

DETAILED METHODS

Study populations

The United Kingdom Biobank (UK Biobank)

UK Biobank is a large, prospective study with extensive genetic and phenotypic data collected on ~500,000 volunteers across the UK aged 40 to 69 at recruitment (**Supplemental Table 1**). The baseline assessment was performed between 2006 and 2010 in 22 assessment centers throughout the UK, covering various settings to represent socioeconomic and racial/ethnic heterogeneity. At the baseline exam, participants completed questionnaires assessing their social backgrounds, lifestyle, cognitive, physical functioning, mood and personality; blood, urine and saliva samples also were collected. All participants were followed up through linkage to health and medical records. The study design and characteristics of UK Biobank have been detailed elsewhere^{1,2}.

The Population Architecture using Genomics and Epidemiology (PAGE) Study

The multi-ethnic PAGE study³ is a consortium funded by the National Institutes of Health to examine the genetic architecture of common complex diseases and traits in diverse populations. PAGE data used in this study included participants enrolled in the following cohort studies:

Atherosclerosis Risk in Communities Study (ARIC)

ARIC is a multi-center prospective epidemiologic cohort study funded by the National Heart, Lung, and Blood Institute (NHLBI) to investigate the causes of atherosclerosis and its clinical outcomes, and variation in cardiovascular risk factors, medical care, and disease by race,

gender, location, and date.⁴ 15,792 participants ages 45-64 of primarily European American and African American descent were recruited between 1987 and 1989 from four communities in the United States: Washington County, MD; Forsyth County, NC; Jackson, MS; and Minneapolis, MN. At study baseline (1987-1989), participants received standardized physical examinations and interviewer-administered questionnaires. Semi-annual telephone follow-up calls are ongoing to maintain contact and assess health status of the cohort.

The Coronary Artery Risk Development in Young Adults Study (CARDIA)

CARDIA is a multi-center prospective cohort study funded by the NHLBI to study the development and distribution of cardiovascular diseases and their risk factors⁵. 5,115 participants ages 18-30 years (52% African American, 55% women) were recruited in 1985-1986 from four communities in the United States: Birmingham, AL; Chicago, IL; Minneapolis, MN; and Oakland, CA. The participants were selected so that there would be approximately the same number of people in subgroups of race, gender, education (high school or less/more than high school) and age (18-24 and 25-30) in each of these 4 centers. Participants were asked to participate in follow-up examinations during 1987-1988 (Year 2), 1990-1991 (Year 5), 1992-1993 (Year 7), 1995-1996 (Year 10), 2000-2001 (Year 15), and 2005-2006 (Year 20), 2010-2011 (Year 25), and 2015-2016 (Year 35). Data have been collected on factors believed to be related to heart disease, including blood pressure, cholesterol and other lipids, and glucose as well as physical measurements such as weight and skinfold fat, as well as lifestyle factors, behavioral and psychological variables, and medical and family history.

Jackson Heart Study (JHS)

The JHS is a longitudinal, population-based cohort designed for prospective research into

the epidemiology and determinants of cardiovascular disease (CVD) in African American populations from the Jackson, Mississippi metropolitan area⁶. The design and sampling of JHS initially only included participants from the Jackson cohort of the ARIC study, random and family components. To reach recruitment goals and address community concerns regarding broad participation, an additional structured volunteer sample was added later⁷. Study baseline data collection began in late 2000 and was completed in early 2004, and a total of 5,306 male and female participants were recruited. The baseline examination included a home interview, a clinic visit, laboratory tests, complete blood cell counts, and a physical examination.

The Mount Sinai BioMe Biobank

The Mount Sinai BioMe Biobank is an ongoing, broadly consented, electronic health record (HER)-linked clinical care Biobank that enrolls participants non-selectively from the Mount Sinai Medical Center patient population. As of Oct 2021, BioMe comprises >60,000 participants, who represent a broad racial, ethnic and socioeconomic diversity, characteristic of the communities served by Mount Sinai Hospital. Participants are predominantly of African (24%), Hispanic/Latino (35%), European (32%), and other backgrounds (10%), and between 18 and 89 years. Enrolled participants consent to be followed throughout their clinical care (past, present, and future) in real-time, allowing us to integrate their genomic information with their EHRs for discovery research and clinical care implementation. Approximately 22% of the BioMe participants have been diagnosed with chronic disease, predominantly diabetes, cardiovascular disease, chronic kidney disease.

Multi-Ethnic Study of Atherosclerosis (MESA)

MESA was initiated in 2000 to investigate subclinical cardiovascular disease and the risk factors that predict progression to clinically overt cardiovascular disease in a multi-ethnic US population free of clinically recognized cardiovascular disease at study baseline.⁸ The population-based cohort recruited 6,814 men and women of European American (38%), African American (28%), Hispanic (22%), and Chinese American (12%) descent, 45-84 years of age from six field centers (Winston-Salem, NC; St. Paul, MN; Chicago, IL; Los Angeles, CA; New York, NY; Baltimore, MD). The baseline examination, which was designed to be the most comprehensive of all examinations, included a physical examination, biospecimen collection, completion of questionnaires, and non-invasive measurement of subclinical disease indicators and risk factors.

The Women's Health Initiative Study (WHI)

WHI is a long-term prospective study to investigate causes of morbidity and mortality among postmenopausal women in the United States⁹. Between 1993 and 1998, 161,808 women ages 50-79 years were recruited from 40 clinical centers and enrolled in randomized clinical trials or an observational cohort study. Women in the observational study received a standardized examination at baseline and interviewer-administered questionnaires. The following ancillary studies were included in this analysis: the Genetics and Epidemiology of Colorectal Cancer Consortium (GECCO), the Genomics and Randomized Trials Networks (GARNET), the Hip Fracture GWAS (HIPFX), the Women's Health Initiative Memory Study (WHIMS), and the Women's Health Initiative-SNP Health Association Resource (WHI-SHARE).

The participants included from GECCO, GARNET, HIPFX and WHIMS were

self-reported White, while participants included from WHI-SHARe were self-reported Black/African American.

Genotyping and imputation

Genotyping platform, quality control, and imputation methods are specified for UK Biobank and each PAGE study in **Supplemental Table 2**.

Lipoprotein (a) measurement

Lipoprotein (a) [Lp(a)] was measured using various assays at baseline visits, except in ARIC, which was measured at visit 4. The assay methods and the distributions of Lp(a) in participating studies are detailed in **Supplemental Table 3**. Participants with Lp(a) values below limits of detection or four standard deviations from the study- and ancestry-specific mean were excluded.

