.046	0.008	1.89E-08
						PLT	0.019	0.006	2.04E-03
rs1935	10	64,927,823	<i>JMJD1C</i>	G/C	0.49	WBC	-0.026	0.005	2.46E-08
						PLT	0.05	0.005	3.11E-25
						MPV	-0.112	0.008	7.64E-41
						RDW	-0.017	0.007	1.75E-02
						MCH	0.017	0.007	1.18E-02
rs4763879	12	9,910,164	<i>CD69</i>	A/G	0.36	LYM	-0.038	0.007	3.08E-08
						HGB	-0.01	0.005	3.44E-02
						MCHC	-0.012	0.006	3.38E-02
rs11625112	14	23,596,740	<i>SLC7A8</i>	G/A	0.46	MON	-0.038	0.007	3.82E-08
						HCT	0.012	0.005	1.76E-02
rs1292053	17	57,963,537	<i>TUBD1</i>	G/A	0.45	WBC	-0.03	0.004	1.28E-11
						PLT	-0.017	0.005	1.94E-04
						RDW	0.024	0.007	3.85E-04
						HCT	-0.015	0.005	2.05E-03
						HGB	-0.016	0.005	5.11E-04
						MCV	-0.012	0.006	4.34E-02
rs3865444	19	51,727,962	<i>CD33</i>	A/C	0.31	WBC	-0.037	0.005	3.51E-12
						PLT	-0.026	0.005	1.11E-06
						MCHC	0.016	0.006	8.70E-03
rs2295764	20	31,025,163	<i>ASXLI</i>	G/A	0.36	BAS	-0.042	0.007	3.28E-09
						RDW	0.034	0.007	2.35E-06
<b>All combined ancestries</b>									
rs2276853	3	47,282,303	<i>KIF9</i>	A/G	0.58	WBC	0.023	0.004	3.65E-08
						HGB	-0.011	0.004	1.14E-02
rs9374080	6	109,616,420	<i>CCDC162P</i>	C/T	0.43	WBC	0.023	0.004	4.01E-08
						PLT	0.015	0.004	3.07E-04
						MPV	-0.024	0.007	9.28E-04
						RBC	-0.043	0.005	3.13E-15
						RDW	-0.041	0.006	6.19E-11

						MCV	0.06	0.006	8.84E-28
						MCH	0.062	0.006	3.10E-26
						MCHC	0.023	0.005	5.13E-06
rs185819	6	32,050,067	<i>TNXB</i>	C/T	0.51	WBC	0.031	0.005	4.02E-10
						PLT	0.017	0.005	6.16E-04
						MPV	-0.023	0.009	8.78E-03
						MCH	-0.015	0.007	2.94E-02
rs1292053	17	57,963,537	<i>TUBD1</i>	G/A	0.45	MON	-0.036	0.006	2.55E-09
						PLT	-0.013	0.004	1.40E-03
						RBC	-0.012	0.005	2.51E-02
						RDW	0.023	0.006	2.30E-04
						HCT	-0.013	0.004	2.97E-03
						HGB	-0.013	0.004	1.02E-03
rs2836878	21	40,465,534	<i>ETS2-PSMG1</i>	A/G	0.26	WBC	-0.025	0.005	8.36E-08
						PLT	-0.014	0.005	3.44E-03
						RDW	-0.025	0.007	3.28E-04
						HCT	0.016	0.005	1.37E-03
						HGB	0.022	0.005	2.72E-06
						MCV	0.014	0.006	2.14E-02
						MCH	0.024	0.007	2.78E-04
						MCHC	0.019	0.006	9.14E-04

Abbreviations: Chr, chromosome; Pos, basepair position; Alt, effect allele; Ref, reference allele; EAF, effect allele frequency; EA, European ancestry, All, combined European, African, Hispanic American, East Asian and South Asian ancestries; BAS, basophil; HCT, hematocrit; HGB, hemoglobin; LYM, lymphocyte; MCH, mean corpuscular hemoglobin; MCHC, mean corpuscular hemoglobin concentration; MCV, mean corpuscular volume; MON, monocytes; MPV, mean platelet volume; PLT, platelet; RBC, red blood cell; RDW, red cell distribution width; WBC, white blood cell.

See Table S13 in the accompanying Excel file.

## **Additional Funding Information**

### **Airwave**

The Airwave Study is funded by the Home Office (grant number 780-TETRA) with additional support from the National Institute for Health Research (NIHR) Imperial College Healthcare NHS Trust (ICHNT) and Imperial College Biomedical Research Centre (BRC) (Grant number BRC-P38084). Paul Elliott is an NIHR Senior Investigator and is supported by the ICHNT and Imperial College BRC, the MRC-PHE Centre for Environment and Health and the NIHR Health Protection Research Unit on Health Impact of Environmental Hazards.

