SUPPLEMENTAL MATERIAL

Supplemental Table 1. Quality control pipeline*

Individuals with phenotypes	51,186
	7,305 individuals' samples not sent to Broad due to lack of patient consent, lack of DNA, or DNA quality issues
Total DNA samples sent to Broad Institute for genotyping (including controls and duplicates)	46,560
	2,679 control samples or duplicates removed

Study	**ARIC**	**CARDIA**	**CFS**	**CHS**	**CSSCD**	**FHS**	**JHS**	**MESA**	**Total**
Samples genotyped (not including controls or duplicates)	14,996	3,520	1,481	5,485	1,707	7,992	2,156	6,544	43,881
Twins removed						23			23
Removed for incomplete family information						436			436
Removed for Mendel errors			7			26			33
Removed for low genotyping rate	287	124	48	183	57	130	36	249	1,114
Final number of genotyped unique individuals (% of samples genotyped)	14,709 (98.1%)	3,396 (96.5%)	1,426 (96.3%)	5,302 (96.7%)	1,650 (96.7%)	7,377 (92.3%)	2,120 (98.3%)	6,295 (96.2%)	42,275 (96.3%)
Self-identified solely as *AA*, with available pilot phenotypes	3,435	1,613	693	794			2,118	1,713	10,366
Self-identified solely as *EA*, with available pilot phenotypes	10,504	1,743	691	4,362		6,914		2,433	26,647
Self-identified solely as *HIS*, with available pilot phenotypes								1,410	1,410
Self-identified solely as *CHI*, with available pilot phenotypes								717	717
Total analyzed[†] (% of final number of genotyped individuals)	13,939 (94.8%)	3,356 (98.8%)	1,384 (97.1%)	5,156 (97.2%)		6,914 (93.7%)	2,118 (99.9%)	6,273 (99.7%)	39,140 (92.6%)

AA = African American; EA = European American or Caucasian; HIS = Hispanic; CHI = Chinese American.

* The Sleep Heart Health Study (SHHS)[11] is not represented in this table because the subgroup of the SHHS cohort with genotype data comprises individuals originally recruited from ARIC, CHS, and FHS (and who are included in this table under these other cohorts).

[†] Because no lipid phenotypes were available for the CSSCD cohort, no analyses were performed for this cohort in the Pilot Study.

