

Supplemental Table 1: Primer sequences for RT-qPCR

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')
Liver, Ileum and Hypothalamus		
IRS-1	CTCTGCTTCTGCTTCTGTTAC	TGGTTATGGTTGGGACTTAGG
IRS-2	AAGATAGCGGGTACATGCGAAT	GCAGCTTAGGGTCTGGGTTCT
ZO-1	AAAGGTGAAACTCTGCTGAG	GATCTCCAGGAAGACACTTG
Occludin	GAGGACTGGCTCAGGGAATATC	TTGTTGACCTCGTCGAGTTCTG
Muc2	CCACCATTACCACCACCTCAG	CGATCACCACCATTGCCATTG
MMP9	CATGCGCTGGGCTTAGATCA	GAGGCCTTGGGTCAGGTTTAGAG
IL-10	AGTCAGCCAGACCCACATG	GCAACCCAAGTAACCCTTAAAG
POMC	AGGTTAAGGAGCAGTGACTAAG	AGCAGAATCTCGGCATCTTC
AGRP	CGTGCTACTGCCGCTTCTTC	CCCTGCCTTTGCCAACATC
NPY	GCTCGTGTGTTTGGGCATTC	GAGATTGATGTAGTGTGCGCAGAG
β -Actin	ATCAAGATCATTGCTCCTCCTG	GACTCATCGTACTCCTGCTTG
18S	TGACTCAACACGGGAAACC	TCGCTCCACCAACTAAGAAC
GAPDH	CAAGTTCAACGGCACAGTCAAG	ACATACTCAGCACCAGCATCAC

Supplemental Table 2: Between-group changes in relative abundance of the 15 most abundant bacterial families in male rats after the first, second, third antibiotic pulse and at the end of the study. (n=8-10 rats per group/time point).

- After first antibiotic exposure

Family/Group	CTR	ABT	PRE	ABT+PRE	LEAN
Peptococcaceae	0.002±0.000 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.002±0.000 ^a
Bifidobacteriaceae	0.000±0.000 ^a	0.000±0.000 ^a	0.004±0.002 ^b	0.000±0.000 ^a	0.000±0.000 ^a
Verrucomicrobiaceae	0.030±0.008 ^a	0.000±0.000 ^b	0.006±0.005 ^b	0.000±0.000 ^b	0.038±0.010 ^a
Enterococcaceae	0.001±0.000 ^a	0.046±0.010 ^{bc}	0.004±0.001 ^{ac}	0.261±0.022 ^b	0.000±0.000 ^a
Porphyromonadaceae	0.043±0.010 ^a	0.000±0.000 ^b	0.016±0.005 ^{ac}	0.006±0.004 ^{bc}	0.014±0.006 ^{ac}
Prevotellaceae	0.068±0.017 ^a	0.000±0.000 ^b	0.001±0.001 ^b	0.000±0.000 ^b	0.118±0.019 ^a
Erysipelotrichaceae	0.021±0.006 ^a	0.002±0.000 ^b	0.066±0.019 ^a	0.001±0.001 ^b	0.015±0.003 ^a
Enterobacteriaceae	0.014±0.003 ^a	0.018±0.008 ^a	0.175±0.031 ^b	0.205±0.025 ^b	0.016±0.004 ^a
Ruminococcaceae	0.051±0.007 ^a	0.035±0.005 ^a	0.001±0.001 ^b	0.002±0.001 ^b	0.063±0.011 ^a
Bacteroidales_S24-7_group	0.121±0.019 ^a	0.003±0.002 ^b	0.003±0.002 ^b	0.000±0.000 ^b	0.121±0.008 ^a
Peptostreptococcaceae	0.041±0.008 ^a	0.003±0.001 ^b	0.033±0.009 ^a	0.000±0.000 ^b	0.059±0.010 ^a
Clostridiaceae_1	0.011±0.003 ^a	0.000±0.000 ^b	0.044±0.011 ^a	0.000±0.000 ^b	0.010±0.002 ^a
Lachnospiraceae	0.187±0.036 ^{ab}	0.203±0.017 ^a	0.120±0.010 ^b	0.196±0.022 ^{ab}	0.130±0.019 ^b
Bacteroidaceae	0.071±0.016 ^b	0.605±0.027 ^a	0.126±0.026 ^{bc}	0.217±0.041 ^{ac}	0.066±0.029 ^b
Lactobacillaceae	0.323±0.042 ^a	0.081±0.012 ^b	0.400±0.025 ^a	0.111±0.025 ^b	0.337±0.049 ^a

