

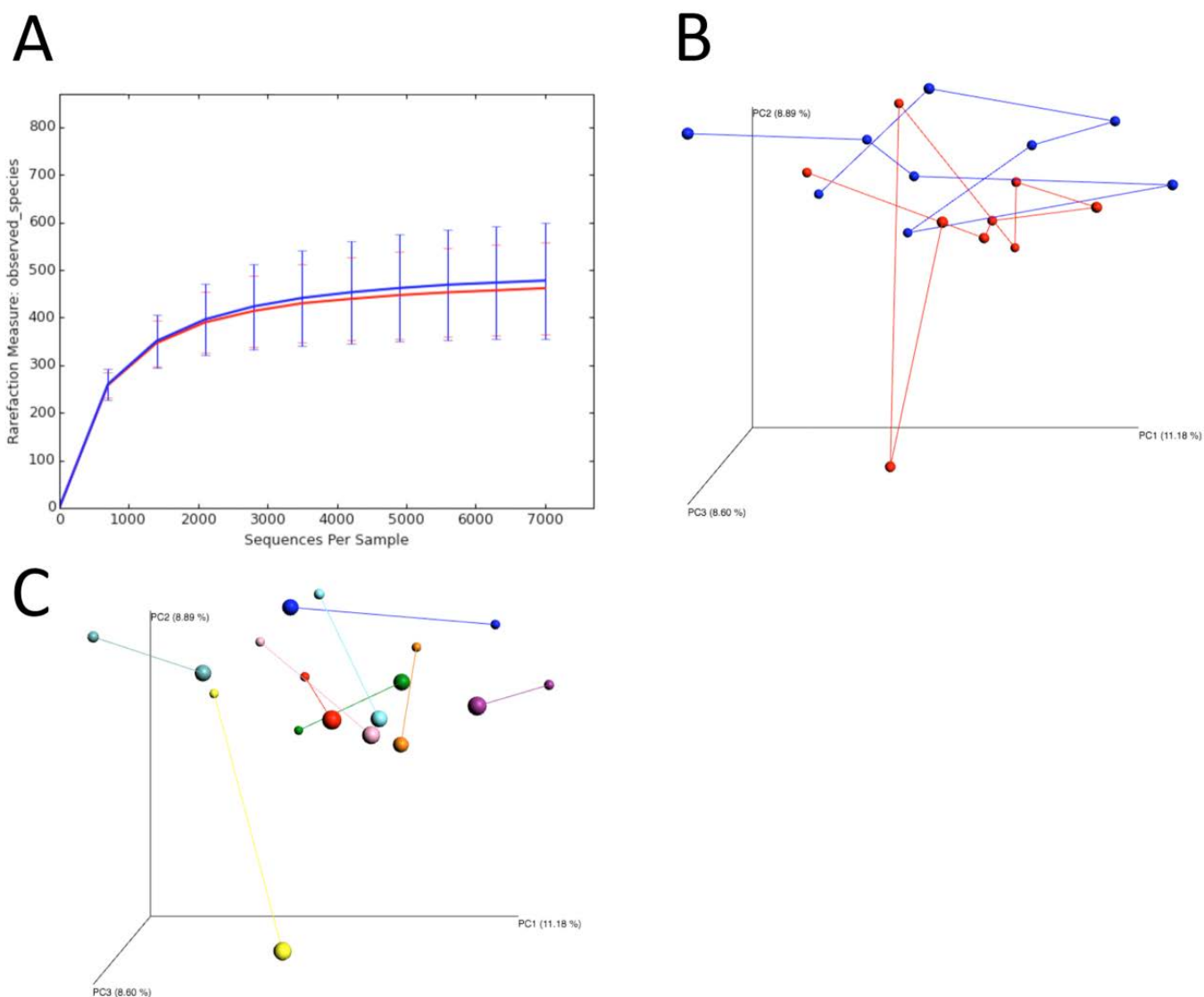
Running Title: Microbial Ecology Network in Diverticulitis

The Microbial Ecosystem Distinguishes Chronically Diseased Tissue from Adjacent Tissue in the Sigmoid Colon of Chronic, Recurrent Diverticulitis Patients

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Supplemental Table S1. PERMANOVA power analysis using the weighted UniFrac distances from our 16S rRNA OTU data table

Subjects/group	Alpha	Average effect size (omega2)	Power
5	0.01	0.059	0.1
9	0.01	0.055	0.4
15	0.01	0.057	1
5	0.05	0.056	0.24
9	0.05	0.059	0.89
15	0.05	0.058	1
5	0.1	0.058	0.5
9	0.1	0.061	0.95
15	0.1	0.059	1



