

Supplementary Material

Genome-wide association study for adiponectin levels in Filipino women identifies *CDH13* and a novel uncommon haplotype at *KNG1-ADIPOQ*

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Supplementary Table 1. Correlation between log adiponectin and other metabolic-related traits

	Mothers samples		Offspring samples	
	Correlation coefficient	<i>P</i>	Correlation coefficient	<i>P</i>
Log_BMI	-0.32	< 0.0001	-0.28	< 0.0001
Waist circumference	-0.33	< 0.0001	-0.28	< 0.0001
Log_triglyceride	-0.34	< 0.0001	-0.24	< 0.0001
Log_HDL-C	0.17	< 0.0001	0.18	< 0.0001
Log_LDL-C	-0.03	0.20	-0.05	0.032
Log_glucose	-0.25	< 0.0001	-0.03	0.21
Log_insulin	-0.37	< 0.0001	-0.18	< 0.0001
Log_HOMA-IR	-0.40	< 0.0001	-0.17	< 0.0001
Log_HOMA- β	-0.19	< 0.0001	-0.16	< 0.0001

Analysis of CLHNS mothers was adjusted for age, age², household assets, log-transformed household income and menopausal status; Analysis of CLHNS offspring was adjusted for sex, household assets and log-transformed household income.

Supplementary Table 2. Association of plasma adiponectin level with covariates, including 10 principal components of population structure in CLHNS mothers ($n = 1,776$)

Covariate	Adjusted for	β (SE)	P
Age*	1	0.015 (0.002)	1.02E-19
Age ² *	2	0.000 (0.000)	0.038
Household assets*	3	-0.289 (0.005)	9.36E-09
Log-transformed household income*	3	-0.049 (0.012)	2.86E-05
Number of Pregnancies (3 categories)	3	----	0.61
Menopausal status*	3	0.070 (0.028)	0.012
PC1	4	0.365 (0.405)	0.37
PC2	4	0.272 (0.397)	0.49
PC3	4	0.629 (0.401)	0.12
PC4	4	-0.333 (0.410)	0.42
PC5	4	-0.305 (0.408)	0.46
PC6	4	0.752 (0.408)	0.066
PC7	4	-0.338 (0.412)	0.41
PC8	4	0.529 (0.412)	0.20
PC9	4	0.128 (0.412)	0.76
PC10	4	-0.094 (0.415)	0.82

Covariate tests adjusted for:

