

**Supplementary Table 4.** Relative abundance (median (%) and range) of the most abundant taxa identified in healthy horses and survival and non-surviving diarrheic horses.

Phylum	Family	Genus	Healthy n = 36	Survivors n = 27	Non-Survivors n = 28
Bacteroidetes	Unclass.	Unclass.	20.5 <sup>a</sup> [12.8 – 35.5]	1.4 <sup>b</sup> [0.014 – 15.9]	0.94 <sup>b</sup> [0.011 – 14.0]
Firmicutes	Lachnospiraceae	Unclass.	8.7 <sup>a</sup> [1.5 – 20.8]	5.2 <sup>a</sup> [0.43 – 18.5]	4.9 <sup>a</sup> [0.023 – 32.2]
Firmicutes	Ruminococcaceae	Unclass.	6.8 <sup>a</sup> [1.4 – 12.5]	3.6 <sup>a</sup> [0.22 – 20.5]	1.6 <sup>a</sup> [0.021 – 22.8]
Firmicutes	Clostridiales Unclass.	Unclass.	5.4 <sup>a</sup> [0.75 – 8.4]	5.3 <sup>a</sup> [0.023 – 21.2]	4.9 <sup>a</sup> [0.014 – 14.0]
Verrucomicrobia	5_family_incertae_sedis	5_genus_incertae_sedis	6.7 <sup>a</sup> [1.7 – 16.5]	1.0 <sup>b</sup> [0.0041 – 9.5]	0.15 <sup>b</sup> [0.0051 – 4.2]
Firmicutes	Streptococcaceae	<i>Streptococcus</i>	0.026 <sup>a</sup> [0 – 7.5]	0.64 <sup>b</sup> [0.01 – 34.7]	1.9 <sup>b</sup> [0.0059 – 54.1]
Firmicutes	Clostridiaceae_1	<i>Clostridium_sensu_stricto</i>	0.058 <sup>a</sup> [0.00090 – 1.6]	1.8 <sup>b</sup> [0.0008 – 66.4]	0.37 <sup>b</sup> [0.0032 – 43.5]
Firmicutes	Enterococcaceae	<i>Enterococcus</i>	0.0014 <sup>a</sup> [0 – 0.026]	0.18 <sup>b</sup> [0.0017 – 17.4]	0.30 <sup>b</sup> [0.0048 – 94.5]
Firmicutes	Unclass.	Unclass.	2.8 <sup>a</sup> [0.43 – 5.8]	2.0 <sup>a</sup> [0.015 – 7.8]	1.5 <sup>a</sup> [0.012 – 8.4]
Bacteroidetes	Bacteroidales Unclass	Unclass.	4.7 <sup>a</sup> [0.49 – 6.9]	0.20 <sup>b</sup> [0.0077 – 14.0]	0.18 <sup>b</sup> [0.0023 – 1.9]
Verrucomicrobia	Verrucomicrobiaceae	<i>Akkermansia</i>	0.061 <sup>a</sup> [0.0026 – 1.8]	0.65 <sup>ab</sup> [0.0085 – 26.5]	0.65 <sup>b</sup> [0.0007 – 46.2]
Spirochaetes	Spirochaetaceae	<i>Treponema</i>	3.4 <sup>a</sup> [1.1 – 7.9]	0.12 <sup>b</sup> [0.0008 – 2.9]	0.055 <sup>b</sup> [0.0007 – 2]
Firmicutes	Lactobacillaceae	<i>Lactobacillus</i>	0.069 <sup>a</sup> [0.0034 – 1.1]	0.15 <sup>b</sup> [0.0063 – 33.3]	0.50 <sup>ab</sup> [0.0051 – 9.4]
Proteobacteria	Moraxellaceae	<i>Acinetobacter</i>	0.016 <sup>a</sup> [0.0006 – 8.8]	0.025 <sup>a</sup> [0.0007 – 40.3]	0.011 <sup>a</sup> [0 – 27.8]
Actinobacteria	Coriobacteriaceae	Unclass.	0.45 <sup>a</sup> [0.040 – 4.2]	1.7 <sup>ab</sup> [0.0048 – 9.5]	1.2 <sup>b</sup> [0.0014 – 17.4]
Verrucomicrobia	Unclass.	Unclass.	0.14 <sup>a</sup> [0.013 – 0.37]	0.0039 <sup>a</sup> [0 – 0.27]	0.0006 <sup>a</sup> [0 – 0.12]
Proteobacteria	Enterobacteriaceae	Unclass.	0.0051 <sup>a</sup> [0 – 0.14]	0.085 <sup>b</sup> [0 – 38.7]	0.17 <sup>b</sup> [0.0046 – 18.8]
Firmicutes	Eubacteriaceae	<i>Mogibacterium</i>	0.21 <sup>a</sup> [0.020 – 2.0]	1.8 <sup>ab</sup> [0.0033 – 12.0]	0.68 <sup>b</sup> [0.0022 – 14.6]
Firmicutes	Lachnospiraceae	<i>Blautia</i>	0.16 <sup>a</sup> [0.013 – 2.2]	1.0 <sup>a</sup> [0.0071 – 46.0]	0.23 <sup>a</sup> [0.0028 – 4.7]

Unclass, Unclassified taxonomy from the from the earlier identified taxonomic group. P-values obtained using Steel Dwass test for multiple comparisons and corrected with Benjamini and Hochberg's false discovery rate analysis (FDR). P-values with a FDR adjustment of < .05 were considered significant. Superscript letters indicate within row comparisons that are significantly different.