Supplemental Figure S1. Microbial alpha and beta diversity analysis. **(A)** Alpha diversity rarefaction plots of observed taxa within diverticulitis (red) tissue and adjacent (blue) tissue were generated within QIIME 1.9.0. Differences in alpha diversity were not found to be statistically significant. **(B)** Principle coordinate analysis plot calculated from weighted UniFrac distances comparing bacterial community structures between diverticulitis (red) tissue and adjacent (blue) tissue. **(C)** Principle coordinate analysis plot calculated from weighted UniFrac distances comparing bacterial community structures between individual patients. Each color is indicative of an individual patient, with large points representing diverticular tissue, and small points representing adjacent tissue. Clustering was not found to be statistically significant based on tissue type nor patient.

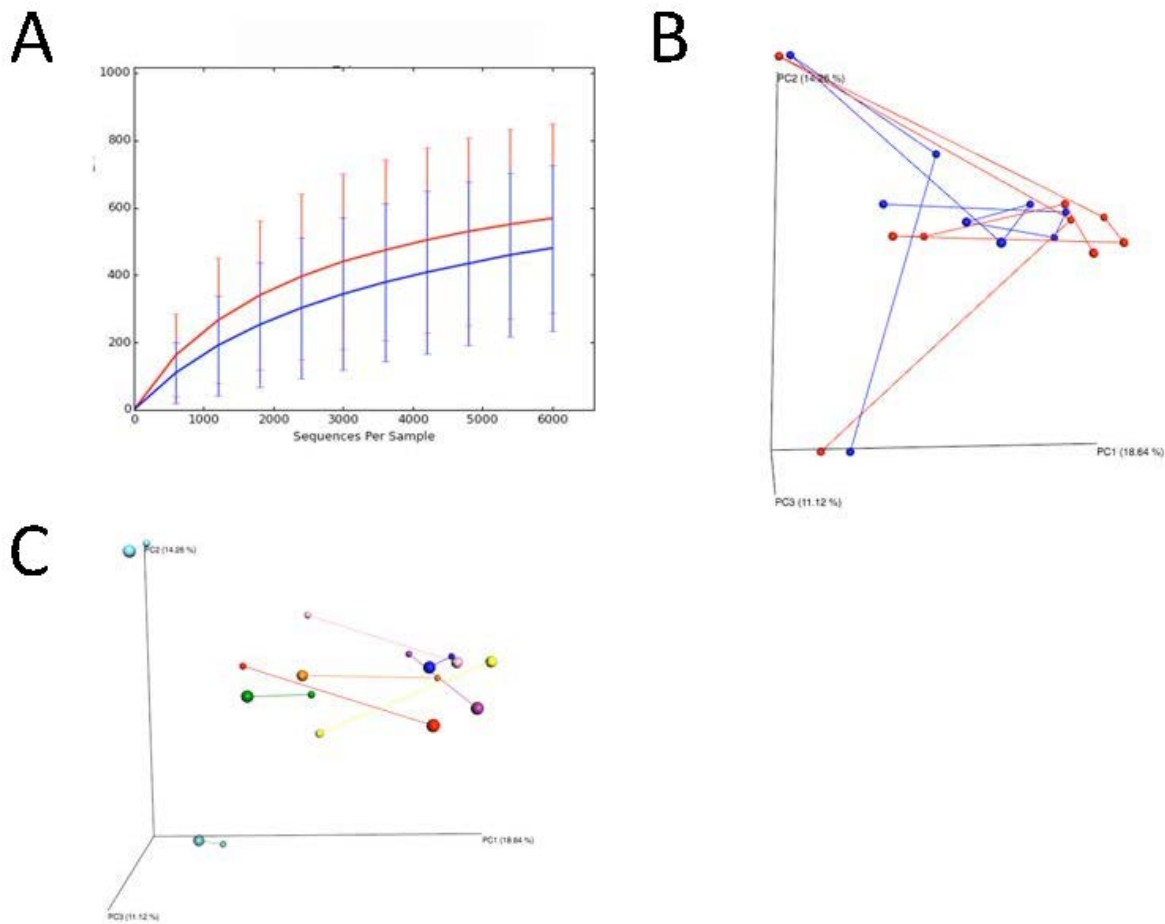
Supplemental Table S2. Differentially expressed bacterial taxa unique between diverticulitis tissue (DT) and adjacent tissue (AT). Only taxonomically assigned OTUs at the kingdom are listed.

