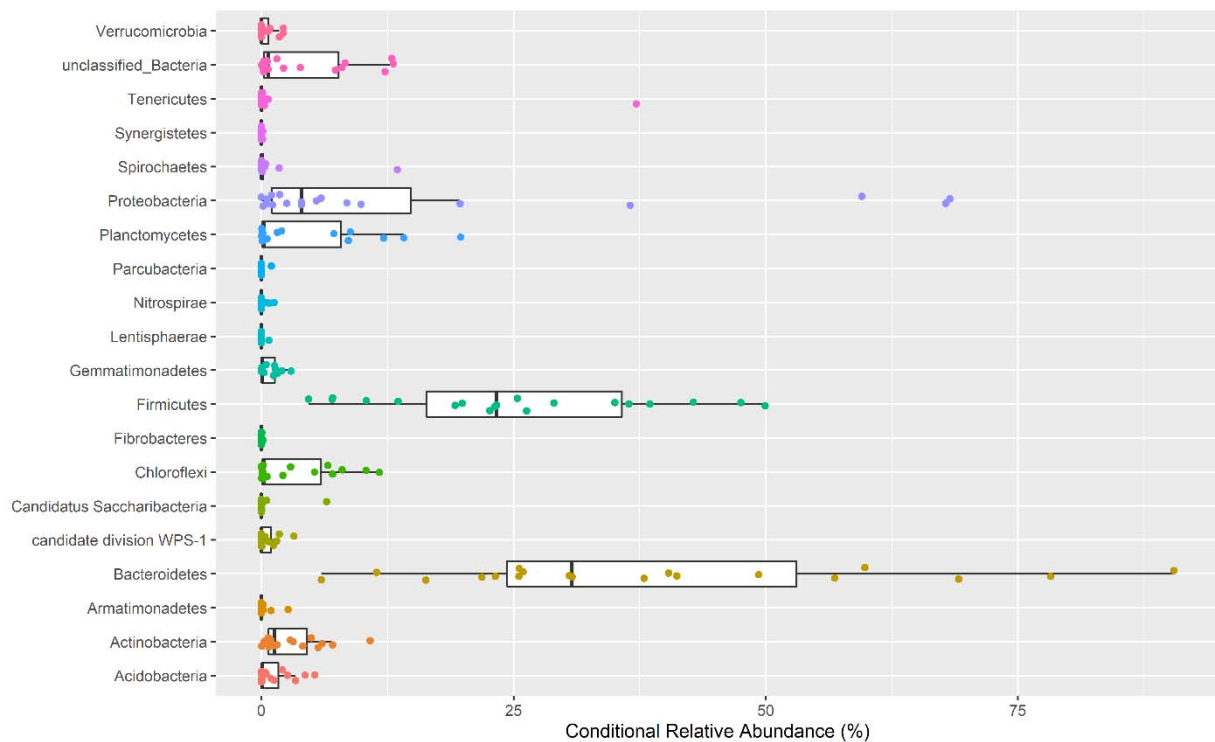


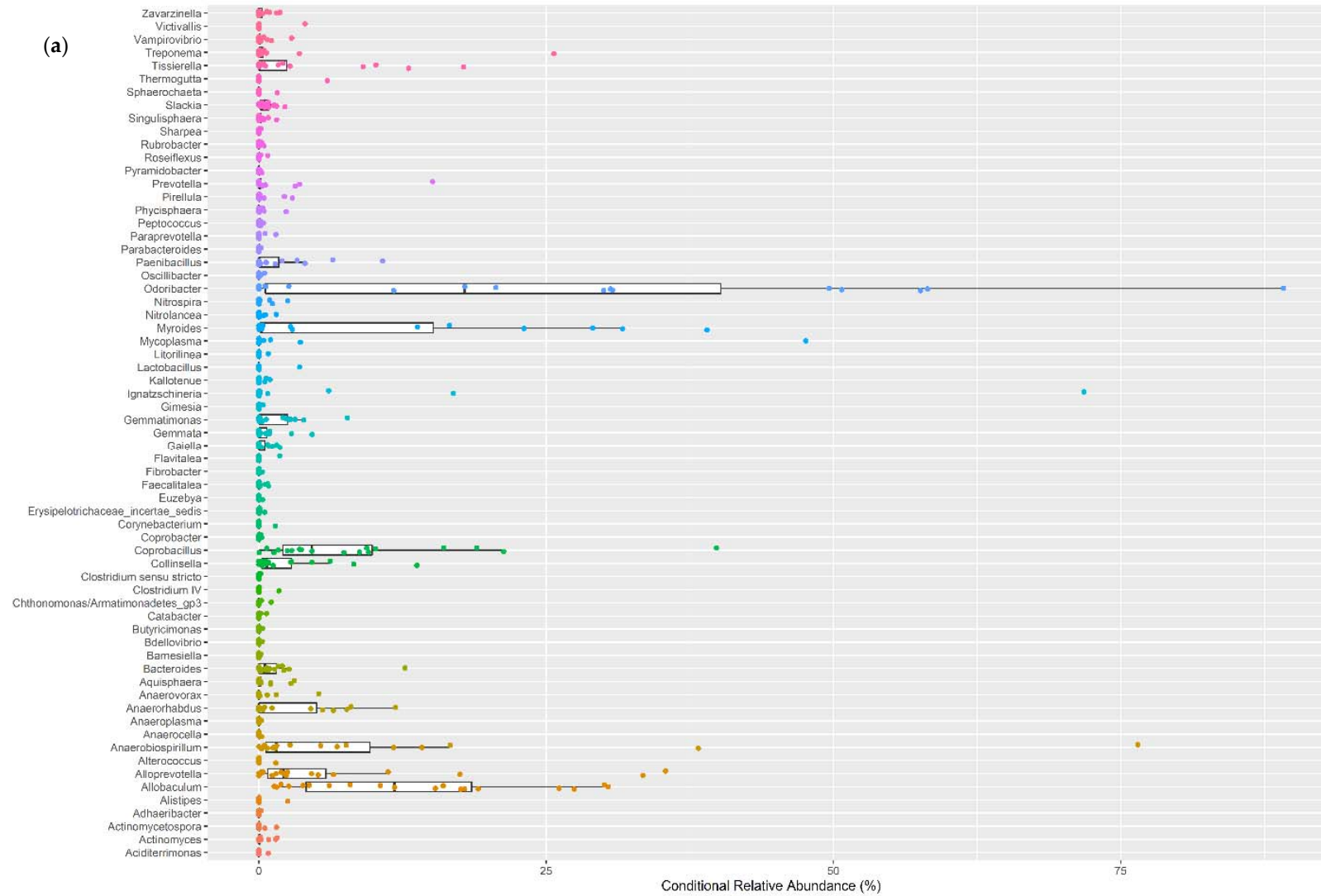
# Fecal Microbial Diversity of Coyotes and Wild Hogs in Texas Panhandle, USA