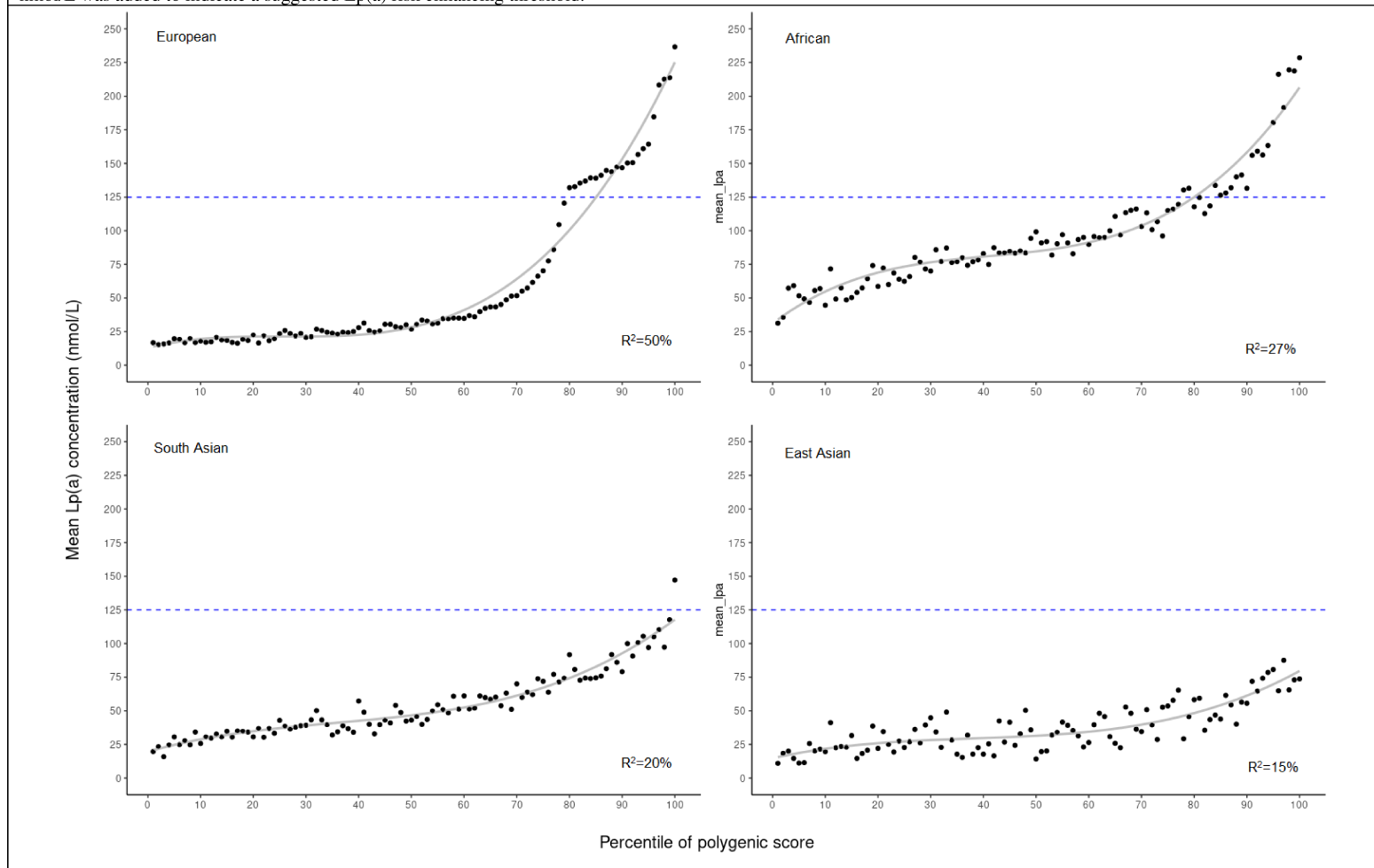
PRS construction

Because of the strong genetic effects of the *LPA* locus, we began by examining five approaches restricted to variants within 2 Mb of *LPA*. The first PRS we examined used data on 43 independent *LPA* variants, was constructed in an external European ancestral population and had the best performance of available Lp(a) PRS ($R^2 = 59\%$).¹⁰ We applied this PRS to African, South Asian, and East Asian participants in the UK Biobank to assess transportability of a European derived PRS across ancestries. Second, we examined two approaches (Pruning and Thresholding¹¹ and LDpred2¹²) that constructed PRS using independent discovery and target data within the same ancestry. Here, PAGE Study data served as our discovery sample and UK Biobank data served as the target sample. Because the PAGE Study did not include data on

participants of South Asian ancestry, we used trans-ethnic PAGE Study results for the discovery population. Our third approach - GWAS significant independent signals - was to construct Lp(a) PRS based on the independently associated variants that were identified across ancestry-specific GWAS meta-analyses using GCTA-COJO. For this approach, we included PAGE Study and UK Biobank participants and applied the cross-validation (Crosspred)¹³ method to account for lack of independence in the discovery and target samples. Fourth, to examine PRS performance in cases where independent discovery and target data are unavailable (e.g., South Asian participants) or when target data have very large sample size that could be informative for PRS construction, we estimated ancestrally specific PRS in UK Biobank participants using Crosspred.

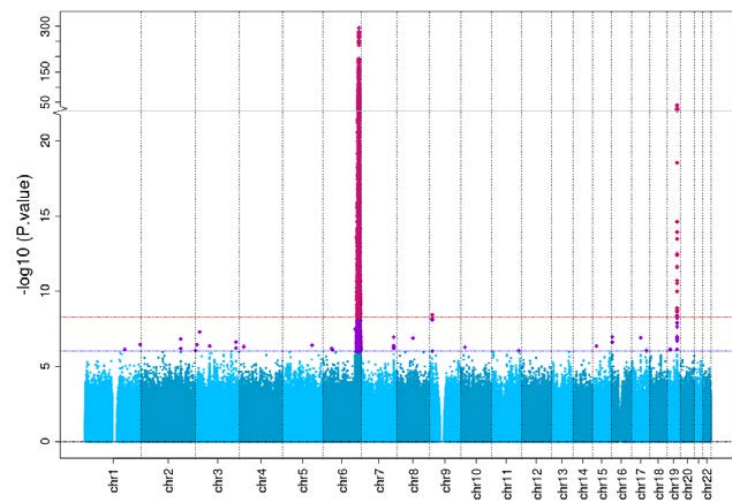
We also examined the accuracy of Lp(a) PRS extended to include variants outside the *LPA* locus. Here, we extended two approaches— GWAS significant independent signals and Crosspred. These methods were prioritized given their improved performance when compared to LDpred2 and Pruning and Thresholding. Briefly, we considered variants in loci harboring at least one genome-wide significant ($P < 5 \times 10^{-9}$) variant for the GWAS significant independent signals approach. For Crosspred, because evaluating all 1000 Genomes-imputed variants was computationally infeasible, we restricted to Hapmap3 variants, but did not impose any *P*-value based criteria.

Supplemental Figure 1. Calibration plots for lipoprotein (a) [Lp(a)] concentration according to the ancestry-specific polygenic risk score percentiles in four ancestral groups in UK Biobank. The agreement between the predicted and observed Lp(a) was assessed using the best-performing polygenic risk score in each ancestry. A blue dotted line at 125 nmol/L was added to indicate a suggested Lp(a) risk enhancing threshold.

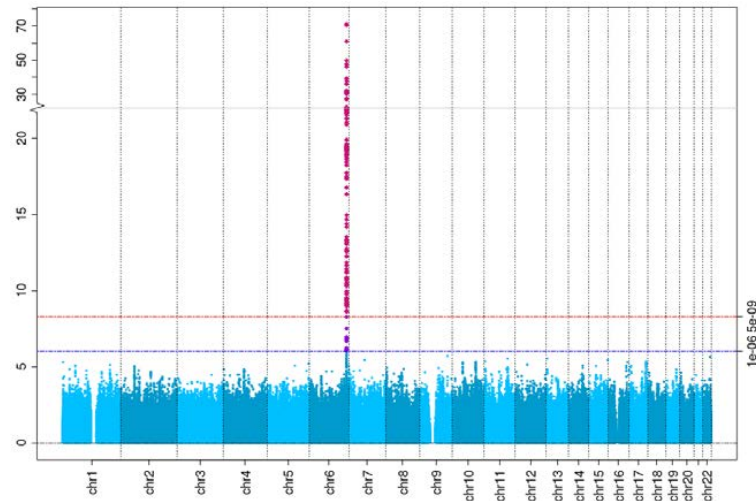


Supplemental Figure 2. Manhattan plots by race/ethnicity for a multi-ethnic GWAS of Lp(a) in (A) African, (B) East Asian, (C) European, and (D) South Asian descent populations. The genome-wide significant ($P < 5 \times 10^{-9}$) and genome-wide suggestive ($P < 5 \times 10^{-6}$) thresholds are shown by the red and blue dashed horizontal lines, respectively.

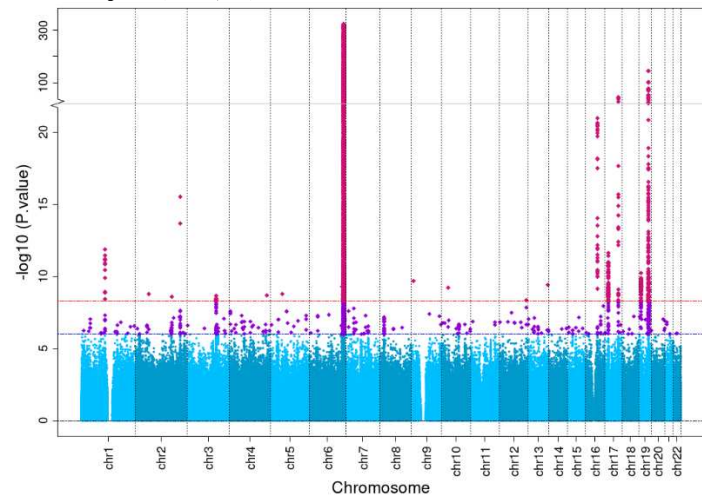
A. Africans (n=18,993)



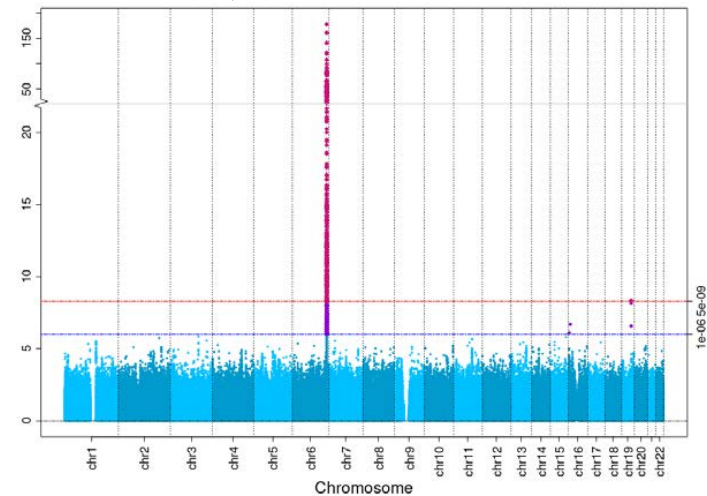
B. East Asians (n=2,189)



C. Europeans (n=354,843)



D. South Asians (n= 8,192)



Supplemental Table 1. Data sources and select characteristics by participating studies. Information on data sources for the United Kingdom Biobank (UK Biobank) and six Population Architecture through Genomics and Environment (PAGE) Study cohorts are described in detail. Distributions of the selected characteristics of the study participants are presented to provide an overall description of the study population.