- After second antibiotic exposure – Males

Family/Group	CTR	ABT	PRE	ABT+PRE	LEAN
Peptococcaceae	0.003±0.001 ^a	0.001±0.001 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.002±0.001 ^a
Bifidobacteriaceae	0.002±0.000 ^{acd}	0.000±0.000 ^b	0.039±0.019 ^c	0.000±0.000 ^b	0.001±0.000 ^{bd}
Verrucomicrobiaceae	0.045±0.014 ^a	0.018±0.014 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.003±0.001 ^{ab}
Enterococcaceae	0.000±0.000 ^a	0.018±0.006 ^{bc}	0.003±0.001 ^{ac}	0.088±0.029 ^b	0.001±0.001 ^a
Porphyromonadaceae	0.096±0.010 ^a	0.000±0.000 ^b	0.021±0.005 ^c	0.105±0.021 ^a	0.004±0.001 ^{bc}
Prevotellaceae	0.065±0.015 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.187±0.006 ^a
Erysipelotrichaceae	0.019±0.004 ^a	0.020±0.016 ^a	0.206±0.025 ^b	0.062±0.035 ^a	0.022±0.002 ^a
Enterobacteriaceae	0.003±0.002 ^a	0.000±0.000 ^a	0.121±0.016 ^{bc}	0.231±0.037 ^b	0.003±0.000 ^{ac}
Ruminococcaceae	0.033±0.006 ^{ac}	0.077±0.015 ^a	0.002±0.000 ^b	0.017±0.006 ^{bc}	0.086±0.015 ^a
Bacteroidales_S24-7_group	0.123±0.021 ^a	0.012±0.004 ^b	0.000±0.000 ^c	0.000±0.000 ^c	0.131±0.007 ^a
Peptostreptococcaceae	0.089±0.008 ^a	0.011±0.007 ^{bc}	0.012±0.005 ^{bc}	0.003±0.003 ^c	0.029±0.008 ^{ab}
Clostridiaceae_1	0.129±0.014 ^a	0.021±0.012 ^b	0.152±0.050 ^a	0.037±0.016 ^b	0.011±0.005 ^b
Lachnospiraceae	0.120±0.024 ^{ac}	0.291±0.026 ^b	0.065±0.025 ^a	0.224±0.024 ^b	0.181±0.019 ^{bc}
Bacteroidaceae	0.043±0.010 ^{ac}	0.477±0.024 ^b	0.142±0.022 ^a	0.181±0.040 ^a	0.010±0.003 ^c
Lactobacillaceae	0.215±0.037 ^a	0.051±0.019 ^b	0.230±0.036 ^a	0.051±0.050 ^b	0.315±0.026 ^a

- After third antibiotic exposure – Males

Family/Group	CTR	ABT	PRE	ABT+PRE	LEAN
Peptococcaceae	0.002±0.001 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.003±0.000 ^a
Bifidobacteriaceae	0.002±0.001 ^a	0.000±0.000 ^a	0.338±0.015 ^b	0.000±0.000 ^a	0.001±0.000 ^a
Verrucomicrobiaceae	0.030±0.012 ^a	0.009±0.005 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.000±0.000 ^b

