Supplementary Data

Supplementary Table S1. Demographics and Biochemical Characteristics for High Triglyceride at the 75TH Percentile and Low High Density Lipoprotein Cholesterol at the 25TH Percentile in Cases and Controls by Gender

	Males						*Females*					
Risk determinant	*High TG_75 (n=60)*	*Non-High TG_75 (n=110)*	P[3]	*Low HDL-C_25 (n=50)*	*Non-Low HDL-C_25 (n=120)*	P[3]	*High TG_75 (n=33)*	*Non-High TG_75 (n=157)*	P[3]	*Low HDL-C_25 (n=21)*	*Non-Low HDL-C_25 (n=169)*	P[3]
Age[1]	12.1 (.41)	13.1 (.32)	0.021	13.0 (0.48)	12.6 (0.31)	0.506	12.8 (0.59)	13.3 (0.26)	0.791	13.4 (0.69)	13.2 (0.26)	0.849
BMI[1]	19.6 (.67)	18.4 (.29)	0.423	20.1 (0.66)	18.3 (0.32)	0.023	20.4 (0.81)	18.7 (0.27)	0.080	21.5 (0.99)	18.7 (0.27)	0.006
Fasting glucose[1]	79. (1.34)	78.6 (0.90)	0.396	77.0 (1.67)	79.9 (0.80)	0.083	74.5 (1.47)	75.4 (0.68)	0.590	71.8 (2.09)	75.7 (0.63)	0.043
Insulin resistance (IR)[2]	[12 (48)]	[13 (97)]	0.150*	[10 (40)]	[15 (105)]	0.208*	[4 (29)]	[12 (145)]	0.487*	[1 (20)]	[15 (154)]	0.522*

High TG_75 definition = Triglyceride (TG) level ≥75th percentile; Low HDL-C_25 = HDL-C level ≤25th percentile. Age and sex specific percentiles were obtained from National Heart Lund and Blood Institute Growth and Health Study (NGHS) data.

[1]Mean (SE) of risk determinant are presented, unless otherwise indicated.

[2]Insulin Resistance: [IR Cases (IR Controls)], IR Case definition is HOMA-IR ≥3.16.

[3]*P* value presented is Student's *t* test *p* value or Wilcoxon Rank Sum test *p* value where appropriate, unless otherwise indicated.

**P* value presented is from Chi-square test or Fisher's Exact test of association where appropriate.

Supplementary Table S2. Single SNP Assocation Analysis for Low HDL-C at the 25TH Percentile and High TG at the 75TH Percentile

			Low HDL-C_25			*High TG_75*		
Gene	*SNP*	*Genotype categories*	*Genotype counts cases (%)*	*Genotype counts controls (%)*	*P*[1] *(Allelic, genotypic)*	*Genotype counts cases (%)*	*Genotype counts controls (%)*	*P*[1] *(Allelic, genotypic)*
ABCA1	rs1800977	CC	33 (46.5)	130 (45.0)	(0.995, 0.859)	41 (44.1)	122 (45.7)	(0.701, 0.902)
		CT	31 (43.6)	135 (46.7)		43 (46.2)	123 (46.1)	
		TT	7 (9.9)	24 (8.3)		9 (9.7)	22 (8.2)	
LPL	rs328	SX	14 (19.7)	55 (19.0)	(0.901, 0.506)	15 (16.1)	54 (20.2)	(0.414, 0.446)
		SS	57 (80.3)	234 (81.0)		78 (83.9)	213 (79.8)	
CETP	rs708272	B1B1	30 (42.2)	78 (27.0)	(0.005, 0.019)	28 (30.1)	80 (30.0)	(0.765, 0.842)
		B1B2	32 (45.1)	142 (49.1)		43 (46.2)	131 (49.1)	
		B2B2	9 (12.7)	69 (23.9)		22 (23.7)	56 (20.9)	
LIPC	rs1800588	CC	42 (59.2)	202 (70.0)	(0.09, 0.184)	63 (67.7)	181 (67.8)	(0.790, 0.665)
		CT	26 (36.6)	79 (27.3)		26 (28.0)	79 (29.6)	
		TT	3 (4.2)	8 (2.7)		4 (4.3)	7 (2.6)	
SHBG	rs1799941	AA	0 (0.0)	8 (2.7)	(0.240, 0.449)	2 (2.2)	6 (2.3)	(0.783, 0.965)
		AG	17 (23.9)	76 (26.3)		23 (24.7)	70 (26.2)	
		GG	54 (76.1)	205 (71.0)		68 (73.1)	191 (71.5)	
	rs6257	CC	1 (1.4)	3 (1.0)	(0.088, 0.111)	3 (3.2)	1 (0.4)	(0.966, 0.067)
		CT	30 (42.3)	89 (30.8)		27 (29.0)	92 (34.5)	
		TT	40 (56.3)	197 (68.2)		63 (67.8)	174 (65.1)	

