Supplemental Figures

Figure S1: Mean θ_{YC} distances from baseline community during saline treatment and recovery.

Based on family-level (A) and 3% OTU-level (B) sequence assignments. An asterisk (*, $p < 0.05$) indicates a significant difference from the mean distance between all day 0 communities (Day 0 to Day 0) by the non-parametric data Kruskal-Wallis test followed by Dunn's Multiple Comparison Test. Error bars represent ± SD.

Table S1: AMOVA *p*-values of distances between consecutive time points during tigecycline treatment.

Table S2: Relative abundances of bacterial families in the fecal microbiota before, during and after tigecycline treatment. Mean percent abundances ± SD.

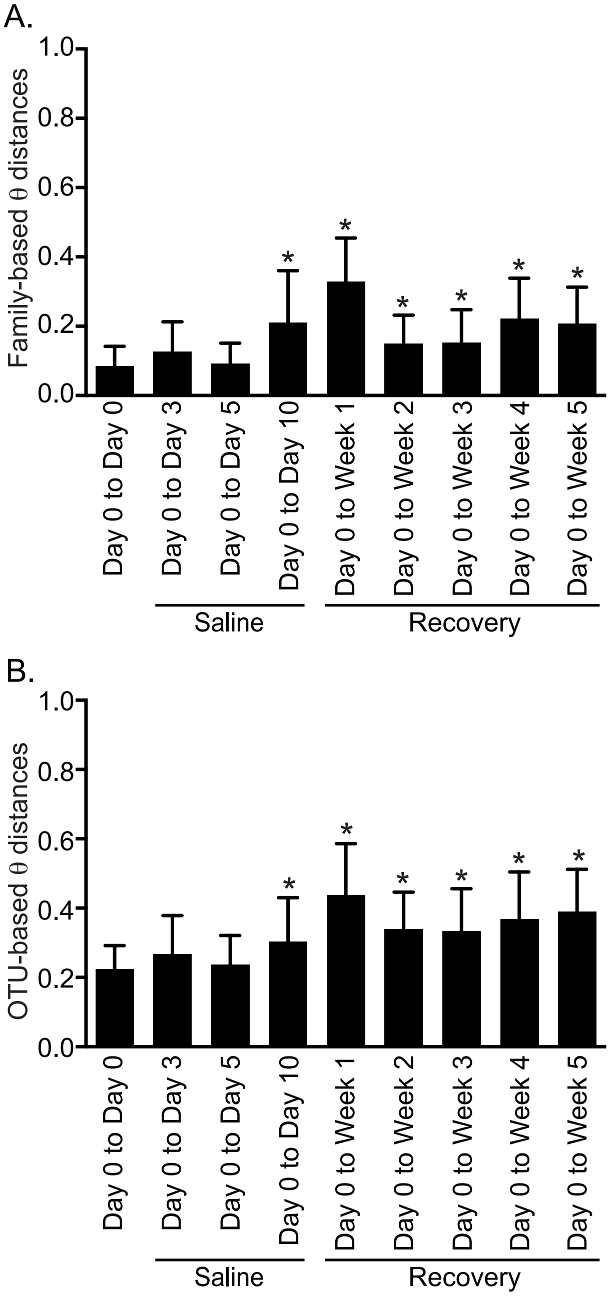

Figure S1: Mean θ_{YC} distances from baseline community during saline treatment and recovery.

Based on family-level (A) and 3% OTU-level (B) sequence assignments. An asterisk (*, $p < 0.05$) indicates a significant difference from the mean distance between all day 0 communities (Day 0 to Day 0) by the non-parametric data Kruskal-Wallis test followed by Dunn’s Multiple Comparison Test. Error bars represent ± SD.