	PAGE (n=50,703)						
	UK Biobank (n=357,096)	ARIC (n=11,457)	CARDIA (n=4,099)	WHI (n=4,361)	JHS (n=3,260)	MESA (n=4,650)	BioMe (n=22,876)
Data sources							
Study type	Longitudinal	Longitudinal	Longitudinal	Cohort and clinical trials	Longitudinal	Longitudinal	Biobank
Study focus	Wide range of complex disease	Cardiovascular disease	Cardiovascular disease	Women's health	Cardiovascular disease	Cardiovascular disease	Wide range of complex disease
Regions	United Kingdom (UK)	Washington County, MD; Forsyth County, NC; Jackson, MS; and Minneapolis, MN	Birmingham, AL; Chicago, IL; Minneapolis, MN; and Oakland, CA	40 Clinical Centers in the United States	Jackson, MS	Six US field centers	New York City, NY
Years of data collection	2006-present	1987-present	1985-present	1993-present	1998-present	2000-present	2007 - present
Follow-up assessment	Initial assessment in 22 centers in UK between 2006-2010; repeat of baseline assessment in 2013; linkages to cancer registry and hospital admissions	Semi-annual interview via telephone; an extensive examination at baseline in 1987-1989 and every 3 years	Follow-up examinations every 2-5 years	Annual in-person interviews, semi-annual phone interviews	Follow-up examinations and questionnaires every 2-5 years. Annual follow-up ongoing	Follow-up examinations and questionnaires every 2-5 years. Annual follow-up ongoing	Enrolled participants consent to be followed throughout their clinical care (past, present, and future) in real-time
Phenotypic data sources	Questionnaire, physical measures, samples, health record linkage (registries, EMR)	In-person examinations, limited CVD surveillance	In-person examinations, limited CVD surveillance	In-person examinations, limited CVD surveillance	In-person examinations, surveillance	In-person examinations, limited CVD surveillance	Electronic medical records
Participant characteristics							
Age - Median (years)	58	54	25	63	54	62	63
Age Range (years)	37-72	44-66	18-35	50-79	34-80+	45-84	18-92
Female - %	55	57	56	100	58	52	59
Race/Ethnicity or ancestry - No.							
African/African American	8,046	2,553	1,982	1,603	3,260	1,549	6,215
East Asian	2,189	0	0	0	0	706	0
European/White	338,669	8,904	2,117	2,758	0	2,395	7,715
South Asian	8,192	0	0	0	0	0	0
Hispanic/Latino	0	0	0	0	0	0	8,946

Supplemental Table 2. Genotyping, imputation, and quality control procedures implemented by UK Biobank and PAGE Study investigators.

	UK Biobank	PAGE Study									
		ARIC	CARDIA	JHS	PAGE MEGA*	MESA	WHI GARNET	WHI GECCO	WHI HIPfx	WHI SHARe	BioMe
Genotyping platform	Affymetrix UI Biobank Axiom array and Axiom UK BiLEVE genotyping array	Affymetrix Gene Chip SNP array 6.0	Affymetrix Gene Chip SNP array 6.0	Affymetrix Gene Chip SNP array 6.0	Infinium Expanded Multi-Ethnic Genotyping Array	Affymetrix Gene Chip SNP array 6.0	Illumina Human Omni 1-Quad v1-0 B	ONCOarray	Illumina 50K and 610K	Affymetrix Gene Chip SNP array 6.0	Regeneron Infinium Global Screening Array
QC filters											
Sample call rate	97	90	95	90	98	90	98	95	98	98	95
HWE threshold	$p > 10^{-6}$	$p > 10^{-6}$	$p > 10^{-6}$	$p > 10^{-6}$	$p > 10^{-6}$	$p > 10^{-6}$	$p > 10^{-6}$	$p > 10^{-7}$	$p > 10^{-6}$	$p > 10^{-6}$	$p > 10^{-5}$
Imputation software	IMPUTE v2.3.1	IMPUTE version 2.3.2	Mach (version 1.0.16)	Minimac3	IMPUTE version 2.3.2	IMPUTE version 2.3.2	IMPUTE version 2.3.2	Minimac2	IMPUTE version 2.3.2	IMPUTE version 2.3.2	IMPUTE 2
Reference panel	1000 Genomes Project Phase 1 and UK10K	1000 Genomes phase 3 v 5	1000 Genomes phase 3 v 5	TopMED	1000 Genomes phase 3 v 5	1000 Genomes phase 3 v 5	1000 Genomes phase 3 v 5	1000 Genomes phase 3 v 5	1000 Genomes phase 3 v 5	1000 Genomes phase 3 v 5	1000 Genomes phase 3 v 5
Build	37	37	37	37	37	37	37	37	37	37	37

*For this study, includes African American participants from the Women's Health Initiative

Supplemental Table 3. Description of methods used to develop polygenic risk score (PRS) of lipoprotein (a) in n=385,263 participants of African (n=19,333), East Asian (n=2,895), European (n=354,843), and South Asian (n=8,192) ancestry from the PAGE Study and UK Biobank.

Approach	Statistical method	Discovery data	Regions examined	Parameters	LD-reference	Software
External PRS	PRS developed using 43 variant identified by conditional analysis ¹⁰	CHD Exome+ Consortium; independent study of European ancestral populations ¹⁴	<i>LPA</i> region*	NA	NA	PLINK
Pruning and Thresholding (P+T)	LD-based clumping and p-value thresholding	Ancestry-specific PAGE Study results; trans-ethnic PAGE Study results for South Asian	<i>LPA</i> region*	P-value thresholds: from $5e^{-50}$ to 0.5; Clumping: $r^2 = 0.2$; window = 250kb	Four ancestral populations in UK Biobank	PRSice
LDpred2	Bayesian shrinkage		<i>LPA</i> region*	Heritability (h^2) and non-zero effect fractions (p) are automatically estimated from the data.	Four ancestral populations in UK Biobank	bigsnpr
Crosspred	Cross-validation method using penalized regression; addresses lack of independence between discovery and target data	Four ancestral populations in UK Biobank	<i>LPA</i> region*; Genome-wide	Tuning parameters for penalized regression using lassosum software; EUR: $\lambda = 0.01$, $s = 0.5$; AFR: $\lambda = 0.04$, $s = 0.2$; SAS: $\lambda = 0.01$, $s = 0.2$; EAS: $\lambda = 0.02$, $s = 0.2$	Ancestry-specific (AFR, EAS, EUR) or EUR (SAS) LD blocks developed based on the 1000 Genome data ¹⁵	lassosum, crosspred
GWAS significant independent signals	Independent signals by GCTA-COJO; PRS estimated using Crosspred	Ancestry-specific PAGE Study results and UK Biobank; trans-ethnic PAGE and UK Biobank study results for South Asian; lack of independence addressed using Crosspred	<i>LPA</i> region*; Genome-wide	Tuning parameters for penalized regression using lassosum software; EUR: $\lambda = 0.007$, $s = 0.2$; AFR: $\lambda = 0.001$, $s = 0.2$; SAS: $\lambda = 0.001$, $s = 0.2$; EAS: $\lambda = 0.04$, $s = 1$	Ancestry-specific (AFR, EAS, EUR) or EUR (SAS) LD blocks developed based on the 1000 Genome data ¹⁵	gcta, lassosum, crosspred

CHD = coronary heart disease; PAGE = Population Architecture using Genomics and Epidemiology; GWAS = genome-wide association study; EUR = European descent; AFR = African descent; SAS = South Asian descent; EAS = East Asian descent

Target data to assess Lp(a) PRS: Four ancestral populations in UK Biobank

**LPA* region \pm 2 Mb

Supplemental Table 4. The assay method, measured unit, and distributions of Lipoprotein (a) in participating studies. The distributions of lipoprotein (a) are further stratified by race and ethnicity in each study to present the variability in levels between different populations.

Participating studies and ancestry	N.	Assay method	Unit reported	Lipoprotein (a)*		
				Mean (SD)	Median (25 th tile-75 th tile)	>150 nmol/L (%)
UK Biobank						
European	338,669			59.5 (72.6)	23.7 (10.0-87.3)	45,804 (14)
African	8,046	Immunturbidimetry (Beckman)	nmol/L	96.7 (76.3)	73.8 (42.9-132.3)	1,667 (21)
South Asian	8,192			54.4 (57.2)	34.3 (14.2-71.6)	665 (8)
East Asian	2,189			36.8 (45.0)	17.6 (9.1-45.7)	97 (4)
ARIC						
European	8,904	Immunturbidimetry (Denka Seiken)	mg/dL	48.2 (28.3)	20.9 (8.9, 62.8)	727 (8.2)
African	2,553			87.4 (32.6)	70.6 (37.7, 116.6)	382 (15.0)
CARDIA						
European	2,117	ELISA	mg/dL	30.5 (17.1)	13.7 (5.7, 43.6)	23 (1.1)
African	1,982			62.1 (23.3)	50.1 (24.0, 88.7)	120 (6.0)
WHI						
European	2,758	ELISA	mg/dL	30.5 (17.1)	13.7 (5.7, 43.6)	23 (1.1)
African	1,603			62.1 (23.3)	50.1 (24.0, 88.7)	120 (6.0)
JHS (African)	3,260	Immunturbidimetry (Denka Seiken)	mg/dL	125.3 (100.2)	98.6 (50.7, 172.7)	1030 (31.6)
MESA						
European	2,395	Immunturbidimetry (Denka Seiken)	mg/dL	49.2 (66.0)	22.8 (8.2, 61.4)	221 (9.2)
African	1,549			98.5 (83.7)	74.1 (39.6, 134.8)	347 (22.4)
East Asian	706			39.8 (49.7)	23.0 (10.6, 46.3)	37 (5.2)

*Lp(a) levels reported in mg/dL was converted to nmol/L using the equation: Lp(a), nmol/L=2.18×Lp(a), mg/dL-3.83 provided by Madsen et al.¹⁶

Supplemental Table 5. Lead variants for genome wide-significant ($P < 5 \times 10^{-8}$) loci discovered in ancestry-specific Lp(a) genome-wide association studies (GWAS) of African (n=18,993), East Asian (n=2,895), European (n=354,843), and South Asian (n=8,192) PAGE Study and UK Biobank participants.