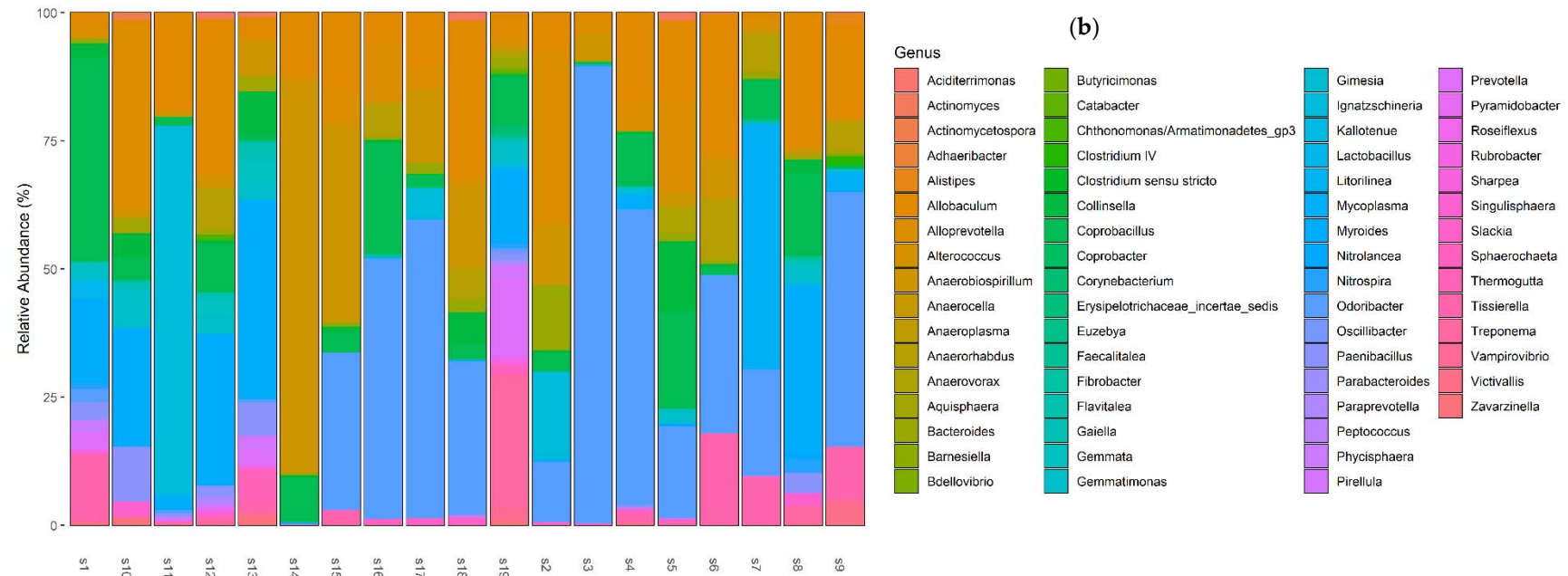
Babafela Awosile, Chiquito Crasto, Md. Kaisar Rahman, Ian Daniel, SaraBeth Boggan, Ashley Steuer and Jason Fritzler

