SUPPLEMENTAL MATERIAL

Table S1. Tests of normality.

Quantitative variables	***p* Shapiro-Wilk test Controls**	**Controls Passed normality test (alpha ≥ 0.05)?**	***p* Shapiro-Wilk test Cases**	**Cases Passed normality test (alpha ≥ 0.05)?**	**Comparison test used in Table 1**
Age, years	0,3266	Yes	0,0241	No	Mann-Whitney test
BMI, kg/m^2	0,212	Yes	0,0148	No	Mann-Whitney test
Systolic blood pressure, mmHg	0,0006	No	0,0004	No	Mann-Whitney test
Diastolic blood pressure, mmHg	0,0023	No	0,1311	Yes	Mann-Whitney test
Total cholesterol, mmol/L	0,2999	Yes	0,0045	No	Mann-Whitney test
Triglycerides, mmol/L	<0,0001	No	<0,0001	No	Mann-Whitney test
LDL cholesterol, mmol/L	0,1825	Yes	0,2887	Yes	Student t test
HDL cholesterol, mmol/L	0,0026	No	0,0199	No	Mann-Whitney test
Fasting blood glucose, mmol/L	<0,0001	No	<0,0001	No	Mann-Whitney test

Table S2. Results of multiple linear regression models predicting 16S in cases as compared to controls.

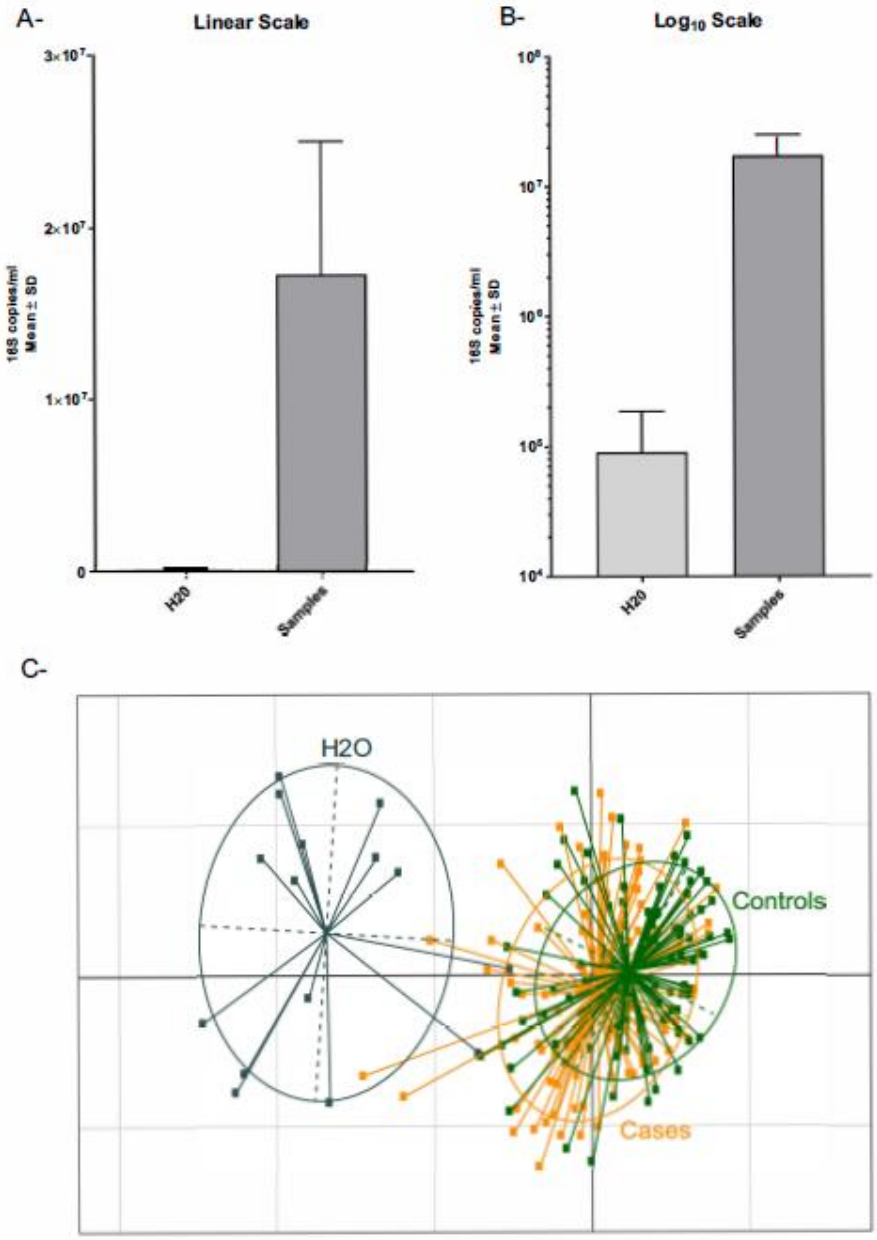
	Model 1			**Model 2**		
	β	**Standard error**	**p-value**	**β**	**Standard error**	**p-value**
Age, years	0.658.10^{5}	0.619.10^{5}	0.290	0.6793.10^{5}	0.624.10^{5}	0.278
BMI, kg/m^{2}	1.475.10^{5}	1.184.10^{5}	0.214	1.433.10^{5}	1.235.10^{5}	0.248
Female vs male	3.624.10^{5}	11.60.10^{5}	0.755	-1.339.10^{5}	12.72.10^{5}	0.916
Smoking vs no smoking	39.56.10^{5}	11.82.10^{5}	0.001	45.83.10^{5}	12.15.10^{5}	<0.0001
Hypertension vs no hypertension	-20.78.10^{5}	12.93.10^{5}	0.110	-24.62.10^{5}	13.15.10^{5}	0.063
Dyslipidemia vs non dyslipidemia	-12.41.10^{5}	11.27.10^{5}	0.272	-14.08.10^{5}	11.61.10^{5}	0.227
Diabetes vs no diabetes	17.62.10^{5}	12.32.10^{5}	0.155	12.55.10^{5}	14.05.10^{5}	0.373
HDL-c, mmol/l				-4.827.10^{5}	15.47.10^{5}	0.755
Fasting glucose, mmol/l				2.149.10^{5}	2.795.10^{5}	0.443
Case vs control	41.51.10^{5}	12.11.10^{5}	0.001	33.04.10^{5}	13.00.10^{5}	0.012