Lead variant	Chr	Position (hg19)	Effect allele	Non-effect allele	Locus	Coded allele effect (SE)	χ^2_Q	Effect allele frequency ¹				P-value			
								AFR	EAS	EUR	SAS	AFR	EAS	EUR	SAS
<i>African</i>															
rs41269135	6	161087440	A	G	<i>LPA</i>	0.94 (0.026)	0.59	0.0494	0	0	0	2.06E-294	.	.	.
rs7039957	9	12728543	T	C	<i>LURAPIL-ASI</i>	-0.19 (0.033)	0.40	0.9674	0.8447	0.9271	0.7349	3.66E-09	0.56	0.9858	0.7703
rs7412	19	45412079	T	C	<i>APOE</i>	-0.26 (0.019)	0.0036	0.1098	0.0853	0.0778	0.0428	2.41E-41	0.000015	6.51E-146	4.58E-09
<i>East Asian</i>															
rs7770628	6	161018174	T	C	<i>LPA</i>	-0.74 (0.041)	0.10	0.7489	0.8856	0.5308	0.6765	0.1738	8.30E-72	9.87E-40	1.16E-140
<i>European</i>															
rs599839	1	109822166	A	G	<i>PSRC1</i>	0.025 (0.0035)	0.52	0.2609	0.9301	0.7725	0.7346	0.3097	0.30	1.33E-12	0.869
rs1047891	2	211540507	A	C	<i>CPSI</i>	-0.026 (0.0031)	0.67	0.363	0.1738	0.3156	0.3016	0.005996	0.60	2.98E-16	0.3489
rs4678322	3	135812523	T	G	<i>PPP2R3A</i>	0.021 (0.0035)	0.32	0.399	0.1383	0.2304	0.2398	0.2459	0.15	2.14E-09	0.01481
rs111321550	4	174514218	A	C	<i>HAND2AS1-MORF4</i>	-0.077 (0.013)	N/a	0	0	0.9847	0.9909	.	.	2.03E-09	0.5903
rs571472683	5	55495591	A	G	<i>ANKRD55</i>	-0.13 (0.021)	N/a	0	0	0.0059	0	.	.	1.64E-09	.
rs10455872	6	161010118	A	G	<i>LPA</i>	-1.21 (0.026)	0.19	0.9882	0	0.9333	0.9891	7.33E-61	.	<1E-300	2.97E-50
rs141546126	9	10599267	A	G	<i>PTPRD</i>	0.14 (0.023)	N/a	0	0	0.0052	0	.	.	2.04E-10	.
rs12412956	10	31009857	A	G	<i>SVIL2P-LINC02644</i>	0.046 (0.0074)	0.083	0.9916	0.9682	0.9525	0.9493	0.2857	0.59	6.02E-10	0.5481
rs141027916	12	125539193	T	C	<i>THRIL-AACS</i>	-0.1 (0.017)	0.74	0	0	0.0088	0	.	.	4.39E-09	.
rs543756678	13	110797505	T	C	<i>LOC101927712-COL4A1</i>	0.13 (0.021)	N/a	0	0.0138	0.0058	0	.	0.87	3.84E-10	.
rs56156922	16	56987369	T	C	<i>HERPUDI1-CETP</i>	0.03 (0.0031)	0.20	0.8472	0.8345	0.6768	0.6669	0.437	0.95	1.06E-21	0.6894
rs8178824	17	64224775	T	C	<i>APOH</i>	0.12 (0.0087)	0.56	0.0051	0	0.0304	0.0162	0.05257	.	1.54E-45	0.05022
rs1065853	19	45413233	T	G	<i>APOE</i>	-0.14 (0.0056)	0.96	0.1156	0.086	0.0777	0.0432	6.12E-41	0.000025	1.00E-145	7.20E-09
<i>South Asian</i>															
rs73596816	6	161017363	A	G	<i>LPA</i>	0.77 (0.027)	N/a	0.0361	0.0419	0.0372	0.0927	1.04E-13	9.60E-47	3.25E-07	2.45E-178
rs7412	19	45412079	T	C	<i>APOE</i>	-0.23 (0.039)	N/a	0.1098	0.0853	0.0778	0.0428	2.41E-41	0.000015	6.51E-146	4.58E-09

¹. Weighted average of PAGE Study and UK Biobank ancestry-specific effect allele frequencies. AFR, African. Chr, chromosome. EAS, East Asian. EUR, European. N/a, not applicable. SAS, South Asian. SE, standard error. χ^2_Q , Cochran's Q test of heterogeneity.

Supplemental Table 6. Number of independent secondary signals, by chromosome, in ancestry specific GWAS of Lp(a) among PAGE study and UK Biobank participants. Results are restricted to loci with at least two independent signals in at least one population.

Ancestry	Chromosome			
	2	6	17	19
African	0	38	0	0
East Asian	0	2	0	0
European	2	276	1	4
South Asian	0	15	0	0

Supplemental Table 7. Primary and secondary signals, by race/ethnicity, for a GWAS of Lp(a). Secondary signals are retained if *P*-value is <5x10⁻⁹ and the variant is independent of other index variants (*r*²<0.1).

Race/ethnicity	SNP ID	Chr	BP	Index allele	Frequency	Beta*	SE*	P-value*
African	6:161010118:A_G	6	161010118	A	0.9882	-1.0337	0.0599	1.24E-66
	6:160986280:A_G	6	160986280	A	0.0294	0.7916	0.0465	5.16E-65
	6:161206375:G_T	6	161206375	T	0.986	0.8037	0.0550	2.82E-48
	6:161022169:C_T	6	161022169	T	0.9785	-0.7777	0.0534	5.02E-48
	6:161031253:C_T	6	161031253	T	0.1428	-0.2514	0.0197	2.71E-37
	6:161016666:C_CTT	6	161016666	CTT	0.9249	0.2884	0.0249	4.02E-31
	6:160650281:A_C	6	160650281	A	0.0078	2.1195	0.1859	4.00E-30
	6:160794891:C_G	6	160794891	C	0.9897	-0.7258	0.0670	2.56E-27
	6:161087440:A_G	6	161087440	A	0.0494	0.3915	0.0376	2.32E-25
	6:161092884:A_G	6	161092884	A	0.9939	-0.9511	0.0923	6.91E-25
	6:160942197:G_T	6	160942197	T	0.9928	0.8944	0.0872	1.11E-24
	6:161067949:C_G	6	161067949	C	0.6107	0.2038	0.0201	4.00E-24
	6:161164187:A_C	6	161164187	A	0.8928	-0.1895	0.0193	1.19E-22
	6:161017363:A_G	6	161017363	A	0.0361	0.3415	0.0352	2.62E-22
	6:160608101:C_T	6	160608101	T	0.0057	-2.0618	0.2180	3.21E-21
	6:160999154:G_T	6	160999154	T	0.9557	-0.2764	0.0297	1.37E-20
	6:161005103:C_CT	6	161005103	CT	0.967	0.3034	0.0327	1.80E-20
	6:160775652:G_T	6	160775652	T	0.4167	0.1154	0.0127	1.36E-19
	6:160986915:A_C	6	160986915	A	0.0417	-0.2945	0.0331	5.61E-19
	6:160595654:A_G	6	160595654	A	0.0771	-0.1982	0.0227	2.57E-18
	6:161113698:C_T	6	161113698	T	0.0447	0.2649	0.0307	6.26E-18
	6:161114553:A_G	6	161114553	A	0.9776	0.3912	0.0455	8.44E-18
	6:160698826:C_T	6	160698826	T	0.1881	0.1429	0.0171	6.08E-17
	6:161119578:C_T	6	161119578	T	0.9595	-0.2622	0.0322	4.22E-16
	6:161100997:G_T	6	161100997	T	0.0208	0.5204	0.0646	7.84E-16
	6:161366947:A_G	6	161366947	A	0.1961	0.1389	0.0173	1.11E-15
	6:161028667:A_G	6	161028667	A	0.8243	-0.1479	0.0188	3.48E-15
	6:160991306:A_G	6	160991306	A	0.0232	-0.3325	0.0427	6.75E-15
	6:161086111:A_G	6	161086111	A	0.9865	0.4476	0.0590	3.44E-14
	6:161240841:A_C	6	161240841	A	0.8989	-0.1445	0.0195	1.29E-13
	6:160929812:C_G	6	160929812	C	0.0557	0.2012	0.0278	4.45E-13
	6:161020158:A_G	6	161020158	A	0.009	0.9252	0.1301	1.13E-12
	6:160810118:C_T	6	160810118	T	0.0115	0.6961	0.1004	4.05E-12
	6:160991302:G_T	6	160991302	T	0.9732	0.2839	0.0411	5.07E-12
	6:161013013:C_T	6	161013013	T	0.9916	-0.7440	0.1140	6.76E-11
	6:161723526:C_T	6	161723526	T	0.9291	0.2250	0.0346	7.46E-11
	6:161125102:C_T	6	161125102	T	0.9929	-0.9176	0.1473	4.74E-10
	6:160882589:A_G	6	160882589	A	0.8838	0.1182	0.0193	8.85E-10
	6:160534942:C_T	6	160534942	T	0.9928	-0.9064	0.1497	1.39E-09
	9:12728543:C_T	9	12728543	T	0.9674	-0.1925	0.0326	3.66E-09
	19:45412079:C_T	19	45412079	T	0.1098	-0.2592	0.0193	4.72E-41
East Asian	6:161018174:C_T	6	161018174	T	0.8836	-0.6832	0.0446	6.17E-53
	6:161087863:C_T	6	161087863	T	0.7738	0.2462	0.0339	3.71E-13
	6:160910517:A_T	6	160910517	A	0.0327	0.4592	0.0737	4.73E-10
European	1:109822166:A_G	1	109822166	A	0.7725	0.0248	0.0035	1.39E-12
	2:211540507:A_C	2	211540507	A	0.3156	-0.0257	0.0031	1.14E-16
	2:64773731:A_C	2	64773731	A	0.9932	0.1211	0.0201	1.70E-09
	2:172266423:C_T	2	172266423	T	0.0112	0.0874	0.0147	2.76E-09
	3:135812523:G_T	3	135812523	T	0.2304	0.0208	0.0035	2.81E-09
	4:174514218:A_C	4	174514218	A	0.9847	-0.0773	0.0129	2.07E-09
	5:55495591:A_G	5	55495591	A	0.0059	-0.1270	0.0211	1.76E-09
	6:160610902:C_T	6	160610902	T	0.9924	-0.9600	0.0247	<1E-300
	6:160627001:C_G	6	160627001	C	0.147	-0.2398	0.0061	<1E-300
	6:160697628:G_T	6	160697628	T	0.2939	0.2366	0.0057	<1E-300
	6:160721376:A_T	6	160721376	A	0.9427	-0.3790	0.0084	<1E-300
	6:160727799:A_G	6	160727799	A	0.9839	-0.9739	0.0190	<1E-300
	6:160789296:A_G	6	160789296	A	0.7117	0.2904	0.0061	<1E-300
	6:160822756:A_T	6	160822756	A	0.0389	0.9555	0.0150	<1E-300
	6:160842725:A_G	6	160842725	A	0.907	-0.7592	0.0098	<1E-300
	6:160868121:A_G	6	160868121	A	0.0294	-1.2331	0.0189	<1E-300
	6:160888021:G_T	6	160888021	T	0.1188	-0.7611	0.0103	<1E-300
	6:160894448:A_G	6	160894448	A	0.9716	0.4333	0.0108	<1E-300
	6:160903421:A_G	6	160903421	A	0.0101	0.9987	0.0203	<1E-300
	6:160915695:A_C	6	160915695	A	0.0332	0.7394	0.0135	<1E-300
	6:160953137:C_T	6	160953137	T	0.9824	-0.6420	0.0144	<1E-300
	6:160974578:A_G	6	160974578	A	0.1413	0.3988	0.0075	<1E-300

