

CTR Group		Time Point				
		BL	ICR	W1	W2	W4
Phylum	<i>Bacteroidetes</i>	58.0 (2.2)	56.0 (2.0)	0.03 (0.03)	2.7 (2.5)	6.9 (6.9)
	<i>Firmicutes</i>	29.9 (2.7)	33.5 (2.6)	68.1 (9.7)	64.8 (6.3)	75.3 (8.7)
	<i>Proteobacteria</i>	2.1 (0.3)	2.2 (0.2)	31.9 (9.7)	32.5 (6.6)	17.7 (7.6)
	<i>Verrucomicrobiota</i>	9.7 (1.3)	8.0 (0.8)	0 (0)	0.02 (0.02)	0 (0)
Class	<i>Alphaproteobacteria</i>	1.0 (0.2)	1.1 (0.2)	0 (0)	0.01 (0.01)	0 (0)
	<i>Bacilli</i>	3.5 (0.7)	3.2 (0.8)	47.7 (8.9)	48.3 (6.1)	44.8 (7.1)
	<i>Bacteroidia</i>	58.0 (2.2)	56.0 (2.0)	0.03 (0.03)	2.7 (2.6)	7.1 (7.1)
	<i>Clostridia</i>	26.3 (2.7)	30.2 (2.2)	20.1 (7.1)	16.1 (7.7)	29.7 (7.0)
	<i>Gammaproteobacteria</i>	1.1 (0.1)	1.1 (0.1)	32.2 (9.7)	33.0 (6.6)	18.4 (7.8)
	<i>Verrucomicrobiae</i>	9.7 (1.3)	8.0 (0.8)	0 (0)	0.02 (0.02)	0 (0)
Family	<i>Akkermansiaceae</i>	9.9 (1.3)	8.1 (0.8)	0 (0)	0.02 (0.02)	0 (0)
	<i>Bacteroidaceae</i>	7.5 (0.7)	7.1 (0.8)	0 (0)	0 (0)	6.3 (6.3)
	<i>Clostridiaceae</i>	0 (0)	0 (0)	3.6 (3.6)	8.3 (8.3)	8.4 (8.4)
	<i>Enterobacteriaceae</i>	0.01 (0.01)	0 (0)	30.6 (9.5)	33.0 (6.7)	18.1 (7.6)
	<i>Enterococcaceae</i>	0 (0)	0 (0)	4.1 (1.4)	8.0 (1.8)	9.6 (2.1)
	<i>Erysipelotrichaceae</i>	0.2 (0.1)	0.1 (0.04)	0.8 (0.6)	2.5 (1.8)	5.2 (3.3)
	<i>Lachnospiraceae</i>	21.8 (2.2)	25.6 (2.3)	0.01 (0.01)	0.3 (0.3)	3.6 (2.3)
	<i>Lactobacillaceae</i>	2.5 (0.7)	2.3 (0.9)	44.0 (8.9)	37.7 (5.0)	30.7 (5.9)
	<i>Muribaculaceae</i>	47.4 (2.1)	46.4 (1.8)	0.03 (0.03)	0 (0)	0 (0)
	<i>Oscillospiraceae</i>	2.9 (0.6)	3.2 (0.3)	0 (0)	0.3 (0.3)	0.2 (0.2)
	<i>Peptostreptococcaceae</i>	0.01 (0.01)	0.01 (0.01)	16.5 (7.3)	7.1 (2.7)	17.1 (3.7)
	<i>Sutterellaceae</i>	1.1 (0.1)	1.1 (0.1)	0 (0)	0 (0)	0 (0)
	<i>Tannerellaceae</i>	3.9 (0.6)	3.1 (0.4)	0 (0)	2.7 (2.7)	0.9 (0.9)
Genus	<i>[Clostridium] inoculum group</i>	0.4 (0.2)	0.3 (0.1)	0 (0)	0.6 (0.4)	1.7 (0.7)
	<i>Akkermansia</i>	32.3 (4.0)	28.2 (2.4)	0 (0)	0.02 (0.02)	0 (0)
	<i>Anaeroplasma</i>	2.7 (1.0)	2.6 (1.1)	0 (0)	0 (0)	0 (0)
	<i>ASF356</i>	2.0 (0.4)	3.0 (0.9)	0 (0)	0 (0)	0 (0)
	<i>Bacteroides</i>	0 (0)	24.9 (2.6)	0 (0)	0 (0)	7.3 (7.3)
	<i>Clostridium sensu stricto 1</i>	0 (0)	0 (0)	2.9 (2.9)	8.2 (8.2)	8.3 (8.3)
	<i>Enterococcus</i>	0 (0)	0 (0)	5.1 (1.8)	9.7 (2.0)	13.1 (2.9)
	<i>Escherichia-Shigella</i>	0.02 (0.02)	0 (0)	17.9 (6.3)	16.6 (5.9)	8.6 (4.7)