Enterococcaceae	0.000±0.000 ^a	0.011±0.006 ^b	0.010±0.003 ^b	0.039±0.008 ^b	0.000±0.000 ^a
Porphyromonadaceae	0.083±0.014 ^a	0.000±0.000 ^b	0.001±0.001 ^{bd}	0.015±0.012 ^{bc}	0.006±0.001 ^{acd}
Prevotellaceae	0.031±0.007 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.150±0.018 ^a
Erysipelotrichaceae	0.007±0.002 ^a	0.038±0.004 ^{bc}	0.041±0.011 ^{bc}	0.134±0.047 ^b	0.016±0.002 ^{ac}
Enterobacteriaceae	0.002±0.000 ^a	0.000±0.000 ^a	0.022±0.008 ^b	0.026±0.011 ^b	0.001±0.000 ^a
Ruminococcaceae	0.029±0.009 ^{ad}	0.069±0.011 ^{ac}	0.000±0.000 ^b	0.003±0.001 ^{bd}	0.120±0.13 ^c
Bacteroidales_S24-7_group	0.131±0.023 ^a	0.021±0.005 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.132±0.017 ^a
Peptostreptococcaceae	0.104±0.012 ^a	0.021±0.015 ^{bc}	0.001±0.001 ^b	0.003±0.002 ^b	0.052±0.012 ^{ac}
Clostridiaceae_1	0.149±0.024 ^a	0.030±0.015 ^b	0.031±0.017 ^b	0.214±0.058 ^a	0.041±0.014 ^b
Lachnospiraceae	0.079±0.024 ^{ac}	0.249±0.014 ^b	0.008±0.005 ^a	0.017±0.010 ^a	0.165±0.011 ^{bc}
Bacteroidaceae	0.030±0.007 ^a	0.452±0.029 ^b	0.017±0.007 ^a	0.049±0.033 ^a	0.006±0.002 ^a
Lactobacillaceae	0.307±0.036 ^a	0.092±0.036 ^b	0.530±0.031 ^c	0.499±0.082 ^{ac}	0.300±0.037 ^a

- End of Study – Males

Family/Group	CTR	ABT	PRE	ABT+PRE	LEAN
Peptococcaceae	0.004±0.000	0.006±0.001	0.004±0.001	0.004±0.000	0.003±0.000
Bifidobacteriaceae	0.000±0.000 ^a	0.000±0.000 ^a	0.000±0.000 ^a	0.000±0.000 ^a	0.000±0.000 ^a
Verrucomicrobiaceae	0.005±0.004 ^a	0.079±0.013 ^b	0.050±0.009 ^b	0.060±0.015 ^b	0.000±0.000 ^a
Enterococcaceae	0.000±0.000 ^a	0.001±0.000 ^a	0.005±0.003 ^a	0.001±0.000 ^a	0.000±0.000 ^a
Porphyromonadaceae	0.023±0.003 ^{ac}	0.051±0.008 ^b	0.037±0.005 ^{ab}	0.034±0.007 ^{ab}	0.007±0.001 ^c
Prevotellaceae	0.019±0.004 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.001±0.000 ^b	0.130±0.012 ^a
Erysipelotrichaceae	0.015±0.006 ^a	0.017±0.004 ^a	0.040±0.010 ^a	0.015±0.003 ^a	0.032±0.013 ^a
Enterobacteriaceae	0.001±0.000 ^{ac}	0.003±0.000 ^b	0.002±0.000 ^{ab}	0.002±0.000 ^{ab}	0.000±0.000 ^c
Ruminococcaceae	0.040±0.005 ^a	0.071±0.011 ^a	0.046±0.007 ^a	0.054±0.011 ^a	0.147±0.018 ^b
Bacteroidales_S24-7_group	0.138±0.013 ^a	0.015±0.002 ^b	0.021±0.010 ^b	0.022±0.004 ^b	0.136±0.021 ^a
Peptostreptococcaceae	0.144±0.013 ^a	0.084±0.012 ^{bc}	0.172±0.012 ^a	0.132±0.017 ^{ac}	0.080±0.019 ^{bc}
Clostridiaceae_1	0.198±0.016 ^a	0.174±0.034 ^a	0.226±0.020 ^a	0.140±0.033 ^a	0.019±0.007 ^b
Lachnospiraceae	0.078±0.006 ^a	0.135±0.017 ^{ab}	0.109±0.014 ^{ab}	0.113±0.018 ^{ab}	0.178±0.026 ^b
Bacteroidaceae	0.017±0.004 ^{ad}	0.172±0.022 ^b	0.064±0.011 ^{cd}	0.128±0.011 ^{bc}	0.008±0.002 ^a
Lactobacillaceae	0.294±0.040	0.183±0.020	0.210±0.037	0.189±0.046	0.249±0.043

