

- Methanobacteriaceae
- Bifidobacteriaceae
- Frankiales
- Brevibacteriaceae
- Jonesiaceae
- Micromonosporaceae
- Solirubrobacterales
- Prevotellaceae
- Chitinophagaceae
- Chlamydiaceae
- Chloroplast
- Bacillales
- Thermoactinomycetaceae
- Lactobacillaceae
- Defluviitaleaceae
- Peptostreptococcaceae
- Veillonellaceae
- Phycisphaeraceae
- Methylobacteriaceae
- Acetobacteraceae
- Sphingomonadaceae
- Oxalobacteraceae
- Desulfovibrionaceae
- Enterobacteriaceae
- Pasteurellaceae
- Xanthomonadales
- Opitutaceae
- Acidobacteria
- Corynebacteriaceae
- Geodermatophilaceae
- Cellulomonadaceae
- Microbacteriaceae
- Nocardiodiaceae
- Bacteroidaceae
- Rikenellaceae
- Lentimicrobiaceae
- Ardenticatenia
- Cyanobacteria
- Paenibacillaceae
- Aerococcaceae
- Leuconostocaceae
- Eubacteriaceae
- Ruminococcaceae
- Fusobacteriaceae
- Caulobacteraceae
- Alcaligenaceae
- Hydrogenophilaceae
- Haliangiaceae
- Legionellaceae
- Moraxellaceae
- Spirochaetaceae
- Chthoniobacteriales
- Acidimicrobiales
- Mycobacteriaceae
- Nakamurellaceae
- Dermabacteraceae
- Micrococcaceae
- Propionibacteriaceae
- Bacteroidales
- Cytophagaceae
- Sphingobacteriaceae
- Chloroflexi
- Planococcaceae
- Carnobacteriaceae
- Streptococcaceae
- Lachnospiraceae
- Erysipelotrichaceae
- Leptotrichiaceae
- Bradyrhizobiaceae
- Burkholderiaceae
- Campylobacteraceae
- Alcanivoracaceae
- Pseudomonadaceae
- Anaeroplasmataceae
- Verrucomicrobia
- Actinomycetaceae
- Tsukamurellaceae
- Kineosporiaceae
- Intrasporangiaceae
- Sanguibacteraceae
- Coriobacteriaceae
- Porphyromonadaceae
- Flavobacteriaceae
- Sphingobacteriales
- Thermomicrobia
- Bacillaceae
- Staphylococcaceae
- Enterococcaceae
- Clostridiales
- Peptococcaceae
- Acidaminococcaceae
- Gemmatimonadetes
- Brucellaceae
- Rhodobacteraceae
- Erythrobacteraceae
- Comamonadaceae
- Rhodocyclaceae
- Helicobacteraceae
- Oceanospirillaceae
- Xanthomonadaceae
- Mollicutes
- Verrucomicrobiaceae

Fig. S1. Relative abundance of bacterial families (in percentage) in the intestinal tracts of EF_{CK135} colonized conventional mice in response to ceftriaxone treatment. EF_{CK135} colonized mice were treated with either saline or ceftriaxone and euthanized at day 4 post-first dose of ceftriaxone administration. 16S rRNA gene sequencing was performed with DNA extracted from the intestinal tissues and relative abundance of bacterial families was determined and represented here in percentage. Note that for readability purposes, these figures show data at the family level while our data (in Fig. 4F) was analyzed at the genus level.

