

Additional file 2. The WGCNA results show that the yellow module is associated with serum TG levels in the Mexican TG cases/controls.

Module(Number, % TG-assoc)

Pink(60, 11.7%)		-0.013 (0.9)	0.035 (0.8)	0.21 (0.08)	0.24 (0.04)
Turquoise(2193, 11.6%)		0.16 (0.2)	0.12 (0.3)	0.17 (0.1)	0.12 (0.3)
Yellow(192, 93.8%)		0.44 (1e-04)	0.42 (3e-04)	0.31 (0.009)	0.15 (0.2)
Brown(434, 5.8%)		-0.15 (0.2)	0.066 (0.6)	-0.31 (0.009)	-0.28 (0.02)
Black(66, 3.0%)		0.051 (0.7)	0.19 (0.1)	0.022 (0.9)	0.0038 (1)
Green(88, 0.0%)		0.016 (0.9)	-0.072 (0.6)	0.092 (0.5)	0.097 (0.4)
Blue(474, 4.2%)		-0.093 (0.4)	0.1 (0.4)	-0.25 (0.04)	-0.23 (0.06)
Red(85, 1.2%)		-0.0074 (1)	0.077 (0.5)	-0.096 (0.4)	-0.1 (0.4)
Grey(11255, 8.9%)		-0.016 (0.9)	0.17 (0.2)	-0.23 (0.06)	-0.25 (0.04)
		TG	logTG_step	BMI	BMI_step

Each row represents a module (labeled by color), and each column represents a trait. The value at the top of each square represents the correlation coefficient between the module eigengene and the trait. Beneath the correlation coefficient in parentheses is the correlation p-value. The red color represents a positive correlation between the module eigengene and the trait, and the green color represents a negative correlation. The number of probes present in each module and the percent of probes correlated with TGs ($p < 0.05$, Pearson correlation) are listed in parenthesis next

to the module color. Genes that cannot be clustered into one of the modules are assigned to the Grey module. TG values were log transformed and corrected for age, sex, TG status, and BMI using stepwise linear regression. BMI values were corrected for age, sex, TG status, and BMI using stepwise linear regression. As the color labels for WGCNA are given based on the number of probes found in the given module, module colors in different study samples are not comparable and thus, comparing the color labels observed between the study samples does not indicate whether the modules are related. The yellow module-TG association passed the Bonferroni multiple testing correction for the 18 statistical tests performed (9 modules, 2 traits); the Bonferroni p-value cut-off = 2.8×10^{-3} .