Supplemental Table 2. Genotype-phenotype associations for lipid traits

Trait	Gene	SNP (minor/major alleles)	*African American*							*European American*							*Hispanic*	*Chinese American*
			ARIC N=3435	JHS N=2118	MESA N=1713	CARDIA N=1613	CHS N=794	CFS N=693	Meta-analysis N=10366	ARIC N=10504	FHS N=6914	CHS N=4362	MESA N=2433	CARDIA N=1743	CFS N=691	Meta-analysis N=26647	MESA N=1410	MESA N=717
HDL	*CETP*	rs4783961 A/G	0.24 (0.02) 4.2E-22 (43%) 0.49	0.21 (0.03) 8.5E-12 (44%) 0.12	0.21 (0.03) 9.6E-10 (44%) 0.59	0.16 (0.04) 6.8E-06 (44%) 0.84	0.22 (0.05) 1.2E-05 (45%) 0.94	0.22 (0.06) 5.7E-05 (41%) 0.16	0.21 (0.01) 1.8E-52 0.64 0%	0.11 (0.01) 1.6E-16 (49.8%) 0.41	0.11 (0.02) 4.1E-10 (49.6%) 0.34	0.15 (0.02) 4.6E-12 (49%) 0.49	0.09 (0.03) 0.003 (49.8%) 0.44	0.13 (0.03) 1.9E-04 (49.7%) 0.67	0.10 (0.06) 0.10 (46%) 1.0	0.12 (0.01) 1.6E-40 0.59 0%	0.12 (0.04) 0.001 (49.5%) 1.0	0.26 (0.05) 1.2E-05 (24%) 0.18
HDL	*CETP*	rs17231506 T/C	0.16 (0.04) 6.9E-06 (14%) 1.0	0.07 (0.04) 0.11 (15%) 0.34	0.10 (0.05) 0.04 (15%) 0.85	0.06 (0.05) 0.18 (16%) 0.35	0.13 (0.07) 0.06 (16%) 0.30	0.26 (0.08) 0.001 (10%) 1.0	0.12 (0.02) 2.5E-09 0.21 30%	0.24 (0.01) 1.7E-60 (32%) 0.71	0.23 (0.02) 9.8E-33 (32%) 0.83	0.28 (0.02) 1.0E-35 (33%) 0.70	0.21 (0.03) 2.9E-11 (31%) 0.78	0.24 (0.04) 5.1E-11 (32%) 0.74	0.26 (0.06) 4.1E-05 (32%) 0.86	0.24 (0.01) 2.0E-148 0.42 0%	0.24 (0.04) 4.7E-09 (29%) 0.40	0.35 (0.07) 3.9E-07 (17%) 1.0
HDL	*LIPC*	rs1800588 T/C	0.09 (0.02) 5.9E-04 (48%) 1.0	0.07 (0.03) 0.03 (49.8%) 0.93	0.11 (0.03) 0.002 (49.9%) 0.81	0.11 (0.03) 0.002 (49.5%) 0.40	0.18 (0.05) 2.1E-04 (45%) 0.22	0.11 (0.06) 0.05 (46%) 0.86	0.10 (0.01) 2.3E-12 0.48 0%	0.13 (0.02) 2.3E-14 (21%) 0.03	0.12 (0.02) 5.7E-08 (21%) 0.93	0.13 (0.03) 2.0E-06 (21%) 0.21	0.08 (0.03) 0.02 (22%) 0.19	0.13 (0.04) 0.001 (21%) 0.14	0.08 (0.07) 0.31 (18%) 0.31	0.12 (0.01) 2.8E-29 0.86 0%	0.14 (0.04) 1.3E-04 (47%) 0.01	0.05 (0.06) 0.35 (35%) 0.12
HDL	*LPL*	rs328 G/C	0.17 (0.05) 5.0E-04 (7%) 0.68	0.20 (0.06) 5.2E-04 (8%) 0.44	0.10 (0.07) 0.13 (7%) 1.0	0.04 (0.07) 0.50 (8%) 0.86	0.06 (0.10) 0.55 (7%) 0.79	0.12 (0.11) 0.28 (7%) 0.48	0.13 (0.03) 1.1E-06 0.46 0%	0.18 (0.02) 2.9E-15 (10%) 0.26	0.19 (0.03) 1.1E-09 (10%) 0.16	0.16 (0.03) 8.9E-06 (11%) 0.38	0.26 (0.05) 2.0E-08 (11%) 0.46	0.06 (0.06) 0.27 (10%) 0.44	0.13 (0.11) 0.21 (9%) 0.63	0.18 (0.01) 1.8E-33 0.13 41%	0.22 (0.07) 0.001 (8%) 0.48	0.11 (0.08) 0.17 (12%) 1.0
LDL	*PCSK9*	rs505151 G/A	0.09 (0.03) 0.002 (25%) 0.26	0.15 (0.04) 3.7E-05 (26%) 0.86	0.09 (0.04) 0.02 (24%) 0.52	0.15 (0.04) 1.6E-04 (25%) 0.01	0.08 (0.06) 0.17 (24%) 0.01	-0.08 (0.09) 0.37 (28%) 1.0	0.11 (0.02) 1.1E-10 0.17 35%	0.09 (0.04) 0.02 (4%) 0.11	0.05 (0.05) 0.36 (4%) 1.0	0.07 (0.05) 0.17 (4%) 0.07	-0.03 (0.07) 0.71 (4%) 1.0	0.12 (0.09) 0.17 (4%) 1.0	0.12 (0.18) 0.49 (4%) 1.0	0.07 (0.02) 0.004 0.76 0%	0.23 (0.08) 0.004 (6%) 0.22	0.24 (0.11) 0.03 (6%) 0.76