Supplemental Table 1	
Comparisons of Consecutive Communities of Tigecyline Treated Mice During Treatment and Recovery	**AMOVA *p*-value**
Day 0 (Baseline) to Day 3 (Tigecycline)	<0.001
Day 3 (Tigecycline) to Day 5 (Tigecycline)	0.017
Day 5 (Tigecycline) to Day 10 (Tigecycline)	<0.001
Day 10 (Tigecycline) to Week 1 (Recovery)	<0.001
Week 1 (Recovery) to Week 2 (Recovery)	0.034
Week 2 (Recovery) to Week 3 (Recovery)	0.025
Week 3 (Recovery) to Week 4 (Recovery)	0.435
Week 4 (Recovery) to Week 5 (Recovery)	0.717

Supplemental Table 2

		Tigecycline Treatment			Recovery				
	Day 0	Day 3	Day 5	Day 10	Week 1	Week 2	Week 3	Week 4	Week 5
Bacteroidetes									
Porphyromonadaceae	55.44 ± 8.31%	19.81 ± 11.27%	26.65 ± 7.48%	31.33 ± 6.38%	44.67 ± 12.36%	58.53 ± 5.52%	63.21 ± 4.55%	60.94 ± 5.90%	58.27 ± 3.82%
Rikenellaceae	5.99 ± 3.52%	0.01 ± 0.02%	0.07 ± 0.13%	0.01 ± 0.02%	0.02 ± 0.02%	0.01 ± 0.02%	0.01 ± 0.01%	0.01 ± 0.01%	0.02 ± 0.03%
Bacteroidaceae	9.43 ± 5.03%	0.03 ± 0.04%	0.06 ± 0.14%	0.02 ± 0.04%	0.00 ± 0.00%	0.02 ± 0.02%	0.01 ± 0.01%	0.02 ± 0.01%	0.01 ± 0.02%
Unclassified Bacteroidales	9.36 ± 2.63%	0.03 ± 0.05%	1.74 ± 3.04%	17.63 ± 6.89%	24.51 ± 2.91%	20.17 ± 1.70%	10.51 ± 2.54%	11.67 ± 5.53%	11.72 ± 2.78%
Unclassified Bacteroidetes	1.96 ± 0.79%	0.02 ± 0.02%	0.08 ± 0.09%	10.44 ± 7.13%	0.23 ± 0.10%	0.22 ± 0.08%	0.09 ± 0.05%	0.18 ± 0.08%	0.15 ± 0.08%
Proteobacteria									
Enterobacteriaceae	0.75 ± 1.58%	57.88 ± 7.31%	53.07 ± 8.96%	30.34 ± 6.93%	12.27 ± 5.05%	4.15 ± 3.87%	0.18 ± 0.30%	2.54 ± 5.03%	0.02 ± 0.02%
Verrucomicrobiae									
Verrucomicrobiaceae	0.73 ± 2.16%	15.87 ± 8.44%	14.61 ± 10.40%	7.06 ± 2.84%	7.46 ± 5.82%	0.41 ± 0.24%	0.27 ± 0.18%	0.45 ± 0.87%	0.03 ± 0.03%
Firmicutes									
Lactobacillaceae	2.96 ± 1.31%	6.25 ± 6.07%	3.02 ± 1.20%	0.95 ± 0.56%	2.05 ± 1.46%	4.28 ± 1.58%	4.32 ± 0.65%	2.06 ± 0.64%	2.36 ± 1.01%
Lachnospiraceae	8.58 ± 6.52%	0.03 ± 0.05%	0.33 ± 0.73	0.27 ± 0.81%	1.09 ± 0.97%	4.41 ± 1.87%	10.18 ± 4.20%	11.56 ± 5.48%	8.98 ± 4.26%
Ruminococcaceae	1.10 ± 1.16%	0.01 ± 0.02%	0.07 ± 0.15%	0.15 ± 0.48%	0.40 ± 0.09%	1.32 ± 0.45%	1.70 ± 0.84%	2.56 ± 1.21%	2.20 ± 0.99%
Unclassified Clostridiales	1.80 ± 1.54%	0.02 ± 0.05%	0.06 ± 0.11%	0.06 ± 0.18%	1.89 ± 1.15%	1.13 ± 0.56%	2.53 ± 1.07%	2.51 ± 1.22%	1.92 ± 0.95%
Erysipelotrichaceae	0.86 ± 1.75%	0.01 ± 0.03%	0.01 ± 0.02%	1.48 ± 1.79%	5.16 ± 2.93%	5.09 ± 2.07%	6.49 ± 1.71%	4.36 ± 1.07%	12.68 ± 4.36%
Unclassified Firmicutes	0.36 ± 0.23%	0.00 ± 0.00%	0.00 ± 0.01%	0.08 ± 0.25%	0.01 ± 0.01%	0.09 ± 0.14%	0.28 ± 0.17%	0.94 ± 0.30%	1.34 ± 1.02%