

Supplementary Materials

Supplemental Figure S1. Alpha-diversity as measured by the Shannon-Wiener diversity index using MEtaGenome Analyzer (Megan, version 5). Donor samples had increased diversity compared with samples from RCDI patients. Donor cohort (red), single FMT cohort (green) and two FMT cohort (blue).

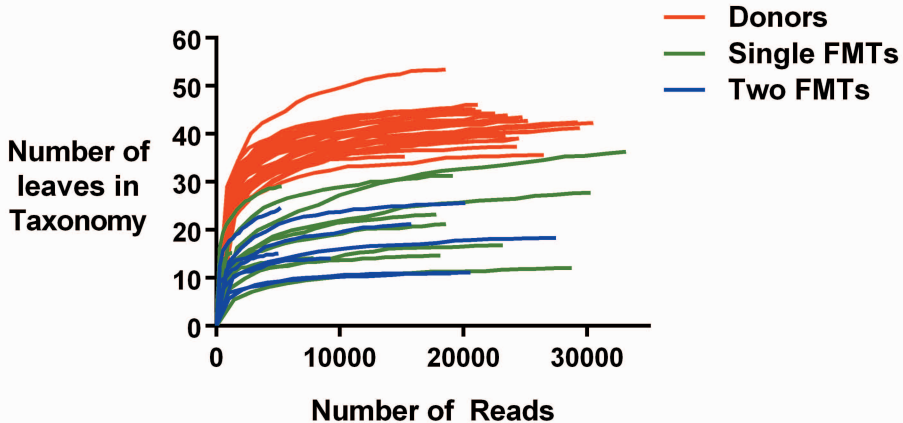
Supplemental Figure S2. Correlations between the number of ABR genes detected in each individual BFT to (A) the duration of their *C. difficile* infection ($R^2 = 0.059$; $p=0.3$) and (B) age ($R^2 = 0.014$; $p=0.6$). Dotted lines show the 95% confidence interval; linear regression was performed calculating to determine the goodness of fit, and R squared of 1 indicates the regression line perfectly fits the data. There were no significant correlations.

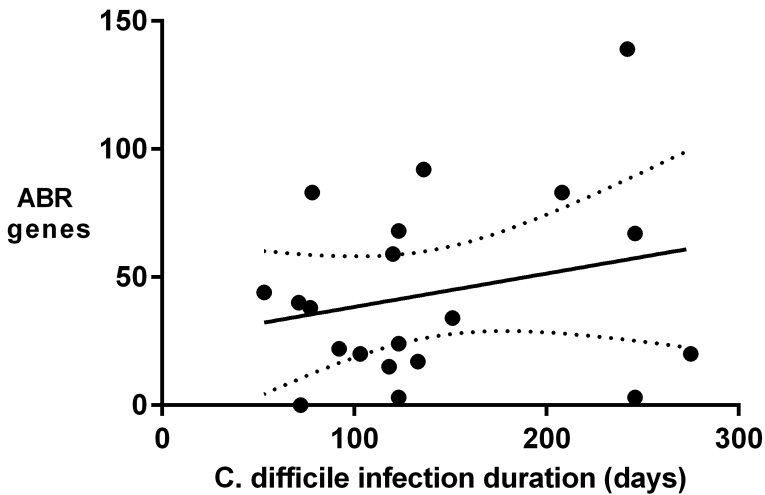
Supplemental Figure S3. The percentage of individuals containing the top 150 antibiotic resistance genes within each of the two experimental cohorts, two FMTs (blue), and single FMT (green), and in donor cohort (red) where samples were taken over time.

Supplemental Figure S4. The number of raw reads detected in RCDI and Donor samples belonging to the phylum Proteobacteria. (A) Following successful FMT, (PFT: 1-4 wks) the number of reads was reduced significantly. (B). In the patients who did not respond to the initial FMT, there was no significant decrease in the number of reads (PFT1). However, following the second successful FMT, a significant decrease was seen in the number of raw reads belonging to the phylum Proteobacteria (PFT2: 1-3 wks).

Donor cohort: $n = 29$; Single FMT Cohort: $n = 11$; Two FMT Cohort $n = 9$.

Whiskers denote mean with the standard deviation. * P -value <0.05 ; ** P -value <0.005 ; *** P -value <0.001 ; **** P -value <0.0001



A**B**