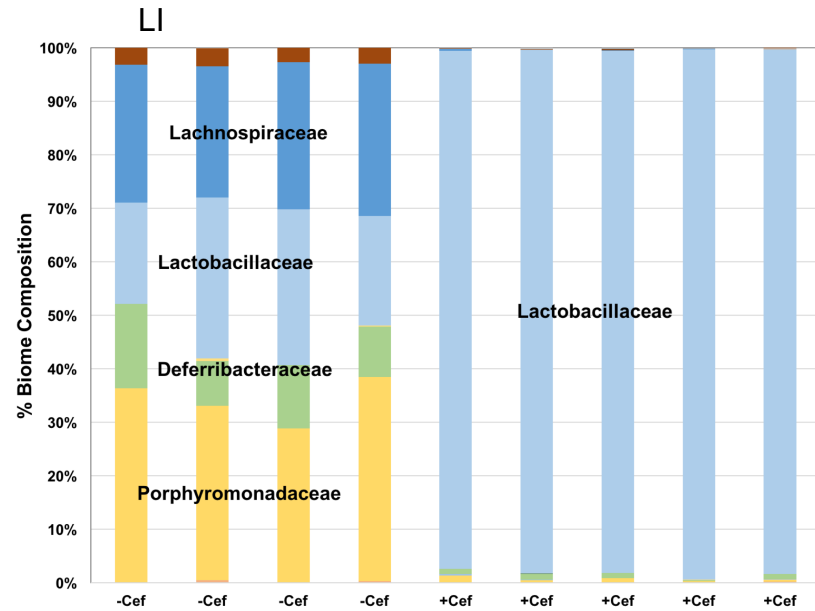
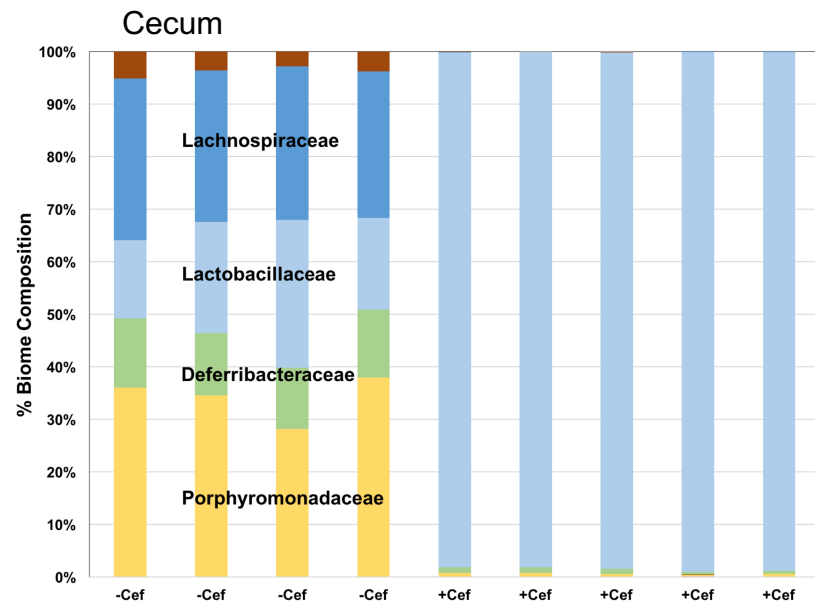
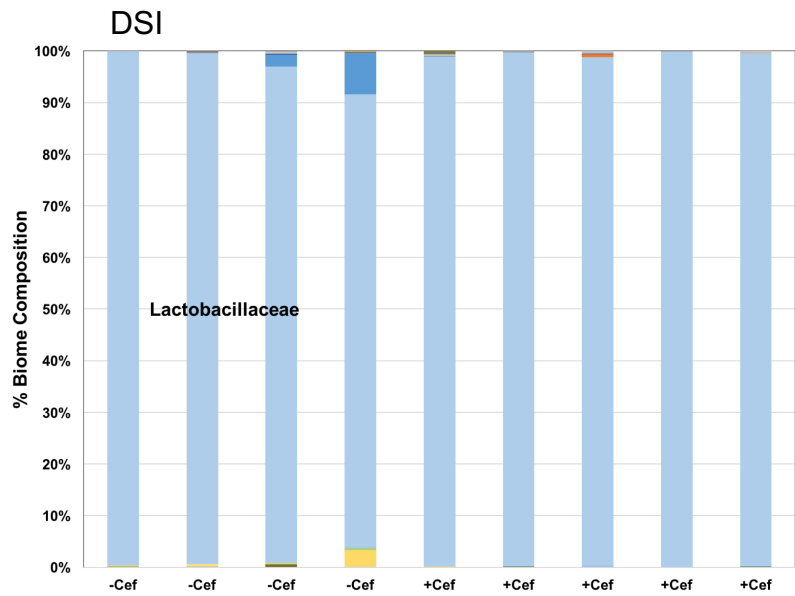


Fig. S2. Relative abundance of bacterial families (in percentage) in the intestinal tracts of defined flora mice in response to ceftriaxone treatment. Defined flora mice (lacking enterococci) were treated with either saline or ceftriaxone and euthanized at day 4 post-first dose of ceftriaxone administration. 16S rRNA gene sequencing was performed with DNA extracted from the intestinal tissues and relative abundance of bacterial families was determined and represented in percentage. *Lactobacillaceae* was found as the dominant taxa in the DSI of these mice before and after ceftriaxone treatment and in the cecum and LI after ceftriaxone administration.

