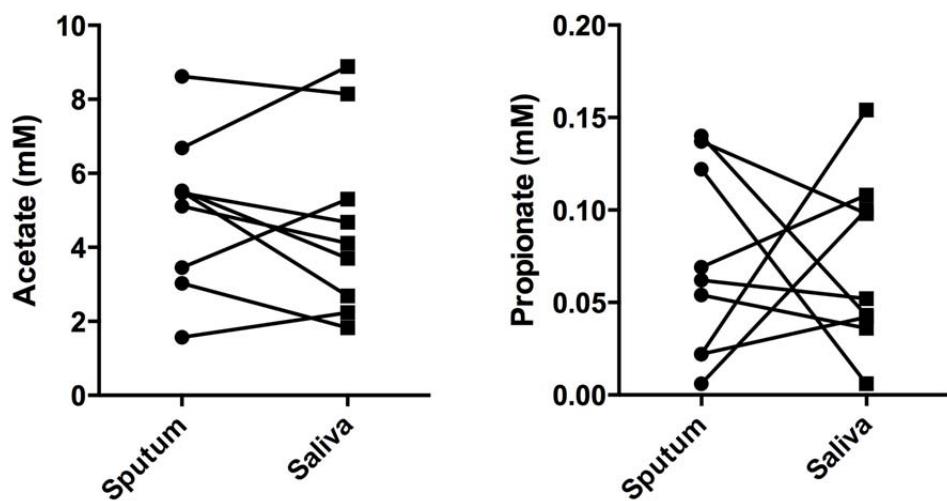


Supplementary Figure 1. Taxonomic composition of the mucin-enriched, saliva-derived bacterial community used in this study.



Supplementary Figure 2. Direct measurements of (a) acetate and (b) propionate in paired sputum and saliva samples between CF patients ($n=9$) without an oral rinse between sampling sites. There were no significant difference between saliva and sputum for either SCFA ($p=0.51$ and 0.98 , respectively).

Supplementary Table 1. Relative abundance of bacterial OTUs in explanted CF lungs.

Patient A

Genus ^a	Right Upper	Right Middle	Right Lower	Left Upper	Left Lingula	Left Lower
<i>Pseudomonas</i>	98.87%	98.53%	97.49%	98.31%	82.75%	96.90%
<i>Streptococcus</i>	0.01%	0.05%	0.14%	0.09%	1.96%	0.03%
<i>Veillonella</i>	-	0.04%	0.10%	-	0.39%	0.45%
<i>Prevotella</i>	-	0.07%	0.12%	0.03%	2.35%	0.48%
<i>Haemophilus</i>	-	-	-	0.01%	3.14%	-
<i>Staphylococcus</i>	0.02%	0.04%	0.06%	0.08%	0.20%	0.15%
<i>Fusobacterium</i>	-	-	0.12%	0.01%	-	-

Patient B

Genus ^a	Right Upper	Right Middle	Right Lower	Left Upper	Left Lingula	Left Lower
<i>Pseudomonas</i>	99.75%	99.32%	99.26%	99.88%	99.34%	86.46%
<i>Streptococcus</i>	-	0.04%	-	0.02%	-	1.61%
<i>Veillonella</i>	-	0.06%	0.09%	-	0.02%	3.83%
<i>Prevotella</i>	-	0.01%	0.02%	-	0.01%	1.45%
<i>Haemophilus</i>	0.03%	-	0.01%	-	-	-
<i>Staphylococcus</i>	0.03%	0.01%	0.02%	-	0.04%	0.31%
<i>Fusobacterium</i>	-	-	0.01%	-	-	0.99%

Patient C

Genus ^a	Right Upper	Right Middle	Right Lower	Left Upper	Left Lingula	Left Lower
<i>Pseudomonas</i>	99.89%	99.87%	99.88%	99.82%	99.86%	99.86
<i>Streptococcus</i>	-	0.01%	-	0.01%	-	-
<i>Veillonella</i>	0.01%	-	-	0.05%	-	0.01%
<i>Prevotella</i>	0.01%	-	-	0.02%	-	-
<i>Haemophilus</i>	-	-	-	-	-	-
<i>Staphylococcus</i>	0.01%	-	-	-	-	-
<i>Fusobacterium</i>	-	-	-	-	-	-

^a Shown are the three most abundant known lung pathogens (*Pseudomonas*, *Haemophilus*, *Staphylococcus*) and the percentage of known mucin-degrading anaerobes (*Prevotella*, *Streptococcus*, *Veillonella* and *Fusobacterium*)

Supplementary Table 2. Oligonucleotide primers used in this study.

qRT-PCR oligonucleotide primers			
Target Gene	Primer	Sequence (5'-3')	Primer Efficiency %
<i>clpX</i>	<i>clpX</i> F	CCTGTGCAATGACATCATCC	91.6
	<i>clpX</i> R	TTCTTGTCACGCTGGTTGAG	
<i>oprI</i>	<i>oprI</i> F	TGCGATCACCACCTTCTACT	
	<i>oprI</i> R	GCCCAGAGCCATGTTGTAC	
<i>prpD</i>	<i>prpD</i> F	GCAGTGGGGTTCTACGATG	96.8
	<i>prpD</i> R	CTTGAACAGCACGTTTCCA	
<i>acsA</i>	<i>acsA</i> F	TGTTCGAGGGCGTACCGAACT	91.6
	<i>acsA</i> R	AGCAGACGCAGGCTGGAA	
16S gene sequencing indexing primers			
Amplification Step	Primer	Sequence (5'-3')	
Primary	V3F Nextera	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTACGGGAGGCAGCAG	
	V5R Nextera	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCGTCAATTCTTTTRAGT	
Indexing	Index F	AATGATACGGCGACCACCGAGATCTACACXXXXXXXXCGTCGGCA GCGTC ^a	
	Index R	GATXXXXXXXXXGTCTCGTGGCTCGG ^a	

^a X marks the position of 8bp indices