Values displayed are mean±SE (relative abundance). Kruskal-Wallis test with Dunn post-hoc tests and Benjamin-Holmes False Discovery Rate (FDR) correction; $P < 0.05$. CTR, control; ABT, antibiotic; PRE, prebiotic; ABT+PRE, antibiotic+prebiotic; LEAN, lean control.

Supplemental Table 3: Between-group changes in relative abundance of the 15 most abundant bacterial families in female rats after the first, second, third antibiotic pulse and at the end of the study. (n=8-10 rats per group/time point).

• After first antibiotic exposure – Females

Family/Group	CTR	ABT	PRE	ABT+PRE	LEAN
Peptococcaceae	0.004±0.001 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.003±0.001 ^a
Bifidobacteriaceae	0.000±0.000 ^a	0.000±0.000 ^a	0.022±0.011 ^b	0.000±0.000 ^a	0.000±0.000 ^a
Enterococcaceae	0.004±0.002 ^a	0.063±0.011 ^b	0.002±0.001 ^a	0.229±0.035 ^b	0.001±0.000 ^a
Verrucomicrobiaceae	0.056±0.017 ^a	0.001±0.000 ^{bd}	0.010±0.004 ^{acd}	0.000±0.000 ^b	0.030±0.011 ^c
Porphyromonadaceae	0.037±0.008 ^a	0.000±0.000 ^b	0.018±0.007 ^{ac}	0.006±0.003 ^{bc}	0.005±0.002 ^{bc}
Enterobacteriaceae	0.014±0.003 ^a	0.014±0.005 ^a	0.126±0.033 ^b	0.193±0.030 ^b	0.008±0.002 ^a
Erysipelotrichaceae	0.021±0.004 ^a	0.001±0.001 ^b	0.078±0.013 ^a	0.008±0.007 ^b	0.009±0.001 ^b
Prevotellaceae	0.065±0.013 ^a	0.000±0.000 ^b	0.001±0.001 ^b	0.000±0.000 ^b	0.131±0.010 ^a
Ruminococcaceae	0.064±0.009 ^a	0.024±0.004 ^{ab}	0.003±0.003 ^b	0.003±0.002 ^b	0.068±0.011 ^a
Peptostreptococcaceae	0.050±0.008 ^a	0.002±0.000 ^b	0.036±0.010 ^a	0.001±0.001 ^b	0.046±0.008 ^a
Bacteroidales_S24-7_group	0.153±0.017 ^a	0.007±0.003 ^b	0.008±0.003 ^b	0.000±0.000 ^b	0.134±0.010 ^a
Clostridiaceae_1	0.048±0.024 ^a	0.000±0.000 ^b	0.022±0.005 ^a	0.000±0.000 ^b	0.0122±0.003 ^a
Bacteroidaceae	0.070±0.009 ^a	0.548±0.031 ^b	0.117±0.023 ^{ac}	0.208±0.019 ^{bc}	0.016±0.009 ^a
Lachnospiraceae	0.168±0.019 ^a	0.189±0.013 ^a	0.132±0.016 ^a	0.162±0.024 ^a	0.143±0.013 ^a
Lactobacillaceae	0.232±0.023 ^a	0.147±0.036 ^a	0.419±0.032 ^b	0.188±0.050 ^a	0.383±0.025 ^b