Table S3. Correlations between lipid parameters and blood microbiota (16S copies/ml of blood and relative proportion of taxa displayed in Figure 3 and Figure 4).

All patients	**R (Spearman)**			
	Total Cholesterol	**HDL Cholesterol**	**LDL cholesterol**	**Triglycérides**
16S copies/ml of blood	-0,11	0,02	-0,12	0,18
Aerococcaceae	-0,21	-0,23	-0,11	0,14
Caulobacteraceae	-0,09	0,06	-0,06	-0,17
Caulobacterales	-0,06	0,07	-0,03	-0,16
Chryseobacterium	0,08	0,02	0,08	-0,09
Clostridia	0,02	-0,04	-0,01	0,03
Clostridiales	0,02	-0,04	-0,01	0,03
Clostridiales is XI	0,02	0,01	0,11	-0,18
Gordonia	-0,03	-0,06	0,07	-0,06
Hymenobacter	0,01	0,04	0,06	-0,14
Neisseriaceae	0,03	-0,02	-0,09	0,14
Neisseriales	0,03	-0,02	-0,09	0,14
Nocardiaceae	0,05	-0,11	0,18	0,00
Propionibacteriaceae	0,15	0,22	0,04	-0,17
Propionibacterium	0,15	0,22	0,05	-0,18
Rhodococcus	0,14	-0,08	0,22	0,13
Sphingobacteria	0,03	0,01	0,14	-0,03
Sphingobacteriales	0,03	0,01	0,14	-0,03

