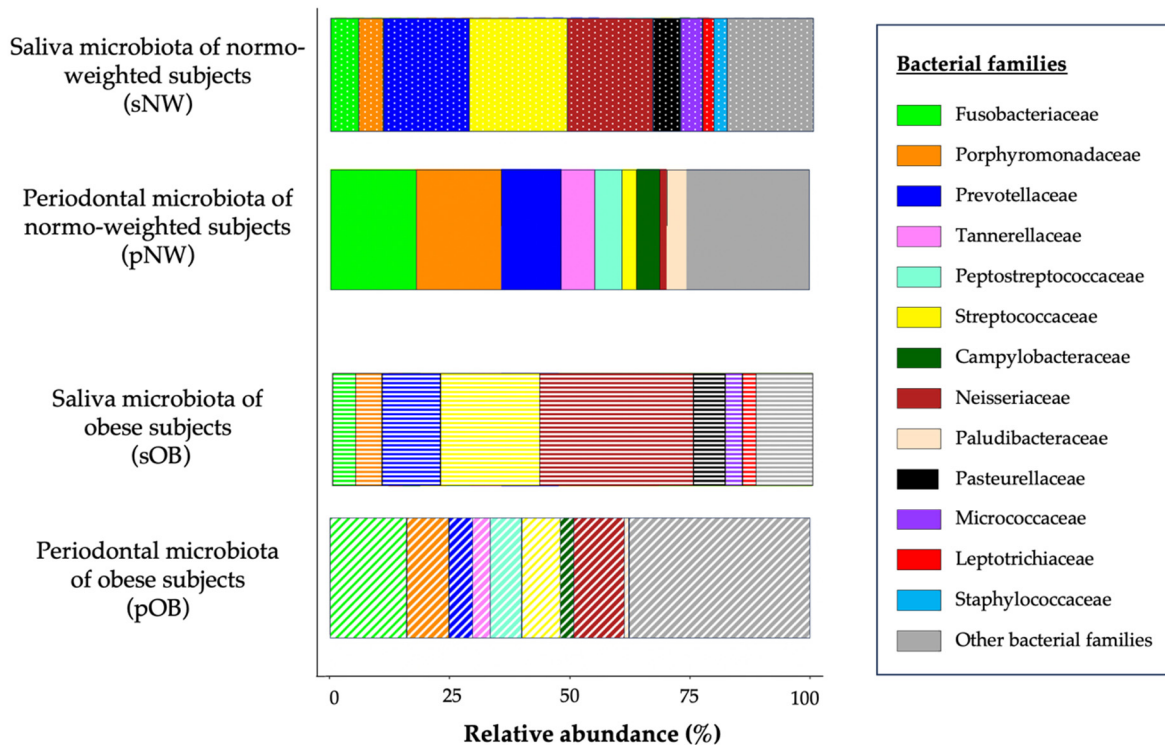
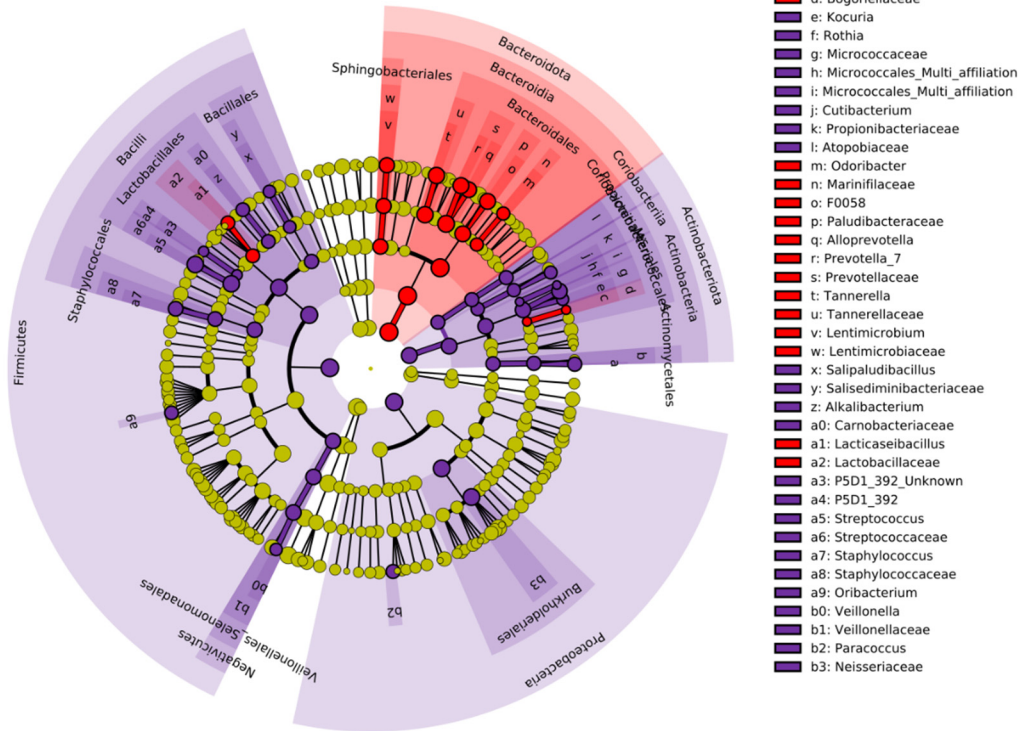