## Supplementary Figures

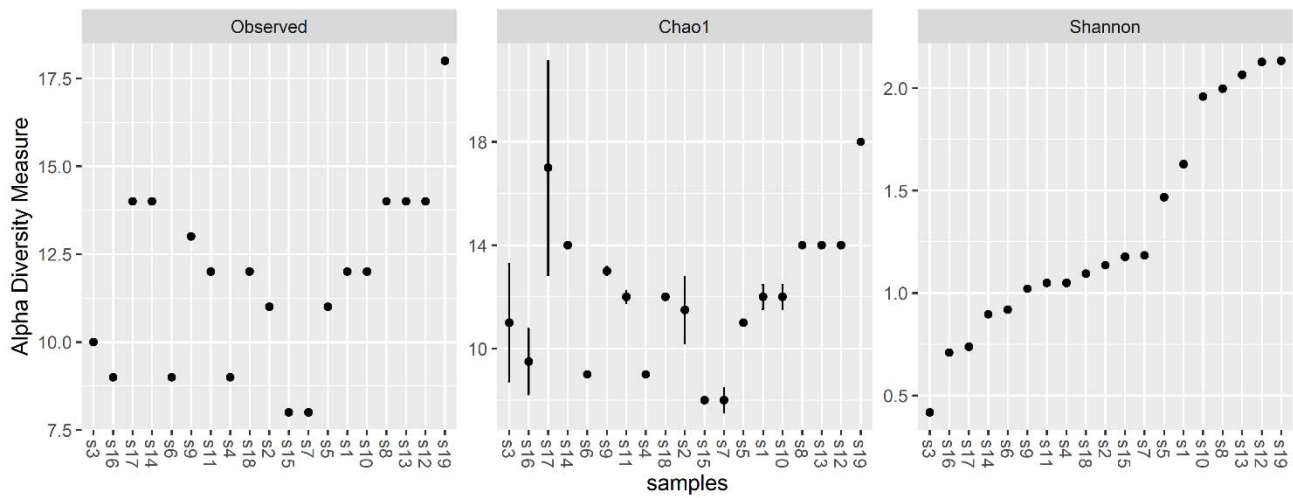


**Figure S1.** Boxplot distribution of relative abundance (%) of each bacteria phylum observed between the 19 Coyote samples. The plot showed *Bacteroidetes*, *Firmicutes*, and *Proteobacteria* as the predominant phyla in fecal microbiome of coyotes in Texas panhandle.

