Supplementary Table S1. Plasma lipids and NMR lipoprotein profiles of participants

Parameter	Fasting (1117)	3.5 h (1044)	6.0 h (1047)
Triglycerides	143.2 ± 31.9	$223.3 \pm 139.4^{\dagger}$	$205.0 \pm 156.6^{\dagger*}$
Total Cholesterol	183.7 ± 38.6	188.5 ± 40.0	$192.4 \pm 41.2^{\dagger*}$
Chylomicrons	4.8 ± 4.9	$58.0 \pm 50.6^{\dagger}$	$49.8 \pm 56.9^{\dagger}$
HDL-C	45.5 ± 13.5	45.6 ± 14.1	$48.2 \pm 14.3^{\dagger*}$
LDL-C	116.5 ± 31.9	118.6 ± 32.7	$121.4\pm32.7^{\dagger}$
VLDL-TG	106.5 ± 105	183.7 ± 135	$164.8 \pm 152.3^{\dagger}$
VLDL particle	74.4 ± 50	68.8 ± 42.6	$63.1 \pm 43.1^{\dagger}$
Small VLDL	33 ± 22	$19.6 \pm 18.1^{\dagger}$	$24\pm18.4^{\dagger*}$
HDL size	8.8 ± 0.5	8.9 ± 0.5	9.0 ± 0.5
VLDL size	59.7 ± 10.4	$51.9 \pm 8.7^{\dagger}$	59.3 ± 11.8

Fasting plasma lipid levels (mg/dl), lipoprotein particle (nmol/l) and size (nm), mean \pm s.d., were measured in participants (number indicated in parentheses) after an overnight fast and at 3.5h and 6h after ingestion of a high fat (83%) milkshake (700 calories/m² body surface area). Abbreviations: High, low and very low density lipoproteins: HDL, LDL and VLDL. †Compared to fasting, p≤ 0.001, *p<0.001 compared to 3.5 h.

Supplementary Table S2: *CD36* tag SNPs related to fasting LDL particle number also associate with postprandial levels of LDL particles

SNP	Effect Allele	MAF	β(se)	<i>p</i> -value
		<u>3.5 h</u>		
rs6970109	C/ <u>A</u>	0.10	0.24 (0.09)	0.0059
rs1722507	A/ <u>G</u>	0.39	0.18 (0.05)	0.0011
rs1761665	T/ <u>C</u>	0.44	0.19 (0.05)	0.0005
rs3211842	$G/\underline{\mathbf{A}}$	0.42	0.16 (0.05)	0.0031
rs7755	$G/\underline{\mathbf{A}}$	0.46	0.14 (0.05)	0.0084
		<u>6.0 h</u>		
rs1722507	A/ <u>G</u>	0.39	0.16 (0.05)	0.0026
rs1761665	T/ <u>C</u>	0.44	0.17 (0.05)	0.0012
rs3211842	$G/\underline{\mathbf{A}}$	0.42	0.15 (0.05)	0.0034
rs7755	$G/\underline{\mathbf{A}}$	0.46	0.14 (0.05)	0.0055

SNPs are listed based on genomic location. Effect allele is bolded. Shown are beta-estimates (β) \pm standard errors and raw p-values for representative *CD36* tag SNPs. *Bonferroni corrections threshold, raw p-value <0.006.

Supplementary Table S3. Associations between rs7755, rs1761665 and adipose tissue CD36 mRNA adjusted for DNA methylation

tissue CD30 inKNA aujusteu for DNA methylation						
		β methylation	βSNP	p-value		
rs7755	cg18508525	1.15	-0.42	6.75×10^{-42}		
	cg25783969	1.65	-0.42	9.62×10^{-42}		
	cg21055948	0.97	-0.42	5.84 x 10 ⁻⁴¹		
	cg19096849	0.35	-0.43	5.28×10^{-42}		
	cg26138637	1.22	-0.42	1.48×10^{-42}		
	cg14093018	0.82	-0.43	3.47×10^{-43}		
	cg05917188	0.77	-0.43	5.03 x 10 ⁻⁴⁴		
rs1761665	cg18508525	1.54	-0.27	8.67×10^{-17}		
	cg25783969	2.21	-0.27	6.9×10^{-17}		
	cg21055948	1.37	-0.26	4.32×10^{-16}		
	cg19096849	0.73	-0.27	1.46×10^{-16}		
	cg26138637	1.63	-0.27	1.90 x 10 ⁻¹⁷		
	cg14093018	1.10	-0.28	3.24×10^{-18}		
	cg05917188	1.09	-0.28	1.02 x 10 ⁻¹⁸		

Given the twin structure of the MuTHER cohort, a mixed-linear model was used to examine SNP effects on *CD36* mRNA levels (ILMN_1784863; NM_001001548.1) adjusted for methylation at the designated CpG sites, p-values represent effect SNP-expression including methylation within the model.