**Figure S1.** Pearson's correlation analysis between PISA index and BMI. We observed a correlation between local inflammatory surface, represented by the PISA index, and BMI. In order to avoid two distinct groups, we took advantage of the epidemiological data of overweight patients to obtain the distribution of local inflammation depending on BMI.



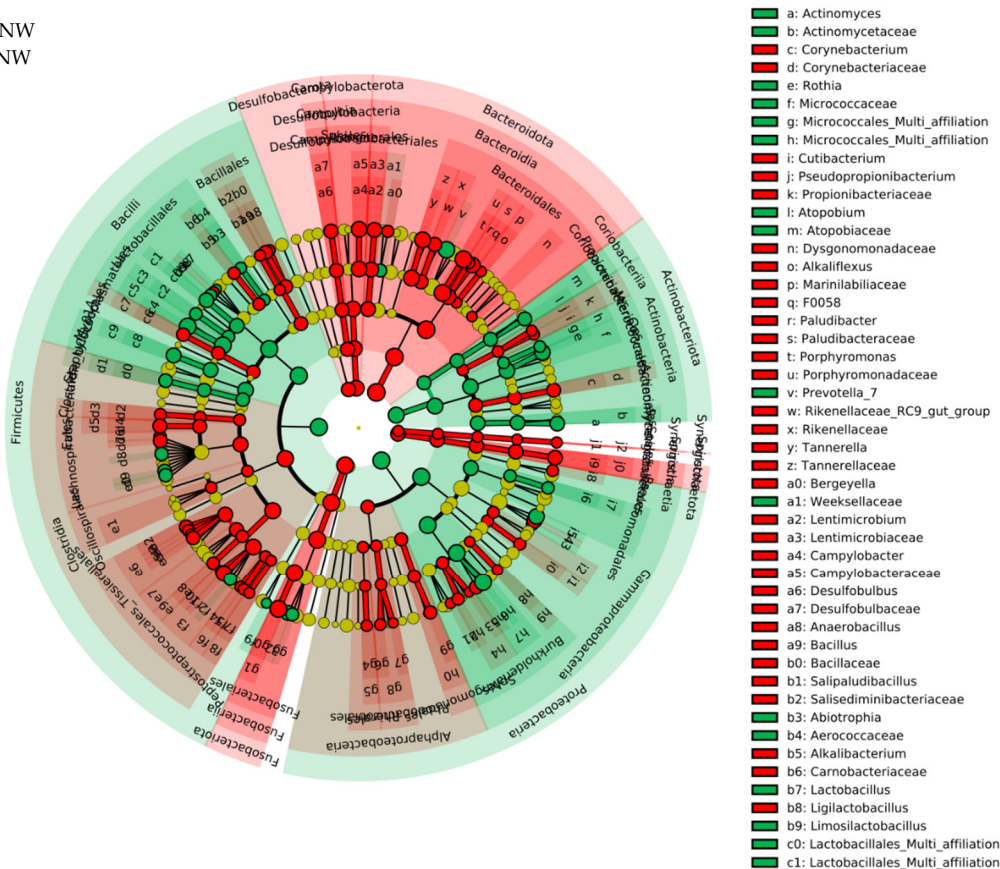
**Figure S2.** Top 10 relative abundances (%) for taxonomic families in salivary and periodontal microbiota of obese and normo-weighted subjects.