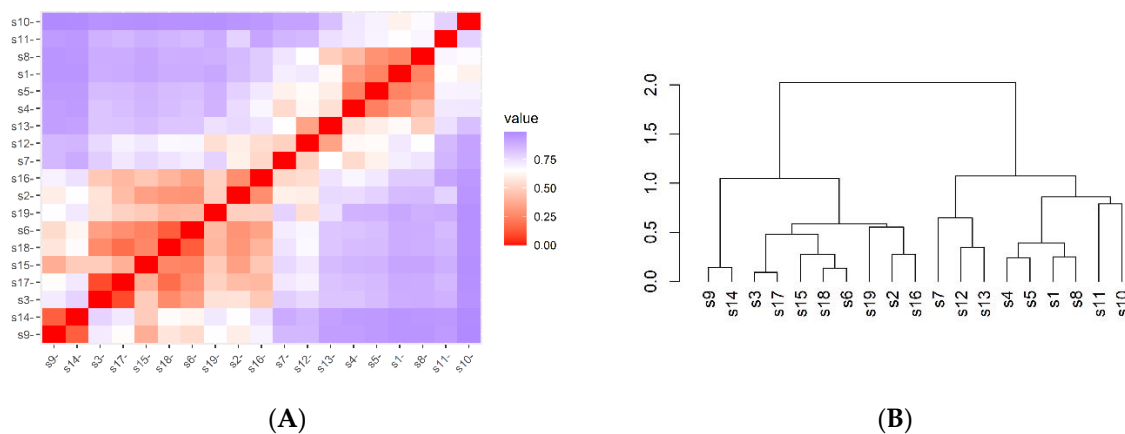




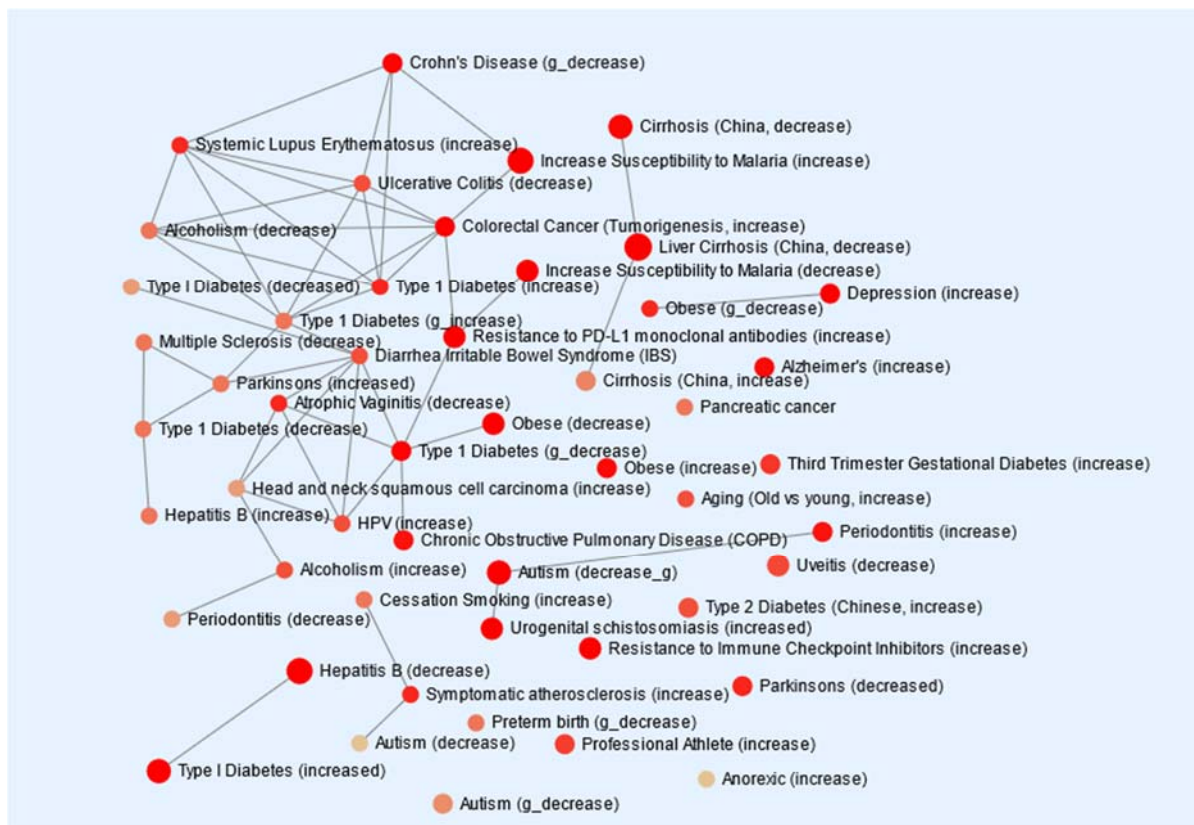
**Figure S2. (a)** Boxplot distribution of genus level relative abundance (%) observed in each 19 Coyote samples. The plot showed *Odoribacter* spp., *Allobaculum* spp., *Coprobacillus* spp., and *Alloprevotella* spp. as the dominant genera in fecal microbiome of coyotes in Texas panhandle. Data on unclassified genera were included in this plot. **(b):** Boxplot distribution of genus level relative abundance (%) observed in each 19 Coyote samples. The plot showed *Odoribacter* spp., *Allobaculum* spp., *Coprobacillus* spp., and *Alloprevotella* spp. as the dominant genera in fecal microbiome of coyotes in Texas panhandle. Data on unclassified genera were included in this plot.



