SUPPLEMENTARY DATA

Supplementary Table 1. Co-variation of Staphylococcus aureus relative abundance with anaerobic species-level taxa and Corynebacterium relative abundance. Rho (ρ) represents the Spearman rank correlation coefficient. *P*-values were calculated by a permutation test. These P-values were then corrected for multiple testing by applying false discovery rate (FDR) control (*q*=0.05).

	ρ	***P*-value**	**FDR-adjusted**
			***P*-value**
Anaerococcus	-0.43	0.001	0.038
Anaerococcus.1	-0.42	0.002	0.047
Anaerococcus.2	-0.46	0.001	0.024
Clostridium	-0.06	0.657	0.917
Enterococcus	-0.15	0.293	0.731
Fastidiosipila	-0.18	0.194	0.631
Finegoldia	-0.15	0.284	0.725
Fusobacterium	-0.16	0.245	0.693
Gemella	-0.10	0.460	0.844
Helcococcus	-0.30	0.030	0.248
Helcococcus.1	-0.40	0.003	0.061
Parvimonas	-0.43	0.002	0.042
Peptoniphilus	-0.34	0.013	0.156
Peptostreptococcus	-0.35	0.011	0.135
Porphyromonas	-0.48	<0.001	0.014
Porphyromonas.1	-0.22	0.124	0.531
Porphyromonas.2	-0.41	0.002	0.051
Prevotella	-0.38	0.005	0.082
Prevotella.1	-0.51	<0.001	0.007
unclassified.Clostridiales	-0.51	<0.001	0.006
unclassified.Clostridiales.1	-0.10	0.469	0.848
unclassified.Incertae.Sedis.XI	-0.38	0.006	0.089
unclassified.Incertae.Sedis.XI.1	-0.17	0.223	0.663
Veillonella	0.14	0.325	0.753
Corynebacterium	0.47	<0.001	0.02
Corynebacterium.1	-0.05	0.703	0.93
Corynebacterium.2	0.30	0.031	0.26

Supplementary Table 2. Analysis of molecular variance (AMOVA) F statistic values and Bonferroni corrected *P*-values. AMOVA was performed on data clustered by the weighted and unweighted UniFrac metric, the Jaccard index, and the Theta index. The UniFrac metric measures shared phylogeny among samples, weighted or unweighted for abundance. The Jacccard index measures shared community membership. The Theta index measures shared community structure. AMOVA detects differences in microbial communities (as measured by the above metrics) with respect to the clinical factor specified. P-values are adjusted for multiple testing using a Bonferroni correction.

	UniFrac-weighted		UniFrac-unweighted		Jaccard		Theta	
	Fs	p-value	Fs	p-value	Fs	p-value	Fs	p-value
Depth	1.31	0.06	1.03	0.27	0.99	0.60	1.35	0.02
Hemoglobin A1c	1.30	0.05	1.02	0.30	1.06	0.11	1.19	0.10
Tissue oxygen	0.71	0.94	1.01	0.45	1.01	0.40	0.87	0.73
Necrosis	1.82	0.01	1.01	0.44	0.94	0.75	1.38	0.07
Surface area	1.32	0.12	0.85	0.99	0.93	0.90	1.27	0.12
Duration	1.20	0.12	0.98	0.67	0.97	0.77	1.21	0.08

Supplementary Table 3. Spearman correlation coefficients (ρ) between DFU clinical factors and bacterial diversity and dominant bacterial taxa. * Indicates significance at a threshold of $P<0.05$ by permutation test.

	Staphylococcus	Streptococcus	Proteobacteria	Anaerobes	Shannon Index	Richness
Duration	-0.31*	0.12	0.38*	0.05	0.32*	0.41*
Depth	-0.47*	0.11	0.25	0.33*	0.27*	0.16
HGBA1c	0.07	0.18	-0.22	-0.07	-0.18	-0.06
Necrosis	-0.16	-0.05	-0.08	0.15	0.20	0.11
Tissue oxygen	-0.12	-0.04	0.12	0.11	0.21	0.24
Surface area	-0.26	0.11	0.20	0.23	0.24	0.27*

SUPPLEMENTARY DATA

Supplementary Figure 1. Co-variation of species-level OTUs colonizing DFUs. Spearman rank correlation coefficients were calculated for the 72 taxa present in >10% of DFU samples and containing greater than 100 sequence counts. Purple and red denote positive and negative correlation, respectively. Columns and rows were hierarchically clustered, as indicated by the dendrograms at the top and to the left of the heatmap. OTUs are classified as Staphylococcus, Anaerobes, Proteobacteria, Streptococcus, or Other, and are indicated by the color strips at the bottom and to the left of the heatmap. Rho values significant after false discovery rate (FDR) control of 5% are indicated by dots.