Description	Query Cover	E value	Percent Identified	Accession
Clostridioides difficile strain FC6877	100%	0.0	100.00%	MN060981.1
Clostridioides difficile MRN121781	100%	0.0	100.00%	MN049824.1
Clostridioides difficile CDT25	100%	0.0	100.00%	MN049583.1

Supplemental table 1. Bacterial CFU from ABX-treated, uninfected mice is confirmed to be *C. difficile* by Sanger sequencing. Sanger sequencing was performed on PCR amplified 16s rDNA gene segments of bacteria isolated from PBS mock infected mice that were culture positive for *C. difficile*. Table shows results of trimmed sequences queried to NCBI BLAST database.

Method	Description	Sequence
Sanger Sequencing	Forward 16s 8F primer	AGAGTTTGATCCTGGCTCAG
	Reverse 16s 1492R primer	GGTTACCTTGTTACGACTT
PCR Ribotyping	16S_Cdiff_Ribo - FWD	GCTGGATCACCTCCTTTCTAAG
	23S_Cdiff_Ribo - REV	TGACCAGTTAAAAAGGTTTGATAGATT
Florescent PCR Ribotyping	16S_Cdiff_Ribo - FWD	GTGCG GCTGGATC ACCTC CT
	23S_Cdiff_Ribo - REV	FAM/CCCTGCAC CCTTAATAACTT GACC

Supplemental table 2. Primers used in this study. Sanger sequencing PCR primers, PCR ribotyping primers, and fluorescent PCR ribotyping.