<i>Lachnospiraceae NK4A136</i> <i>group</i>	2.4 (1.0)	4.2 (1.5)	0 (0)	0 (0)	0 (0)
<i>Lactobacillus</i>	7.9 (2.4)	7.8 (2.7)	72.3 (7.8)	59.3 (8.5)	53.7 (9.7)
<i>Muribaculum</i>	2.8 (1.0)	4.1 (1.3)	0 (0)	0 (0)	0 (0)
<i>Parabacteroides</i>	12.3 (1.9)	10.6 (1.4)	0 (0)	2.9 (2.9)	1.0 (1.0)
<i>Parasutterella</i>	3.5 (0.4)	3.9 (0.2)	0 (0)	0 (0)	0 (0)
<i>Turicibacter</i>	0 (0)	0 (0)	1.0 (0.7)	2.2 (1.7)	6.2 (3.9)

**Supplemental Table 1. Shifts in microbial taxa from BL to W4 in CTR mice.** Values reported as median and standard error measurement.

PRE Group		Time Point				
		BL	ICR	W1	W2	W4
Phylum	<i>Bacteroidetes</i>	61.2 (0.9)	60.8 (2.2)	0 (0)	0 (0)	0 (0)
	<i>Firmicutes</i>	24.6 (2.0)	28.1 (2.0)	79.0 (6.9)	68.3 (7.8)	73.7 (8.3)
	<i>Proteobacteria</i>	3.4 (0.7)	3.0 (0.3)	20.9 (6.9)	31.7 (7.8)	26.3 (8.3)
	<i>Verrucomicrobiota</i>	10.4 (1.9)	7.8 (1.4)	0 (0)	0 (0)	0 (0)
Class	<i>Alphaproteobacteria</i>	1.9 (0.6)	1.5 (0.3)	0 (0)	0 (0)	0 (0)
	<i>Bacilli</i>	3.3 (1.0)	2.4 (0.4)	55.8 (6.2)	58.3 (6.9)	56.9 (7.6)
	<i>Bacteroidia</i>	61.2 (0.9)	60.8 (2.2)	0 (0)	0 (0)	0 (0)
	<i>Clostridia</i>	21.3 (2.0)	25.7 (2.1)	23.0 (8.4)	9.5 (3.1)	16.3 (5.4)
	<i>Gammaproteobacteria</i>	1.5 (0.1)	1.5 (0.2)	21.1 (6.9)	32.3 (7.9)	26.8 (8.3)
	<i>Verrucomicrobiae</i>	10.4 (1.9)	7.8 (1.4)	0 (0)	0 (0)	0 (0)
Family	<i>Akkermansiaceae</i>	10.8 (1.9)	8.0 (1.4)	0 (0)	0 (0)	0 (0)
	<i>Bacteroidaceae</i>	12.6 (1.8)	11.5 (1.3)	0 (0)	0 (0)	0 (0)
	<i>Clostridiaceae</i>	0 (0)	0 (0)	0 (0)	0.1 (0.1)	0 (0)
	<i>Enterobacteriaceae</i>	0.1 (0.1)	0.02 (0.02)	21.1 (6.9)	31.4 (7.7)	26.4 (8.4)
	<i>Enterococcaceae</i>	0 (0)	0 (0)	1.9 (0.9)	4.6 (1.3)	7.2 (1.3)