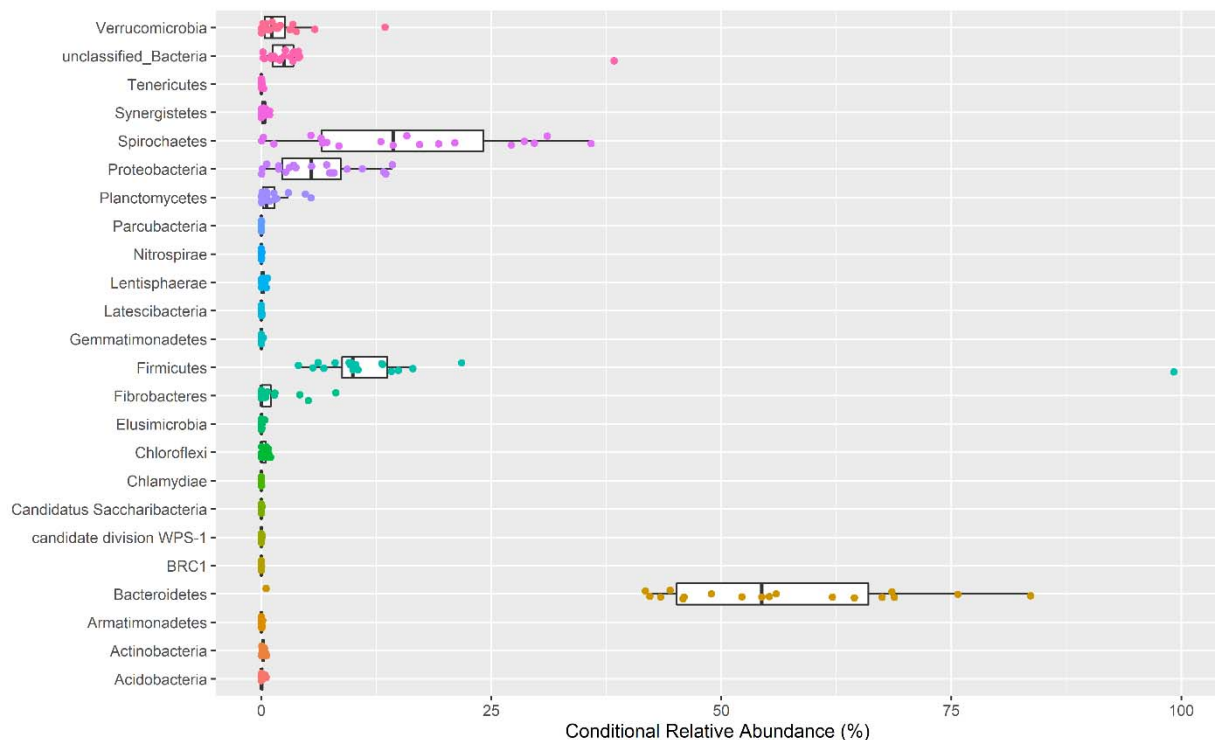
**Figure S3.** Alpha Diversity Index using Chao's and Shannon Indices as a measure of microbial richness and evenness within each of 19 coyote samples. Higher alpha diversity measure represents sample(s) with greater microbial species richness and/or evenness.