• After second antibiotic exposure – Females

Family/Group	CTR	ABT	PRE	ABT+PRE	LEAN
Peptococcaceae	0.004±0.001 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.004±0.001 ^a
Bifidobacteriaceae	0.001±0.000 ^a	0.000±0.000 ^a	0.071±0.028 ^b	0.000±0.000 ^a	0.000±0.000 ^a
Enterococcaceae	0.001±0.001 ^{ac}	0.009±0.004 ^b	0.003±0.001 ^{bc}	0.059±0.016 ^b	0.000±0.000 ^a
Verrucomicrobiaceae	0.060±0.017 ^a	0.015±0.012 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.001±0.001 ^b
Porphyromonadaceae	0.089±0.010 ^a	0.000±0.000 ^b	0.019±0.004 ^c	0.149±0.023 ^a	0.005±0.001 ^{bc}
Enterobacteriaceae	0.005±0.002 ^{ac}	0.000±0.000 ^a	0.094±0.014 ^{bc}	0.215±0.036 ^b	0.002±0.001 ^a
Erysipelotrichaceae	0.022±0.004 ^a	0.011±0.003 ^a	0.195±0.035 ^b	0.083±0.045 ^a	0.015±0.035 ^a
Prevotellaceae	0.056±0.015 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.191±0.009 ^a
Ruminococcaceae	0.032±0.004 ^{ac}	0.075±0.011 ^a	0.002±0.001 ^b	0.013±0.005 ^{bc}	0.087±0.008 ^a
Peptostreptococcaceae	0.089±0.006 ^a	0.030±0.026 ^b	0.009±0.003 ^{bc}	0.000±0.000 ^c	0.038±0.013 ^{ab}
Bacteroidales_S24-7_group	0.120±0.014 ^{ac}	0.009±0.003 ^{ab}	0.000±0.000 ^b	0.000±0.000 ^b	0.153±0.010 ^c
Clostridiaceae_1	0.125±0.021 ^a	0.026±0.014 ^b	0.144±0.022 ^a	0.078±0.034 ^{ab}	0.017±0.009 ^b
Bacteroidaceae	0.068±0.018 ^{ac}	0.477±0.029 ^b	0.131±0.067 ^c	0.152±0.043 ^c	0.009±0.002 ^a
Lachnospiraceae	0.109±0.017 ^a	0.270±0.017 ^b	0.064±0.016 ^a	0.238±0.031 ^b	0.135±0.016 ^a
Lactobacillaceae	0.203±0.002 ^{ac}	0.067±0.016 ^{bc}	0.262±0.056 ^a	0.012±0.004 ^b	0.327±0.018 ^a

