SUPPLEMENTAL MATERIALS

SUPPLEMENTAL FIG 1. Gross morphology of the intestinal tract, spleen and MLN of ampicillin-treated CBA/J mice infected with *C. jejuni* at 2, 7, and 35 dpi. Mice were inoculated PBS (untreated), a *C. jejuni* wild-type strain, a *ΔflgL* mutant, and the *ΔflgL* + *flgL* isolate by oral gavage. The colons of animals infected with the *C. jejuni* wild-type strain or the *ΔflgL* + *flgL* complemented isolate showed signs of edema and apparent stool softening compared to uninfected mice or mice given the *ΔflgL* mutant. MLN = mesenteric lymph nodes.

SUPPLEMENTAL FIG 2. Histopathology of the ileocecocolic junction of ampicillin-treated CBA/J mice infected with *C. jejuni* at 7 dpi. Microscopy images are shown of longitudinal ileocecocolic junction sections of CBA/J mice inoculated by oral gavage with *C. jejuni* wild-type strain or PBS (uninfected) at 7 dpi. Scale bar = 50 µm; GC = Globular Cell; L = Lymphocyte (mucosal); EC = Epithelial Cell.

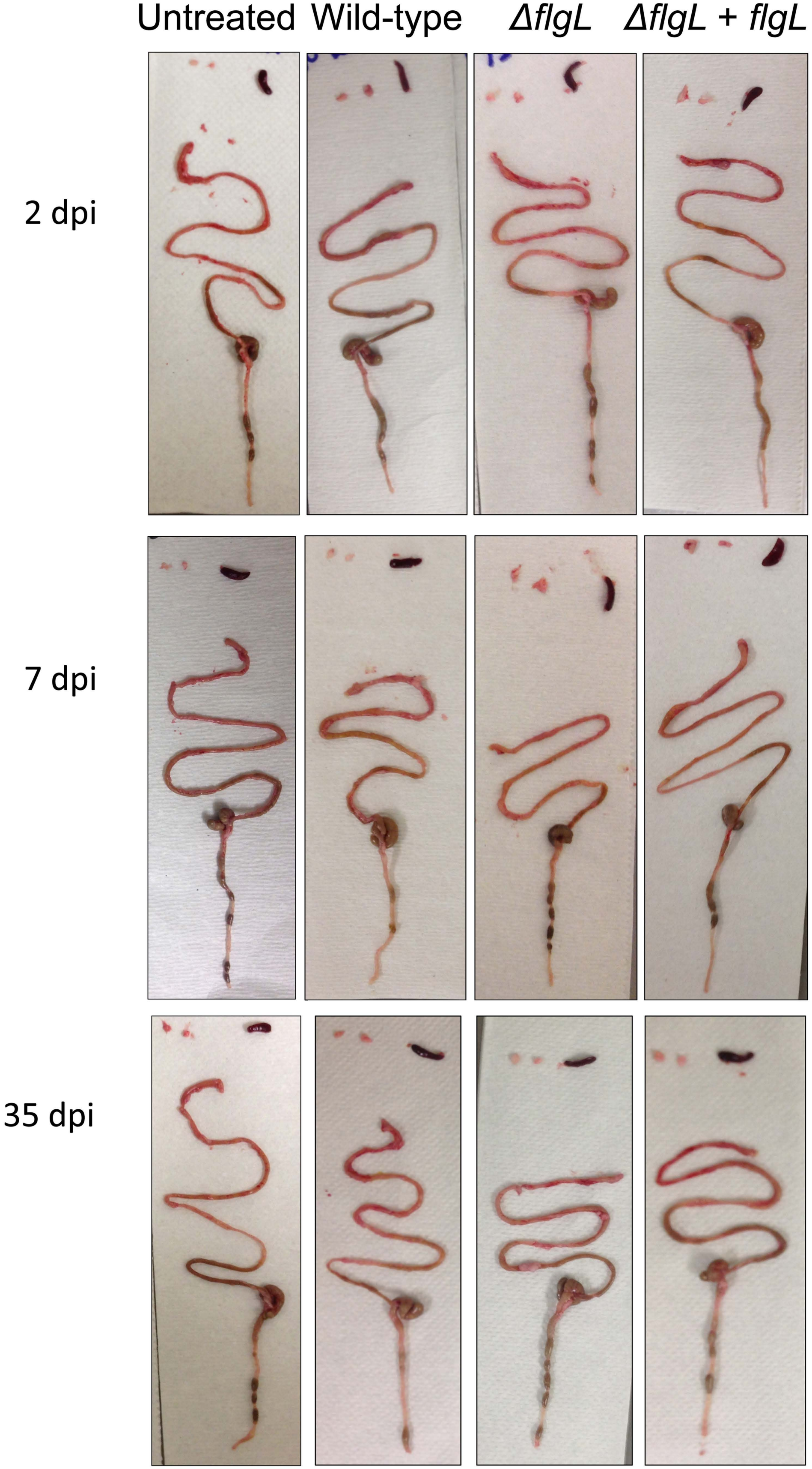
SUPPLEMENTAL TABLE 1. Murine intestinal isolates recovered from CBA/J mice treated with ampicillin.