[1]Chi-Square or Fisher's Exact test *p* value is presented where appropriate for indicated test, either allelic or genotypic.
[2]Allelic test: Compares the frequencies of alleles at the specified marker in cases versus controls using a Chi-Square test with 1 degree of freedom; *M* versus *m* (*M* = major allele, *m* = minor allele).
[3]Genotypic test: Compares the frequencies of genotypes at a specifed marker in cases versus controls using a Chi-Square test with 2 degrees of freedom; *MM* versus *Mm* versus *mm* (*M* = major allele, *m* = minor allele).

Supplementary Table S3. Prevalence Based Association Test (PRAT) Results for Single Variant Assocation Between Genotyped SNPs and Low HDL-C at the 25TH Percentile and High TG at the 75TH Percentile

		Low HDL-C_25		*High TG_75*	
Gene	*SNP*	*PRAT P cases*[1]	*PRAT P controls*[2]	*PRAT P cases*[1]	*PRAT P controls*[2]
ABCA1	rs1800977	1.000	0.411	0.828	0.502
LPL	rs328	0.687	0.621	0.789	0.247
CETP	rs708272	0.022	0.014	0.675	0.942
LIPC	rs1800588	0.255	0.167	0.751	0.651
SHBG	rs1799941	0.327	0.333	0.968	0.940
	rs6257	0.060	0.784	1.000	0.032

[1]PRAT *p* value from case only analysis in selected phenotype, *p* value presented is permutation based pvalue ($n = 1000$).
[2]PRAT *p* value from control only anlaysis in selected phenotype, *p* value presented is permutaiton based pvalue ($n = 1000$).

Supplementary Table S4. Logistic Regression Results for Low HDL-C at 25TH Percentile and High TG at the 75TH Percentile Among Girls and Boys

		Low HDL-C_25						*High TG_75*					
		Males			*Females*			*Males*			*Females*		
Gene	*SNP*	OR[1]	*95% Confidence interval*	P[2]	OR[1]	*95% Confidence interval*	P[2]	OR[1]	*95% Confidence interval*	P[2]	OR[1]	*95% Confidence interval*	P[2]
ABCA1	rs1800977	0.84	0.50–1.41	0.51	0.99	0.44–2.23	0.98	0.86	0.51–1.43	0.56	1.02	0.52–2.00	0.95
LPL	rs328	1.54	0.66–3.62	0.32	0.56	0.14–2.18	0.40	0.36	0.13–1.00	0.05	1.49	0.60–3.73	0.39
CETP	rs708272	0.62	0.37–1.02	0.06	0.39	0.18–0.84	0.02	1.12	0.70–1.81	0.63	0.95	0.55–1.63	0.84
LIPC	rs1800588	1.56	0.85–2.85	0.15	1.44	0.58–3.58	0.44	0.87	0.46–1.64	0.66	1.10	0.53–2.29	0.80
SHBG	rs1799941	1.71	0.77–3.79	0.19	0.93	0.36–2.39	0.88	0.78	0.39–1.57	0.49	1.26	0.57–2.77	0.57
	rs6257	0.54	0.28–1.06	0.07	0.65	0.26–1.61	0.35	0.68	0.35–1.33	0.26	1.67	0.71–3.89	0.24

All analyses were adjusted for age, BMI, and HOMA-IR measurements.

*Logistic regression models tested were coded additively using three independant genotype categories for each marker, with the homozygous major genotype group as the reference. Genotype group categorizates were as follows; homozygous major = 0, heterozygote = 1, homozygous minor = 2. *OR* presented above represent the change in odds per each 1 unit change in genotype group.

[1]*OR* = Odds ratio; [2]*P* value presented is from adjusted logistic regression analysis for association with the specified phenotype.