Table S1. List of qRT-PCR primers to determine copy number of bacterial 16S rRNA genes or host transcripts

Gene	Primer	Sequence	Primer conc. (nM)	Annealing temp (°C)
Universal	UniF340	5'-ACTCCTACGGGAGGCAGCAGT-3'	100	63
	UniR514	5'-ATTACCGCGGCTGCTGGC-3'		
Cryptdin-1	Crypt-1 FWD	5'-TCAAGAGGCTGCAAAGGAAGAGAAC-3'	200	60
	Crypt-1 REV	5'-TGGTCTCCATGTTTCAGCGACAGC-3'		
RegIIIy	RegIIIy-FWD	5'-CCTCAGGACATCTTGTGTCTGTGCTC-3'	150	62
	RegIIIy-REV	5'-TCCACCTCTGTTGGGTTTCATAGCC-3'		
pLysozyme (pLys)	pLys-FWD	5'-GCCAAGGTCTAACAATCGTTGTGAGTTG-3'	150	62
	pLys-REV	5'-CAGTCAGCCAGCTTGACACCACG-3'		
Muc2	Muc2-Fwd	5'-GCTGACGAGTGGTTGGTGAATG-3'	400	60
	Muc2-Rev	5'-GATGAGGTGGCAGACAGGAGAC-3'		
ZO-1	ZO-1 Fwd	5'-CCACCTCTGTCCAGCTCTTC-3'	200	60
	ZO-1 Rev	5'-CACCGGAGTGATGGTTTTCT-3'		
JAM-A	JAM-A Fwd	5'-CTGATCTTTGACCCCGTGAC-3'	400	56
	JAM-A Rev	5'-ACCAGACGCCAAAAATCAAG-3'		
TNF- α	TNF- α Fwd	5'-TCCCAGGTTCTCTTCAAGGGA-3'	300	60
	TNF- α Rev	5'-GGTGAGGAGCACGTAGTCGG-3'		
GAPDH	GAPDH Fwd	5'-GAGAACTTTGGCATTGTGG-3'	400	60
	GAPDH Rev	5'-ATGCAGGGATGATGTTCTG-3'		
β -actin	β -actin Fwd	5'-GGCTGTATTCCCCTCCATCG-3'	400	56
	β -actin Rev	5'-CCAGTTGGTAACAATGCCATGT-3'		

Table S2. List of intestinal bacterial OTUs whose relative abundance was increased in ceftriaxone treated mice compared with the saline treated controls. Log change represents ratio of relative abundance of bacterial OTUs in ceftriaxone versus saline treated mice converted to a log scale. OTU identification information is included in parentheses following individual bacterial OTUs. P-values were calculated using Students' t-test. False discovery rate (q-values) are included to minimize identification of false positives during microbiome analyses.

OTU (DSI)-Day 4	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Enterococcus (GBKMun50)	1.7105234	0.636929233	2.918019	0.7772225	1.207495138	0.006278	0.012491
Lactobacillus (Unc00cd4)	2.1059925	0.882466804	4.125314	0.1495342	2.019315236	0.002311	0.005714
Lachnospiraceae (Unc04psg)	0	0	0.23921	0.2957954	0.239209908	0.041454	0.047633
OTU (DSI)-Day 8	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Enterococcus (GBKMun50)	0.2689741	0.537948209	1.315896	0.5629018	1.046922284	0.026166	0.033886
Bacteroides (GG7Spe54)	0.38636798	0.041565533	0.946175	0.3423907	0.559806743	0.020966	0.028843
Bifidobacterium (GWMPse11)	0.75081651	0.552096577	3.12227	0.4792632	2.371453291	0.000482	0.001974
Streptococcus (S53Therm)	0.48235648	0.385303399	1.172027	0.227287	0.689670545	0.027694	0.035326
Blautia (Unc01277)	0.9265062	0.377770924	2.700325	0.3224475	1.773818886	0.000301	0.001451
Lachnospiraceae (Unc01474)	0.74258963	0.150075423	1.205254	0.3011088	0.462664391	0.02355	0.031444
Lachnospiraceae (Unc01672)	1.47771494	0.34646108	2.102796	0.1561232	0.625081498	0.028927	0.03628
Clostridiales (Unc01dte)	0	0	0.768584	0.5048353	0.768583981	0.02717	0.034997
Lachnospiraceae (Unc01kix)	1.12977944	0.136184811	1.794126	0.3943489	0.664346175	0.016321	0.025484
Turicibacter (Unc05n97)	2.58233104	0.469163406	3.520004	0.6270846	0.937672566	0.037336	0.045102
Lachnospiraceae (Unc41630)	1.56173476	0.26714071	2.184129	0.2231601	0.622394641	0.009993	0.016835
Alistipes (Unc44045)	0	0	0.715176	0.4826585	0.715176013	0.029564	0.036592
Lachnoclostridium (UncO6361)	0.14285135	0.285702698	1.056582	0.5547901	0.913730211	0.01803	0.025997
Lachnospiraceae (Unc89386)	0.51098797	0.341176744	1.192683	0.3543646	0.68169502	0.023295	0.031209
OTU (DSI)-Day 14	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Enterococcus (GBKMun50)	0.14436989	0.250055982	1.268096	0.4854756	1.123726328	0.005075	0.010135
Lachnoclostridium (UncO6361)	0.98198336	0.45898131	2.558811	0.9109636	1.576827752	0.017733	0.025832
Bacteroidales (Unc00kyo)	0	0	0.586232	0.4111267	0.586232091	0.033266	0.040116
Lachnospiraceae (Unc02k9w)	0	0	0.721499	0.4820754	0.72149931	0.028659	0.03628

Table S2 cont.