	<i>Erysipelotrichaceae</i>	0.2 (0.1)	0.08 (0.03)	4.1 (3.1)	5.7 (3.6)	10.4 (5.8)
	<i>Lachnospiraceae</i>	17.9 (2.1)	21.1 (2.2)	0 (0)	1.0 (1.0)	3.0 (2.0)
	<i>Lactobacillaceae</i>	2.6 (1.0)	1.8 (0.4)	49.6 (5.8)	48.8 (8.0)	40.0 (8.6)
	<i>Muribaculaceae</i>	45.2 (1.5)	45.4 (2.1)	0 (0)	0 (0)	0 (0)
	<i>Oscillospiraceae</i>	2.0 (0.4)	2.9 (0.6)	0 (0)	0 (0)	0.2 (0.2)
	<i>Peptostreptococcaceae</i>	0.04 (0.03)	0.1 (0.03)	22.9 (8.4)	8.4 (2.8)	12.8 (4.4)
	<i>Sutterellaceae</i>	1.5 (0.1)	1.4 (0.2)	0 (0)	0 (0)	0 (0)
	<i>Tannerellaceae</i>	5.8 (0.9)	5.4 (0.2)	0 (0)	0 (0)	0 (0)
Genus	<i>[Clostridium] inoculum group</i>	0.4 (0.1)	0.2 (0.1)	0 (0)	0.8 (0.5)	1.7 (0.9)
	<i>Akkermansia</i>	28.2 (4.4)	24.3 (3.6)	0 (0)	0 (0)	0 (0)
	<i>Anaeroplasma</i>	1.8 (0.8)	2.0 (1.1)	0 (0)	0 (0)	0 (0)
	<i>ASF356</i>	1.4 (0.3)	3.5 (0.9)	0 (0)	0 (0)	0 (0)
	<i>Bacteroides</i>	33.4 (3.2)	33.8 (2.4)	0 (0)	0 (0)	0 (0)
	<i>Clostridium sensu stricto 1</i>	0 (0)	0 (0)	0.1 (0.1)	0.1 (0.1)	0 (0)
	<i>Enterococcus</i>	0 (0)	0 (0)	2.7 (1.1)	5.3 (1.1)	10.0 (2.9)
	<i>Escherichia-Shigella</i>	0.1 (0.1)	0 (0)	16.6 (5.2)	12.2 (5.6)	8.6 (3.6)
	<i>Lachnospiraceae NK4A136 group</i>	1.3 (0.7)	1.3 (0.7)	0 (0)	0 (0)	0 (0)
	<i>Lactobacillus</i>	6.9 (2.3)	5.1 (0.8)	75.8 (6.3)	75.4 (8.7)	65.2 (8.8)

<i>Muribaculum</i>	1.8 (1.0)	2.2 (1.1)	0 (0)	0 (0)	0 (0)
<i>Parabacteroides</i>	15.2 (1.8)	15.9 (1.8)	0 (0)	0 (0)	0 (0)
<i>Parasutterella</i>	4.1 (0.3)	4.4 (0.5)	0 (0)	0 (0)	0 (0)
<i>Turicibacter</i>	0 (0)	0 (0)	4.3 (3.1)	6.1 (3.7)	14.0 (7.1)

**Supplemental Table 2. Shifts in microbial taxa from BL to W4 in PRE mice.** Values reported as median and standard error measurement.