■ pNW  
■ pOB

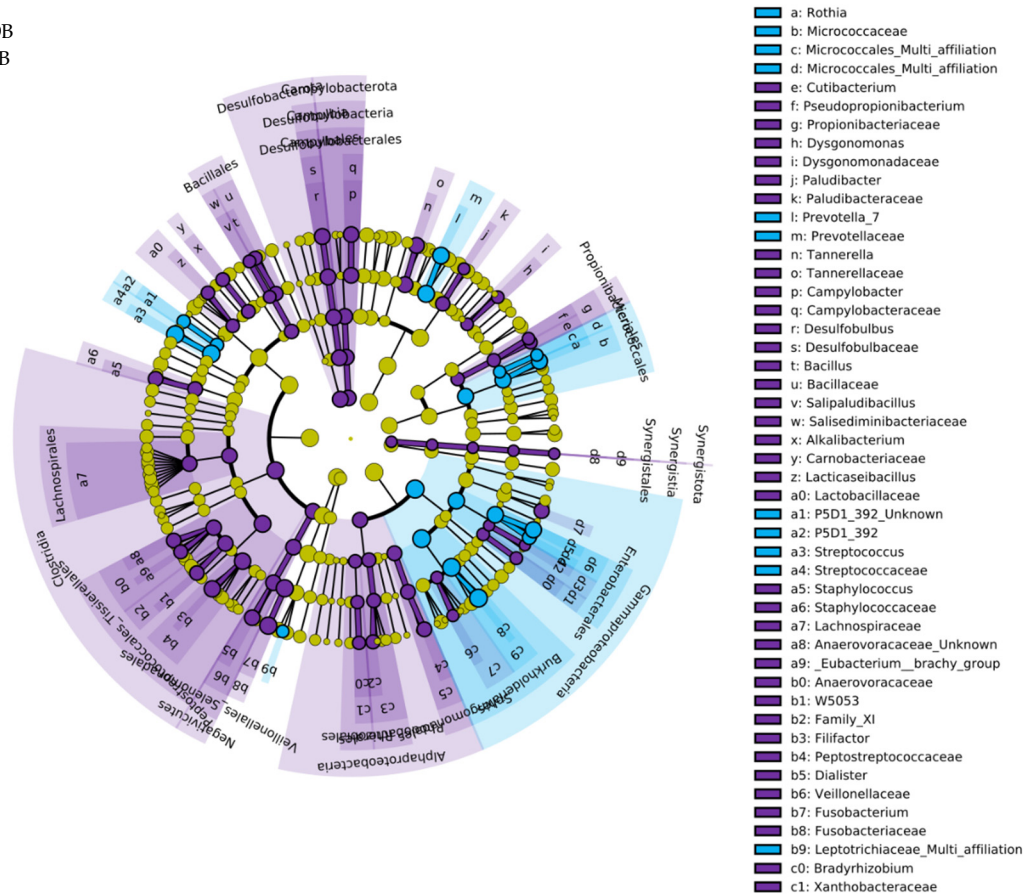


**Figure S3.** Linear discriminant analysis effect size (LEfSe) analysis-based cladogram for periodontal microbiota of obese and normo-weighted subjects

■ pNW  
■ sNW



**Figure S4.** Linear discriminant analysis effect size (LEfSe) analysis-based cladogram of periodontal and salivary microbiota in normo-weighted subjects.



**Figure S5.** Linear discriminant analysis effect size (LEfSe) analysis-based cladogram of periodontal and salivary microbiota in obese subjects.

