

Table S1. Mean relative abundance of taxa correspondence for OTUs identified in fecal samples in 7 hospitalized neonatal foals before and after broad-spectrum antimicrobial treatment (ampicillin + gentamicin/amikacin. IV).

#OTU	Ta	Te	Td
Phyla %			
Actinobacteria	4.48	3.03	6.35
Bacteroidetes	7.55	11.37	7.66
Firmicutes	48.19	38.93	61.58
Fusobacteria	0.14	3.44	0.82
Proteobacteria	31.56	38.31	11.44
TM7	0.12	0.08	0.68
Verrucomicrobia	1.79	3.95	10.28
Other	0.28	0.03	0.37
Unassigned; Other	5.89	0.86	0.82
Familia %			
Aerococcaceae	1.88	0.01	0.05
Bacteroidaceae	4.78	11.21	4.72
Bifidobacteriaceae	0.46	1.83	1.99
Carnobacteriaceae	0.12	0.34	0.95
Chitinophagaceae	0.51	0.01	0.00
Clostridiaceae	6.29	2.45	8.32
Members of Clostridiales	0.90	1.17	3.42
Comamonadaceae	0.51	0.00	0.00
Coriobacteriaceae	0.53	0.88	2.94
Corynebacteriaceae	0.46	0.01	0.05
Dermabacteraceae	0.35	0.00	0.00
Enterobacteriaceae	17.55	37.64	10.85
Enterococcaceae	13.23	13.75	7.98
Eubacteriaceae	0.03	0.04	0.37
Erysipelotrichaceae	1.60	1.26	2.20
F16	0.09	0.08	0.68
Fusobacteriaceae	0.14	3.44	0.82
Lachnospiraceae	7.07	4.94	13.00

Lactobacillaceae	1.63	2.56	7.42
Microbacteriaceae	0.68	0.02	0.07
Micrococcaceae	0.31	0.04	1.14
[Mogibacteriaceae]	0.56	0.59	2.69
Moraxellaceae	0.99	0.01	0.04
[Odoribacteraceae]	0.01	0.01	0.41
Peptococcaceae	0.01	0.00	0.01
Peptostreptococcaceae	3.56	1.14	2.47
Pseudomonadaceae	6.40	0.19	0.00
Porphyromonadaceae	0.16	0.09	1.68
Rhizobiaceae	0.67	0.01	0.02
Rikenellaceae	0.09	0.03	0.55
Ruminococcaceae	3.80	3.03	6.47
Sphingobacteriaceae	1.05	0.00	0.00
Sphingomonadaceae	1.16	0.00	0.00
Streptococcaceae	5.32	7.46	4.64
Streptomycetaceae	0.77	0.00	0.01
Turicibacteraceae	0.46	0.00	0.00
Verrucomicrobiaceae	1.76	3.94	10.22
Xanthomonadaceae	2.14	0.01	0.01
Other	6.11	0.94	2.97
Unassigned; Other	5.89	0.86	0.82
Genera %			
<i>Acinetobacter</i>	0.95	0.00	0.02
<i>Aerococcus</i>	1.54	0.01	0.01
<i>Akkermansia</i>	1.76	3.94	10.22
<i>Arthrobacter</i>	0.22	0.02	0.96
<i>Bacteroides</i>	4.76	11.21	4.67
<i>Bifidobacterium</i>	0.46	1.83	1.99
<i>Blautia</i>	1.11	0.31	1.35
<i>Brachybacterium</i>	0.35	0.00	0.00
<i>Butyricimonas</i>	0.01	0.01	0.34
<i>Clostridium</i>	1.34	0.20	3.90

Members of Clostridiaceae	4.90	2.22	2.42
Members of Coriobacteriaceae	0.13	0.07	0.47
<i>Coprococcus</i>	0.28	0.06	0.79
<i>Corynebacterium</i>	0.46	0.01	0.05
<i>Curtobacterium</i>	0.50	0.01	0.02
<i>Delftia</i>	0.34	0.00	0.00
<i>Dorea</i>	0.67	0.41	3.52
<i>Eggerthella</i>	0.16	0.79	2.26
Members of Enterobacteriaceae	17.08	35.94	9.73
<i>Enterococcus</i>	13.23	13.75	7.98
<i>Epulopiscium</i>	2.40	0.01	0.07
<i>Erwinia</i>	0.39	0.00	0.00
Members of Erysipelotrichaceae	0.85	0.51	1.42
<i>Eubacterium</i>	0.66	0.69	0.51
Members of F16	0.09	0.08	0.68
<i>Faecalibacterium</i>	0.77	0.01	0.01
<i>Fusobacterium</i>	0.14	3.44	0.82
<i>Klebsiella</i>	0.07	1.35	1.06
Members of Lachnospiraceae	0.81	0.80	3.04
<i>Lactobacillus</i>	1.62	2.54	7.41
Members of Mogibacteriaceae	0.55	0.59	2.64
<i>Oscillospira</i>	0.49	1.01	1.52
<i>Parabacteroides</i>	0.16	0.09	1.67
Members of Peptostreptococcaceae	3.56	1.14	2.45
<i>Pseudomonas</i>	6.33	0.18	0.00
Members of Rikenellaceae	0.09	0.03	0.55
<i>[Ruminococcus]</i>	1.41	3.27	4.16
<i>Ruminococcus</i>	0.81	0.24	1.47
Members of Ruminococcaceae	1.71	1.75	3.38
<i>Sarcina</i>	0.05	0.03	1.94
<i>Sphingobacterium</i>	0.61	0.00	0.00
<i>Sphingomonas</i>	0.98	0.00	0.00
<i>Sediminibacterium</i>	0.51	0.01	0.00

<i>Stenotrophomonas</i>	1.43	0.01	0.01
<i>Streptococcus</i>	5.30	7.44	4.61
<i>Streptomyces</i>	0.77	0.00	0.01
<i>Turicibacter</i>	0.46	0.00	0.00
Members of Xanthomonadaceae	0.63	0.00	0.00
Other	9.31	1.89	5.24
Unassigned; Other	5.89	0.86	0.82

Ta: time (hours) of antimicrobial treatment start; Te: end of antimicrobial treatment; Td: day of hospital discharge.