POS Group		Time Point				
		BL	ICR	W1	W2	W4
Phylum	<i>Bacteroidetes</i>	59.6 (2.2)	58.5 (3.7)	0 (0)	6.1 (4.9)	6.4 (6.4)
	<i>Firmicutes</i>	24.7 (2.5)	30.2 (3.9)	82.9 (6.7)	64.7 (8.2)	64.2 (7.8)
	<i>Proteobacteria</i>	3.0 (0.5)	2.7 (0.6)	17.1 (6.7)	29.2 (8.2)	29.4 (8.1)
	<i>Verrucomicrobiota</i>	12.5 (1.8)	8.1 (1.4)	0 (0)	0 (0)	0 (0)
Class	<i>Alphaproteobacteria</i>	1.6 (0.4)	1.6 (0.5)	0 (0)	0 (0)	0 (0)
	<i>Bacilli</i>	2.6 (0.5)	1.7 (0.4)	62.7 (6.4)	47.4 (6.0)	46.7 (7.4)
	<i>Bacteroidia</i>	59.4 (2.2)	58.5 (3.7)	0 (0)	6.3 (5.1)	6.5 (6.5)
	<i>Clostridia</i>	22.1 (2.6)	28.4 (4.1)	20.1 (8.5 )	16.9 (6.2)	16.9 (6.5)
	<i>Gammaproteobacteria</i>	1.4 (0.3)	1.1 (0.1)	17.2 (6.6)	29.4 (8.2)	29.9 (8.1)
	<i>Verrucomicrobiae</i>	12.5 (1.8)	8.1 (1.4)	0 (0)	0 (0)	0 (0)
Family	<i>Akkermansiaceae</i>	12.9 (1.9)	8.3 (1.4)	0 (0)	0 (0)	0 (0)
	<i>Bacteroidaceae</i>	9.7 (1.9)	9.4 (1.6)	0 (0)	6.4 (5.1 )	6.7 (6.7)
	<i>Clostridiaceae</i>	0 (0)	0 (0)	0 (0)	0.7 (0.7)	0 (0)
	<i>Enterobacteriaceae</i>	0.1 (0)	0 (0)	14.0 (6.4)	16.5 (6.7)	29.7 (8.1)
	<i>Enterococcaceae</i>	0 (0)	0 (0)	3.9 (1.5)	8.2 (0.9)	8.9 (3.5)
	<i>Erysipelotrichaceae</i>	0.2 (0.1)	0.1 (0)	2.8 (2.7)	3.2 (1.9)	3.8 (1.9)
	<i>Lachnospiraceae</i>	18.5 (2.7)	24.3 (4.0)	0 (0)	0.5 (0.5)	2.3 (1.3)
	<i>Lactobacillaceae</i>	2.1 (0.6)	1.4 (0.4)	58.5 (7.6)	49.4 (8.5)	34.4 (4.0)
	<i>Muribaculaceae</i>	46.8 (1.7)	46.5 (3.1)	0 (0)	0 (0)	0 (0)
	<i>Oscillospiraceae</i>	2.0 (0.4)	2.7 (0.6)	0 (0)	0.1 (0)	0 (0)
	<i>Peptostreptococcaceae</i>	0.1 (0)	0.1 (0)	20.0 (8.5)	15.1 (5.6)	14.1 (6.4)
	<i>Sutterellaceae</i>	1.3 (0.2)	1.2 (0.1)	0 (0)	0 (0)	0 (0)
	<i>Tannerellaceae</i>	5.2 (0.6)	4.4 (0.5)	0 (0)	0 (0)	0 (0)
Genus	<i>[Clostridium] inoculum group</i>	0.3 (0.1)	0.2 (0.1)	0.2 (0.2)	1.8 (1.3)	1.6 (0.6)
	<i>Akkermansia</i>	37.7 (5.0)	29.4 (4.7)	0 (0)	0 (0)	0 (0)
	<i>Anaeroplasma</i>	1.4 (0.7)	0.9 (0.6)	0 (0)	0 (0)	0 (0)
	<i>ASF356</i>	2.3 (0.7)	4.4 (1.3)	0 (0)	0 (0)	0 (0)
	<i>Bacteroides</i>	27.3 (4.3)	31.5 (4.1)	0 (0)	11.4 (7.6)	8.5 (8.5)
	<i>Clostridium sensu stricto 1</i>	0 (0)	0 (0)	0 (0)	1.1 (1.0)	0 (0)
	<i>Enterococcus</i>	0 (0)	0.1 (0)	4.9 (2.1)	9.0 (1.1)	11.1 (3.3)
	<i>Escherichia-Shigella</i>	0 (0)	0 (0)	14.4 (6.3)	11.6 (5.1)	14.6 (6.3)
	<i>Lachnospiraceae NK4A136 group</i>	1.2 (0.6)	0.7 (0.5)	0 (0)	0 (0)	0 (0)
	<i>Lactobacillus</i>	5.6 (1.3)	4.8 (1.4)	77.0 (7.0)	62.4 (8.2)	60.8 (8.7)