LDL	*PCSK9*	rs11591147 T/G	-0.52 (0.17) 0.002 (0.5%) 0.07	-0.14 (0.21) 0.50 (0.5%) 1.0	-0.27 (0.26) 0.30 (0.4%) 1.0	-0.38 (0.21) 0.08 (0.6%) 0.06	-0.70 (0.45) 0.12 (0.3%) 1.0	— — — — —	-0.38 (0.10) 1.8E-04 0.62 0%	-0.47 (0.06) 1.9E-17 (1.6%) 0.53	-0.47 (0.08) 6.5E-10 (1.5%) 1.0	-0.50 (0.09) 3.7E-08 (1.4%) 0.60	-0.25 (0.12) 0.05 (1.4%) 1.0	-0.61 (0.14) 1.6E-05 (1.5%) 1.0	-0.50 (0.26) 0.05 (1.1%) 1.0	-0.46 (0.04) 2.3E-37 0.50 0%	-0.21 (0.20) 0.30 (1.0%) 1.0	— — — — —
TG	*LPL*	rs328 G/C	-0.21 (0.05) 3.5E-05 (7%) 0.68	-0.18 (0.06) 0.003 (8%) 0.44	-0.13 (0.07) 0.07 (7%) 1.0	-0.18 (0.07) 0.007 (8%) 0.86	0.00 (0.10) 0.99 (7%) 0.79	-0.36 (0.16) 0.02 (7%) 0.48	-0.17 (0.03) 1.3E-09 0.35 10%	-0.20 (0.02) 1.1E-17 (10%) 0.26	-0.19 (0.03) 8.5E-09 (10%) 0.16	-0.22 (0.03) 2.8E-10 (11%) 0.38	-0.23 (0.05) 4.9E-07 (11%) 0.46	-0.09 (0.06) 0.10 (10%) 0.44	-0.25 (0.17) 0.14 (9%) 0.63	-0.20 (0.01) 2.7E-39 0.41 0.5%	0.27 (0.07) 7.23E-05 (8%) 0.48	-0.04 (0.08) 0.59 (12%) 1.0
TG	*APOA5*	rs3135506 C/G	0.22 (0.05) 2.3E-05 (6%) 0.37	0.31 (0.06) 1.6E-06 (6%) 0.57	0.39 (0.07) 4.0E-08 (6%) 1.0	0.29 (0.08) 1.2E-04 (6%) 0.70	0.14 (0.10) 0.16 (7%) 0.26	0.23 (0.14) 0.09 (5%) 1.0	0.27 (0.03) 2.6E-20 0.30 17%	0.28 (0.03) 2.6E-24 (7%) 0.94	0.22 (0.04) 1.1E-08 (7%) 1.0	0.26 (0.05) 1.1E-08 (6%) 0.19	0.18 (0.06) 0.002 (6%) 0.61	0.29 (0.07) 5.3E-05 (6%) 0.38	0.48 (0.14) 9.4E-04 (7%) 0.59	0.26 (0.02) 1.3E-45 0.36 8.9%	0.37 (0.05) 1.2E-11 (13%) 0.09	— — — — —

For each study cohort/ethnicity with each phenotype, the five numbers are (1) effect size (beta-coefficient), (2) standard error for the effect size, (3) *P* value for genotype-phenotype association, (4) allele frequency for the allele designated in the *SNP* column as the minor allele, and (5) the Hardy-Weinberg *P* value for the SNP. For the meta-analyses, the five numbers are (1) the overall effect size, (2) the overall standard error, (3) the overall *P* value for the ethnicity, (4) the Cochran's Q *P* value for heterogeneity among the cohorts for the ethnicity, and (5) the I^2 inconsistency metric for heterogeneity. The numbers of DNA samples successfully genotyped and passing QC criteria for each cohort are indicated in the top row. HDL = high-density lipoprotein cholesterol; LDL = low-density lipoprotein cholesterol; TG = triglyceride

SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure 1. Governance structure of CARe.

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