1: Nothing

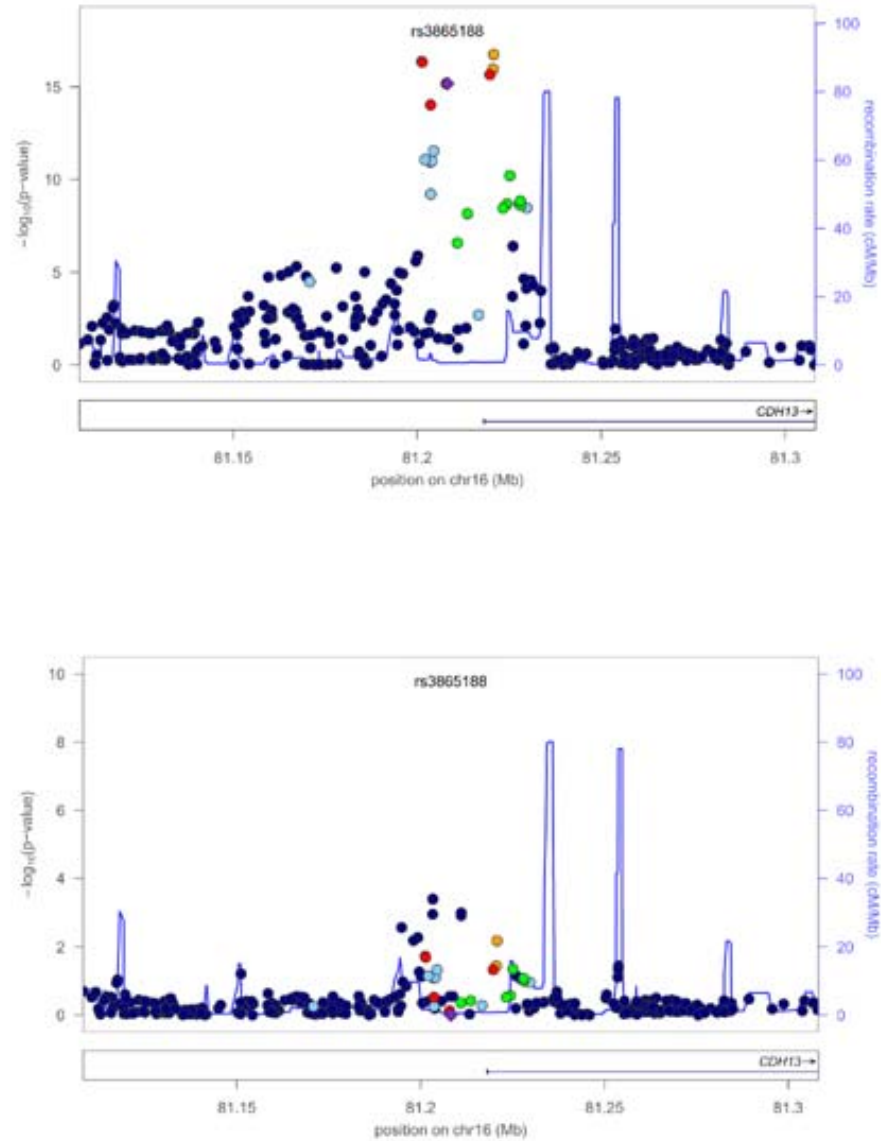
2: Age

3: Age, age²

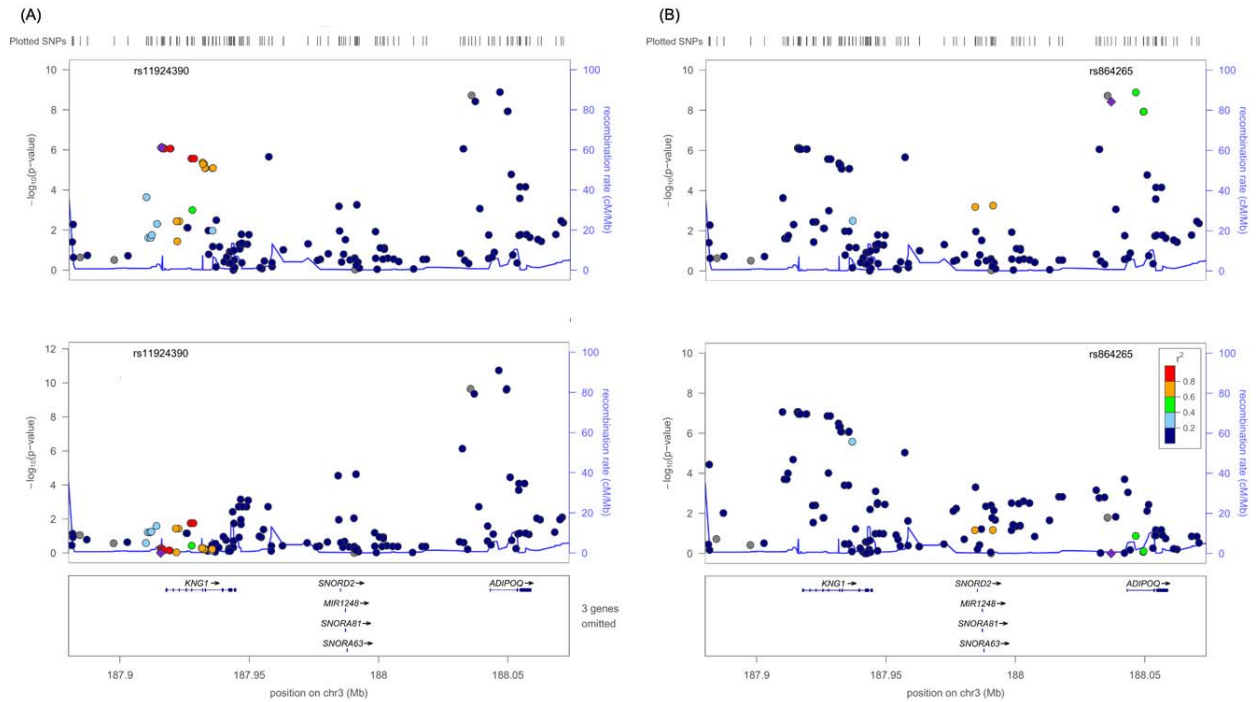
4: Age, age², all other PCs

PC1-10 are the EIGENSTRAT principal components

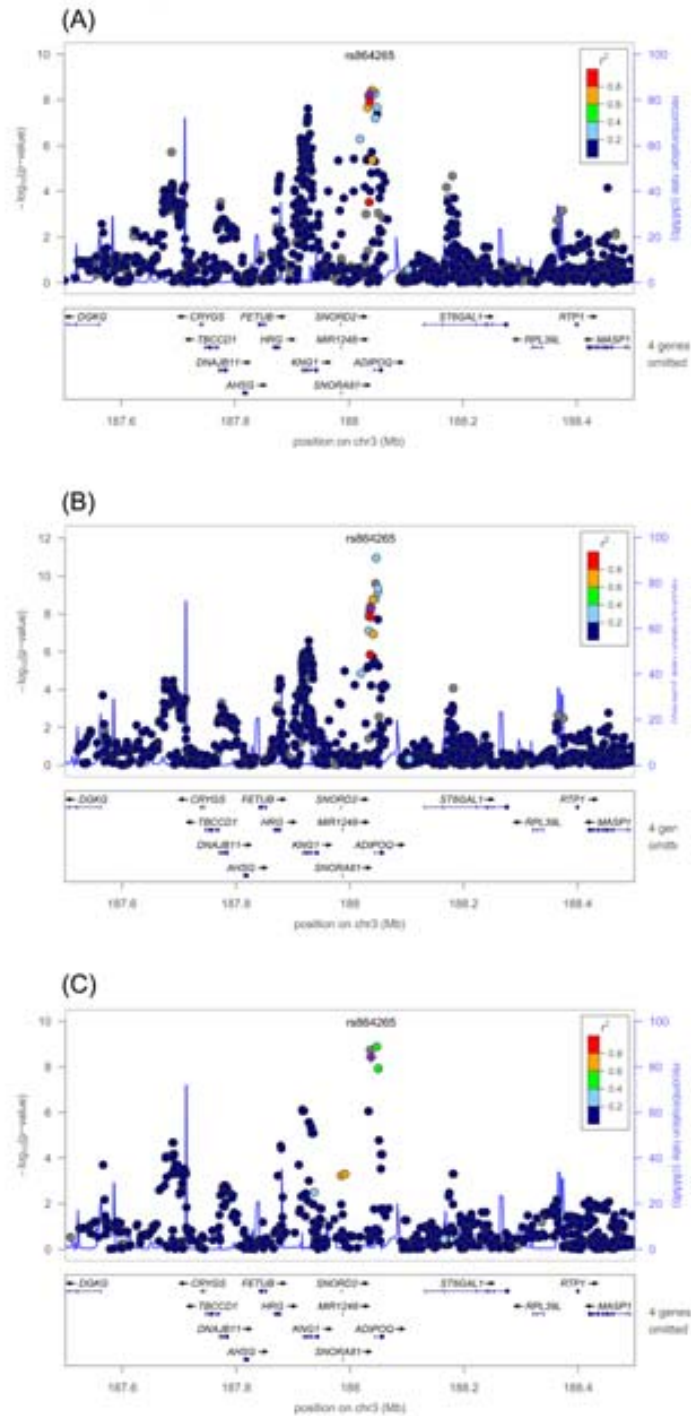
* Covariates used in analysis for plasma adiponectin



Supplementary Figure 1. Evidence of association between adiponectin and SNPs within the *CDH13* (chromosome 16: 81,107 kb - 81,309 kb) with and without conditional analysis. SNPs are colored based on HapMap CHB+JPT linkage disequilibrium with the index SNP in each plot. Upper panel, initial evidence of association; lower panel, evidence of association conditioning on SNP rs3865188.



Supplementary Figure 2. Evidence of association between adiponectin and SNPs within the *KNG1-ADIPOQ* gene locus (chromosome 3: position 187,880 kb-188,080 kb) with and without conditional analysis. SNPs are colored based on HapMap CHB+JPT linkage disequilibrium with the index SNP in each plot. (A) index SNP rs11924390; upper panel, initial evidence of association; lower panel, evidence of association conditioning on SNP rs11924390. (B) index SNP rs864265; upper panel, initial evidence of association; lower panel, evidence of association conditioning on SNP rs864265.



Supplementary Figure 3. Association with adiponectin for SNPs imputed based on HapMap or 1000 Genomes Project pilot data (August 2009 Release). (A) 1000 Genomes Project CHB+JPT combined samples; (B) 1000 Genomes Project CEU+CHB+JPT combined samples; (C) HapMap CEU+CHB+JPT combined samples. The purple diamond represents the index SNP rs864265. SNPs showing stronger association with adiponectin are either in high linkage disequilibrium with rs864265 ($r^2 > 0.8$) or poorly imputed (MACH quality $r^2 < 0.6$), and thus unlikely to represent a novel signal or potential functional variant.