<i>Muribaculum</i>	0.7 (0.7)	0.7 (0.7)	0 (0)	0 (0)	0 (0)
<i>Parabacteroides</i>	14.7 (1.3)	15.3 (1.5)	0 (0)	0 (0)	0 (0)
<i>Parasutterella</i>	3.5 (0.6)	4.1 (0.2)	0 (0)	0 (0)	0 (0)
<i>Turicibacter</i>	0 (0)	0 (0)	2.7 (2.7)	2.4 (1.9)	3.3 (1.6)

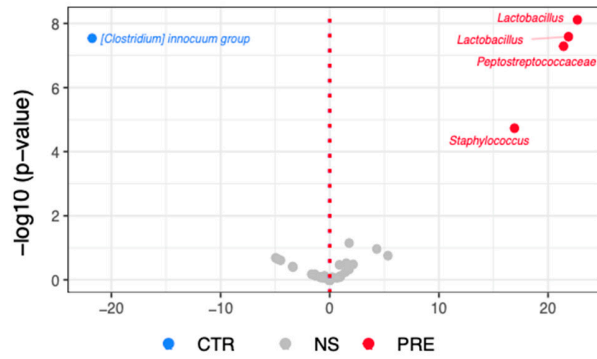
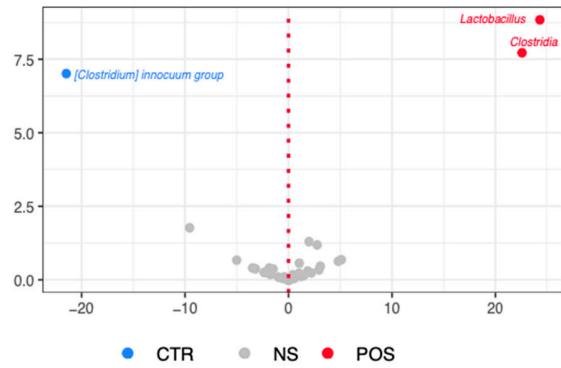
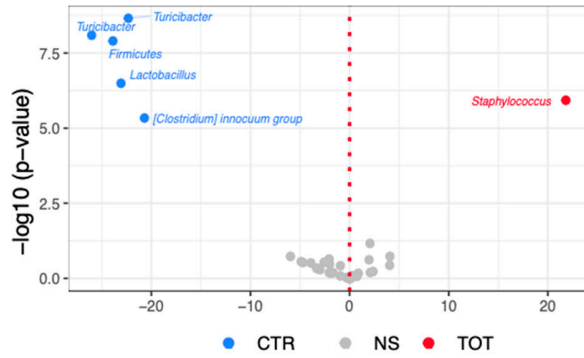
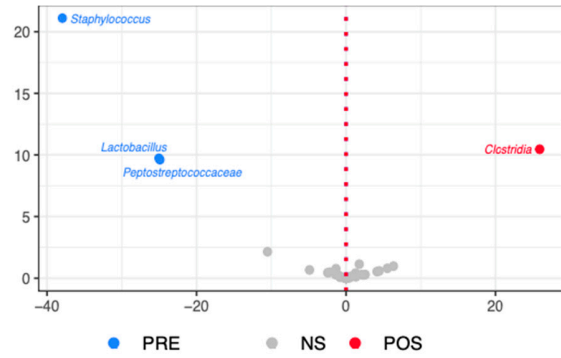
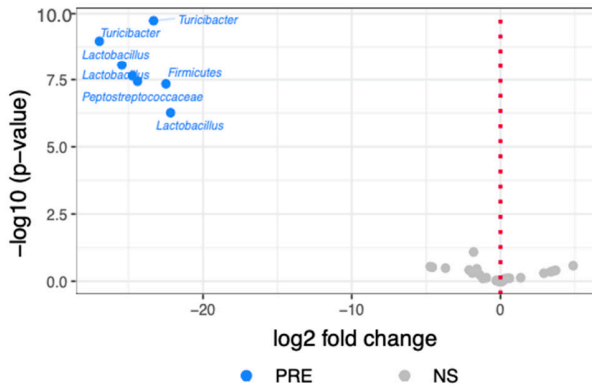
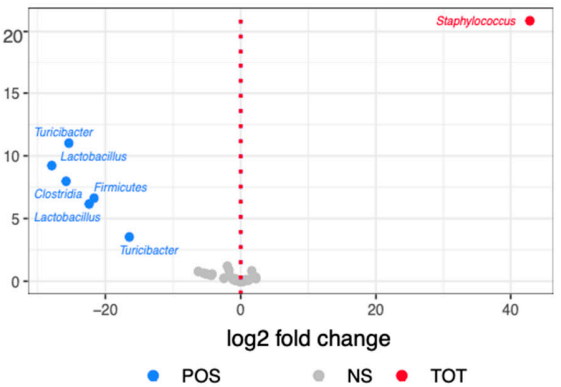
**Supplemental Table 3. Shifts in microbial taxa from BL to W4 in POS mice.** Values reported as median and standard error measurement.

