

Characteristic	ARIC	FHS Offspring, Gen 3	MONICA/KORA
Study Design reference	<sup>1</sup>	<sup>3,4,8</sup>	<sup>5-7</sup>
LADS	<a href="http://www.nhlbi.nih.gov/resources/deca/descriptions/aric.htm">http://www.nhlbi.nih.gov/resources/deca/descriptions/aric.htm</a>	<a href="http://www.nhlbi.nih.gov/resources/deca/descriptions/framoff.htm">http://www.nhlbi.nih.gov/resources/deca/descriptions/framoff.htm</a>	
Genetics web	--	<a href="http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?id=phs000007">http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?id=phs000007</a>	<a href="http://epi.helmholtz-muenchen.de/kora-gen/index_e.php">http://epi.helmholtz-muenchen.de/kora-gen/index_e.php</a>
Website	<a href="http://www.csc.unc.edu/aric/">http://www.csc.unc.edu/aric/</a>	<a href="http://www.framinghamheartstudy.org/ab-out/index.html">http://www.framinghamheartstudy.org/ab-out/index.html</a>	<a href="http://www.helmholtz-muenchen.de/kora/en/index.html">http://www.helmholtz-muenchen.de/kora/en/index.html</a>
GWAS reference	<sup>9</sup>	<sup>9,10</sup>	--
Genotyping			
Genotyping platforms, SNP panel	Affymetrix 6.0	Affymetrix 500K, MIPS 50K	Affymetrix 500K
Genotyping center	Broad Institute of Harvard and Massachusetts Institute of Technology	Affymetrix	Affymetrix
Genotyping calling algorithm	Bird Seed	BRLMM	BRLMM
QC filters on individual level	1st degree relatives: 297 Discordant with previous genotyping: 123 Genetic outliers (based on average IBS and Eigenstrat run if PC>8SD): 322 Gen. sex did not match phen sex: 40	Call rate, heterozygosity rate, Mendelian errors	Gender discordance, error in chip comparison
Call rate (filter / N individuals excluded)	95%/none	97%/97	93% / 153
Heterozygosity (filter / N individuals excluded)	--	5 SD from mean (<25.758% or >29.958%)/15	--
Exclusion on race/ethnicity	--	none	--
Other exclusions	--	>1000 Mendelian errors/1	--
Individuals for analysis	8861	6771	1644
QC filters on SNP level			
Test for HWE	Exact HWE test (implemented in Plink)	exact HWE test (implemented in R) <sup>11</sup>	exact HWE test (implemented in R) <sup>11</sup>
MAF (filter / N SNPs excluded)	0% / 74	1% / 68,953	5% / 109,681
HWE (filter / N SNPs excluded)	10 <sup>-6</sup> (only for MAF >0.05)/21220	10 <sup>-6</sup> / 21,002	10 <sup>-6</sup> / 21,752
Call rate (filter / N SNPs excluded)	90%/26274	95% / 23,312	95% / 49,325

Characteristic	ARIC	FHS Offspring, Gen 3	MONICA/KORA
Other (filter / N SNPs excluded)	Difference between two data freezes: 21395*	--	--
N SNPs for imputation	589,253	378,163	380,407
Imputation			
Imputation software	Mach1 v1.0.1.5 <a href="http://www.sph.umich.edu/csg/abecasis/MaCH/index.html">http://www.sph.umich.edu/csg/abecasis/MaCH/index.html</a>	Mach1 v1.0.1.5 <a href="http://www.sph.umich.edu/csg/abecasis/MaCH/index.html">http://www.sph.umich.edu/csg/abecasis/MaCH/index.html</a>	Mach1 v1.0.1.5 <a href="http://www.sph.umich.edu/csg/abecasis/MaCH/index.html">http://www.sph.umich.edu/csg/abecasis/MaCH/index.html</a>
Imputation quality metrics	-	$r^2_{\text{hat}} \geq 0.3$	--
Other SNP quality filters	-	MAF $\geq 1\%$	--
N imputed SNPs for analysis	2,516,204	2,540,223	2,557,252
Phenotypes			
Individuals for analysis, N	729	6771	1,625
Trait transformation	Log-transformed	Log-transformed (unstandardized residuals)	Log-transformed (unstandardized)
Cohort-specific adjustments	Age, sex, case status	Cohort –specific residuals Model 1: age, sex Model 2: age, sex, smoking, SBP, DBP, HTN treatment, BMI, waist circumference, total/HDL cholesterol, triglyceride, lipid lowering medication, glucose, diabetes, aspirin, hormone replacement therapy and prevalent CVD	age, sex, smoking, SBP, DBP, HTN treatment, BMI, waist circumference, total/HDL cholesterol, triglyceride, lipid lowering medication, diabetes, aspirin, hormone replacement therapy and prevalent CVD
Analysis method	Linear regression	Linear mixed effect models to account for family structure	Linear regression
Analysis software	Probabel ( <a href="http://mga.bionet.nsc.ru/~yurii/ABEL/">http://mga.bionet.nsc.ru/~yurii/ABEL/</a> ) <sup>12</sup>	SAS version 8.1 (Cary, North Carolina, <a href="http://www.sas.com/presscenter/guidelines.html">http://www.sas.com/presscenter/guidelines.html</a> ) <sup>13</sup> R version 2.6.1 ( <a href="http://www.r-project.org">www.r-project.org</a> ) <sup>14</sup>	SAS version 9.1 (Cary, North Carolina, <a href="http://www.sas.com/presscenter/guidelines.html">http://www.sas.com/presscenter/guidelines.html</a> )
Genomic control ( $\lambda$ ), age- and sex-adjusted (multivariable-adjusted)	0.999 (0.999)	1.017 (1.011)	Plasma 0.977 (0.977) Serum 1.016 (1.016)

\*Genotyping was performed in two steps (two sets of individuals). HWE indicates Hardy-Weinberg equilibrium. LADS indicates limited access data set.