• After third antibiotic exposure – Females

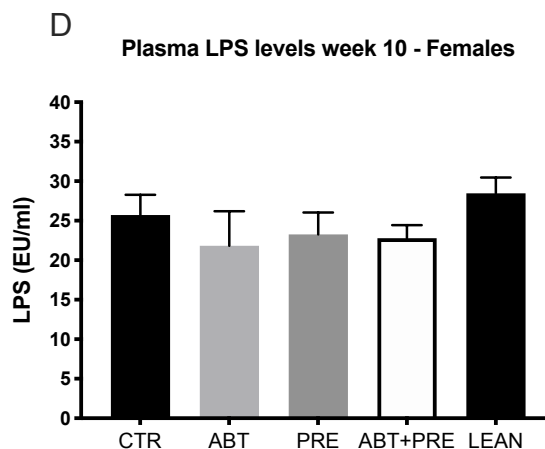
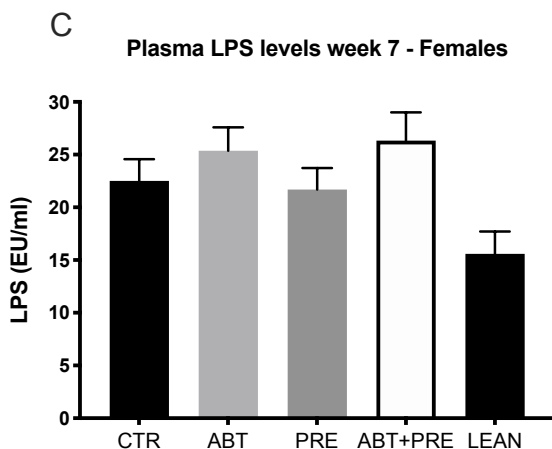
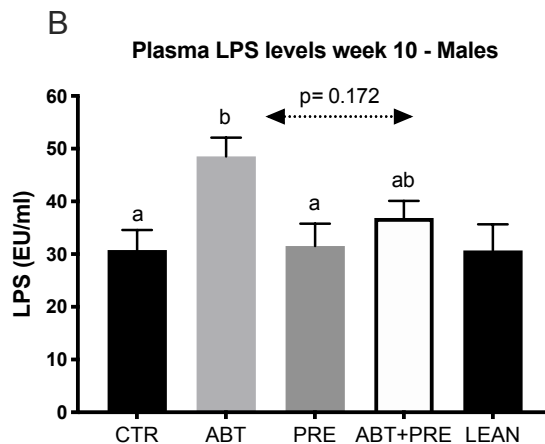
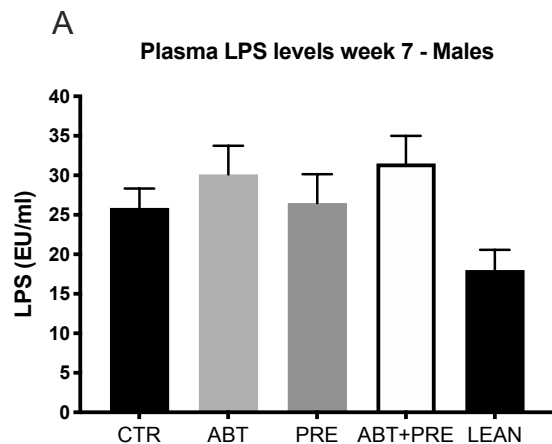
Family/Group	CTR	ABT	PRE	ABT+PRE	LEAN
Peptococcaceae	0.003±0.001 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.002±0.000 ^a
Bifidobacteriaceae	0.001±0.001 ^a	0.000±0.000 ^a	0.308±0.047 ^b	0.000±0.000 ^a	0.000±0.000 ^a

Enterococcaceae	0.000±0.000 ^a	0.001±0.000 ^{ab}	0.011±0.003 ^{bc}	0.050±0.013 ^c	0.000±0.000 ^a
Verrucomicrobiaceae	0.068±0.027 ^a	0.035±0.015 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.001±0.001 ^b
Porphyromonadaceae	0.093±0.022 ^a	0.000±0.000 ^b	0.001±0.001 ^b	0.001±0.000 ^b	0.007±0.001 ^a
Enterobacteriaceae	0.006±0.002 ^{bc}	0.000±0.000 ^a	0.024±0.006 ^b	0.004±0.001 ^{ab}	0.001±0.000 ^{ac}
Erysipelotrichaceae	0.008±0.001 ^a	0.029±0.006 ^a	0.112±0.026 ^a	0.092±0.016 ^a	0.008±0.002 ^a
Prevotellaceae	0.036±0.003 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.000±0.000 ^b	0.182±0.010 ^a
Ruminococcaceae	0.028±0.006 ^{ab}	0.1503±0.015 ^a	0.001±0.000 ^b	0.004±0.001 ^b	0.094±0.016 ^a
Peptostreptococcaceae	0.127±0.015 ^a	0.011±0.008 ^b	0.014±0.006 ^{bc}	0.002±0.001 ^b	0.050±0.017 ^{ac}
Bacteroidales_S24-7_group	0.123±0.019 ^{ab}	0.014±0.002 ^b	0.000±0.000 ^c	0.000±0.000 ^c	0.150±0.007 ^a
Clostridiaceae_1	0.138±0.019 ^{ac}	0.018±0.013 ^b	0.112±0.038 ^{ad}	0.493±0.056 ^c	0.019±0.012 ^{bd}
Bacteroidaceae	0.030±0.009 ^a	0.459±0.017 ^b	0.016±0.010 ^a	0.013±0.005 ^a	0.008±0.002 ^a
Lachnospiraceae	0.073±0.008 ^{ac}	0.245±0.019 ^b	0.006±0.002 ^a	0.016±0.008 ^a	0.128±0.015 ^{bc}
Lactobacillaceae (Adjusted p value between C and A =0.06)	0.253±0.030 ^{ac}	0.079±0.020 ^{bc}	0.394±0.047 ^a	0.326±0.045 ^a	0.342±0.038 ^a

