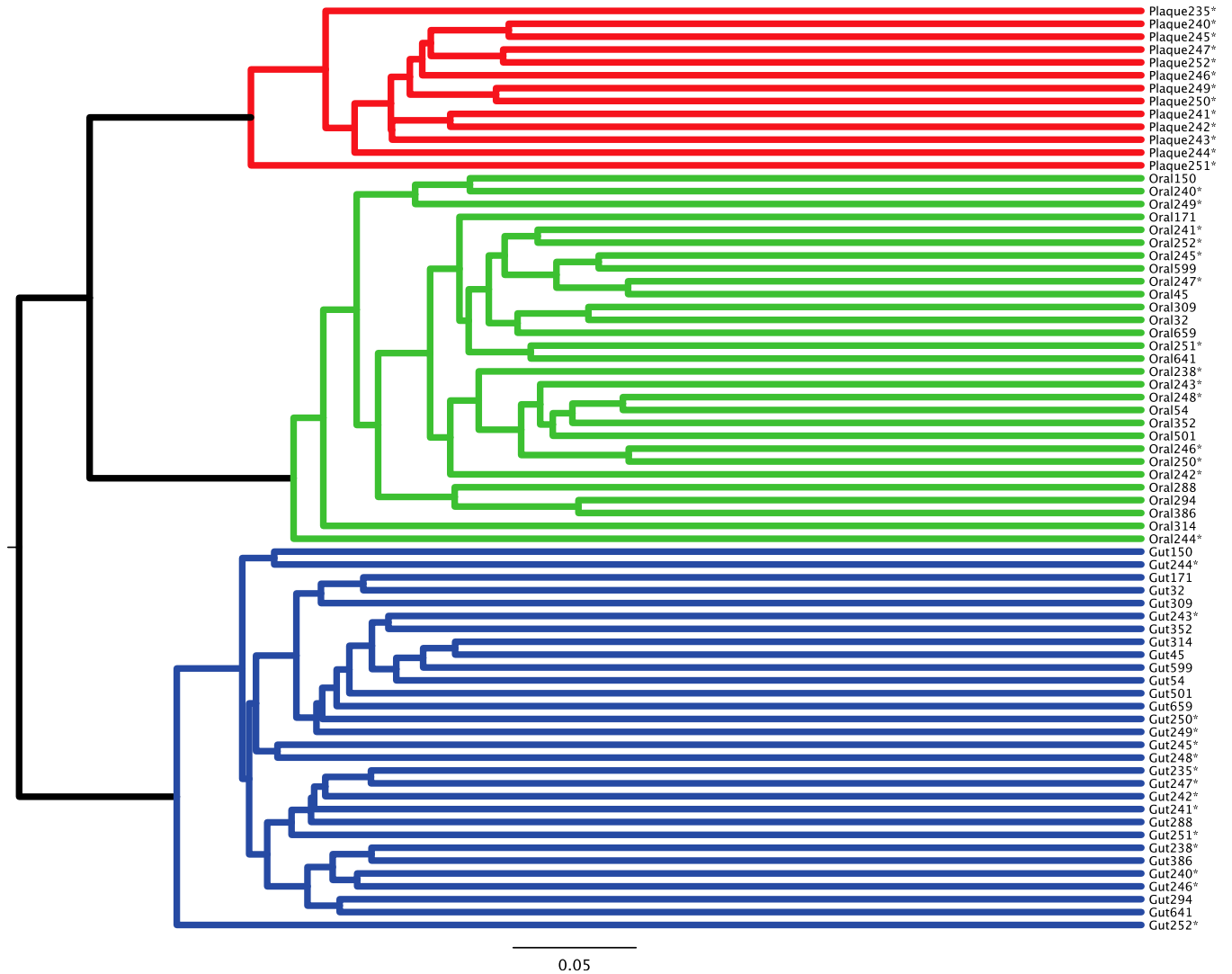


# Supporting Information

Koren et al. 10.1073/pnas.1011383107



**Fig. S1.** Clustering of bacterial communities from atherosclerotic plaques, oral cavity, and gut samples. UPGMA clustering of samples using the unweighted UniFrac distances between samples. Branches are colored by body site, and numbers in labels refer to subject numbers in the study. All atherosclerotic plaque samples are from patients; oral and gut samples from patients are noted with an asterisk.

**Table S1. Number of sequences per sample**

Subject ID	Feces	Mouth	Plaque
235	3,813	ND	26,100
238	3,418	4,191	1,037
240	3,471	5,632	5,583
241	3,142	4,871	3,914
242	4,140	4,298	4,074
243	3,212	3,587	7,357
244	3,837	5,540	29,070
245	3,604	4,947	12,845
246	3,393	4,835	5,462
247	2,874	4,486	6,501
248	3,708	4,954	ND
249	3,758	5,862	5,909
250	3,501	7255	5,292
251	3,999	4419	46,279
252	4,735	4,890	1,796
150	3,432	3,851	
171	2,576	3,936	
288	2,462	3,586	
294	3,327	3,916	
309	2,751	3,473	
314	2,795	3,456	
32	2,894	3,215	
352	2,789	3,193	
386	3,291	3,312	
45	2,946	3,648	
501	2,051	2,522	
54	2,921	2,508	
599	2,338	3,758	
641	3,400	3,504	
659	3,448	3,611	

**Table S2. Presence of *Chlamydia* DNA in atherosclerotic plaques**

Patient	<i>Chlamydia</i> DNA, pg/ $\mu$ L
235	1.25
238	3.67
240	1.07
241	1.48
242	0.96
243	0.6
244	2.16
245	1.11
246	0.787
247	1.19
249	0.92
250	1.34
251	0.937
252	0.84