### **ARIC**

The Atherosclerosis Risk in Communities (ARIC) Study is carried out as a collaborative study supported by National Heart, Lung, and Blood Institute (NHLBI) contracts (HHSN268201100005C, HHSN268201100006C, HHSN268201100007C, HHSN268201100008C, HHSN268201100009C, HHSN268201100010C, HHSN268201100011C, and HHSN268201100012C), R01HL087641, R01HL59367 and R01HL086694; National Human Genome Research Institute contract U01HG004402; and National Institutes of Health contract HHSN268200625226C.

### **BioMe**

The Mount Sinai Institute for Personalized Medicine Biobank Program is supported by The Andrea and Charles Bronfman Philanthropies.

### **BIOVU**

The dataset used in the analyses described were obtained from Vanderbilt University Medical Center's BioVU which is supported by institutional funding and by the Vanderbilt CTSA grant UL1 TR000445 from NCATS (National Center for Advancing Translational Sciences)/National Institutes of Health (NIH). Genome-wide genotyping was funded by NIH grants RC2GM092618 from NIGMS/OD and U01HG004603 from the National

Human Genome Research Institute (NHGRI)/ National Institute of General Medical Sciences (NIGMS).

Funding for TLE and DRVE was provided by 1R21HL12142902 from NHLBI/NIH. Funding for the BioVU replication cohort was provided by 5R01HD074711 from National Institute of Child Health and Human Development (NICHD)/NIH.

## **CARDIA**

The CARDIA Study is conducted and supported by the NHLBI in collaboration with the University of Alabama at Birmingham (HHSN268201300025C & HHSN268201300026C), Northwestern University (HHSN268201300027C), University of Minnesota (HHSN268201300028C), Kaiser Foundation Research Institute (HHSN268201300029C), and Johns Hopkins University School of Medicine (HHSN268200900041C). CARDIA is also partially supported by the Intramural Research Program of the National Institute on Aging (NIA). Exome Chip genotyping was supported from grants R01-HL093029 and U01- HG004729 to MF. This manuscript has been reviewed and approved by CARDIA for scientific content.

## **CHS**

This CHS research was supported by NHLBI contracts HHSN268201200036C, HHSN268200800007C, N01HC55222, N01HC85079, N01HC85080, N01HC85081, N01HC85082, N01HC85083, N01HC85086; and NHLBI grants HL080295, HL087652, HL103612, HL105756, HL120393 with additional contribution from the National Institute of Neurological Disorders and Stroke (NINDS). Additional support was provided through AG023629 from the NIA. A full list of CHS investigators and institutions can be found at <http://chs-nhlbi.org/>. The provision of genotyping data was supported in part by the National Center for Advancing Translational Sciences, CTSI grant UL1TR000124, and the National Institute of Diabetes and Digestive and Kidney Disease Diabetes Research Center (DRC) grant DK063491 to the Southern California Diabetes Endocrinology Research Center.

## **EGCUT**

This study was supported by EU H2020 grants 692145, 676550, 654248, Estonian Research Council Grant IUT20-60, NIASC, EIT – Health and NIH-BMI grant 2R01DK075787-06A1.

### **FINCAVAS**

This work was supported by the Competitive Research Funding of the Tampere University Hospital (Grant 9M048 and 9N035), the Finnish Cultural Foundation, the Finnish Foundation for Cardiovascular Research, the Emil Aaltonen Foundation, Finland, and the Tampere Tuberculosis Foundation.

### **FramHS**

Genotyping, quality control and calling of the Illumina HumanExome BeadChip in the Framingham Heart Study was supported by funding from the National Heart, Lung and Blood Institute Division of Intramural Research (Daniel Levy and Christopher J. O'Donnell, Principle Investigators). Support for the centralized genotype calling was provided by Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium through the NIH American Recovery and Reinvestment Act of 2009 (5RC2HL102419). The NHLBI's Framingham Heart Study is a joint project of the National Institutes of Health and Boston University School of Medicine and was supported by contract N01-HC-25195.

### **GeneSTAR**

GeneSTAR was supported by the NIH/NHLBI (U01 HL72518, HL087698, and HL112064) and by a grant from the NIH/National Center for Research Resources (M01-RR000052) to the Johns Hopkins General Clinical Research Center. Genotyping services were provided through the RS&G Service by the Northwest Genomics Center at the University of Washington, Department of Genome Sciences, under U.S. Federal Government contract number HHSN268201100037C from the National Heart, Lung, and Blood Institute.

### **GSK-STABILITY and SOLID TIMI-52**

The GSK-STABILITY and SOLID TIMI-52 studies were funded by GlaxoSmithKline.

