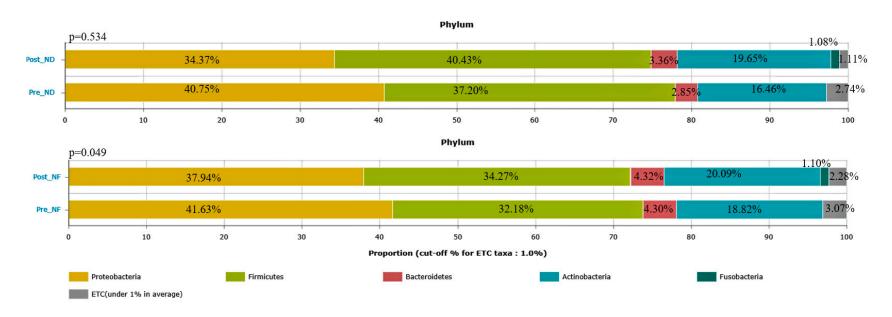


Sup. 1. The relative abundance of the most prevalent bacterial groups associated with each microenvironment depicted for all the subjects investigated. Superscripts indicate phylum.

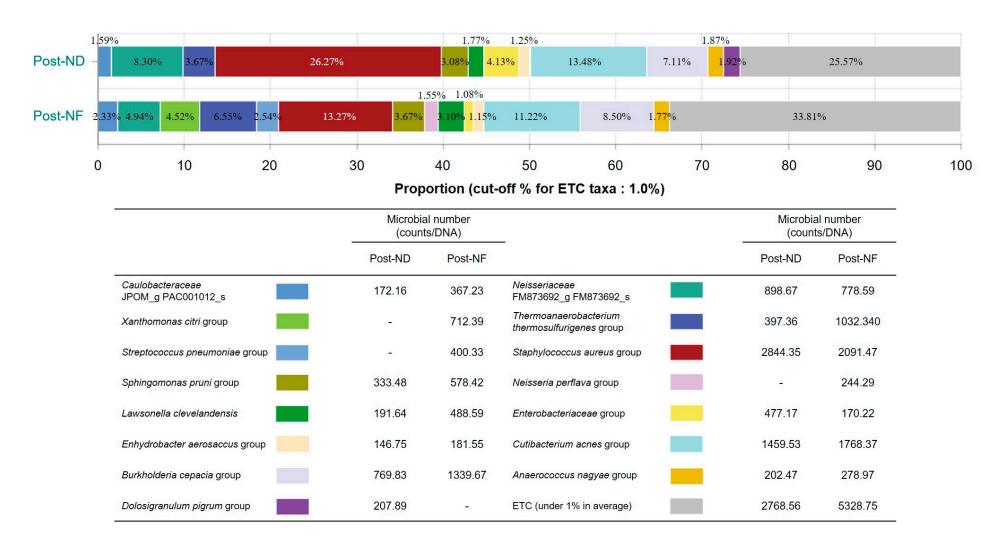


Sup. 2. The relative abundance of the most prevalent bacterial groups in each group.

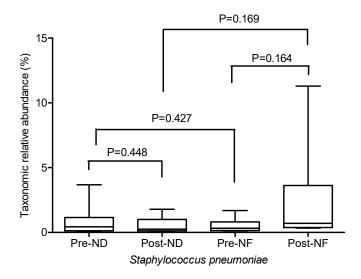
Sup. 3. The relative abundance of the main genera of bacteria in post-treatment groups (post-ND and post-NF)

Phylum	Genus	Group	Abundance (%)	P value	Phylum	Genus	Group	Abundance (%)	P value
Firmicutes	Staphylococcus*	Post-ND	26.32 ± 12.06	0.027	Proteobacteria	Burkholderia	Post-ND	7.10 ± 3.01	0.462
		Post-NF	13.18 ± 8.85				Post-NF	8.42 ± 5.56	
	Streptococcus	Post-ND	1.63 ± 1.08	0.208		Sphingomonas	Post-ND	3.29 ± 1.01	0.462
		Post-NF	4.25 ± 4.29				Post-NF	3.83 ± 2.02	
	Thermoanaerobacterium	Post-ND	3.74 ± 2.05	0.074		Enterobacteriaceae_g	Post-ND	4.11 ± 2.61	0.753
		Post-NF	6.67 ± 4.27				Post-NF	1.06 ± 1.02	
	Anaerococcus	Post-ND	2.53 ± 2.07	0.916	Actinobacteria	Cutibacterium	Post-ND	13.69 ± 12.27	0.916
		Post-NF	2.33 ± 2.57				Post-NF	11.44 ± 8.17	
Bacteroidetes	Prevotella	Post-ND	1.60 ± 1.17	1.00		Corynebacterium	Post-ND	1.54 ± 0.79	0.674
		Post-NF	1.72 ± 2.24				Post-NF	0.93 ± 0.51	
						Lawsonella	Post-ND	1.77 ± 2.76	0.600
							Post-NF	3.08 ± 2.05	

The asterisks indicate significant differences (*p < 0.05) between the NF and the ND groups in the indicated Genus.



Sup. 4. The relative abundance of the main species of bacteria in post-treatment groups (post-ND and post-NF)



Sup. 5. *Staphylococcus pneumoniae* difference within and between groups. ND (control serum); NF (cosmetic serum containing GOS).