

Supplemental Table 1: Taxa showing significant differences among the cohort groups using DESeq2 analysis.

Controls Compared fCDI		
	Taxonomic Level	Adjusted p-value
Higher in Controls		
Asaccharobacter	genus	0.001010093
Collinsella	genus	2.28E-07
Coriobacteriaceae	family	0.001446745
Barnesiella	genus	0.001820101
Prevotellaceae	family	0.045160392
Bacteroidales	order	0.006587203
Anaerostipes	genus	1.94E-11
Clostridium_XIVb	genus	0.035027962
Coprococcus	genus	2.85E-11
Dorea	genus	0.006049567
Pseudobutyrvibrio	genus	0.001693646
Roseburia	genus	3.10E-07
Lachnospiraceae	family	0.068095429
Clostridium_IV	genus	0.088374326
Faecalibacterium	genus	0.019262066
Ruminococcus	genus	3.98E-09
Ruminococcaceae	family	0.008294786
Clostridiales	Order	3.34E-06
Turicibacter	genus	0.02607887
Erysipelotrichaceae	family	0.000101813
Phascolarctobacterium	genus	0.0001296
Acidaminococcaceae	family	0.009621216
Firmicutes	phylum	1.84E-07
Alphaproteobacteria	class	0.003072667
Betaproteobacteria	class	0.067949259
Pasteurellaceae	family	0.009651848
Akkermansia	genus	0.010595299
Higher in fCDI		
Methanobrevibacter	genus	4.89E-05
Bacteroidetes	phylum	3.41E-06
Gemella	genus	0.000796493
Staphylococcus	genus	0.000419077

Enterococcus	genus	3.58E-17
Lactobacillus	genus	0.000247622
Anaerococcus	genus	0.089911946
Eubacteriaceae	family	0.061768263
Clostridium_XIVa	genus	0.006119287
Clostridium_XI	genus	0.053097977
Anaerotruncus	genus	0.007593418
Subdoligranulum	genus	0.000352895
Acidaminococcus	genus	0.007314414
Megamonas	genus	0.03507509
Veillonella	genus	3.31E-06
Fusobacterium	genus	4.70E-07
Burkholderiales	order	0.003154702
Desulfovibrio	genus	0.009651848
Enterobacteriaceae	family	0.01449686
Pyramidobacter	genus	0.013483575
TM7_genus_incertae_sedis	genus	0.042975897
Controls Compared to rCDI		
Higher in Control		
Methanobrevibacter	genus	0.035319197
Asaccharobacter	genus	0.009155028
Collinsella	genus	2.91E-05
Eggerthella	genus	0.056433765
Coriobacteriaceae	family	4.11E-05
Bacteroides	genus	0.045160392
Barnesiella	genus	0.000196
Butyricimonas	genus	0.00053362
Odoribacter	genus	8.20E-07
Parabacteroides	genus	8.16E-07
Alistipes	genus	2.14E-18
Clostridium_sensu_stricto	genus	0.051136343
Anaerostipes	genus	1.28E-14
Blautia	genus	0.009160824
Clostridium_XIVa	genus	0.088374326
Clostridium_XIVb	genus	1.17E-08
Coprococcus	genus	1.08E-14
Dorea	genus	0.000387117
Lachnospiracea_incertae_sedis	genus	1.69E-05
Pseudobutyrvibrio	genus	0.006542324
Roseburia	genus	3.86E-05

Lachnospiraceae	family	8.07E-05
Clostridium_XI	genus	0.078180456
Butyricoccus	genus	0.005184213
Clostridium_IV	genus	1.41E-12
Faecalibacterium	genus	0.001730092
Flavonifractor	genus	0.001452964
Oscillibacter	genus	5.46E-09
Ruminococcus	genus	2.41E-10
Sporobacter	genus	0.002415051
Ruminococcaceae	family	2.15E-05
Clostridiales	order	2.66E-13
Clostridia	class	0.015509886
Coprobacillus	genus	0.060667481
Erysipelotrichaceae	family	1.40E-05
Phascolarctobacterium	genus	0.036980555
Firmicutes	phylum	2.74E-13
Alphaproteobacteria	class	0.005710105
Oxalobacteraceae	family	0.087091276
Parasutterella	genus	0.033727006
Pasteurellaceae	family	0.009651848
Anaeroplasma	genus	0.009363913
Bacteria;unclassified	domain	1.09E-06
Akkermansia	genus	0.002324539
Higher in rCDI		
Actinomyces	genus	0.003916282
Atopobium	genus	0.00200702
Prevotella	genus	1.22E-08
Abiotrophia	genus	0.010077468
Enterococcus	genus	3.96E-12
Lactobacillus	genus	1.75E-15
Pediococcus	genus	0.000146118
Lactobacillaceae	family	0.001010093
Lactococcus	genus	0.076885097
Lactobacillales	order	1.02E-05
Oribacterium	genus	0.00059166
Catenibacterium	genus	0.091508083
Acidaminococcus	genus	0.00028368
Anaeroglobus	genus	0.026082477
Megamonas	genus	0.086470202