6:160976262:C_T	6	160976262	T	0.9892	0.8183	0.0191	<1E-300
6:160980330:C_T	6	160980330	T	0.4771	0.4148	0.0052	<1E-300
6:161027131:A_C	6	161027131	A	0.9927	0.8728	0.0207	<1E-300
6:161071982:A_G	6	161071982	A	0.0638	-0.5145	0.0100	<1E-300
6:161078754:A_G	6	161078754	A	0.016	-0.8697	0.0177	<1E-300
6:161097590:A_T	6	161097590	A	0.8416	0.6813	0.0115	<1E-300
6:161105200:A_G	6	161105200	A	0.8299	-0.7215	0.0104	<1E-300
6:161118190:G_T	6	161118190	T	0.9945	1.1445	0.0260	<1E-300
6:161257961:A_G	6	161257961	A	0.5566	0.2257	0.0047	<1E-300
6:161280379:C_T	6	161280379	T	0.1912	0.3727	0.0067	<1E-300
6:161475692:A_T	6	161475692	A	0.0072	1.0530	0.0205	<1E-300
6:160991737:A_C	6	160991737	A	0.015	0.5541	0.0151	5.98E-295
6:161154450:A_G	6	161154450	A	0.0297	-0.3912	0.0108	4.70E-286
6:161106730:G_T	6	161106730	T	0.01	-0.6892	0.0191	3.75E-285
6:160712481:A_G	6	160712481	A	0.0167	0.4639	0.0131	1.49E-273
6:161112805:A_G	6	161112805	A	0.0162	0.4952	0.0141	2.62E-268
6:160877594:G_T	6	160877594	T	0.008	0.6960	0.0201	3.33E-262
6:160642103:C_G	6	160642103	C	0.2393	0.1766	0.0052	1.54E-255
6:161231196:A_G	6	161231196	A	0.0102	-0.5693	0.0167	7.30E-255
6:161127501:A_G	6	161127501	A	0.9944	0.7682	0.0225	8.70E-255
6:160910517:A_T	6	160910517	A	0.04	-0.5131	0.0151	2.70E-254
6:161286623:A_G	6	161286623	A	0.0076	0.6613	0.0195	5.32E-253
6:160699471:C_T	6	160699471	T	0.9919	0.9672	0.0285	8.67E-252
6:161608252:A_G	6	161608252	A	0.0879	-0.2468	0.0073	3.27E-250
6:160697866:C_G	6	160697866	C	0.9885	-0.6289	0.0188	6.16E-245
6:161078894:C_T	6	161078894	T	0.9912	-0.5798	0.0174	7.76E-245
6:160734662:A_G	6	160734662	A	0.9924	0.6409	0.0195	1.63E-237
6:161632692:C_T	6	161632692	T	0.9916	-0.6031	0.0184	4.77E-235
6:161237578:C_CA	6	161237578	CA	0.7929	-0.1804	0.0056	1.27E-228
6:161272446:A_G	6	161272446	A	0.0242	-0.5956	0.0185	8.49E-228
6:160975629:A_G	6	160975629	A	0.025	-0.4438	0.0138	2.08E-227
6:161186302:A_G	6	161186302	A	0.9548	0.2877	0.0091	2.12E-221
6:161548026:A_G	6	161548026	A	0.0065	0.6943	0.0222	2.73E-214
6:161124143:G_T	6	161124143	T	0.0233	-0.3804	0.0122	3.09E-213
6:160710480:A_G	6	160710480	A	0.0272	-0.4328	0.0142	6.56E-205
6:161125631:C_T	6	161125631	T	0.7658	-0.1960	0.0064	5.29E-204
6:161618071:A_G	6	161618071	A	0.0125	0.4582	0.0151	2.40E-203
6:161339399:A_G	6	161339399	A	0.9731	0.3600	0.0119	1.70E-202
6:160952816:C_T	6	160952816	T	0.9852	0.5368	0.0179	6.81E-198
6:160841075:A_G	6	160841075	A	0.0144	-0.5460	0.0183	5.19E-196
6:160599325:A_AAG	6	160599325	A	0.6377	0.1226	0.0041	5.10E-195
6:161017825:C_T	6	161017825	T	0.0053	-0.7300	0.0246	5.72E-194
6:161640802:C_T	6	161640802	T	0.0168	0.3887	0.0133	1.60E-187
6:161159619:C_T	6	161159619	T	0.9936	0.7021	0.0241	1.89E-186
6:161074983:A_T	6	161074983	A	0.0375	-0.2975	0.0104	5.62E-180
6:161147619:T_TA	6	161147619	T	0.9944	-0.6285	0.0220	6.37E-179
6:160231601:C_G	6	160231601	C	0.0316	-0.2791	0.0098	1.74E-177
6:160938131:A_C	6	160938131	A	0.0105	0.5039	0.0184	7.12E-166
6:161330808:C_G	6	161330808	C	0.0069	-0.5633	0.0206	2.57E-165
6:161236385:C_T	6	161236385	T	0.982	-0.6101	0.0223	7.70E-165
6:161206068:A_G	6	161206068	A	0.0104	-0.4631	0.0170	3.09E-164
6:160809918:A_G	6	160809918	A	0.0075	-0.5521	0.0202	1.13E-163
6:160696919:C_T	6	160696919	T	0.0717	0.2632	0.0097	1.74E-162
6:161285786:C_T	6	161285786	T	0.9903	0.5333	0.0198	3.41E-159
6:161556852:C_T	6	161556852	T	0.0476	-0.2140	0.0080	1.08E-158
6:161225253:A_G	6	161225253	A	0.992	0.6081	0.0229	2.00E-155
6:160818614:A_C	6	160818614	A	0.9949	0.6299	0.0239	5.96E-153
6:160953642:A_G	6	160953642	A	0.9833	0.4602	0.0180	7.86E-144
6:160469853:C_CAA	6	160469853	CAA	0.9599	0.2139	0.0084	2.01E-143
6:160966409:C_T	6	160966409	T	0.6627	0.1404	0.0056	2.27E-139
6:160628128:C_T	6	160628128	T	0.0121	-0.4397	0.0175	5.82E-139
6:161127106:C_T	6	161127106	T	0.0157	-0.4013	0.0161	1.15E-136
6:161645205:C_T	6	161645205	T	0.174	-0.1181	0.0048	5.54E-136
6:160287100:G_GTTT	6	160287100	G	0.833	0.1160	0.0047	2.92E-132
6:161126323:C_T	6	161126323	T	0.0626	-0.1942	0.0079	8.08E-132
6:161024293:C_T	6	161024293	T	0.2453	-0.1173	0.0049	6.22E-126
6:161351132:C_T	6	161351132	T	0.0056	-0.5360	0.0226	2.24E-124
6:160592112:A_G	6	160592112	A	0.0074	-0.4742	0.0202	6.97E-122
6:160707986:C_T	6	160707986	T	0.9818	-0.3066	0.0132	1.50E-119
6:161068235:A_T	6	161068235	A	0.987	0.3450	0.0149	6.40E-118

