SUPPLEMENTAL MATERIAL

Table S1. Univariate Analyses in Twin and SNP Models.

Traits	rMZ/rDZ*	BM	a^2 (se)			d^2 (se)	
			Twin	SNP	LDSC[†]	Twin	SNP
Triglycerides	2.27	ADE	42% (7%)*	31% (6%)*	15% (2%)*	14% (8%)	28% (9%)*
Total cholesterol	2.50	ADE	28% (8%)*	15% (6%)*	15% (2%)*	19% (8%)*	0% (9%)
LDL	2.64	ADE	23% (8%)*	16% (6%)*	13% (2%)*	24% (8%)*	0% (9%)
Apolipoprotein B	2.24	ADE	39% (7%)*	14% (6%)*	11% (3%)*	14% (8%)	0% (9%)
nonHDL	2.61	ADE	24% (8%)*	13% (6%)*	NA	25% (8%)*	0% (9%)
HDL	2.17	AE	66% (2%)*	24% (6%)*	16% (2%)*	-	1% (9%)
Apolipoprotein A1	1.93	AE	66% (2%)*	17% (6%)*	9% (3%)*	-	9% (9%)
Hemoglobin	2.24	ADE	41% (7%)*	21% (6%)*	NA	15% (8%)	0% (9%)
Hemoglobin A1c	2.50	ADE	37% (7%)*	20% (6%)*	7% (1%)*	35% (7%)*	0% (9%)
Glucose	2.55	ADE	24% (7%)*	17% (6%)*	10% (2%)*	30% (8%)*	15% (9%)
Creatinine	2.41	ADE	35% (7%)*	18% (6%)*	11% (2%)*	24% (8%)*	0% (9%)
Cystatin C	2.19	ADE	42% (7%)*	27% (6%)*	NA	18% (8%)*	5% (9%)
eGFR	2.35	ADE	38% (7%)*	32% (6%)*	NA	21% (8%)*	3% (9%)
C-reactive protein	2.19	ADE	30% (7%)*	37% (6%)*	NA	14% (8%)	0% (9%)
Height	1.81	ACE	77% (3%)*	62% (6%)*	27% (1%)*	-	0% (9%)
Weight	2.66	ADE	37% (7%)*	26% (6%)*	NA	35% (7%)*	11% (9%)
Body mass index	2.80	ADE	28% (7%)*	21% (6%)*	19% (1%)*	41% (7%)*	3% (9%)
Waist circumference	3.14	ADE	15% (7%)*	16% (6%)*	12% (0%)*	49% (7%)*	19% (9%)*
Hip circumference	2.86	ADE	24% (7%)*	22% (6%)*	13% (1%)*	40% (8%)*	13% (9%)
Waist-hip ratio	3.12	ADE	13% (7%)	19% (6%)*	11% (1%)*	40% (8%)*	3% (9%)
SBP	2.50	ADE	27% (8%)*	10% (6%)	NA	15% (9%)	0% (9%)
DBP	2.33	AE	37% (2%)*	8% (6%)	NA	-	0% (10%)
MAP	2.50	AE	39% (2%)*	8% (6%)	NA	-	0% (9%)
Pulse pressure	2.17	AE	36% (2%)*	12% (6%)*	NA	-	2% (9%)

rMZ/rDZ, ratio of intra-pair correlation in monozygotic and dizygotic twin pairs; BM, the best-fitted model according to Akaike information criterion; SNP, single nucleotide polymorphism-based genomic-relatedness-matrix restricted maximum likelihood model; LDSC: linkage disequilibrium score regression model; a^2, additive genetic variance; d^2, dominant genetic variance; se, standard error; ADE, model including a^2, d^2 and non-shared environmental (e^2) components; AE, model including a^2 and e^2; ACE, model including a^2, c^2 and e^2; LDL, low-density lipoprotein; HDL, high-density lipoprotein; SBP, systolic blood pressure; DBP, diastolic blood pressure; MAP, mean arterial pressure; NA, not available from LD Hub.

* Statistically significant estimates (P-value<0.05).

[†] Estimates are based on the largest European ancestry genome-wide association study reported from LD Hub.

Table S2. LDSC-based Estimates of Cardiometabolic Traits from European Ancestry Data in the LD Hub.

Traits	Consortium	Sample size	N_{SNP}	h^2	SE	λ_{GC}	PMID
Triglycerides	GLGC	96598	2692561	15%	2%	1.1294	20686565
	Kettunen	21545	11820641	12%	3%	1.0195	27005778
Total Cholesterol	GLGC	99900	2692414	15%	2%	1.1232	20686565
	Kettunen	21491	11866342	9%	3%	1.0225	27005778
Low-density lipoprotein	GLGC	95454	2692565	13%	2%	1.1151	20686565
Apolipoprotein B	Kettunen	20690	11813266	11%	3%	1.0255	27005778
High-density lipoprotein	GLGC	100184	2692430	16%	2%	1.1622	20686565
Apolipoprotein A1	Kettunen	20687	11760646	9%	3%	1.0165	27005778
Hemoglobin A1c	MAGIC	46368	2576680	7%	1%	1.0405	20858683
Glucose	MAGIC	58074	2628880	10%	2%	1.0679	22581228
	Kettunen	24679	12052259	9%	2%	1.0315	27005778
Creatinine	Kettunen	24810	12087816	11%	2%	1.0496	27005778
Height	GIANT	133859	2469636	27%	1%	1.4122	20881960
Body mass index	GIANT	123912	2471517	19%	1%	1.3675	20935630
Waist circumference	GIANT	232101	2565409	12%	0%	1.1085	25673412
Hip circumference	GIANT	213038	2559740	13%	1%	1.1085	25673412
Waist-hip ratio	GIANT	212244	2560783	11%	1%	1.1617	25673412

LDSC, linkage disequilibrium score regression model; N_{SNP}, number of single nucleotide polymorphisms; h^2, estimate of heritability; SE, standard error; λ_{GC}, genomic inflation factor; PMID, PubMed Unique Identifier; GLGC, the Global Lipids Genetics Consortium; MAGIC, the Meta-Analyses of Glucose and Insulin-related traits Consortium; GIANT, the Genetic Investigation of ANthropometric Traits consortium.