



**Supplementary Figure 1: Abundances of bacterial genera identified in fecal samples collected from feral horses on Sable Island, Nova Scotia, Canada, using 16S rRNA sequencing.** Samples from eight horses were divided into aliquots, stored at both -20°C and -80°C for four years, and characterized using 16S amplicon sequencing. Taxonomy was assigned to amplicon sequence variants (ASVs), and abundances were made proportional then aggregated to the family level. Genera with low abundances (< 1% within a sample) were pooled for clarity.