6:160444632:A_G	6	160444632	A	0.0064	0.5407	0.0235	7.71E-117
6:160643819:C_T	6	160643819	T	0.1738	-0.1229	0.0054	1.23E-115
6:161534516:A_G	6	161534516	A	0.9916	0.4452	0.0196	6.81E-114
6:161478381:C_T	6	161478381	T	0.9936	-0.4398	0.0200	1.29E-107
6:160906922:G_T	6	160906922	T	0.043	-0.2745	0.0125	6.33E-107
6:161565731:C_G	6	161565731	C	0.9945	0.5059	0.0232	4.30E-105
6:160300221:A_G	6	160300221	A	0.2314	-0.0918	0.0042	1.75E-104
6:160475532:C_CGTT	6	160475532	CGTT	0.9943	-0.4888	0.0226	1.65E-103
6:160505317:A_G	6	160505317	A	0.9921	0.4819	0.0224	1.11E-102
6:159956709:C_G	6	159956709	C	0.0327	0.1949	0.0091	3.06E-101
6:161352234:A_G	6	161352234	A	0.034	-0.2149	0.0101	3.63E-101
6:160251955:C_T	6	160251955	T	0.6969	0.0813	0.0038	1.82E-100
6:161544035:A_G	6	161544035	A	0.038	0.2230	0.0105	2.73E-100
6:161490712:G_T	6	161490712	T	0.9918	-0.4057	0.0192	3.66E-99
6:161294759:G_GCA	6	161294759	G	0.8963	0.1465	0.0069	1.03E-98
6:161389720:A_G	6	161389720	A	0.0059	0.4718	0.0225	6.14E-98
6:160185151:A_C	6	160185151	A	0.9817	-0.2679	0.0128	2.23E-97
6:161299811:A_G	6	161299811	A	0.9769	0.2622	0.0127	2.06E-94
6:161172374:C_T	6	161172374	T	0.0147	-0.3037	0.0149	3.89E-92
6:161004630:C_T	6	161004630	T	0.9939	0.4622	0.0228	1.08E-91
6:160918070:G_GT	6	160918070	G	0.0325	0.2555	0.0126	9.33E-91
6:161006979:T_TAAAC	6	161006979	T	0.0106	-0.4260	0.0211	2.12E-90
6:160740880:A_G	6	160740880	A	0.0075	-0.4142	0.0207	3.65E-89
6:160955713:G_T	6	160955713	T	0.0227	0.2486	0.0124	7.19E-89
6:161005272:C_T	6	161005272	T	0.0724	0.1482	0.0074	8.70E-89
6:160455976:A_G	6	160455976	A	0.9542	0.1605	0.0081	1.88E-88
6:160915513:C_G	6	160915513	C	0.9888	0.3595	0.0182	6.08E-87
6:160486533:C_T	6	160486533	T	0.0061	-0.5379	0.0272	7.19E-87
6:161606358:C_T	6	161606358	T	0.0098	-0.3385	0.0172	2.04E-86
6:161089817:A_G	6	161089817	A	0.1653	0.1501	0.0077	1.40E-85
6:161312655:C_T	6	161312655	T	0.9239	-0.1728	0.0089	2.15E-83
6:161565180:A_G	6	161565180	A	0.0261	-0.2293	0.0119	1.88E-82
6:161278005:G_T	6	161278005	T	0.9946	0.4336	0.0226	5.57E-82
6:160310512:C_T	6	160310512	T	0.006	-0.4504	0.0236	2.56E-81
6:161157310:C_T	6	161157310	T	0.0125	-0.2801	0.0148	5.53E-80
6:160529016:A_G	6	160529016	A	0.0081	-0.4625	0.0245	2.35E-79
6:161689812:G_GTCCA TATAATT	6	161689812	G	0.8102	-0.0813	0.0044	1.10E-77
6:161480419:C_T	6	161480419	T	0.9945	0.4057	0.0219	1.15E-76
6:161366675:C_G	6	161366675	C	0.9852	-0.2692	0.0145	1.72E-76
6:159754524:C_CA	6	159754524	CA	0.1211	-0.0892	0.0048	2.72E-76
6:161215480:A_G	6	161215480	A	0.9949	-0.4523	0.0246	3.24E-75
6:160655331:C_G	6	160655331	C	0.0126	0.2828	0.0156	2.35E-73
6:169290804:C_T	6	169290804	T	0.0061	-0.3628	0.0201	1.70E-72
6:161320210:A_G	6	161320210	A	0.2907	-0.0885	0.0049	1.71E-72
6:160401264:A_G	6	160401264	A	0.9335	0.1287	0.0072	1.64E-71
6:161453525:C_T	6	161453525	T	0.0134	0.2625	0.0147	1.80E-71
6:161101714:A_G	6	161101714	A	0.9924	0.3602	0.0202	3.78E-71
6:160907681:A_G	6	160907681	A	0.0051	-0.4494	0.0254	2.67E-70
6:159958502:A_C	6	159958502	A	0.0288	0.1867	0.0106	8.30E-70
6:166966915:A_C	6	166966915	A	0.9927	0.3088	0.0180	2.61E-66
6:160426622:C_T	6	160426622	T	0.0273	0.1691	0.0099	4.39E-65
6:160604202:C_T	6	160604202	T	0.0055	-0.4070	0.0241	6.97E-64
6:160489092:T_TGG	6	160489092	T	0.8965	-0.0953	0.0057	4.74E-63
6:161989710:C_T	6	161989710	T	0.6812	-0.0543	0.0033	1.61E-60
6:167599101:A_G	6	167599101	A	0.3165	-0.0534	0.0033	1.50E-59
6:160633223:A_G	6	160633223	A	0.0274	-0.1805	0.0113	1.56E-57
6:162808219:A_G	6	162808219	A	0.0061	0.3067	0.0194	3.03E-56
6:161155264:C_T	6	161155264	T	0.9836	0.2408	0.0153	1.61E-55
6:161368353:A_G	6	161368353	A	0.0475	-0.1563	0.0100	5.44E-55
6:160783782:C_T	6	160783782	T	0.0153	0.2557	0.0164	7.15E-55
6:167813541:C_T	6	167813541	T	0.0073	-0.3012	0.0193	1.26E-54
6:161727383:A_T	6	161727383	A	0.0083	0.2856	0.0184	1.80E-54
6:161314984:C_T	6	161314984	T	0.9902	0.2997	0.0194	7.70E-54
6:160712416:A_T	6	160712416	A	0.9492	0.1589	0.0103	9.62E-54
6:161700177:A_G	6	161700177	A	0.9693	-0.1483	0.0096	2.49E-53
6:166157448:C_T	6	166157448	T	0.01	-0.2552	0.0166	2.77E-53
6:161491684:G_T	6	161491684	T	0.006	0.3242	0.0212	1.11E-52
6:151591640:C_T	6	151591640	T	0.9868	-0.2023	0.0133	1.33E-52
6:161279121:G_T	6	161279121	T	0.9949	-0.3633	0.0239	2.68E-52