OTU (Cecum)-Day 4	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Enterococcus (GBKMun50)	0.5569895	0.599941888	2.87370907	0.9807967	2.316719547	7.73E-05	0.000653887
Bacteroides (GG7Spe54)	0.3316087	0.213684387	3.80531242	0.2577674	3.473703679	1.58862E-12	6.31598E-10
Lactobacillus (Unc00cd4)	0.2912832	0.15186304	3.54702331	0.4366218	3.25574012	6.81238E-10	6.77111E-08
OTU (Cecum)-Day 8	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Enterococcus (GBKMun50)	0	0	1.6902668	0.5953879	1.6902668	0.003154664	0.007293807
Bifidobacterium (GWMPse11)	0.1625165	0.325032961	2.34108752	0.5471132	2.178571038	0.000196948	0.001118599
Enterobacter (GWTAmn51)	0	0	1.81573983	0.7620556	1.815739829	0.005973899	0.01136403
Blautia (Unc01277)	0	0	2.98028609	0.5003121	2.980286094	0.000183653	0.001118599
Lachnoclostridium (Unc02rbn)	2.1158569	0.1915214	2.78551167	0.1975817	0.669654764	0.001558876	0.004334135
Turicibacter (Unc05n97)	2.1794384	0.430668459	3.03073302	0.4108864	0.851294645	0.021938861	0.02991761
Ruminococcaceae (Unc69200)	0.086128	0.172256063	1.14628808	0.7149396	1.06016005	0.027199921	0.03523511
OTU (Cecum)-Day 14	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Enterococcus (GBKMun50)	0.1590985	0.275566719	0.7633595	0.3786363	0.604260977	0.04372785	1

OTU (LI)-Day 4	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Enterococcus (GBKMun50)	0.718051	0.661289418	2.991569	1.0735021	2.273517963	0.000215359	0.001150764
Bacteroides (GG7Spe54)	0.3062003	0.222331919	3.763798	0.1901905	3.457598174	5.23975E-11	6.77111E-08
Lactobacillus (Unc00cd4)	0.387171	0.256160963	3.67041	0.3715078	3.283239261	3.47236E-11	6.90265E-09
OTU (LI)-Day 8	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Enterococcus (GBKMun50)	0	0	1.772004	0.6244737	1.772003608	0.00316017	0.007293807
Bifidobacterium (GWMPse11)	0.2276964	0.455392874	2.466465	0.717913	2.238768927	0.000843812	0.00295076
Enterobacter (GWTAmn51)	0	0	2.145996	0.6023088	2.145996392	0.001344871	0.003948508
Blautia (Unc01277)	0.2945333	0.252883314	3.260945	0.4125014	2.966412107	4.81706E-06	0.000137127
Enterorhabdus (Unc01zsp)	0.808694	0.226549077	1.365798	0.2917835	0.557104452	0.014571505	0.02219651
Lachnociostriidium (Unc02rbn)	1.9367194	0.163813745	2.522531	0.3245784	0.585812007	0.012179356	0.01960416
Turicibacter (Unc05n97)	2.4349946	0.402085192	3.158246	0.3490635	0.723251291	0.029206208	0.03640033
Ruminococcaceae (Unc69200)	0	0	1.359381	0.8969931	1.359380633	0.027562287	0.03523511
OTU (LI)-Day 14	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Enterococcus (GBKMun50)	0	0	1.073979	0.4754974	1.073978953	0.007228654	0.01314479
Lachnoclostridium (UncO6361)	0.3197894	0.280945886	2.71652	1.7133014	2.396731077	0.0337221	0.04110619

Table S3. List of intestinal bacterial OTUs whose relative abundance was decreased in ceftriaxone treated mice compared with the saline treated controls. Log change represents ratio of relative abundance of bacterial OTUs in ceftriaxone versus saline treated mice converted to a log scale. OTU identification information is included in parentheses following individual bacterial OTUs. P-values were calculated using Students' t-test. False discovery rate (q-values) are included to minimize identification of false positives during microbiome analyses.