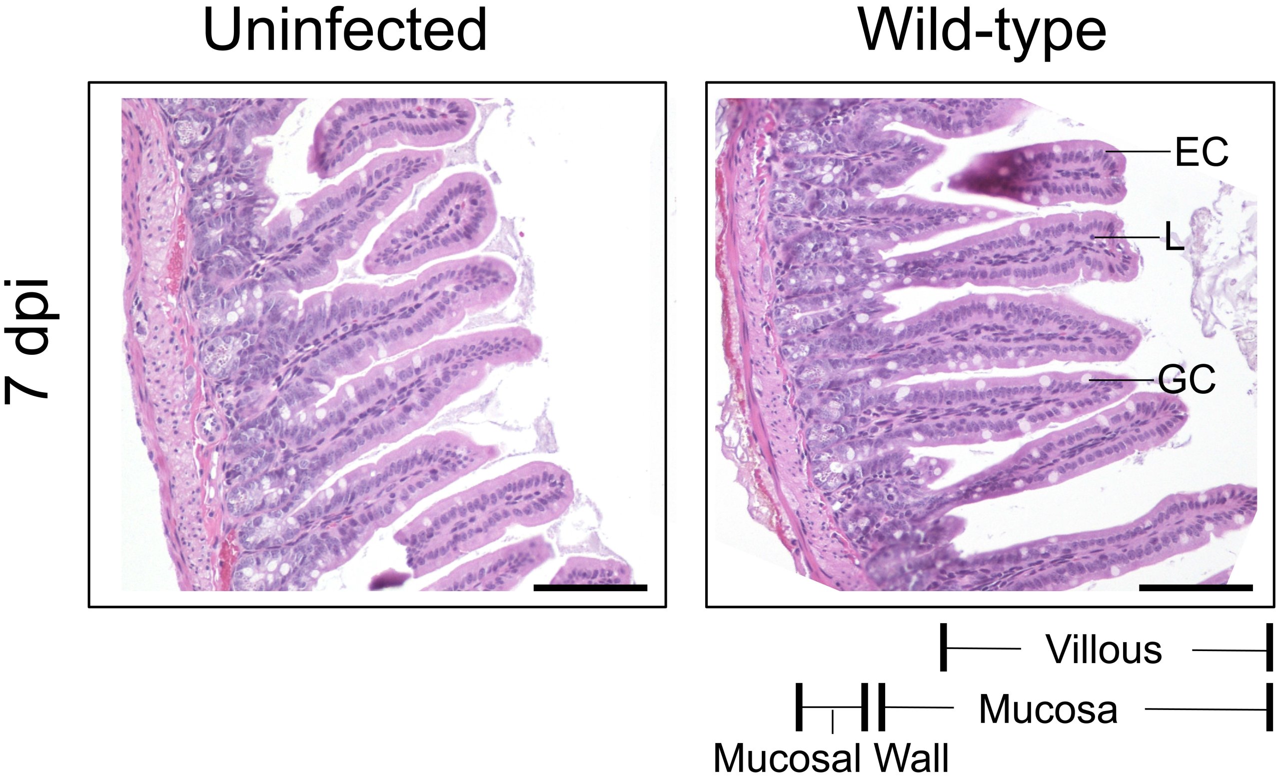
SUPPLEMENTAL TABLE 2. Alignment of the 16S rRNA gene fragment from *E. faecalis* MEK1 (KLC3001) to the 16S rRNA gene from *E. faecalis* ATCC 29212.

