

Supplementary Material

Table S1. Relative abundances of the bacterial genera in the microbiome of Necrotizing Fasciitis.

Genus.	Pat. No. 2	Pat. No. 3	Pat. No. 4	Mean
<i>Prevotella</i>	11.5017	6.4085	46.7153	21.5418
<i>Porphyromonas</i>	16.4081	25.7687	0.0092	14.0620
<i>Peptostreptococcus</i>	14.8501	6.3073	8.1825	9.7800
<i>Parvimonas</i>	10.1047	2.3329	3.0086	5.1487
<i>Erysipelothrix</i>	13.9398	0.0000	0.5520	4.8306
<i>Coriobacterium</i>	0.8435	0.0000	12.8167	4.5534
<i>Pyramidobacter</i>	0.0009	13.5196	0.0000	4.5068
<i>Veillonella</i>	1.1946	4.0980	7.9985	4.4304
<i>Fusobacterium</i>	5.4298	0.0000	6.5724	4.0007
<i>Moryella</i>	0.0000	9.9162	0.0000	3.3054
<i>Slackia</i>	6.3279	0.2305	1.7175	2.7586
<i>Peptoniphilus</i>	0.0000	6.2173	0.0000	2.0724
<i>Oceanivirga</i>	0.0000	5.9812	0.0000	1.9937
<i>Atopobium</i>	3.7758	1.6190	0.0000	1.7983
<i>Lachnospira</i>	0.8614	0.3485	3.6128	1.6076
<i>Ezakiella</i>	0.0000	4.3679	0.0000	1.4560
<i>Mogibacterium</i>	3.3645	0.0000	0.9569	1.4405
<i>Bacteroides</i>	0.0715	3.9463	0.0061	1.3413
<i>Filifactor</i>	3.2731	0.0000	0.0000	1.0910
<i>Eubacterium</i>	1.2031	0.2136	1.6469	1.0212
<i>Alloprevotella</i>	0.0047	0.0000	2.5915	0.8654
<i>Oribacterium</i>	0.0047	2.4228	0.0000	0.8092
<i>Dialister</i>	0.0038	0.0000	2.2818	0.7619
<i>Streptococcus</i>	0.2052	0.0000	1.1777	0.4610
<i>Treponema</i>	1.2756	0.0000	0.0031	0.4262
<i>Olsenella</i>	0.0038	1.2704	0.0000	0.4247
<i>Family_XIII_ge</i>	1.2228	0.0000	0.0000	0.4076
<i>DNF00809</i>	0.0000	1.1580	0.0000	0.3860
<i>Corynebacterium</i>	1.0694	0.0000	0.0000	0.3565
<i>Rikenella</i>	1.0477	0.0000	0.0000	0.3492
<i>Selenomonas</i>	0.9809	0.0000	0.0215	0.3341
<i>Prevotella_7</i>	0.0000	0.7982	0.0000	0.2661
<i>Solobacterium</i>	0.0000	0.6127	0.0000	0.2042
<i>Actinomyces</i>	0.0028	0.4666	0.0000	0.1565
<i>Catonella</i>	0.4255	0.0000	0.0000	0.1418
<i>Lachnospiraceae FE2018 group</i>	0.0000	0.4104	0.0000	0.1368
<i>Peptococcus</i>	0.3427	0.0675	0.0000	0.1367
<i>Eggerthia</i>	0.0000	0.3092	0.0000	0.1031
<i>Candidatus Saccharimonas</i>	0.0000	0.2811	0.0000	0.0937
<i>Rikenellaceae RC9 gut group</i>	0.0000	0.2530	0.0000	0.0843
<i>Sphaerochaeta</i>	0.0000	0.2080	0.0000	0.0693
<i>Gemella</i>	0.1845	0.0000	0.0061	0.0635
<i>Escherichia-Shigella</i>	0.0000	0.1518	0.0000	0.0506
<i>Finegoldia</i>	0.0000	0.1349	0.0000	0.0450
<i>Neisseria</i>	0.0038	0.0843	0.0092	0.0324
<i>Family XIII AD3011 group</i>	0.0000	0.0787	0.0000	0.0262
<i>Mycoplasma</i>	0.0000	0.0000	0.0644	0.0215
<i>Campylobacter</i>	0.0235	0.0000	0.0000	0.0078
<i>Rothia</i>	0.0000	0.0000	0.0184	0.0061
<i>Anaerococcus</i>	0.0000	0.0169	0.0000	0.0056
<i>Lactobacillus</i>	0.0038	0.0000	0.0123	0.0054

<i>Fretibacterium</i>	0.0038	0.0000	0.0061	0.0033
<i>Staphylococcus</i>	0.0038	0.0000	0.0031	0.0023
<i>Clostridium</i>	0.0066	0.0000	0.0000	0.0022
<i>Moraxella</i>	0.0038	0.0000	0.0000	0.0013
<i>Listeria</i>	0.0038	0.0000	0.0000	0.0013
<i>Ruminococcus</i>	0.0038	0.0000	0.0000	0.0013
<i>Acidibacter</i>	0.0038	0.0000	0.0000	0.0013
<i>Bifidobacterium</i>	0.0000	0.0000	0.0031	0.0010
<i>Haemophilus</i>	0.0000	0.0000	0.0031	0.0010
<i>Clostridiales bacterium</i>	0.0000	0.0000	0.0031	0.0010
<i>Enterococcus</i>	0.0028	0.0000	0.0000	0.0009
<i>Acinetobacter</i>	0.0019	0.0000	0.0000	0.0006
<i>Pseudomonas</i>	0.0019	0.0000	0.0000	0.0006
<i>Pasteurella</i>	0.0019	0.0000	0.0000	0.0006
<i>Defluviitaleaceae_UCG-012</i>	0.0019	0.0000	0.0000	0.0006
<i>Burkholderia-Paraburkholderia</i>	0.0019	0.0000	0.0000	0.0006
<i>Bradyrhizobium</i>	0.0009	0.0000	0.0000	0.0003
<i>Comamonas</i>	0.0009	0.0000	0.0000	0.0003
<i>Howardella</i>	0.0009	0.0000	0.0000	0.0003