OTU (DSI)-Day 4	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Bacteroidales (Unc00h6h)	1.903469002	0.232229561	0.2274835	0.453757248	-1.675985523	5.28E-07	1.85261E-05
Desulfovibrio (Unc00hwx)	2.609076228	0.474642296	0.3513406	0.63135655	-2.257735641	3.01E-06	6.63907E-05
Bacteroidales (Unc00krl)	3.34333574	0.21656796	0.9787363	1.204736588	-2.364599487	3.05E-04	0.001450681
Parasutterella (Unc00mei)	2.687716346	0.673675191	0.6954127	1.382158831	-1.992303661	2.87E-03	0.006758691
Bacteroidales (Unc00mpd)	2.323606912	0.368220485	0.3569782	0.621191826	-1.966628698	3.60E-06	9.57575E-05
Lachnospiraceae (Unc011hu)	1.519066303	0.852006234	0	0	-1.519066303	7.24E-03	0.01314479
Bacteroidales (Unc16803)	2.938475753	0.081057149	0.8378664	0.939329002	-2.100609387	1.42E-04	0.000959561
Bacteroidales (Unc58327)	2.657737561	0.329257041	0.2814836	0.446787998	-2.376253934	2.93E-08	1.7745E-06
Bacteroidales (Unc74089)	1.989978136	0.674383474	0.4864203	0.719298192	-1.503557791	1.59E-03	0.00455285
OTU (DSI)-Day 8	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Erysipelotrichaceae (GJ1Bac11)	2.2380248	0.277808975	0.2335762	0.320763168	-2.004448622	2.27E-05	0.000280466
Bacteroidales (Unc00h6h)	1.682768629	0.373167694	0.0911723	0.203867402	-1.591596355	1.04E-03	0.003436248
Desulfovibrio (Unc00hwx)	2.043531683	0.670631716	0.1099	0.245743805	-1.933631713	7.03E-03	0.01298555
Lachnospiraceae (Unc00v94)	1.933665423	0.27070271	0.1872238	0.418645141	-1.746441624	1.51E-04	0.000960488
Bacteroidales (Unc04v7r)	2.660149024	0.269729924	0.7001482	0.681893188	-1.960000778	1.52E-03	0.004274294
Bacteroidales (Unc05qy3)	3.000531663	0.270592721	1.2985508	0.337177336	-1.701980878	6.71E-05	0.000634958
Lachnospiraceae (Unc05sfe)	3.025879159	0.290783358	1.1109734	0.179887862	-1.914905719	1.14E-04	0.000823453
Bacteroidales (Unc16803)	2.580692994	0.191582769	1.0597937	0.142721968	-1.520899341	2.40E-05	0.000308802
Bacteroidales (Unc37317)	2.86300901	0.364295986	1.1143897	0.393973652	-1.748619356	2.66E-04	0.001373313
Bacteroidales (Unc38684)	2.075661231	0.168112965	0.2148485	0.299752124	-1.86081275	1.37E-05	0.000237059
OTU (DSI)-Day 14	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Lachnospiraceae (Unc00v94)	1.759697821	0.067599403	0	0	-1.759697821	4.92E-04	0.002031418
Marvinbryantia (Unc03ak3)	2.368753267	0.241944124	0.2350101	0.525498536	-2.133743177	2.61E-04	0.001315611
Bacteroidales (Unc16803)	2.740684286	0.126416769	0.5627257	0.586356504	-2.177958606	7.29E-04	0.002655886
Bacteroidales (Unc38684)	2.125151897	0.321828123	0.4237682	0.436965109	-1.7013837	1.03E-03	0.003293779
Bacteroidales (Unc58327)	2.707766342	0.098835175	0.3901495	0.569459068	-2.317616807	5.75E-04	0.002310727
Bacteroidales (Unc74089)	2.276943301	0.067684258	0.3453248	0.357609791	-1.931618519	1.60E-04	0.00099693

Table S3. cont.