SUPPLEMENTAL TABLE 3. Multilocus sequence typing (MLST) of *Enterococcus faecalis* KLC3001.

SUPPLEMENTAL TABLE 4. Complete taxon identification of intestinal samples with and without ampicillin treatment.

SUPPLEMENTAL TABLE 5. Intestinal taxa (OTUs) common to all animals within a treatment group.


Untreated
Wild-type
ΔflgL
ΔflgL + flgL
2 dpi
7 dpi
35 dpi


Uninfected
Wild-type
7 dpi
EC
L
GC
Villous
Mucosa
Mucosal Wall

Supplemental Table 1. Murine intestinal isolates recovered from CBA/J mice treated with ampicillin.*

Intestinal Isolate	Plate Type	Inhibition
MEK1	MHB	Yes
MEK2	MHB	Yes
MEK3	MRS	Yes
MEK4	MHB	Yes
MEK5	LB	Yes
MEK6	MRS	No
MEK7	LB	No
MEK8	LB	No
MEK9	MHB	No
MEK10	MHB	No
MEK11	LB	No
MEK12	MHB	No
MEK13	MHB	No

*Isolates recovered from 5 mice (*n* = 5)

Supplemental Table 2. Alignment of the 16S rRNA gene fragment from *E. faecalis* MEK1 (KLC3001) to the 16S rRNA gene from *E. faecalis* ATCC 29212.*

```
MEK1        1       CTGGCGGCGTGCCTAATACATGCAAGTCGAACGCTTCTTTCCTCCCGAGTGCTTGCACTC  60
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108195  CTGGCGGCGTGCCTAATACATGCAAGTCGAACGCTTCTTTCCTCCCGAGTGCTTGCACTC  108254

MEK1        61      AATTGGAAAGAGGAGTGGCGGACGGGTGAGTAACACGTGGGTAACCTACCCATCAGAGGG  120
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108255  AATTGGAAAGAGGAGTGGCGGACGGGTGAGTAACACGTGGGTAACCTACCCATCAGAGGG  108314

MEK1        121     GGATAACACTTGGAAACAGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGA  180
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108315  GGATAACACTTGGAAACAGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGA  108374

MEK1        181     GTGAAAGGCGCTTTCGGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTG  240
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108375  GTGAAAGGCGCTTTCGGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTG  108434

MEK1        241     AGGTAACGGCTCACCAAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACT  300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108435  AGGTAACGGCTCACCAAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACT  108494

MEK1        301     GGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGG  360
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108495  GGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGG  108554

MEK1        361     ACGAAAGTCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCT  420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108555  ACGAAAGTCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCT  108614

MEK1        421     GTTGTTAGAGAAGAACAAGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGA  480
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108615  GTTGTTAGAGAAGAACAAGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGA  108674

MEK1        481     AAGCCACGGCTAACTACGAGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCG  540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108675  AAGCCACGGCTAACTACGAGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCG  108734

MEK1        541     GAATTATTGGGCGTAAAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGG  600
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108735  GAATTATTGGGCGTAAAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGG  108794

MEK1        601     CTCAACCGGGGAGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAAT  660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108795  CTCAACCGGGGAGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAAT  108854