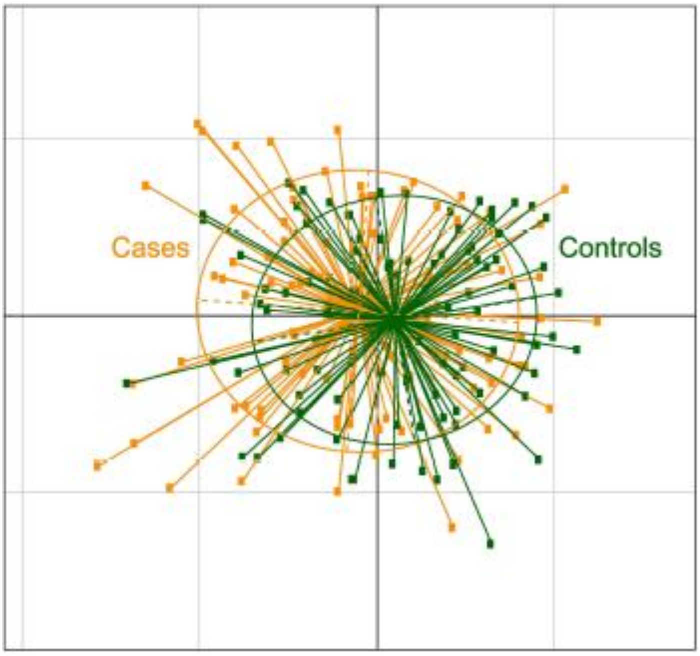
Cases	**R (Spearman)**			
	Total Cholesterol	**HDL Cholesterol**	**LDL cholesterol**	**Triglycérides**
16S copies/ml of blood	0,17	-0,11	0,23	0,07
Aerococcaceae	0,07	0,01	0,08	0,15
Caulobacteraceae	0,10	0,04	0,07	-0,04
Caulobacterales	0,08	0,04	0,04	-0,01
Chryseobacterium	0,11	-0,01	0,06	-0,06
Clostridia	-0,04	-0,01	-0,02	-0,06
Clostridiales	-0,04	-0,01	-0,02	-0,06
Clostridiales is XI	0,10	-0,03	0,11	0,01
Gordonia	0,10	0,06	0,05	0,05
Hymenobacter	0,02	-0,04	0,01	-0,03
Neisseriaceae	0,03	0,08	0,04	-0,03
Neisseriales	0,03	0,09	0,04	-0,03
Nocardiaceae	0,07	0,12	0,03	-0,02
Propionibacteriaceae	-0,03	-0,12	-0,05	-0,09
Propionibacterium	0,02	-0,07	-0,02	-0,11
Rhodococcus	-0,13	0,14	-0,14	-0,11
Sphingobacteria	0,11	0,03	0,09	0,04
Sphingobacteriales	0,11	0,03	0,09	0,04

Figure S1. Assessment of the background of the 16S qPCR and sequencing assays.



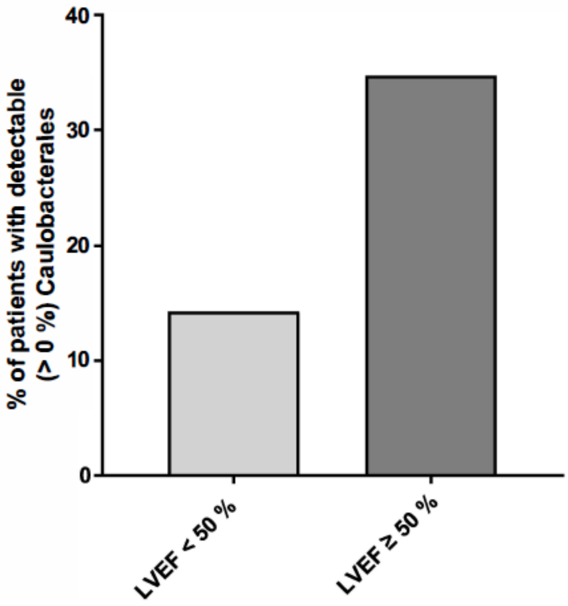
Comparison in linear scale (A) and log scale (B) by 16S qPCR between the blood samples from this study and the negative controls ran at the same time (negative controls were molecular grade water added in an empty tube, extracted and analyzed at the same time as the samples). (C) Comparison by PCoA analysis of the 16S sequencing of the blood samples (Control and Case) and water (H20) using distance calculated with Generalized UniFrac with alpha=0.2. qPCR: quantitative polymerase chain reaction; PCoA: principal coordinate analysis.

Figure S2. PCoA analysis of the 16S sequencing of the blood samples (Controls and Cases) using distance calculated with Generalized UniFrac with alpha=0.2.