6:162723021:C_T	6	162723021	T	0.9352	-0.0921	0.0061	1.77E-51
6:160180003:C_T	6	160180003	T	0.0068	0.3057	0.0203	4.70E-51
6:167732122:A_C	6	167732122	A	0.2747	0.0545	0.0036	1.05E-50
6:162254160:A_G	6	162254160	A	0.3763	0.0468	0.0031	1.89E-50
6:160761788:C_T	6	160761788	T	0.0059	-0.3661	0.0245	2.29E-50
6:154484259:A_G	6	154484259	A	0.011	-0.2117	0.0145	1.63E-48
6:160575008:C_G	6	160575008	C	0.9886	0.2567	0.0176	2.06E-48
6:155231603:C_T	6	155231603	T	0.0056	-0.3252	0.0223	4.52E-48
6:161998222:A_G	6	161998222	A	0.9948	0.3216	0.0221	7.88E-48
6:169914012:C_T	6	169914012	T	0.0053	0.3270	0.0226	1.66E-47
6:159955911:A_G	6	159955911	A	0.0051	-0.3399	0.0236	6.13E-47
6:160412524:A_G	6	160412524	A	0.0085	-0.2450	0.0170	6.22E-47
6:156104230:A_G	6	156104230	A	0.9852	0.1831	0.0128	2.95E-46
6:156771172:C_T	6	156771172	T	0.0061	-0.2919	0.0206	1.04E-45
6:162639223:C_T	6	162639223	T	0.0468	0.1049	0.0074	1.13E-45
6:153219139:C_T	6	153219139	T	0.0126	0.1981	0.0140	1.25E-45
6:165822976:C_T	6	165822976	T	0.0415	-0.1108	0.0079	8.19E-45
6:158739931:A_ATTTT TTTTT	6	158739931	A	0.9392	0.0897	0.0064	8.37E-45
6:152794383:C_T	6	152794383	T	0.9727	-0.1277	0.0091	1.10E-44
6:156936954:C_T	6	156936954	T	0.0367	0.1109	0.0079	1.13E-44
6:152775812:C_T	6	152775812	T	0.0063	0.2918	0.0208	1.48E-44
6:160340256:A_C	6	160340256	A	0.9873	-0.2072	0.0148	1.86E-44
6:160258860:C_G	6	160258860	C	0.0212	0.1560	0.0112	1.87E-44
6:166522384:A_C	6	166522384	A	0.9929	0.2587	0.0185	2.77E-44
6:160606105:A_G	6	160606105	A	0.9613	0.1360	0.0097	2.99E-44
6:158570503:C_G	6	158570503	C	0.9903	-0.2228	0.0160	5.07E-44
6:156788129:C_CA	6	156788129	CA	0.8298	-0.0563	0.0041	8.56E-44
6:163565779:C_T	6	163565779	T	0.1256	0.0632	0.0046	8.90E-44
6:159430012:A_G	6	159430012	A	0.9859	0.1815	0.0131	1.19E-43
6:160467243:A_G	6	160467243	A	0.9897	0.2338	0.0169	1.32E-43
6:161656909:C_G	6	161656909	C	0.0187	-0.1647	0.0119	1.80E-43
6:161551024:A_G	6	161551024	A	0.0834	-0.0919	0.0067	1.93E-43
6:166366905:C_T	6	166366905	T	0.0186	-0.1540	0.0111	1.93E-43
6:161709278:A_G	6	161709278	A	0.017	0.1782	0.0129	2.08E-43
6:161751750:G_T	6	161751750	T	0.9933	0.2684	0.0195	3.16E-43
6:151724302:A_G	6	151724302	A	0.9943	-0.3005	0.0218	3.22E-43
6:160159702:A_G	6	160159702	A	0.0079	-0.2599	0.0189	5.13E-43
6:164993256:A_C	6	164993256	A	0.9898	-0.2216	0.0162	1.09E-42
6:153090789:A_G	6	153090789	A	0.9901	0.2202	0.0161	1.16E-42
6:162280076:A_G	6	162280076	A	0.7117	0.0443	0.0033	7.24E-42
6:161830218:C_T	6	161830218	T	0.0062	0.2856	0.0212	1.66E-41
6:165198415:C_T	6	165198415	T	0.0103	0.2077	0.0154	1.66E-41
6:161343833:A_G	6	161343833	A	0.0065	0.2838	0.0211	2.75E-41
6:155513629:C_T	6	155513629	T	0.0301	-0.1205	0.0090	2.84E-41
6:160180095:A_C	6	160180095	A	0.0084	-0.2469	0.0185	7.90E-41
6:170379025:C_T	6	170379025	T	0.1355	-0.0580	0.0043	1.43E-40
6:159134426:C_T	6	159134426	T	0.0113	0.1943	0.0146	2.66E-40
6:161330413:C_T	6	161330413	T	0.0069	0.2642	0.0199	3.35E-40
6:161712208:C_T	6	161712208	T	0.9929	0.2759	0.0208	3.67E-40
6:155378316:C_T	6	155378316	T	0.024	-0.1322	0.0100	4.49E-40
6:160427234:A_C	6	160427234	A	0.0075	0.3048	0.0231	6.88E-40
6:162280401:C_T	6	162280401	T	0.0136	-0.1799	0.0136	9.25E-40
6:157637814:A_G	6	157637814	A	0.3604	0.0427	0.0032	1.66E-39
6:166365978:C_T	6	166365978	T	0.0132	-0.1733	0.0132	4.43E-39
6:161010118:A_G	6	161010118	A	0.9333	-0.3663	0.0281	7.94E-39
6:162696500:A_C	6	162696500	A	0.0083	-0.2199	0.0169	1.24E-38
6:158838475:A_G	6	158838475	A	0.0052	0.2902	0.0223	1.42E-38
6:166133878:C_T	6	166133878	T	0.0482	-0.0911	0.0070	1.65E-38
6:159888248:C_T	6	159888248	T	0.199	0.0510	0.0039	2.71E-38
6:161307185:C_T	6	161307185	T	0.9842	0.1758	0.0136	3.56E-38
6:151845594:A_T	6	151845594	A	0.9721	0.1176	0.0091	3.61E-38
6:152626726:C_T	6	152626726	T	0.0083	-0.2227	0.0173	7.36E-38
6:164982125:A_T	6	164982125	A	0.0212	-0.1341	0.0104	8.04E-38
6:169461339:A_ATATT ATTAT	6	169461339	A	0.812	-0.0494	0.0038	9.90E-38
6:159730210:C_G	6	159730210	C	0.9916	-0.2298	0.0179	1.08E-37
6:151566735:G_GCACC ACTGCAGT	6	151566735	G	0.583	0.0386	0.0030	5.49E-37
6:161006077:C_T	6	161006077	T	0.0318	-0.5223	0.0411	6.50E-37

6:161724214:A_G	6	161724214	A	0.0231	0.1304	0.0103	6.51E-37
6:161769835:C_T	6	161769835	T	0.9002	-0.0642	0.0051	7.34E-37
6:157954366:T_TATG	6	157954366	T	0.007	0.2436	0.0192	9.71E-37
6:151261708:C_CTTT	6	151261708	CTTTA	0.2886	0.0419	0.0033	2.47E-36
A							
6:163750378:C_CG	6	163750378	CG	0.4138	0.0403	0.0032	5.78E-36
6:169889938:C_T	6	169889938	T	0.0108	-0.1872	0.0150	7.44E-36
6:159942186:C_T	6	159942186	T	0.0065	-0.2378	0.0190	7.47E-36
6:161475423:A_G	6	161475423	A	0.9942	0.2980	0.0239	1.08E-35
6:164397666:A_C	6	164397666	A	0.0148	0.1600	0.0129	1.51E-35
6:152508715:A_T	6	152508715	A	0.005	0.2717	0.0219	1.76E-35
6:164441428:C_G	6	164441428	C	0.9213	0.0677	0.0055	3.57E-35
6:156446478:G_T	6	156446478	T	0.0096	0.1969	0.0159	3.66E-35
6:156517922:A_G	6	156517922	A	0.0069	0.2263	0.0183	5.98E-35
6:158887057:A_G	6	158887057	A	0.9883	-0.1772	0.0144	8.37E-35
6:152428704:C_G	6	152428704	C	0.5463	-0.0372	0.0030	1.55E-34
6:160747986:A_C	6	160747986	A	0.9896	0.2154	0.0176	2.68E-34
6:163789882:A_AT	6	163789882	A	0.6999	0.0418	0.0034	2.74E-34
6:151602279:C_T	6	151602279	T	0.0065	0.2451	0.0202	6.88E-34
6:160503002:C_G	6	160503002	C	0.9675	-0.1123	0.0093	7.35E-34
6:159164512:G_GTT	6	159164512	G	0.7622	-0.0436	0.0036	2.00E-33
6:157809830:A_G	6	157809830	A	0.9943	0.2359	0.0202	1.61E-31
6:154186805:G_T	6	154186805	T	0.041	0.0876	0.0075	1.83E-31
6:169498637:C_T	6	169498637	T	0.9782	-0.1203	0.0104	6.94E-31
6:166970144:A_T	6	166970144	A	0.0082	-0.2014	0.0176	2.83E-30
6:157411848:C_G	6	157411848	C	0.0133	-0.1589	0.0139	2.89E-30
6:154565935:C_G	6	154565935	C	0.9813	0.1301	0.0114	4.20E-30
6:166554017:C_T	6	166554017	T	0.0847	0.0629	0.0055	7.50E-30
6:160535532:A_G	6	160535532	A	0.0199	-0.1348	0.0120	2.50E-29
6:168591107:A_G	6	168591107	A	0.8119	0.0444	0.0040	2.63E-29
6:155767053:A_G	6	155767053	A	0.9833	0.1399	0.0125	3.19E-29
6:154126632:C_CA	6	154126632	CA	0.9041	0.0561	0.0051	2.11E-28
6:164531965:C_T	6	164531965	T	0.0401	-0.0846	0.0077	4.79E-28
6:155134201:A_G	6	155134201	A	0.9899	-0.1697	0.0155	5.84E-28
6:160472415:A_G	6	160472415	A	0.0058	0.2797	0.0260	5.48E-27
6:165970588:C_T	6	165970588	T	0.0897	-0.0563	0.0053	1.33E-26
6:157177304:A_T	6	157177304	A	0.0196	0.1167	0.0109	1.65E-26
6:161704533:C_T	6	161704533	T	0.5459	0.0333	0.0032	1.11E-25
6:167871963:G_T	6	167871963	T	0.9408	0.0732	0.0072	1.62E-24
6:166680929:A_T	6	166680929	A	0.0941	-0.0513	0.0053	2.20E-22
6:169039497:C_T	6	169039497	T	0.7722	-0.0344	0.0036	6.87E-22
6:152063998:A_G	6	152063998	A	0.4426	0.0282	0.0029	1.07E-21
6:162567622:C_T	6	162567622	T	0.0073	-0.1809	0.0190	1.39E-21
6:158891086:C_T	6	158891086	T	0.0347	-0.0778	0.0083	4.08E-21
6:169435687:A_G	6	169435687	A	0.0107	-0.1356	0.0147	2.66E-20
6:166638596:C_G	6	166638596	C	0.9752	-0.0944	0.0103	4.07E-20
6:163483731:A_G	6	163483731	A	0.5505	0.0312	0.0035	7.86E-19
6:163612103:C_T	6	163612103	T	0.0092	-0.1370	0.0159	7.56E-18
6:163539289:G_T	6	163539289	T	0.3629	0.0313	0.0037	1.36E-17
6:161665020:A_G	6	161665020	A	0.928	-0.0531	0.0063	2.28E-17
6:162251557:A_T	6	162251557	A	0.9148	0.0443	0.0058	2.49E-14
6:151467182:C_T	6	151467182	T	0.4779	0.0211	0.0029	5.68E-13
6:162047938:C_T	6	162047938	T	0.294	-0.0232	0.0033	1.78E-12
6:160698937:G_GTTTT	6	160698937	G	0.0245	-0.0985	0.0145	1.05E-11
TTC							
6:167501529:C_G	6	167501529	C	0.9708	-0.0597	0.0088	1.33E-11
6:166650293:A_G	6	166650293	A	0.8392	-0.0267	0.0041	6.34E-11
6:159005685:A_G	6	159005685	A	0.2725	0.0208	0.0034	1.23E-09
9:10599267:A_G	9	10599267	A	0.0052	0.1434	0.0226	2.23E-10
10:31009857:A_G	10	31009857	A	0.9525	0.0460	0.0074	5.11E-10
12:125539193:C_T	12	125539193	T	0.0088	-0.1004	0.0171	4.33E-09
13:110797505:C_T	13	110797505	T	0.0058	0.1312	0.0210	4.18E-10
16:56987369:C_T	16	56987369	T	0.6768	0.0301	0.0031	2.78E-22
17:64224775:C_T	17	64224775	T	0.0304	0.1238	0.0087	6.35E-46
17:17432744:A_G	17	17432744	A	0.5481	-0.0207	0.0029	9.51E-13
19:45413233:G_T	19	45413233	T	0.0777	-0.1480	0.0057	2.40E-150
19:45441283:G_T	19	45441283	T	0.1442	0.0291	0.0044	5.58E-11
19:49189315:A_AG	19	49189315	A	0.3146	-0.0222	0.0034	7.23E-11
19:45421650:A_G	19	45421650	A	0.0284	0.0591	0.0091	8.56E-11
19:11196651:A_AT	19	11196651	A	0.143	-0.0292	0.0045	8.67E-11