### **HABC**

HABC funding/acknowledgement: The Health ABC Study was supported by NIA contracts N01AG62101, N01AG62103, and N01AG62106 and, in part, by the NIA Intramural Research Program. The genome-wide association study was funded by NIA grant 1R01AG032098-01A1 to Wake Forest University Health Sciences and genotyping services were provided by the Center for Inherited Disease Research (CIDR). CIDR is fully funded through a federal contract from the National Institutes of Health to The Johns Hopkins University, contract number HHSN268200782096C. This study utilized the high-performance computational capabilities of the Biowulf Linux cluster at the National Institutes of Health, Bethesda, Md. (<http://biowulf.nih.gov>).

## **HANDLS**

The Healthy Aging in Neighborhoods of Diversity across the Life Span Study (HANDLS) research was supported by the Intramural Research Program of the NIH, NIA and the National Center on Minority Health and Health Disparities (project # Z01-AG000513 and human subjects protocol # 2009-149). Data analyses for the HANDLS study utilized the computational resources of the NIH HPC Biowulf cluster at the National Institutes of Health, Bethesda, MD (<http://hpc.nih.gov>).

## **JHS**

We thank the Jackson Heart Study (JHS) participants and staff for their contributions to this work. The JHS is supported by contracts HHSN268201300046C, HHSN268201300047C, HHSN268201300048C, HHSN268201300049C, HHSN268201300050C from the National Heart, Lung, and Blood Institute and the National Institute on Minority Health and Health Disparities.

## **LBC1921 and LBC1936**

Phenotype collection in the Lothian Birth Cohort 1921 was supported by the UK's Biotechnology and Biological Sciences Research Council (BBSRC), The Royal Society and The Chief Scientist Office of the Scottish Government. Phenotype collection in the Lothian Birth Cohort 1936 was supported by Age UK (The Disconnected Mind project). Genotyping was supported by Centre for Cognitive Ageing and Cognitive Epidemiology (Pilot Fund award), Age UK, and the Royal Society of Edinburgh. The work was undertaken by



The University of Edinburgh Centre for Cognitive Ageing and Cognitive Epidemiology, part of the cross council Lifelong Health and Wellbeing Initiative (MR/K026992/1). Funding from the BBSRC and Medical Research Council (MRC) is gratefully acknowledged. WDH is supported by a grant from Age UK (Disconnected Mind Project).

## **MESA**

MESA and the MESA SHARe project are conducted and supported by the NHLBI in collaboration with MESA investigators. Support for MESA is provided by contracts HHSN268201500003I, N01-HC-95159, N01-HC-95160, N01-HC-95161, N01-HC-95162, N01-HC-95163, N01-HC-95164, N01-HC-95165, N01-HC-95166, N01-HC-95167, N01-HC-95168, N01-HC-95169, UL1-TR-001079, UL1-TR-000040, and DK063491. MESA Family is conducted and supported by the NHLBI in collaboration with MESA investigators. Support is provided by grants and contracts R01HL071051, R01HL071205, R01HL071250, R01HL071251, R01HL071258, R01HL071259, by the National Center for Research Resources, Grant UL1RR033176, and the NCATS, Grant UL1TR000124. Funding support for the inflammation dataset was provided by grant HL077449. The MESA Epigenomics & Transcriptomics Study was funded by NIA grant 1R01HL101250-01 to Wake Forest University Health Sciences.

## **MHIBB**

This work was supported by the Fonds de Recherche du Québec–Santé (FRQS, scholarship to NC), the Canadian Institute of Health Research (Banting-CIHR, scholarship to SL and operating grant MOP#123382 to GL), the Canada Research Chair program (to GL, JDR, and JCT), and the Montreal Heart Institute (MHI) Foundation.

## **REGARDS**

The genotyping for this project was provided by NIH/NCRR grant 5U54RR026137-03.

## **RS**

The generation and management of the Illumina exome chip v1.0 array data for the Rotterdam Study (RS-I) was executed by the Human Genotyping Facility of the Genetic Laboratory of the Department of Internal Medicine, Erasmus MC, Rotterdam, The Netherlands. The Exome chip array data set was funded by the Genetic Laboratory of the Department of Internal Medicine, Erasmus MC, from the Netherlands Genomics Initiative (NGI)/Netherlands Organisation for Scientific Research (NWO)-sponsored Netherlands Consortium for Healthy Aging (NCHA; project nr. 050-060-810); the Netherlands Organization for Scientific Research (NWO; project number 184021007) and by the Rainbow Project (RP10; Netherlands Exome Chip Project) of the Biobanking and Biomolecular Research Infrastructure Netherlands (BBMRI-NL; [www.bbMRI.nl](http://www.bbMRI.nl)). The Rotterdam Study is funded by Erasmus Medical Center and Erasmus University, Rotterdam, Netherlands Organization for the Health Research and Development (ZonMw), the Research Institute for Diseases in the Elderly (RIDE), the Ministry of Education, Culture and Science, the Ministry for Health, Welfare and Sports, the European Commission (DG XII), and the Municipality of Rotterdam.