OTU (Cecum)-Day 4	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Helicobacter (JT1Muris)	2.489590135	1.400518503	0.08809796	0.136566543	-2.401492176	8.37E-03	0.01445993
Desulfovibrio (Unc00hwx)	2.295180115	0.613536789	0.38377764	0.787906318	-1.911402471	1.71E-04	0.001048587
Bacteroidales (Unc00kr)	2.767204326	0.16013478	1.11702056	1.382126195	-1.65018377	7.09E-03	0.01298555
Prevotellaceae (Unc00md9)	2.735566011	0.600953373	0.07395968	0.111081084	-2.661606334	9.30E-05	0.00078073
Bacteroidales (Unc00mpd)	2.075233205	0.287059084	0.57702305	0.904913545	-1.498210154	8.83E-04	0.003084058
Lachnospiraceae (Unc011hu)	1.648966048	0.813737806	0	0	-1.648966048	4.23E-03	0.009068162
Bacteroidales (Unc58327)	1.906272422	0.809708278	0.19687468	0.344131202	-1.709397747	2.49E-03	0.006007972
OTU (Cecum)-Day 8	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Bacteroides (GG7Spe54)	2.635345198	0.063527264	0.32122508	0.350382985	-2.314120119	7.91E-05	0.000655185
Bacteroidales (Unc00h6h)	1.776650518	0.223759905	0	0	-1.776650518	5.43E-04	0.002136713
Lachnospiraceae (Unc00qjy)	2.830650916	0.185852948	0.05037913	0.112651152	-2.780271789	2.67E-06	6.25163E-05
Lachnospiraceae (Unc00v94)	1.633981098	0.201628876	0	0	-1.633981098	5.11E-04	0.002031418
Lachnospiraceae (Unc00zhm)	1.929935992	0.140019664	0	0	-1.929935992	1.05E-04	0.00078073
Roseburia (Unc013hc)	2.21459729	0.322192937	0.06974159	0.155946929	-2.144855703	2.16E-04	0.001150764
Oscillibacter (Unc0149o)	1.870297607	0.101619527	0.17252723	0.38578262	-1.697770374	3.21E-04	0.001477075
Lachnospiraceae (Unc014mj)	2.414007276	0.107651277	0.74879739	1.150873643	-1.665209883	3.14E-02	0.03850314
Ruminococcaceae (Unc018ao)	1.566169385	0.219749533	0	0	-1.566169385	7.48E-04	0.002655886
Clostridiales (Unc01w9e)	1.68061033	0.375848803	0	0	-1.68061033	2.95E-03	0.007293807
Blautia (Unc02e8n)	1.656456101	0.112229301	0	0	-1.656456101	8.54E-05	0.000725239
Blautia (Unc03n9t)	1.881445902	0.167806437	0.05037913	0.112651152	-1.831066775	7.24E-06	0.000137127
Anaeroplasm (Unc04puc)	1.913133825	0.299515777	0.05037913	0.112651152	-1.862754698	4.67E-04	0.001974028
Bacteroidales (Unc04v7r)	2.297849987	0.186801949	0	0	-2.297849987	1.47E-04	0.000960488
Bacteroidales (Unc05qy3)	2.913958363	0.105935999	0.20195122	0.192699868	-2.712007141	8.46E-08	1.3279E-05
Lachnospiraceae (Unc05sfe)	2.769337577	0.076693231	0.70628916	1.114165622	-2.063048417	1.42E-02	0.02191742
Bacteroidales (Unc16803)	2.508905615	0.300180724	0.50790293	0.146683475	-2.00100269	2.10E-04	0.001150764
Lachnospiraceae (Unc18783)	2.178100263	0.166586715	0	0	-2.178100263	1.23E-04	0.000855724
Bacteroidales (Unc37317)	2.703319465	0.203371482	0.10522066	0.235280556	-2.598098802	5.02E-07	1.85261E-05
Ruminiclostridium (Unc38007)	1.906195689	0.100762221	0.37476022	0.585030265	-1.531435466	3.65E-03	0.008157034
Bacteroidales (Unc38684)	1.961058868	0.19362373	0.05037913	0.112651152	-1.910679742	2.22E-05	0.000273194
Lachnospiraceae (Unc66707)	1.824452662	0.149975821	0	0	-1.824452662	1.52E-04	0.000960488
Lachnospiraceae (Unc70129)	1.879097187	0.24536773	0	0	-1.879097187	6.04E-04	0.002310727
Lachnospiraceae (Uncide598)	2.217052671	0.161496521	0	0	-2.217052671	1.06E-04	0.00078073
OTU (Cecum)-Day 14	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Lachnospiraceae (CsrSpec9)	1.536737926	0.196595896	0	0	-1.536737926	5.41E-03	0.01059782
Lachnospiraceae (Unc00v94)	1.605536428	0.09184442	0	0	-1.605536428	1.09E-03	0.003436248
Lachnospiraceae (Unc00zhm)	2.137564077	0.049222901	0	0	-2.137564077	1.77E-04	0.001058205
Oscillibacter (Unc0149o)	1.723252289	0.468940285	0	0	-1.723252289	2.38E-02	0.03144438
Alistipes (Unc01fwp)	2.544897423	0.306692279	0.21432705	0.197643169	-2.330570374	1.26E-03	0.003863649
Clostridiales (Unc01w9e)	1.953447505	0.239084145	0	0	-1.953447505	4.96E-03	0.01002282
Lachnospiraceae (Unc02pki)	1.58836377	0.102323187	0	0	-1.58836377	1.38E-03	0.003948508
Marvinbryantia (Unc03ak3)	2.289011257	0.058730994	0	0	-2.289011257	2.19E-04	0.001150764
Lachnospiraceae (Unc03imb)	2.480897998	0.756664972	0	0	-2.480897998	2.96E-02	0.03659198
Blautia (Unc03n9t)	2.359500529	0.139951635	0	0	-2.359500529	1.17E-03	0.003596677
Lachnospiraceae (Unc03t7x)	1.809289697	0.218430977	0	0	-1.809289697	4.82E-03	0.00983391
Anaeroplasm (Unc04puc)	2.359223339	0.149757783	0	0	-2.359223339	1.34E-03	0.003902841
Bacteroidales (Unc16803)	2.471632278	0.179624713	0.13039854	0.198939421	-2.341233742	1.90E-05	0.00027062
Lachnospiraceae (Unc18783)	2.137922167	0.082001497	0	0	-2.137922167	4.90E-04	0.001974028
Lachnospiraceae (Unc32085)	1.608329119	0.2980807	0.05611169	0.125469543	-1.552217434	7.09E-03	0.01298555
Lachnospiraceae (Unc36755)	1.513792301	0.227483942	0	0	-1.513792301	7.44E-03	0.01341012
Bacteroidales (Unc38684)	1.617588463	0.212387546	0	0	-1.617588463	5.70E-03	0.01094277
Bacteroidales (Unc58327)	2.185653604	0.167064867	0	0	-2.185653604	1.94E-03	0.005131439
Lachnospiraceae (Unc70129)	1.66209729	0.110283432	0	0	-1.66209729	1.46E-03	0.004184662