- End of Study – Females

Family/Group	CTR	ABT	PRE	ABT+PRE	LEAN
Peptococcaceae	0.007±0.001 ^{ab}	0.008±0.001 ^a	0.007±0.001 ^{ab}	0.009±0.001 ^a	0.004±0.000 ^b
Bifidobacteriaceae	0.001±0.000 ^a	0.000±0.000 ^a	0.000±0.000 ^a	0.000±0.000 ^a	0.000±0.000 ^a
Enterococcaceae	0.002±0.001 ^a	0.000±0.000 ^b	0.000±0.000 ^b	0.002±0.001 ^a	0.000±0.000 ^b
Verrucomicrobiaceae	0.007±0.003 ^a	0.068±0.015 ^b	0.062±0.018 ^b	0.066±0.014 ^b	0.000±0.000 ^a
Porphyromonadaceae	0.030±0.005 ^a	0.051±0.011 ^a	0.057±0.005 ^a	0.048±0.009 ^a	0.003±0.001 ^b
Enterobacteriaceae	0.001±0.000 ^a	0.001±0.000 ^a	0.002±0.001 ^a	0.003±0.001 ^a	0.001±0.000 ^a
Erysipelotrichaceae	0.029±0.006 ^a	0.007±0.002 ^b	0.048±0.008 ^a	0.009±0.002 ^b	0.054±0.025 ^a
Prevotellaceae	0.032±0.008 ^{ac}	0.004±0.004 ^b	0.007±0.004 ^b	0.024±0.016 ^{ab}	0.160±0.020 ^c
Ruminococcaceae	0.064±0.008 ^a	0.086±0.013 ^a	0.048±0.007 ^a	0.069±0.006 ^a	0.159±0.018 ^b
Peptostreptococcaceae	0.164±0.015 ^{ab}	0.117±0.017 ^b	0.223±0.006 ^a	0.126±0.020 ^b	0.087±0.024 ^b
Bacteroidales_S24-7_group	0.214±0.014 ^a	0.032±0.005 ^b	0.107±0.026 ^{bc}	0.060±0.012 ^b	0.146±0.012 ^{ac}
Clostridiaceae_1	0.160±0.016 ^a	0.127±0.025 ^a	0.158±0.017 ^a	0.155±0.023 ^a	0.034±0.015 ^b
Bacteroidaceae	0.012±0.002 ^{ac}	0.187±0.014 ^b	0.052±0.006 ^{cd}	0.141±0.021 ^{bd}	0.010±0.003 ^a
Lachnospiraceae	0.105±0.016 ^a	0.147±0.016 ^a	0.102±0.012 ^a	0.144±0.009 ^a	0.111±0.017 ^a
Lactobacillaceae	0.150±0.024 ^{ab}	0.151±0.035 ^{ab}	0.119±0.015 ^a	0.134±0.014 ^{ab}	0.222±0.022 ^b

Values displayed are mean±SE (relative abundance). Kruskal-Wallis test with Dunn post-hoc tests and Benjamin-Holmes False Discovery Rate (FDR) correction; $P < 0.05$. CTR, control; ABT, antibiotic; PRE, prebiotic; ABT+PRE, antibiotic+prebiotic; LEAN, lean control.



Supplemental Figure 1: ABT male offspring display increased endotoxemia at the end of the study. (A and B) Circulating LPS levels in males at (A) week 7 of life and (B) end of the study (n=8-10 rats per group/time point). (C and D) Circulating LPS levels in females at (C) week 7 of life and (D) end of the study (n=8-10 rats per group/time point). Different superscript letters denote significant differences between the groups, $p < 0.05$. CTR, control; ATB, antibiotic; PRE, prebiotic; ATB+PRE, antibiotic+prebiotic; LEAN, lean control.