## **SHIP**

SHIP is part of the Community Medicine Research net of the University of Greifswald, Germany, which is funded by the Federal Ministry of Education and Research (grants no. 01ZZ9603, 01ZZ0103, and 01ZZ0403), the Ministry of Cultural Affairs as well as the Social Ministry of the Federal State of Mecklenburg-West Pomerania, and the network 'Greifswald Approach to Individualized Medicine (GANI\_MED)' funded by the Federal Ministry of Education and Research (grant 03IS2061A). ExomeChip data have been supported by the Federal Ministry of Education and Research (grant no. 03Z1CN22) and the Federal State of Mecklenburg-West Pomerania.

## **WHI**

The WHI program is funded by the NHLBI, NIH, and the US Department of Health and Human Services (HHSN268201100046C, HHSN268201100001C, HHSN268201100002C, HHSN268201100003C,

HHSN268201100004C and HHSN271201100004C). Exome chip data and analysis were supported through the Exome Sequencing Project (NHLBI RC2 HL-102924, RC2 HL-102925 and RC2 HL-102926), the Genetics and Epidemiology of Colorectal Cancer Consortium (National Cancer Institute CA137088), and the Genomics and Randomized Trials Network (NHGRI U01-HG005152). A full listing of WHI investigators can be found at:

<http://www.whi.org/researchers/Documents%20%20Write%20a%20Paper/WHI%20Investigator%20Short%20List.pdf>

### **Supplemental Acknowledgments**

The MHI Biobank thanks all participants and staff of the MHI Biobank and acknowledges the technical support of the Beaulieu-Saucier MHI Pharmacogenomic Center. The WHI study thanks investigators and staff for their dedication in making the program possible. The FHS authors are pleased to acknowledge the Shared Computing Cluster, which is administered by Boston University's Research Computing Services. URL:

[www.bu.edu/tech/support/research/](http://www.bu.edu/tech/support/research/). The views expressed in this manuscript are those of the authors and do not necessarily represent the views of the National Heart, Lung, and Blood Institute; the National Institutes of Health; or the U.S. Department of Health and Human Services. ARIC thanks the staff and participants of the ARIC study for their important contributions. Infrastructure was partly supported by Grant Number UL1RR025005, a component of the National Institutes of Health and NIH Roadmap for Medical Research. The meta-analysis and meta-regression analyses were funded by grant R01 HL086694 from the National Heart, Lung, and Blood Institute. Airwave study thanks all participants in the Airwave Health Monitoring Study; Louisa Cavaliero who assisted in data collection and management as well as Peter McFarlane and the Glasgow CARE, Patricia Munroe at Queen Mary University of London, Joanna Sarnecka and Ania Zawodniak at Northwick Park for their contributions to the study. GeneSTAR thanks all of our participating families. MESA thanks its Coordinating Center, MESA investigators, and study staff for their valuable contributions. A full list of participating MESA investigators and institutions can be found at <http://www.mesa-nhlbi.org>. A full list of CHS investigators and institutions can be found at <http://chs-nhlbi.org/>. SOLID-TIMI-52 and GSK-

STABILITY thank Liling Warren for contributions to the genetic analysis of the study datasets. The University of Greifswald is a member of the 'Center of Knowledge Interchange' program of the Siemens AG and the Caché Campus program of the InterSystems GmbH. The SHIP and SHIP-TREND samples were genotyped at the Helmholtz Zentrum München, Germany. EGCUT thanks all the participants and co-workers at Estonian Biobank, especially Mr. V. Soo, Mr. S. Smith and Dr. L. Milani. FINCAVAS thanks the staff at the Department of Clinical Physiology for data collection. LBC thanks the cohort participants and team members who contributed to these studies. RS thanks Ms. Mila Jhamai, Ms. Sarah Higgins, and Mr. Marijn Verkerk for their help in creating the exome chip database, and Carolina Medina-Gomez, MSc, Lennard Karsten, MSc, and Linda Broer Ph.D. for quality control and variant. RS is also grateful to the study participants, the staff from the Rotterdam Study and the participating general practitioners and pharmacists. REGARDS thanks the investigators, staff and participants of the study for their valuable contributions. A full list of participating REGARDS investigators and institutions can be found at <http://www.regardsstudy.org>.