Relative abundance of Staphylococcaceae				p-value
Periodontal microbiota		Salivary microbiota		
pNW (n = 34)	pOB (n = 11)	sNW (n = 34)	sOB (n = 11)	
0	5,54917240202491	0	0	
0	2,20167958748987	0	0,04770739	
0,0017690974065032	1,30684174153421	0	0	
0,0059349529160402	0,0507283136459164	42,4307036	0	
0,00132329394328362	0,178422205659823	0	0	
0	2,12809286223399	0	0	
1,68074563988388	0,953972020984262	0	0	
0,00077210537694184 5	0,113687659873272	0	0	
1,7507311405793	0	11,1088317	0	
0,625988490317779	0	20,4362078	0,00525127	
0	0	0		
0,003180358108323		0		
0,00135987815491732		0		
0		0		
0		0		
0		0		
0		0		
0,0873871249635887		0		
0		0		
11,5166551030563		0		
0,792546967790361		0		
0		0		
0		0		
0		20,4362078		
		0		
0,00177604120415594		0		
0,0039714058776807		0		
0		0		
0		0		
0		0		
0		0,00549843		
0		0		
0		15,423589		
0		0		
0		0		
<b>Mean ± SD</b>	0,484533576 ± 1,996730174	1,134781527 ± 1,693212834	2,629695849 ± 8,428264644	0,004814424 ± 0,014312952 <b>pNW vs. pOB * p = 0,006</b>
<b>Ratio Perio/Saliva</b>	<b>-4,427272695</b>	<b>0,9957574</b>		

**Table S1.** Relative abundance of Staphylococcaceae in periodontal microbiota.

Relative abundance of Flavobacteriaceae				p-value
Periodontal microbiota		Salivary microbiota		
pNW (n = 34)	pOB (n = 11)	sNW (n = 34)	sOB (n = 11)	
0,00077715777857220 6	0	0,260704692684468	1,45	
0,308523562887653	0	0,730273141122914	0,01060164325470 45	
12,5004422743516	2,28956461644782	0,246347751360642	1,09434895511314	
1,29381973569676	0,0710196391042829	0,0147048011175649	0,92430433936563 5	
0,919689290582117	0,185197732457032	0,212862026704509	0,24791231732776 6	
0,087830584561335	3,50269829956216	0,281728853157425	0	
0,178988496714906	0,0780664501623782	0,207845044885685	6,58859470468432	
6,56289570400568	2,12328423586846	0,176645593157307	3,20090572251955	
0,0480749969953127	5,36531813510231	0	1,11051502145923	
0	0,425408996612484	0	3,05624113847608	
1,23046711790758	1,61754855994642	1,2126627521062	0,14116887831242 7	
7,69964698024998		0,578679125079635		
0,0720735422106179		1,01419878296146		
0,152296885684093		0,028169014084507		
0		0,313686643552914		
0,36246476037052		2,24211629970159		
2,39599276471407		3,19783573806881		
0,0606855034469366		0		
1,56167045648058		0,495635449030922		
0		0,8		
0		0		
0,20995597697257		0,978574371652246		
1,41497045305319		0,342625759227535		
0,234279823821573		0,420066631258751		
0,43690613622236		12,1785894347656		
0,631453534551231		0,0558174150334904		
0,062439295129735		1,34044393196887		
5,31077024756974		0,257450460290217		
0,301309905166672		0,789714450811383		
0,0753078763178878		0,197943586077968		
0,180813318777293		2,01454659620114		
0,607889442840899		1,37857900318134		
0,682790391576176		0,53194210014833		
2,84802739086452		1,26008778139601		
<b>Mean ± SD</b>	1,467674352 ± 2,73873931	1,423464242 ± 1,770878136	0,992955213 ± 2,105828083	<b>pNW vs. pOB p = 0,8307</b>
<b>Ratio Perio/Saliva</b>	<b>0,323449911</b>	<b>-0,138361943</b>		

**Table S2.** Relative abundance of Flavobacteriaceae in periodontal microbiota.