MEK1        661     TCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTC  720
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108855  TCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTC  108914

MEK1        721     TCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCC  780
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108915  TCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCC  108974

MEK1        781     TGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGC  840
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  108975  TGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGC  109034

MEK1        841     TGCAGCAAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAG  900
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  109035  TGCAGCAAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAG  109094

MEK1        901     GAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTGATTCGAAGCAACGCGAAG  960
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  109095  GAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTGATTCGAAGCAACGCGAAG  109154

MEK1        961     AACCTTACCAGGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCGGGGA  1020
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  109155  AACCTTACCAGGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCGGGGA  109214
```

```
MEK1        1021    CAAAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTC  1080
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  109215  CAAAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTC  109274

MEK1        1081    CCGCAACGAGCGCAACCCTTATTGTTAGTTGCCATCATTTAGTTGGGCACTCTAGCGAGA  1140
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  109275  CCGCAACGAGCGCAACCCTTATTGTTAGTTGCCATCATTTAGTTGGGCACTCTAGCGAGA  109334

MEK1        1141    CTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGAC  1200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  109335  CTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGAC  109394

MEK1        1201    CTGGGCTACACACGTGCTACAATGGGAAGTACAACGAGTCGCTAGACCGCGAGGTCATGC  1260
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  109395  CTGGGCTACACACGTGCTACAATGGGAAGTACAACGAGTCGCTAGACCGCGAGGTCATGC  109454

MEK1        1261    AAATCTCTTAAAGCTTCTCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCA  1312
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCC 29212  109455  AAATCTCTTAAAGCTTCTCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCA  109506
```

---

* The numbers to the left and right of the nucleotide sequence of the *E. faecalis* ATCC 29212 16S rRNA gene indicate the locus within the complete genomic sequence. The two gene fragments showed 100% identity, as indicated by the vertical lines.

Supplemental Table 3. Multilocus sequence typing (MLST) of *Enterococcus faecalis* KLC3001.

Name	**Primer Sequence**	**Sequence Type: 55**
gdh-1	5'-GGCGCACTAAAAGATATGGT-3'	3
gdh-2	5'-CCAAGATTGGGCAACTTCGTCCCA-3'	
gyd-1	5'-CAAACTGCTTAGCTCCAATGGC-3'	7
gyd-2	5'-CATTTCGTTGTCATACCAAGC-3'	
pstS-1	5'-CGGAACAGGACTTTCGC-3'	23
pstS-2	5'-ATTTACATCACGTTCTACTTGC-3'	
gki-1	5'-GATTTTGTGGGAATTGGTATGG-3'	1
gki-2	5'-ACCATTAAAGCAAAATGATCGC-3'	
aroE-1	5'-TGGAAAACTTTACGGAGACAGC-3'	9
aroE-2	5'-GTCCTGTCCATTGTTCAAAAGC-3'	
xpt-1	5'-AAAATGATGGCCGTGTATTAGG-3'	16
xpt-2	5'-AACGTCACCGTTCCTTCACTTA-3'	
yqiL-1	5'-CAGCTTAAGTCAAGTAAGTGCCG-3'	7
yqiL-2	5'-GAATATCCCTTCTGCTTGTGCT-3'	

Supplemental Table 4. Complete taxon identification of intestinal samples with and without ampicillin treatment