TOT Group	Phylum	Time Point				
		BL	ICR	W1	W2	W4
Class	<i>Bacteroidetes</i>	58.8 (2.0)	59.4 (5.5)	0 (0)	0 (0)	18.8 (12.1)
	<i>Firmicutes</i>	27.1 (2.2)	30.4 (5.9)	77.4 (6.1)	82.1 (7.4)	61.0 (11.3)
	<i>Proteobacteria</i>	2.7 (0.7)	3.1 (0.7)	22.6 (6.1)	17.9 (7.4)	20.2 (7.9)
	<i>Verrucomicrobiota</i>	11.0 (2.5)	6.1 (0.7)	0 (0)	0 (0)	0 (0)
	<i>Alphaproteobacteria</i>	1.4 (0.6)	2.0 (0.6)	0 (0)	0 (0)	0 (0)
	<i>Bacilli</i>	3.6 (1.3)	2.8 (0.8)	54.4 (6.9)	65.1 (5.9)	48.0 (13.4)
Family	<i>Bacteroidia</i>	58.9 (2.0)	59.5 (5.5)	0 (0)	0 (0)	18.9 (12.1)
	<i>Clostridia</i>	23.4 (3.0)	27.6 (5.6)	22.6 (10.6)	16.9 (8.4)	12.6 (4.1)
	<i>Gammaproteobacteria</i>	1.3 (0.2)	1.2 (0.1)	23.0 (6.2)	18.0 (7.4)	20.4 (8.1)
	<i>Verrucomicrobiae</i>	11.0 (2.6)	6.1 (0.7)	0 (0)	0 (0)	0 (0)
	<i>Akkermansiaceae</i>	11.4 (2.6)	6.4 (0.8)	0 (0)	0 (0)	0 (0)
	<i>Bacteroidaceae</i>	15.0 (3.1)	13.1 (4.1)	0 (0)	0 (0)	9.3 (9.3)
	<i>Clostridiaceae</i>	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
	<i>Enterobacteriaceae</i>	0 (0)	0 (0)	22.4 (5.9)	18.0 (7.5)	20.1 (8.0)
	<i>Enterococcaceae</i>	0 (0)	0 (0)	0 (0.0)	9.4 (6.2)	3.1 (1.0)
	<i>Erysipelotrichaceae</i>	0.1 (0.1)	0 (0)	0 (0)	0.2 (0.2)	0.4 (0.3)
	<i>Lachnospiraceae</i>	19.5 (3.5)	22.9 (4.7)	0 (0)	0 (0)	5.1 (2.7)
	<i>Lactobacillaceae</i>	2.5 (1.0)	1.3 (0.4)	53.4 (6.9)	56.0 (10.0)	44.6 (13.1)
	<i>Muribaculaceae</i>	40.0 (3.3)	42.4 (2.1)	0 (0)	0 (0)	0 (0)
	<i>Oscillospiraceae</i>	1.7 (0.5)	2.6 (1.0)	0 (0)	0 (0)	0.2 (0.2)
Genus	<i>Peptostreptococcaceae</i>	0.1 (0.1)	0 (0)	22.6 (10.6)	16.5 (8.1)	7.1 (2.8)
	<i>Sutterellaceae</i>	1.4 (0.2)	1.2 (0.1)	0 (0)	0 (0)	0 (0)
	<i>Tannerellaceae</i>	5.4 (1.4)	5.4 (1.5)	0 (0)	0 (0)	10.0 (8.2)
	<i>[Clostridium] inoculum group</i>	0.2 (0.1)	0.3 (0.1)	0 (0)	0.3 (0.3)	0.5 (0.3)
	<i>Akkermansia</i>	28.0 (7.0)	19.0 (3.1)	0 (0)	0 (0)	0 (0)
	<i>Anaeroplasma</i>	2.4 (0.8)	3.9 (1.2)	0 (0)	0 (0)	0 (0)
	<i>ASF356</i>	2.4 (0.9)	2.6 (1.1)	0 (0)	0 (0)	0 (0)
	<i>Bacteroides</i>	35.8 (7.1)	34.2 (7.7)	0 (0)	0 (0)	12.8 (12.8)
	<i>Clostridium sensu stricto 1</i>	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
	<i>Enterococcus</i>	0 (0)	0 (0)	1.6 (1.2)	14.5 (11.0)	3.1 (0.8)
	<i>Escherichia-Shigella</i>	0 (0)	0 (0)	16.7 (8.4)	11.2 (5.7)	8.4 (5.8)
	<i>Lachnospiraceae NK4A136 group</i>	1.9 (1.1)	3.8 (1.8)	0 (0)	0 (0)	0 (0)
	<i>Lactobacillus</i>	5.7 (2.2)	4.0 (1.4)	81.1 (9.0)	74.0 (10.9)	61.2 (16.0)