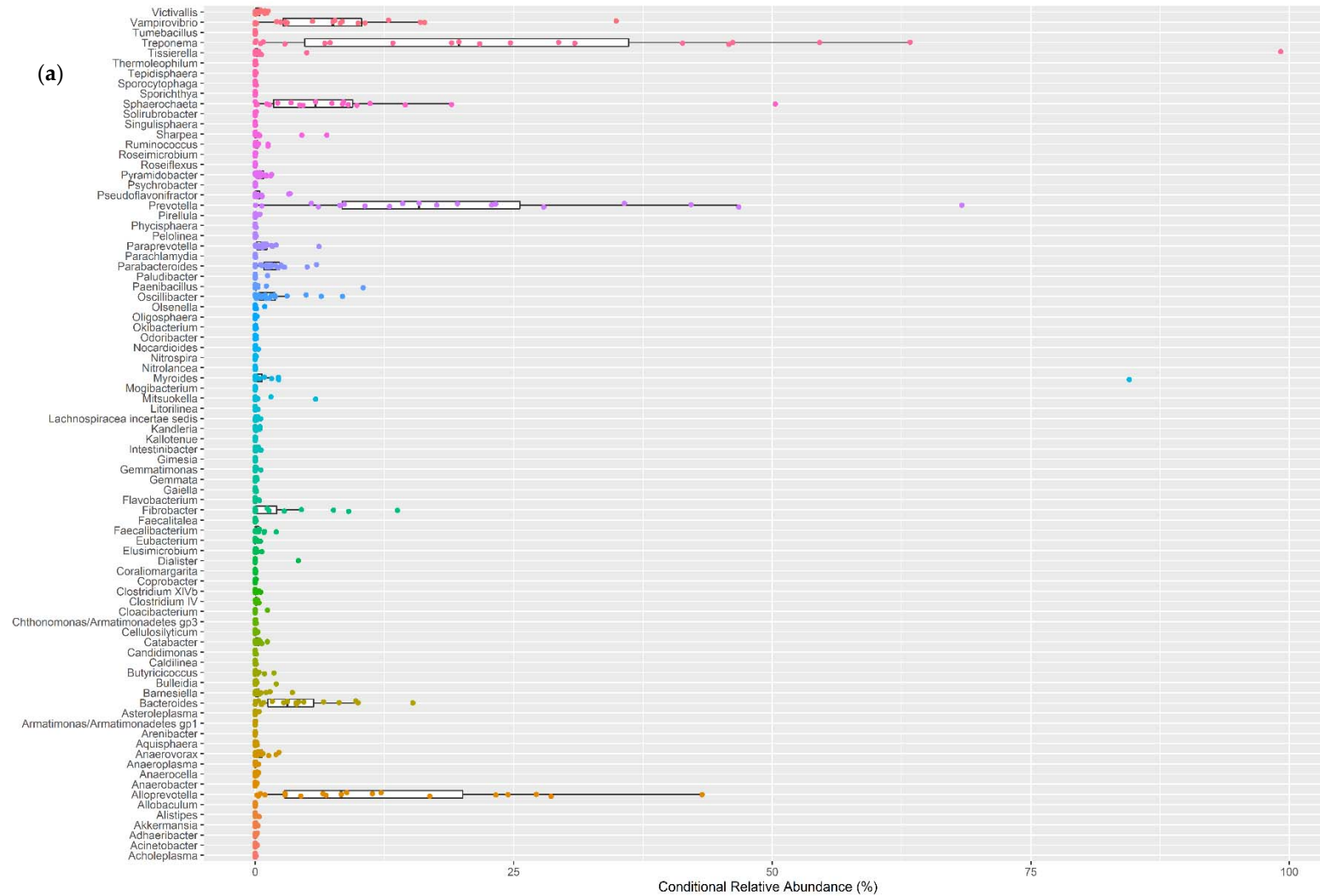
**Figure S4.** (A) Bray-Curtis Dissimilarity matrix and (B) hierarchical clustering dendrogram as measures of beta-diversity index of Coyote fecal microbiota. (A) Value close to 1 showed two sample are dissimilar in microbial diversity and value close to 0 show correlation and similarity between two samples. (B) the higher the Ward's minimum variance value between two samples, the farther the clustering compared to another one or more samples.



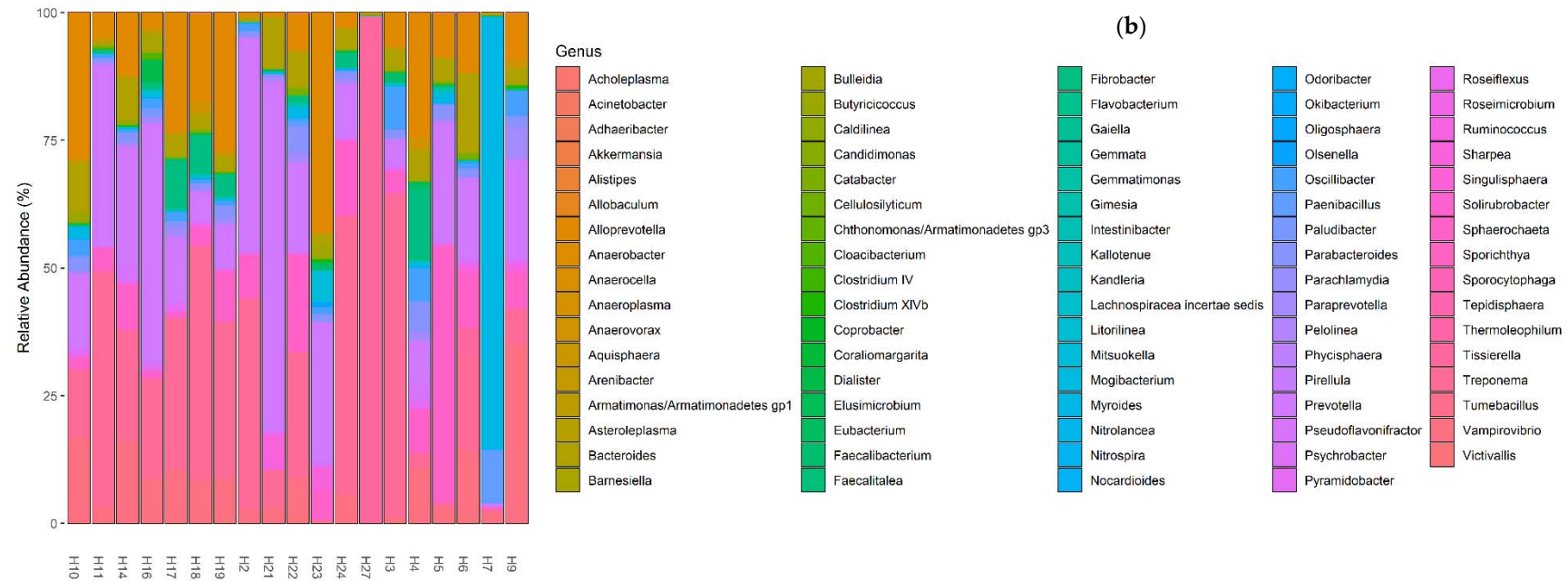
**Figure S5.** Predictive functional profile of coyote microbiota in relation to certain human related diseases. Each node represents a taxon set with its color based on its p-value and its size based on the number of hits in the query. Two taxon sets are connected by an edge if the number of shared taxon hits is over 20% of the total number of their combined taxa (Chong et al., 2020).



