

Supplementary Table 1. Characteristics of genotyping, imputation, quality control, and statistical analysis in discovery and second-stage studies.

	ARIC	CHS	HVH	RSI	RSII	WGHS	Mayo_genotyping	Mayo_GWAS	MARTHA	EOVT
Platform and version	Affymetrix 6.0	Illumina 370CNV	Illumina 370CNV	Illumina 550k	Illumina 610k	Illumina HumanHap300 DuoPlus	Illumina Viracode	Illumina Human 610 Quad	Illumina Human 610 Quad/660W Quad	Illumina Sentrix HumanHap300 Beadchip
Genotype calling	Birdseed	BeadStudio	BeadStudio	BeadStudio	GenomeStudio	BeadStudio	BeadStudio	BeadStudio	BeadStudio	BeadStudio
Sample call rate filter	<95%	<95%	<95%	<98%	<98%	<95%	<94%	<85%	<95%	<95%
SNPs genotyped, n	841,820	346,831	312,004	561,466	531,405	363,808	729	589,945	567,589	317,139
SNP filters for imputation							N/A	> 0.28		
Call rate, %	<95%	<97%	<97%	<98%	<98%	<95%	<95%	<98%	<99%	<97%
MAF	<1%	NA*	NA**	<1%	<1%	N/A	<0.5%	<0.5%	<1%	<1%
HWE p-value	<10 ⁻⁵	<10 ⁻⁵	<10 ⁻⁵	<10 ⁻⁶	<10 ⁻⁶	<10 ⁻⁶	<10 ⁻³	<10 ⁻⁵	<10 ⁻⁵	<10 ⁻⁵
SNPs included in imputation, n	669,450	306,655	305,353	512,349	466,389	331,959	N/A	325	491,258	291,872
Imputation software and version	MACH v1.0.16	BIMBAM v0.99	BIMBAM V0.99	MACH v1.0.15	MACH v1.0.16	MACH v.1.0.16	N/A	MACH v.1.0.16	MACH v1.0.16	MACH v1.0.16
NCBI build	Build 36	Build 36	Build 36	Build 36	Build 36	Build 36	Build 36	Build 36	Build 35	Build 35
Final SNPs for analysis, n	2,543,887	2,543,909	2,543,885	2,543,887	2,543,887	2,608,509	699	318	1,031	1,030
Statistical analysis	ProbABEL	ProbABEL	R	ProbABEL	ProbABEL	ProbABEL	PLINK	PLINK	Eigenstrat/PLINK/Mach2dat	Eigenstrat/PLINK/Mach2dat
Covariate Adjustment	Age, gender, and field center	Age, gender, field center, and CHD status	Age, age by decade, hypertension status, menopausal status, and index year	Age and gender	Age and gender	Age and a single eigenvector†	Age and gender	Age and gender	First four principal components	First four principal components
Genome control lambda (λ)	1.013	1.018	1.058	0.992	0.938	1.009	NA‡	NA‡	NA‡	NA‡

*Not screening on MAF but based on heterozygote frequency = 0;

**No screening on MAF but betas and SEs were set to missing for SNPs with a dosage variance <0.01;

†Significantly associated with VTE among the first 10 vectors;

‡Not applicable because look-up of the high signal SNPs was conducted.