DT Core (80%) Bacteria	Phylum	Class	Order	Family	Genus	Species
	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Enterobacteriales</i>	<i>Enterobacteriaceae</i>		
	<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridiales</i>	<i>Peptococcaceae</i>	<i>Desulfosporosinus</i>	<i>meridiei</i>
	<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridiales</i>	<i>Syntrophomonadaceae</i>	<i>Syntrophomonas</i>	
	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Alteromonadales</i>	<i>Shewanellaceae</i>	<i>Shewanella</i>	
	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Bradyrhizobiaceae</i>		
	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Oxalobacteraceae</i>		
	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Oxalobacteraceae</i>		
	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>		
	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>		
	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>		
	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonadales</i>	<i>Pseudomonadaceae</i>	<i>Pseudomonas</i>	<i>veronii</i>
	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>		
	<i>Synergistetes</i>	<i>Synergistia</i>	<i>Synergistales</i>	<i>Synergistaceae</i>	<i>vadinCA02</i>	
	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylococcales</i>	<i>Methylococcaceae</i>		
	<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	<i>Microbacteriaceae</i>		
	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfobacterales</i>	<i>Desulfobulbaceae</i>		
	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caulobacterales</i>	<i>Caulobacteraceae</i>		
	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	<i>Sphingomonas</i>	
	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caulobacterales</i>	<i>Caulobacteraceae</i>		
	<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales</i>	<i>Bacillaceae</i>	<i>Bacillus</i>	<i>foraminis</i>
AT Core (80%) Bacteria	Phylum	Class	Order	Family	Genus	Species
	<i>Bacteroidetes</i>	<i>Cytophagia</i>	<i>Cytophagales</i>	<i>Cytophagaceae</i>	<i>Hymenobacter</i>	
	GN04					
	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>		
	<i>Proteobacteria</i>	<i>Epsilonproteobacteria</i>	<i>Campylobacteriales</i>	<i>Campylobacteraceae</i>	<i>Arcobacter</i>	
	<i>Bacteroidetes</i>	<i>Sphingobacteriia</i>	<i>Sphingobacteriales</i>			
	<i>Proteobacteria</i>	<i>Epsilonproteobacteria</i>	<i>Campylobacteriales</i>	<i>Helicobacteraceae</i>		
	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>			
	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Methylophilales</i>	<i>Methylophilaceae</i>	<i>Methylothena</i>	<i>mobilis</i>
	<i>Cyanobacteria</i>	<i>Chloroplast</i>	<i>Stramenopiles</i>			
	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfuromonadales</i>	<i>Geobacteraceae</i>	<i>Geobacter</i>	
	<i>Chloroflexi</i>	<i>Anaerolineae</i>	H39			
	<i>Bacteroidetes</i>	<i>Flavobacteriia</i>	<i>Flavobacteriales</i>	<i>Cryomorphaceae</i>	<i>Fluviicola</i>	
	<i>Bacteroidetes</i>	<i>Flavobacteriia</i>	<i>Flavobacteriales</i>	<i>Cryomorphaceae</i>	<i>Fluviicola</i>	
	<i>Acidobacteria</i>	[<i>Chloracidobacteria</i>]	Ellin7246			
	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Rhodoferrax</i>	

Supplemental Table S3. Enriched bacterial and archaeal taxa identified by LefSe analysis.