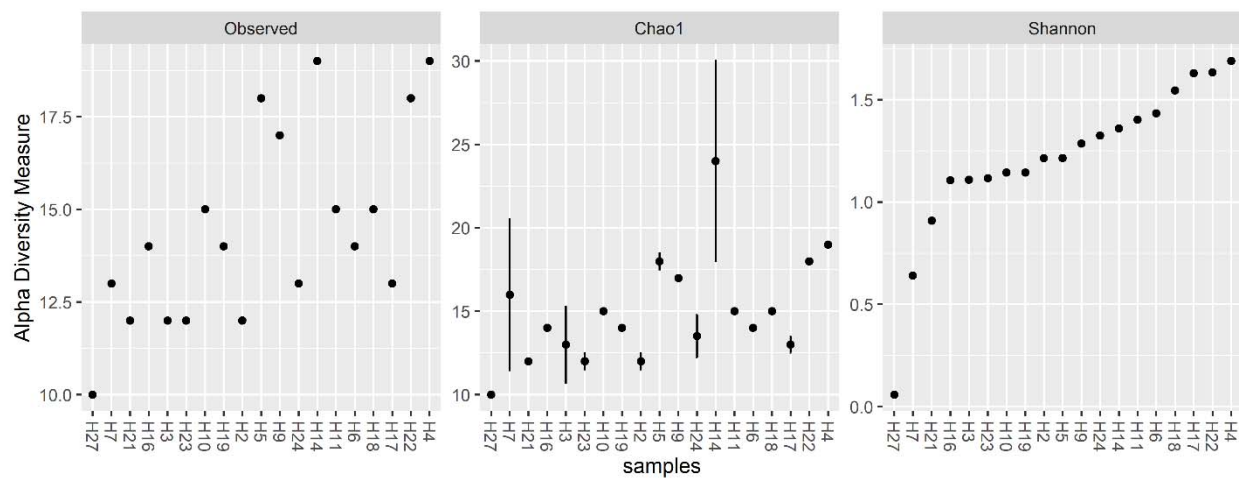
**Figure S6.** Boxplot distribution of relative abundance (%) of each bacteria phylum observed between the 19 wild hog samples. The plot showed *Bacteroidetes*, *Firmicutes*, and *Spirochaetes* as the predominant phyla in fecal microbiome of wild hogs in Texas panhandle.



