

SUPPLEMENTARY TABLE S4. DIFFERENCES
IN THE CHARACTERISTICS BETWEEN CASES
AND CONTROLS AFTER PROPENSITY SCORE MATCHING

<i>Variable</i>	<i>CHISQ</i>	<i>CHISQ_P</i>
Categorical_age	6.678	1.000
Categorical_TG	41.920	0.057
Categorical_HDL	6.248	1.000
Categorical_LDL	7.692	1.000
Categorical_apoA	4.082	1.000
Categorical_apoB	6.956	1.000
Categorical_LP(a)	32.268	0.308
Categorical_PT	23.845	0.301
Categorical_Fg	22.534	0.547
Categorical_Glu	6.261	1.000
EH	1.882	0.170
Race	0.026	0.872
Sex	0.065	0.799

p values were calculated using χ^2 test.
p > 0.05.

We used the SAS “pscore” command to generate propensity scores, and the code and output were produced by the “pscore” command as described in the literature (Coca-Perraillon, 2007). This procedure automatically tests for balance between the case and control groups on covariates used to predict the propensity score, and when we controlled the difference in the pscore from 0 to 0.1, our 596 samples (298 controls and 298 CHD patients) remained to the end.

The Chi-square (χ^2) test is used to compare the independent variable (previously segmented) between the case and control after matching (Table S4), and we observed no significant difference (*p* > 0.05).