Veillonellaceae	family	1.13E-10
Veillonella	genus	1.08E-14
Fusobacterium	genus	1.13E-10
Fusobacteriaceae	family	0.058216139
Leptotrichia	genus	0.035548366
Microvirgula	genus	2.62E-05
Neisseriaceae	family	2.09E-05
Desulfovibrio	genus	0.009651848
Campylobacter	genus	8.07E-05
Morganella	genus	1.13E-10
Proteus	genus	8.16E-07
Enterobacteriaceae	family	7.26E-10
fCDI compared to rCDI		
Higher in fCDI		
Methanobrevibacter	genus	8.03E-10
Bacteria;AEggerthella	genus	0.04293734
Bacteroides	genus	0.078621197
Butyricimonas	genus	1.85E-05
Odoribacter	genus	4.11E-05
Parabacteroides	genus	1.03E-08
Alistipes	genus	2.54E-13
Bacteroidetes	phylum	4.46E-07
Gemella	genus	0.035548366
Staphylococcus	genus	0.002407477
Clostridium_sensu_stricto	genus	0.000149739
Clostridium_XIVa	genus	3.41E-06
Clostridium_XIVb	genus	0.000665842
Lachnospiracea_incertae_sedis	genus	0.001010093
Lachnospiraceae	family	0.067102654
Clostridium_XI	genus	9.31E-05
Anaerotruncus	genus	0.002776403
Clostridium_IV	genus	2.50E-07
Flavonifractor	genus	1.09E-06
Oscillibacter	genus	3.16E-07
Sporobacter	genus	0.057568121
Subdoligranulum	genus	4.39E-07
Clostridiales	order	0.014134195
Firmicutes	phylum	0.036250203
Burkholderiales	order	3.49E-05
Desulfovibrionales	order	0.044252578

Cloacibacillus	genus	0.078180456
Pyramidobacter	genus	0.043466053
Anaeroplasm	genus	0.027283946
Higher in rCDI		
Actinomyces	genus	0.009962328
Atopobium	genus	0.036761739
Prevotella	genus	2.09E-08
Lactobacillus	genus	3.62E-05
Pediococcus	genus	0.000134328
Lactobacillaceae	family	0.000133636
Lactococcus	genus	0.003862545
Lactobacillales	order	0.004384771
Oribacterium	genus	0.033048728
Catenibacterium	genus	0.092841286
Acidaminococcaceae	family	0.050294454
Veillonellaceae	family	1.55E-09
Veillonella	genus	0.004462161
Fusobacteriaceae	family	0.046977027
Leptotrichia	genus	0.063885526
Microvirgula	genus	2.62E-05
Neisseriaceae	family	0.000226356
Campylobacter	genus	0.0001584
Morganella	genus	7.26E-10
Proteus	genus	2.81E-05
Enterobacteriaceae	family	0.000638747

Supplemental Table 2. Taxonomic classification results for the OTUs listed in Table 3. For each OTU, the possible placements reported by pplacer (10) to a reference tree generated using full-length or near full-length 16S rDNA sequences of type strains are listed. Likelihood weight ratios (LWR) approximate the posterior probability of the attachment of the sample to an edge of the tree. Only placements with LWR > 0.1 are shown for brevity.

OTU	Taxonomic level	Identification	LWR
Otu00002	species	<i>Bacteroides dorei</i>	1.0
Otu00007	species	<i>Eubacterium rectale</i>	0.946
Otu00008	species	<i>Blautia wexlerae</i>	1.0
Otu00011	genus	<i>Bifidobacterium</i>	0.496
Otu00011	species	<i>Bifidobacterium dentium</i>	0.504
Otu00016	species	<i>Parabacteroides distasonis</i>	1.0

Otu00017	species	<i>Akkermansia muciniphila</i>	1.0
Otu00018	species	<i>Ruminococcus bromii</i>	1.0
Otu00021	family	Lachnospiraceae	0.811
Otu00021	genus	<i>Blautia</i>	0.159
Otu00035	species	<i>Blautia luti</i>	0.976
Otu00134	species	<i>Eubacterium coprostanoligenes</i>	0.967