South Asian	6:161017363:A_G	6	161017363	A	0.0927	0.7442	0.0343	3.02E-104
	6:161010118:A_G	6	161010118	A	0.9891	-1.0834	0.0773	1.29E-44
	6:161079176:C_G	6	161079176	C	0.979	-0.7733	0.0606	2.70E-37
	6:161162495:C_T	6	161162495	T	0.0063	1.2125	0.1011	3.69E-33
	6:161006077:C_T	6	161006077	T	0.025	-0.4819	0.0522	2.78E-20
	6:161024026:G_GT	6	161024026	G	0.5315	-0.1775	0.0198	3.41E-19
	6:160953642:A_G	6	160953642	A	0.9671	0.3693	0.0447	1.49E-16
	6:161033124:A_G	6	161033124	A	0.7422	0.1611	0.0201	1.17E-15
	6:160720804:C_G	6	160720804	C	0.0069	0.8667	0.1085	1.36E-15
	6:160911596:A_G	6	160911596	A	0.0097	0.6926	0.0894	9.24E-15
	6:161030686:C_T	6	161030686	T	0.005	1.1238	0.1454	1.07E-14
	6:160971286:C_G	6	160971286	C	0.8687	0.2067	0.0273	3.81E-14
	6:160960359:C_T	6	160960359	T	0.0441	-0.2991	0.0398	5.48E-14
	6:161126741:C_T	6	161126741	T	0.9602	-0.3048	0.0422	5.00E-13
	6:161212477:A_G	6	161212477	A	0.0056	0.8013	0.1244	1.17E-10
	6:161124143:G_T	6	161124143	T	0.0075	-0.6503	0.1044	4.65E-10
	19:45412079:C_T	19	45412079	T	0.0428	-0.2286	0.0391	4.92E-09

*Conditioned value. BP, base pair (build 37). Chr, chromosome

Supplemental Table 8. Estimated % variance explained in a Lp(a) genome-wide association studies in populations of African, East Asian, European, and South Asian ancestry. Estimates are presented overall and after restriction to the *LPA* locus.

Ancestry	Estimated heritability (variance %, SE)*			
	Genome-wide		<i>LPA</i> locus	
African	38.4%	5.7%	45.7%	1.7%
East Asian	13.1%	10.0%	22.5%	3.3%
European	28.3%	1.0%	76.1%	0.5%
South Asian	19.6%	4.2%	56.3%	1.7%

*Ratio of additive genetic variance to phenotypic variance, estimate and SE;

Supplemental Table 9. Prediction performance of the genetic scores across four ancestral populations in UK Biobank. Score performance was assessed by estimating the incremental R² while accounting for age, sex, population structure and study centers and AUC for dichotomized Lp(a) at 125nmol/L.

PRS methods	Genetic regions	No. of SNPs				R ²				AUC*			
		EUR	AFR	SAS	EAS	EUR	AFR	SAS	EAS	EUR	AFR	SAS	EAS
External PRS	<i>LPA</i> gene [≡]	43	43	43	43	50%	2%	11%	2%	0.90	0.55	0.70	0.54
P+T	<i>LPA</i> gene	196	9	237	2	30%	12%	5%	10%	0.82	0.66	0.61	0.55
LDpred2	<i>LPA</i> gene	14,849	23,929	13,502	8,620	31%	17%	4%	10%	0.83	0.70	0.60	0.56
GWAS significant independent signals [‡]	<i>LPA</i> gene	200	39	16	3	37%	25%	16%	12%	0.87	0.74	0.70	0.58
GWAS significant independent signals	Genome-wide	245	40	17	3	37%	27%	17%	12%	0.87	0.75	0.70	0.58
Crosspred	<i>LPA</i> gene	18,193	28,075	17,214	13,640	42%	24%	20%	15%	0.88	0.74	0.72	0.66
Crosspred [†]	Genome-wide	1,094,755	1,094,755	1,094,75	1,094,755	29%	11%	10%	9%	0.84	0.66	0.66	0.53

AUC = area under the receiver operator curve; EUR = European ancestry; AFR = African ancestry; SAS = South Asian ancestry; EAS = East Asian ancestry

[≡]*Lp(a)* levels were dichotomized using a threshold of 150 nmol/L.

[†]hapmap3 SNPs across all chromosomes were included.

[‡]Genome-wide significant secondary signals were identified in trans-ethnic populations.

Supplemental Table 10. Nominally significant results from a phenome-wide association study of genetically inferred lipoprotein(a) in a maximum of N=8,946 Hispanic/Latino, N=6,215 African American, and N=7,715 Whites restricting to circulatory system phenotypes.

Phenotype	Description	Group	N cases	Hispanic/Latino		African American		White			
				Beta (SE)	P-value	N cases	Beta (SE)	P-value	N cases	Beta (SE)	P-value
394	Rheumatic disease of the heart valves	Circulatory system	120	0.059 (0.096)	0.54	71	-0.44 (0.16)	0.0054	160	-0.016 (0.084)	0.85
394.2	Mitral valve disease	Circulatory system	76	0.069 (0.12)	0.55	52	-0.41 (0.18)	0.023	110	-0.077 (0.11)	0.47
395	Heart valve disorders	Circulatory system	370	0.11 (0.054)	0.034	240	-0.1 (0.071)	0.15	520	0.091 (0.045)	0.044
395.2	Nonrheumatic aortic valve disorders	Circulatory system	200	0.088 (0.074)	0.23	120	-0.099 (0.1)	0.33	290	0.19 (0.057)	0.0012
395.6	Heart valve replaced	Circulatory system	85	0.26 (0.1)	0.01	53	-0.26 (0.17)	0.12	130	0.2 (0.084)	0.016
411	Ischemic Heart Disease	Circulatory system	1400	0.11 (0.034)	0.00083	680	0.017 (0.043)	0.69	740	0.025 (0.043)	0.57
411.2	Myocardial infarction	Circulatory system	150	0.21 (0.079)	0.0078	92	-0.014 (0.11)	0.9	72	-0.11 (0.14)	0.42
411.3	Angina pectoris	Circulatory system	360	0.15 (0.057)	0.009	170	-0.0067 (0.08)	0.93	100	-0.025 (0.11)	0.82
411.4	Coronary atherosclerosis	Circulatory system	1200	0.12 (0.036)	0.001	620	0.012 (0.045)	0.79	710	0.036 (0.044)	0.42
426.32	Left bundle branch block	Circulatory system	34	0.48 (0.16)	0.0033				23	0.26 (0.17)	0.12
426.92	Cardiac defibrillator in situ	Circulatory system	130	0.22 (0.09)	0.016	85	0.044 (0.11)	0.69	62	-0.08 (0.14)	0.57
427	Cardiac dysrhythmias	Circulatory system	1300	0.082 (0.033)	0.013	790	-0.0063 (0.039)	0.87	930	-0.061 (0.039)	0.11
427.7	Tachycardia NOS	Circulatory system	170	0.23 (0.076)	0.0023	130	-0.026 (0.092)	0.78	77	-0.22 (0.14)	0.11
429.1	Heart transplant/surgery	Circulatory system	32	-0.067 (0.2)	0.74	27	0.006 (0.2)	0.98	24	0.33 (0.16)	0.031
430	Intracranial hemorrhage	Circulatory system	73	-0.0041 (0.11)	0.97	29	0.42 (0.13)	0.0015	28	0.096 (0.18)	0.59
433.2	Occlusion of cerebral arteries	Circulatory system	380	0.022 (0.058)	0.7	320	-0.026 (0.06)	0.67	99	-0.29 (0.13)	0.033
433.21	Cerebral artery occlusion, with cerebral infarction	Circulatory system	370	0.028 (0.059)	0.63	310	-0.017 (0.06)	0.78	90	-0.31 (0.14)	0.03
440	Atherosclerosis	Circulatory system	200	0.1 (0.077)	0.19	110	-0.068 (0.11)	0.53	67	0.21 (0.11)	0.047
443.1	Raynaud's syndrome	Circulatory system	34	-0.044 (0.18)	0.81	21	-0.77 (0.32)	0.016	52	-0.21 (0.17)	0.23
446.9	Arteritis NOS	Circulatory system	23	-0.77 (0.39)	0.045						
447.7	Aortic ectasia	Circulatory system	22	-1 (0.47)	0.029	20	-0.61 (0.32)	0.053	37	-0.084 (0.19)	0.65
456	Chronic venous insufficiency [CVI]	Circulatory system	360	-0.16 (0.065)	0.014	200	-0.062 (0.075)	0.41	130	-0.24 (0.11)	0.032
459.7	Blood vessel replaced	Circulatory system	48	0.43 (0.13)	0.00075	24	0.12 (0.19)	0.53	22	-0.67 (0.4)	0.094

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