Table S3. cont.

OTU (LI)-Day 4	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Helicobacter (JT1Muris)	1.825817649	1.214099873	0.1173481	0.15366658	-1.708469502	1.80E-02	0.02618725
Desulfovibrio (Unc00hwx)	2.108196118	0.479851789	0.252277	0.75683098	-1.855919124	6.08E-05	0.000589158
Bacteroidales (Unc00krl)	2.946747511	0.341249352	1.0849407	1.43324033	-1.861806805	4.35E-03	0.00919635
Prevotellaceae (Unc00md9)	2.994755478	0.362854096	0.0619255	0.12319226	-2.932829942	1.94E-06	5.34953E-05
Bacteroidales (Unc00mpd)	2.299510398	0.488111003	0.6258156	0.93681024	-1.673694831	6.34E-04	0.002351603
Lachnospiraceae (Unc011hu)	1.624069931	0.684772899	0.0248111	0.07443326	-1.599258845	2.21E-03	0.005595958
Bacteroidales (Unc58327)	2.074833862	0.661842813	0.2048259	0.41862924	-1.870008004	3.23E-04	0.001521651
OTU (LI)-Day 8	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Bacteroides (GG7Spe54)	3.036439947	0.218969658	0.1617687	0.36172573	-2.874671282	2.56E-06	6.25163E-05
Erysipelotrichaceae (GJ1Bac11)	1.818922968	0.511547875	0.0769916	0.17215844	-1.741931371	4.30E-03	0.009133044
Bacteroidales (Unc00h6h)	2.138285606	0.110205052	0	0	-2.138285606	3.76E-05	0.000404548
Lachnospiraceae (Unc00qjy)	2.540523759	0.53634478	0	0	-2.540523759	2.49E-03	0.006007972
Lachnospiraceae (Unc00zhm)	1.880463326	0.164082087	0	0	-1.880463326	1.82E-04	0.001058205
Roseburia (Unc013hc)	1.532401099	0.834070812	0	0	-1.532401099	3.49E-02	0.04392226
Oscillibacter (Unc0149o)	1.599076691	0.176805388	0.0528304	0.11813229	-1.546246324	2.22E-05	0.000273194
Lachnospiraceae (Unc014mj)	2.092124488	0.323882312	0.5139518	1.00807585	-1.578172725	2.17E-02	0.02981082
Ruminococcaceae (Unc01yw3)	1.540508715	0.301090975	0	0	-1.540508715	1.99E-03	0.005376124
Blautia (Unc03n9t)	1.516189805	0.370156011	0	0	-1.516189805	3.81E-03	0.008872273
Anaeroplasm (Unc04puc)	1.833794937	0.230485432	0.0769916	0.17215844	-1.75680334	2.95E-05	0.000325624
Bacteroidales (Unc04v7r)	2.455890211	0.225876501	0	0	-2.455890211	2.13E-04	0.001150764
Bacteroidales (Unc05qy3)	3.100096068	0.047323372	0.0939512	0.2100813	-3.006144855	2.02E-06	5.34953E-05
Lachnospiraceae (Unc05sfe)	2.498661443	0.270942193	0.8376895	0.81585411	-1.660971958	7.78E-03	0.01380633
Bacteroidales (Unc16803)	2.745597915	0.424940449	0.2329531	0.32795453	-2.51264486	1.03E-04	0.00078073
Lachnospiraceae (Unc18783)	1.819724667	0.217616677	0	0	-1.819724667	4.65E-04	0.001954876
Bacteroidales (Unc37317)	3.048147726	0.085038488	0.0528304	0.11813229	-2.995317359	8.67E-10	1.7745E-06