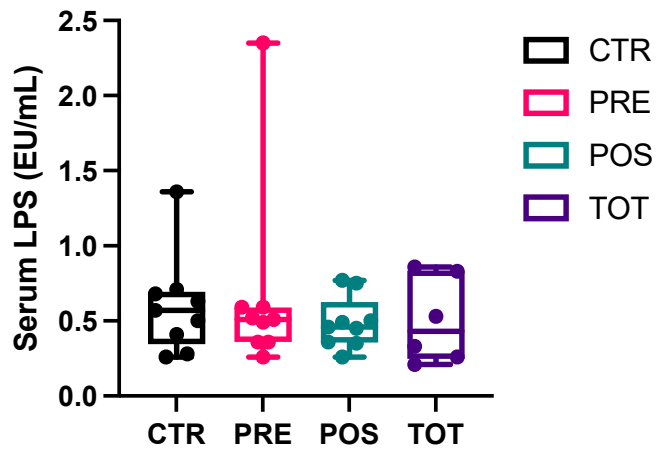
<i>Muribaculum</i>	1.6 (1.1)	2.8 (1.8)	0 (0)	0 (0)	0 (0)
<i>Parabacteroides</i>	12.5 (3.3)	14.1 (2.7)	0 (0)	0 (0)	11.8 (9.3)
<i>Parasutterella</i>	3.2 (0.3)	3.6 (0.3)	0 (0)	0 (0)	0 (0)
<i>Turicibacter</i>	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)

**Supplemental Table 4. Shifts in microbial taxa from BL to W4 in TOT mice.** Values reported as median and standard error measurement.

