

1 **Expression of immune regulatory genes correlates with the abundance**
2 **of specific Clostridiales and Verrucomicrobia species in the equine**
3 **ileum and cecum**

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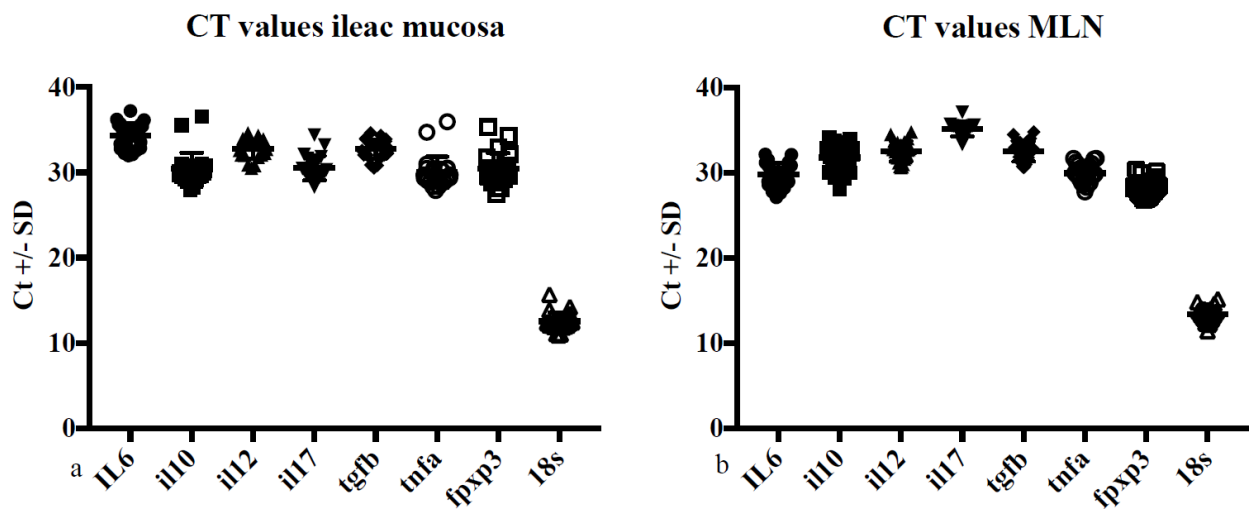
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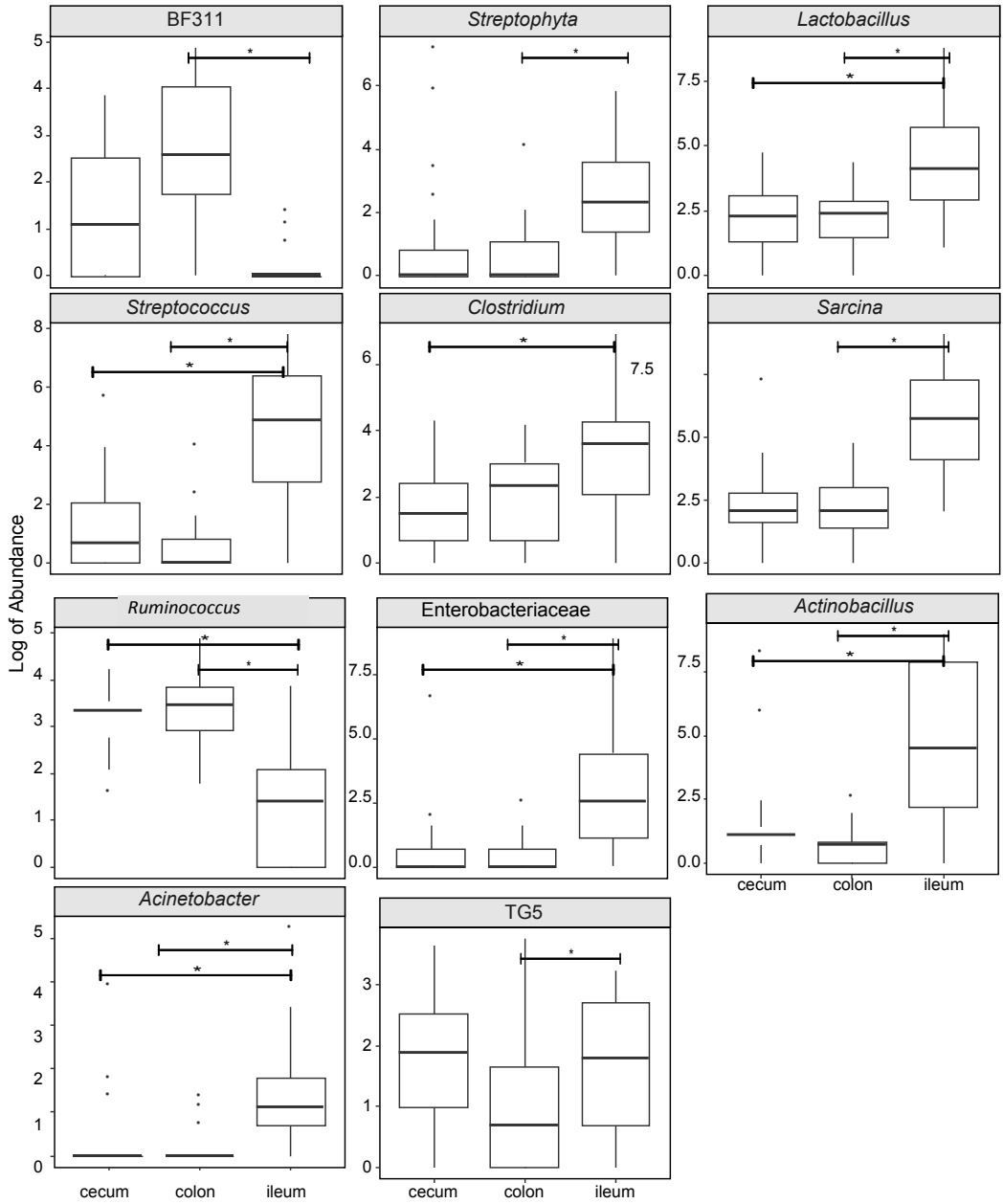
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 41 Supplementary figure S1: Gene-expression of *foxp3*, *tnfa*, *tgfb*, *il17*, *il12*, *il10*, and *il6* in ileal
 42 mucosa (a) and mesenteric lymph nodes (b) measured by qPCR and expressed as mean Ct +/- SD.
 43 In horse number 1 and 2 ileal expression of *il12*, *il17*, and *tgfb* and *il6*, *il1,2* and *il17* respectively
 44 were not detected for unexplained reasons nor was expression of *il17* in horse 24. In the colon *il17*
 45 expression was not detected in horses number 4, 5, 11, 17, 20, 22, 23, and 24.

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65 Supplementary Figure S2:

66 Figures shows box plots of species found to differ significantly between the ileum, cecum, and
 67 colon. Significantly different abundances were found between the ileum and the cecum and the
 68 ileum and colon, denoted by * (ANCOM, FDR $p < 0.05$). There were no major differences
 69 observed between the colon and the cecum microbiota composition. Box plots show log abundance
 70 (ANCOM analysis) on amplicon sequencing of 16S rRNA gene (V3-V4 region) within three
 71 sections of horse gastrointestinal tract (box limits represent upper and lower quartiles, bold line the
 72 median, whiskers the 1.5 IQR and dots the extremes).

