Supplementary Table S3. Multiple Logistic Regression Analyses of the Relationships between the Variables and CHD

Variable	*Test*	*ChiSq*	*ProbChiSq*
Categorical_age	Likelihood ratio	78.7059	<0.0001
	Score	77.1535	<0.0001
	Wald	73.4980	<0.0001
Categorical_TG	Likelihood ratio	45.6614	0.0253
	Score	45.2680	0.0277
	Wald	44.3095	0.0343
Categorical_HDL	Likelihood ratio	106.7197	<0.0001
	Score	103.3709	<0.0001
	Wald	96.7890	<0.0001
Categorical_LDL	Likelihood ratio	90.9864	<0.0001
	Score	88.0533	<0.0001
	Wald	80.3914	<0.0001
Categorical_apoA	Likelihood ratio	381.3593	<0.0001
	Score	352.3160	<0.0001
	Wald	275.6331	<0.0001
Categorical_apoB	Likelihood ratio	381.2923	<0.0001
	Score	345.0423	<0.0001
	Wald	244.9612	<0.0001
Categorical_LP(a)	Likelihood ratio	47.6518	0.0160
	Score	46.8807	0.0191
	Wald	45.3734	0.0271
Categorical_PT	Likelihood ratio	34.2652	0.0339
	Score	33.5720	0.0402
	Wald	32.4564	0.0526
Categorical_Fg	Likelihood ratio	46.2952	0.0041
	Score	45.7184	0.0048
	Wald	44.4870	0.0067
Categorical_Glu	Likelihood ratio	78.6578	<0.0001
	Score	77.1570	<0.0001
	Wald	74.5038	<0.0001
EH	Likelihood ratio	12.9393	0.0003
	Score	12.9167	0.0003
	Wald	12.8783	0.0003
Race	Likelihood ratio	11.0412	0.0009
	Score	11.0250	0.0009
	Wald	10.9971	0.0009
Sex	Likelihood ratio	54.8800	<0.0001
	Score	54.6235	<0.0001
	Wald	53.7569	<0.0001
Categorical_TP	Residual Chi-square test	53.0746	0.2900

Supplementary Table S3 shows that multiple logistic regression analyses were further done with the variables listed in Supplementary Table S2. Because log odds change linearly as a function of explanatory variables (i.e., the relationship between the logit(P) and the independent variable is assumed to be linear), we segmented the independent variable equidistant over 50 and then replaced the original continuous variables with generated categorical variables. For variables for which $p < 0.1$, we used propensity score matching techniques to match the cases and controls (except TP because $p = 0.29$ in residual Chi-square test, and no effects met the 0.1 significance level for entry into the model). At last, age, race, sex, EH, Glu, TG, HDL, LDL, LP(a), apoA, apoB, PT, and Fg did not differ significantly between those with and without CHD; we next analyzed the interaction between the gene and environment.