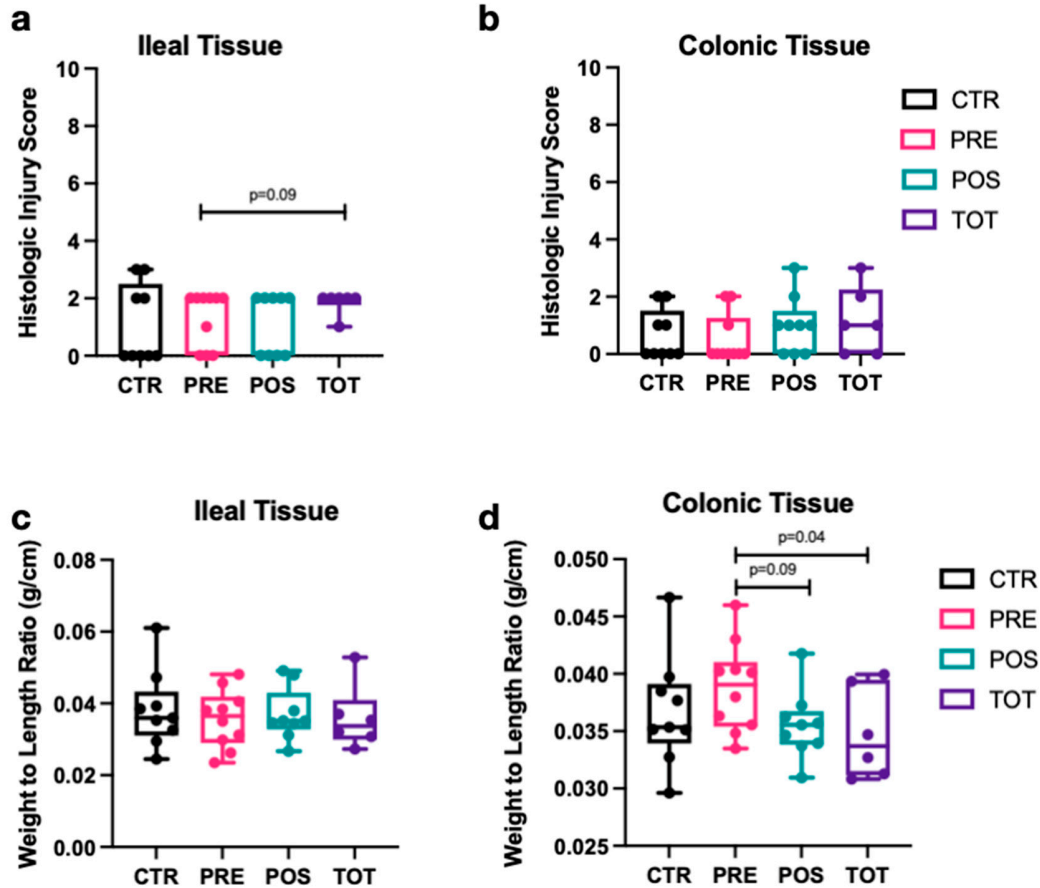


**a CTR vs PRE****b CTR vs POS****c CTR vs TOT****d PRE vs POS****e PRE vs TOT****f POS vs TOT**

**Supplemental Figure 1. Volcano plots demonstrating differences in relative abundance between groups at W4 using DESeq2 analysis. a. CTR vs. PRE. b. CTR vs. POS. c. CTR vs. TOT. d. PRE vs. TOT e. PRE vs TOT f. POS vs. TOT.**



**Supplemental Figure 2.** Differences in serum LPS between groups at W4. Box-and-whisker plots represent the distribution of each group at W4. The median is represented by the middle line while the upper and lower borders of the box plot identify the 75<sup>th</sup> and 25<sup>th</sup> percentile, respectively. The whiskers correspond to the maximal and minimal values.



**Supplemental Figure 3. Perianastomotic ileal and colonic tissue histologic injury scoring and weight to length ratios.** Box-and-whisker plots represent the distribution of each group at week 4. The median is represented by the middle line while the upper and lower borders of the box plot identify the 75<sup>th</sup> and 25<sup>th</sup> percentile, respectively. The whiskers correspond to the maximal and minimal values. **a-b.** Histologic injury scoring for ileal and colonic tissues, respectively. **c-d.** Weight to length ratio for ileal and colonic tissue, respectively.