Bacteroidales (Unc38684)	2.003770256	0.259114619	0.0939512	0.2100813	-1.909819044	2.72E-05	0.000308802
Lachnospiraceae (Unc66707)	1.725732477	0.166798013	0	0	-1.725732477	2.47E-04	0.001274455
Lachnospiraceae (Unc70129)	1.559149149	0.309734588	0	0	-1.559149149	2.09E-03	0.005387323
Lachnospiraceae (Unide598)	1.930173642	0.391861896	0	0	-1.930173642	2.22E-03	0.005595958
OTU (LI)-Day 14	Avg. Saline	St.dev. Saline	Avg. Cef	St.dev. Cef	Log change (cef vs saline)	p-value	q-value
Lachnospiraceae (Unc00myz)	3.647032542	0.0669999565	1.5901733	1.44799248	-2.05685929	3.35E-02	0.0401201
Lachnospiraceae (Unc00v94)	1.538081194	0.034024411	0	0	-1.538081194	1.63E-04	0.000997477
Lachnospiraceae (Unc00zhm)	2.233544209	0.064723646	0	0	-2.233544209	2.80E-04	0.001373313
Roseburia (Unc013hc)	1.916071587	0.021855041	0.4064874	0.57039643	-1.50958418	4.04E-03	0.008872273
Alistipes (Unc01fwp)	2.747251401	0.242556234	0.2107066	0.22126932	-2.536544803	1.22E-04	0.000855724
Clostridiales (Unc01w9e)	1.747880758	0.137916766	0	0	-1.747880758	2.07E-03	0.005376124
Lachnospiraceae (Unc02pki)	1.657221822	0.052985981	0	0	-1.657221822	3.41E-04	0.001521651
Marvinbryantia (Unc03ak3)	2.341864134	0.066468763	0.0449847	0.10058879	-2.296879462	3.12E-08	4.20339E-06
Lachnospiraceae (Unc03imb)	2.482135584	0.718594299	0.1380963	0.12828198	-2.344039253	2.80E-02	0.03605721
Blautia (Unc03n9t)	2.423462245	0.088810273	0	0	-2.423462245	4.47E-04	0.001929768
Lachnospiraceae (Unc03t7x)	1.673319575	0.331306412	0	0	-1.673319575	1.28E-02	0.0203657
Anaeroplasm (Unc04puc)	2.299172535	0.09914121	0	0	-2.299172535	6.19E-04	0.002344619
Lachnospiraceae (Unc05sfe)	2.201634333	0.586926403	0.4183286	0.52158084	-1.783305735	1.30E-02	0.02057513
Bacteroidales (Unc16803)	2.640770358	0.090833952	0.3488702	0.22195045	-2.291900121	1.61E-06	5.34953E-05
Lachnospiraceae (Unc18783)	2.071843655	0.120101704	0	0	-2.071843655	1.12E-03	0.003490595
Lachnospiraceae (Unc32085)	1.54925203	0.291465156	0	0	-1.54925203	1.16E-02	0.01889013
Lachnospiraceae (Unc36755)	1.534865919	0.179870739	0	0	-1.534865919	4.55E-03	0.009626327
Bacteroidales (Unc38684)	1.886799807	0.236006063	0	0	-1.886799807	5.17E-03	0.01023568
Bacteroidales (Unc58327)	2.297618285	0.069687345	0	0	-2.297618285	3.07E-04	0.001477075
Lachnospiraceae (Unc70129)	1.620448288	0.070883135	0	0	-1.620448288	6.37E-04	0.002351603
Bacteroidales (Unc74089)	1.988679145	0.077938249	0.3558723	0.1180314	-1.632806878	5.59E-07	4.91766E-05
Lachnospiraceae (Unc89386)	2.104632166	0.193771771	0.5898628	0.72734781	-1.514769388	7.45E-03	0.0136161