	Enriched Bacterial and Archaeal Taxonomy	LDA Score	LefSe P value
DT	<i>Archaea.Crenarchaeota.Thaumarchaeota</i>	3.22	0.007
	<i>Archaea.Crenarchaeota.Thaumarchaeota.Cenarchaeales</i>	2.87	0.031
	<i>Archaea.Crenarchaeota.Thaumarchaeota.Cenarchaeales.Cenarchaeaceae</i>	2.73	0.039
	<i>Archaea.Euryarchaeota.Thermoplasmata</i>	2.82	0.029
	<i>Bacteria.Acidobacteria.Acidobacteria_6</i>	3.07	0.038
	<i>Bacteria.Actinobacteria.Acidimicrobiia.Acidimicrobiales</i>	3.15	0.020
	<i>Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae</i>	3.42	0.019
	<i>Bacteria.Proteobacteria.Alphaproteobacteria.Rhodeobacterales.Rhodobacteraceae.Pseudoruegeria</i>	2.84	0.031
	<i>Bacteria.Proteobacteria.Betaproteobacteria_SC_I_84</i>	2.89	0.029
	<i>Bacteria.Proteobacteria.Deltaproteobacteria.Desulfobacterales.Desulfobulbaceae</i>	3.03	0.024
	<i>Bacteria.Spirochaetes.Leptospirae.Leptospirales_Sediment_4_SJA_88</i>	2.88	0.029
AT	<i>Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Kineosporiaceae</i>	2.87	0.031
	<i>Bacteria.Actinobacteria.Thermoleophilia</i>	3.18	0.038
	<i>Bacteria.Actinobacteria.Thermoleophilia.Gaiellales.Gaiellaceae</i>	2.99	0.007
	<i>Bacteria.Armatimonadetes_0319_6E2</i>	2.97	0.012
	<i>Bacteria.Chloroflexi.Anaerolineae_H39</i>	2.92	0.047
	<i>Bacteria.Cyanobacteria_4C0d_2_MLE1_12</i>	2.85	0.029
	<i>Bacteria.Gemmatimonadetes_Gemm_5</i>	2.75	0.029
	<i>Bacteria.Planctomycetes_OM190</i>	2.97	0.024
	<i>Bacteria.Planctomycetes.Phycisphaerae.Phycisphaerales</i>	2.75	0.029
	<i>Bacteria.Proteobacteria.Alphaproteobacteria.Rhizobiales.Hyphomicrobiaceae.Parvibaculum</i>	2.85	0.029
	<i>Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales</i>	2.89	0.018
	<i>Bacteria.Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae</i>	2.75	0.012
	<i>Bacteria.Proteobacteria.Gammaproteobacteria.Alteromonadales.Alteromonadaceae.Marinobacter</i>	2.91	0.008
	<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonas</i>	3.31	0.038

Supplemental Table S4. Enriched predicted function from PICRUSt analysis.			
	Enriched Function	LDA Score	LefSe <i>P</i> value
DT	C5 Branched dibasic acid metabolism	1.60	0.009
	Methane metabolism	2.30	0.047
	Valine, leucine, and isoleucine biosynthesis	1.85	0.031
AT	Carbohydrate metabolism	1.58	0.024
	Glycosyltransferases	1.85	0.002



Supplemental Figure S2. Fungal alpha and beta diversity analysis. **(A)** Alpha diversity rarefaction plots of observed taxa within diverticulitis (red) tissue and adjacent (blue) tissue were generated within QIIME 1.9.0. Differences in alpha diversity were not found to be statistically significant. **(B)** Principle coordinate analysis plot calculated from weighted UniFrac distances comparing bacterial community structures between diverticulitis (red) tissue and adjacent (blue) tissue. **(C)** Principle coordinate analysis plot calculated from weighted UniFrac distances comparing bacterial community structures between individual patients. Each color is indicative of an individual patient, with large points representing diverticular tissue, and small points representing adjacent tissue. Clustering was not found to be statistically significant based on tissue type, but was found to be statistically significant based on patient ID (ANOSIM $P=0.01$).

Supplemental Table S5. Differentially expressed fungal taxa unique between diverticulitis tissue (DT) and adjacent tissue (AT). Only taxonomically assigned OTUs at the kingdom are listed.

DT Core (80%) Fungi	Phylum	Class	Order	Family	Genus	Species
	<i>Ascomycota</i>	<i>Leotiomycetes</i>				

AT Core (80%) Fungi	Phylum	Class	Order	Family	Genus	Species
	<i>Ascomycota</i>	<i>Saccharomycetes</i>	<i>Saccharomycetales</i>	<i>Incertae sedis</i>	<i>Cyberlindnera</i>	<i>jadinii</i>
	<i>Ascomycota</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	<i>Trichocomaceae</i>	<i>Aspergillus</i>	<i>subversicolor</i>

Supplemental Table S6. Enriched fungal taxonomy from LefSe analysis.

	Enriched function	LDA score	LefSe P value
DT	<i>Fungi.Ascomycota.Chaetothyriomycetes.Chaetothyriales.Herpotrichiellaceae.Exophiala</i>	4.11	0.037
AT	<i>Fungi.Basidiomycota.Agaricomycetes. Agaricomycetidae.Agaricales</i>	4.04	0.039
	<i>Fungi.Basidiomycota.Agaricomycetes.Agaricomycetidae.Agaricales.Plutaceae</i>	4.24	0.039
	<i>Fungi.Basidiomycota.Agaricomycetes.Agaricomycetidae.Agaricales.Plutaceae.Pluteus</i>	4.21	0.039