Figure S1. Fecal bacterial communities are altered after initiating UDCA. A) Relative abundance of sequences from bacterial phyla in patient feces before and after start of UDCA therapy. See legend below for list of phyla. B) Relative abundance of sequences from bacterial families in patient feces before and after start of UDCA therapy. See legend below for list of families. Significant clinical events are noted above.

Figure S2. α- and β-diversity of patient fecal samples do not normalize following UDCA therapy. A) Shannon diversity indices of healthy (●) and patient (♦) fecal samples before and after initiating UDCA therapy. Healthy donors were all qualified FMT donors. Significant clinical events are noted above. Healthy data represent mean ± SEM. B) Principal coordinate analysis of healthy (●) and patient fecal communities before (▲) and after (♦) initiating UDCA therapy.

Figure S3. Growth of all *C. difficile* isolates is inhibited by UDCA. Hourly OD_{600} measurements for cells in BHIS alone (●) or BHIS with 2 mM UDCA (▲) A) NAP1 isolate, B-C) NAP2 isolates. D) NAP10 isolate. E-G) NAP6 isolates. H-J) NAP7 isolates. * = $p<0.001$; ** = $p<0.0001$ Experiments performed in triplicate. Data represent mean ± SEM.