Taxon	+Amp	-Amp
Bacteria;Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;Asaccharobacter	0.00%	0.00%
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	0.00%	0.00%
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Barnesiella	71.90%	52.79%
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Tannerella	0.00%	0.00%
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Prevotella	0.00%	0.00%
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Elizabethkingia	0.00%	0.00%
Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Flavobacterium	0.23%	0.00%
Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Pedobacter	0.00%	0.00%
Bacteria;Cyanobacteria_Chloroplast;Chloroplast;Chloroplast_order_incertae_sedis;Chloroplast;Streptophyta	1.93%	0.01%
Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	0.01%	0.00%
Bacteria;Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	12.46%	0.04%
Bacteria;Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Melissococcus	0.00%	0.00%
Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	5.40%	0.78%
Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	0.00%	0.00%
Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	0.04%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridium_sensu_stricto	0.00%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales_Incertae_Sedis_XII;Acidaminobacter	0.16%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Eubacteriaceae;Eubacterium	0.03%	0.29%
Bacteria;Firmicutes;Clostridia;Clostridiales;Gracilibacteraceae;Gracilibacter	0.39%	0.51%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Acetitomaculum	0.00%	0.07%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Anaerostipes	0.04%	0.15%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Blautia	0.00%	0.54%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Butyrivibrio	0.01%	0.26%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Clostridium_XlVa	1.27%	11.94%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Clostridium_XlVb	0.02%	0.71%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Coprococcus	0.18%	4.71%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Dorea	0.00%	0.02%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Hespellia	0.00%	0.02%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Johnsonella	0.01%	0.24%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiracea_incertae_sedis	1.12%	5.78%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lactonifactor	0.00%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Marvinbryantia	0.06%	0.53%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Moryella	0.00%	0.33%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Oribacterium	0.00%	0.23%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Parasporobacterium	0.00%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Robinsoniella	0.00%	0.16%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Roseburia	0.00%	0.14%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Shuttleworthia	0.00%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Syntrophococcus	0.12%	5.02%
Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;Clostridium_XI	0.00%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;Peptostreptococcus	0.00%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Acetanaerobacterium	0.00%	0.24%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Acetivibrio	0.30%	2.64%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerofilum	0.00%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	0.02%	0.46%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Butyricicoccus	0.00%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Clostridium_IV	0.37%	3.10%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ethanoligenens	0.00%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Flavonifractor	1.31%	1.61%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Hydrogenoanaerobacterium	0.07%	0.96%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillibacter	0.45%	3.39%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Papillibacter	0.00%	0.02%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Pseudoflavonifractor	0.37%	1.49%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcus	0.00%	0.00%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Saccharofermentans	0.04%	0.27%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Subdoligranulum	0.00%	0.00%
Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Bulleidia	0.00%	0.00%
Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Clostridium_XVIII	0.96%	0.02%
Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Coprobacillus	0.51%	0.06%
Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Erysipelotrichaceae_incertae_sedis	0.03%	0.27%
Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Holdemania	0.00%	0.00%
Bacteria;Firmicutes;Negativicutes;Selenomonadales;Acidaminococcaceae;Phascolarctobacterium	0.00%	0.00%
Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Megasphaera	0.00%	0.00%
Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Propionispira	0.00%	0.10%
Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Zymophilus	0.00%	0.01%
Bacteria;Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;Fusobacterium	0.00%	0.00%
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas	0.01%	0.00%
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Gemmiger	0.00%	0.01%
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Blastomonas	0.00%	0.00%
Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Delftia	0.00%	0.00%
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia_Shigella	0.00%	0.00%
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	0.00%	0.00%
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	0.02%	0.00%
Bacteria;Tenericutes;Mollicutes;Anaeroplasmatales;Anaeroplasmataceae;Anaeroplasma	0.13%	0.05%

Supplemental Table 5. Intestinal taxa (OTUs) common to all animals within a treatment group.

Untreated	**Ampicillin**
Barnesiella	*Barnesiella*
Clostridium_XlVa	*Clostridium_XlVa*
Acetivibrio	*Anaeroplasma*
Clostridium_XVIII	*Enterococcus*
Coprococcus	*Lactobacillus*
Gracilibacter	
Hespellia	
Lachnospiracea	
Roseburia	