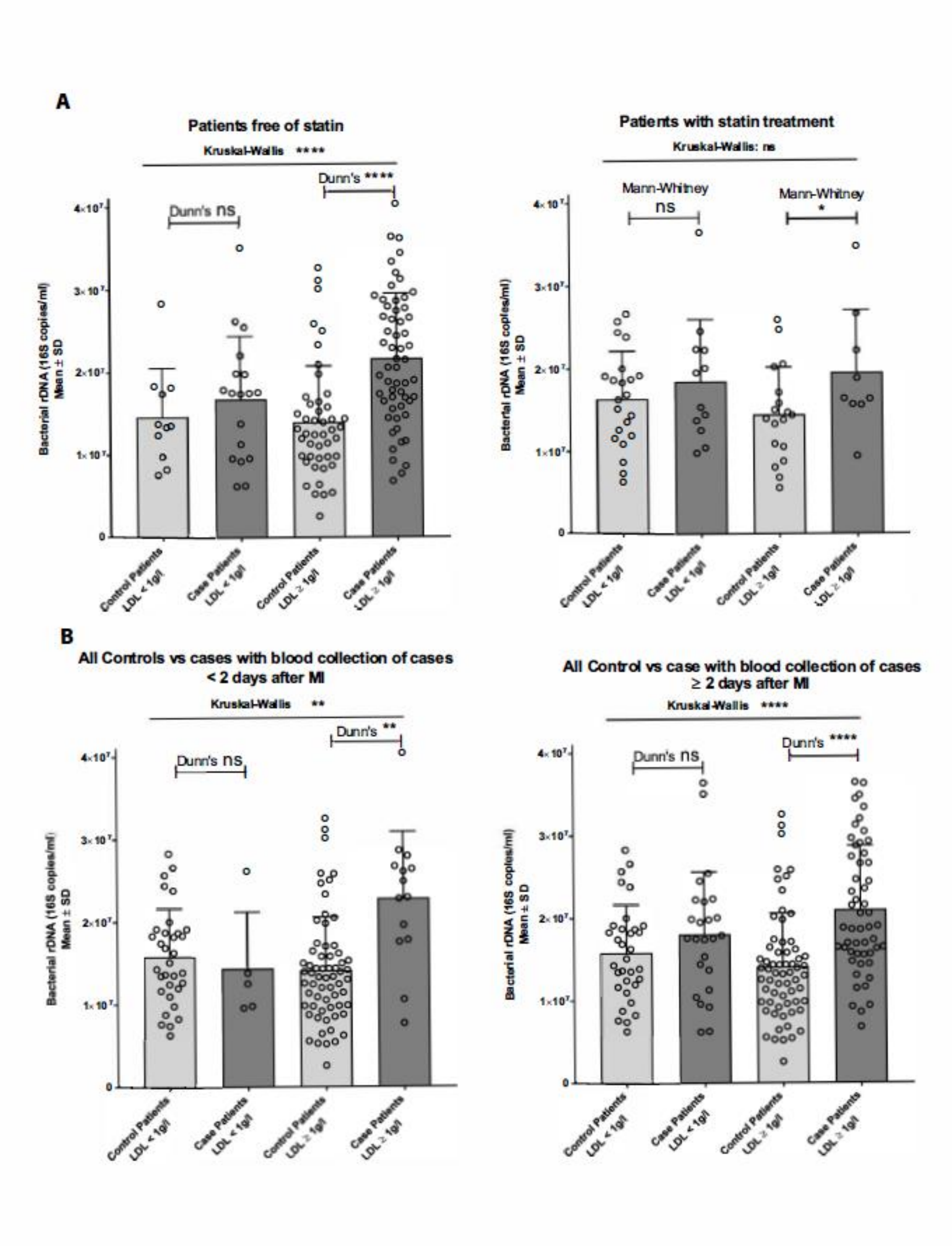
PCoA: principal coordinate analysis.

Figure S3. Presence of Caulobacterales in blood of patient with MI tended to correlate with LVEF.



Mean of relative proportion of the Caulobacterales order in MI patients with LVEF inferior or superior/equal to 50 %. MI: myocardial infarction; LVEF: left ventricular ejection fraction.

Figure S4. Interaction between LDL concentration and modification of blood bacterial 16S rDNA concentration in patients who underwent MI does not depend on statin treatment or time of sampling.



Mean concentrations (bar plots) and individual values (dot plots) of bacterial 16S rDNA assessed by qPCR in patients after myocardial infarction or control patients in subgroup of patients depending on LDL cholesterol concentration (* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$; ns : not significant). **(A)** According to the statin treatment. **(B)** According to the time (<2 days or ≥ 2 days) of blood collection after MI for case patients. LDL: low density lipoprotein; rDNA: ribosomal deoxyribonucleic acid; MI: myocardial infarction; qPCR: quantitative polymerase chain reaction.