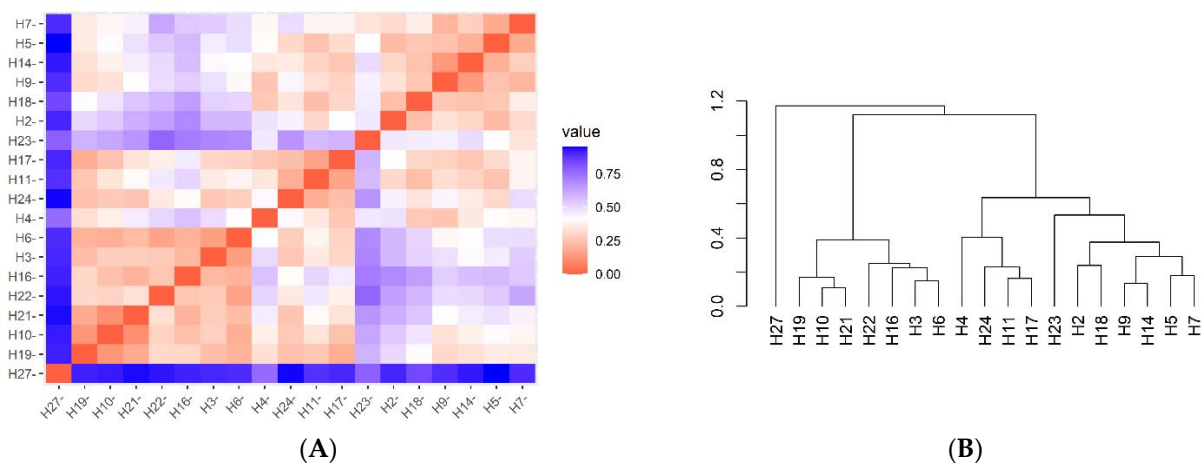




**Figure 7.** (a) Boxplot distribution of genus level relative abundance (%) observed in each 19 wild hog samples. The plot showed *Treponema*, *Prevotella*, *Alloprevotella*, *Vampirovibrio*, *Sphaerochaeta*, and *Bacteroides*, as the dominant genera in fecal microbiome of wild hogs in Texas panhandle. Data on unclassified genera were included in this plot. (b). Barplot distribution of genus level relative abundance (%) observed in each 19 wild hog samples. The plot showed *Treponema*, *Prevotella*, *Alloprevotella*, *Vampirovibrio*, *Sphaerochaeta*, and *Bacteroides*, as the dominant genera in fecal microbiome of wild hogs in Texas panhandle. Data on unclassified genera were included in this plot.

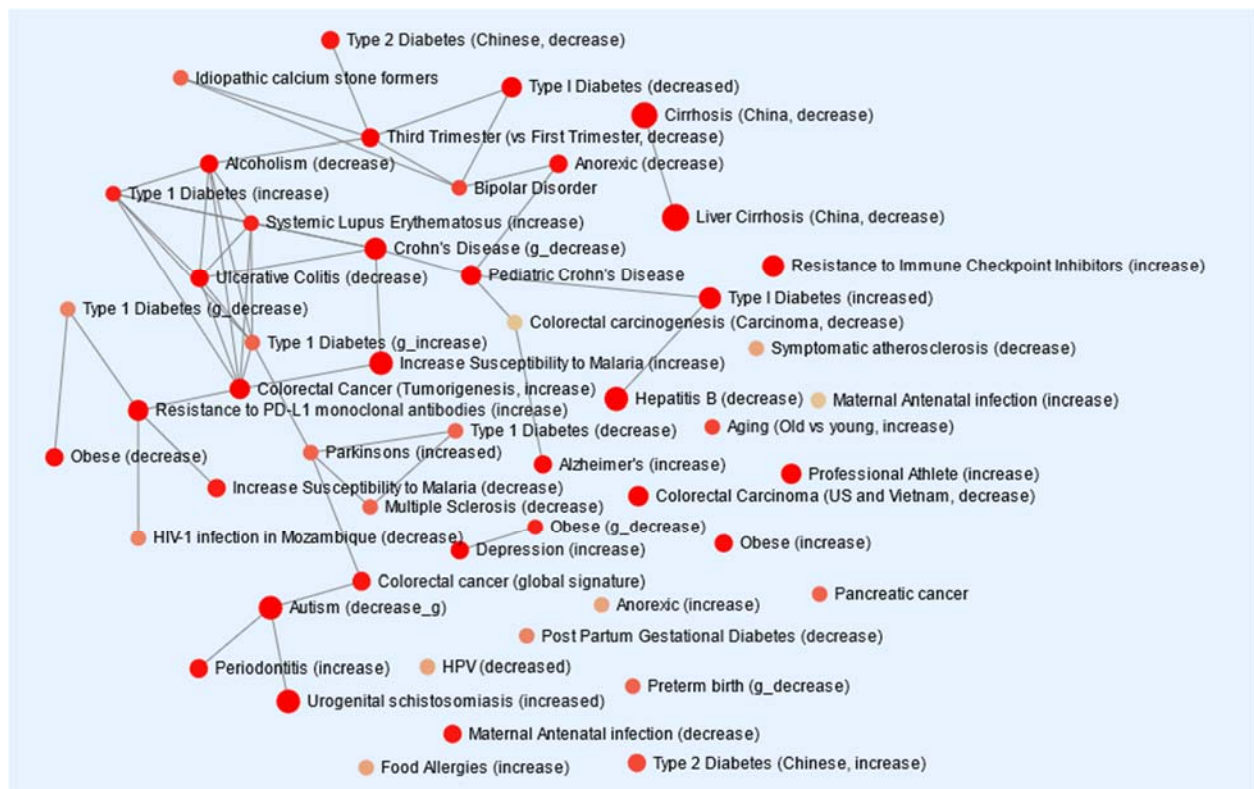


**Figure S8.** Alpha Diversity Index using Chao's and Shannon Indices as a measure of microbial richness and evenness within each of 19 wild hog samples. Higher alpha diversity measure represents sample(s) with greater microbial species richness and/or evenness.



**Figure S9.** (A) Bray-Curtis Dissimilarity matrix and (B) hierarchical clustering dendrogram as measures of beta-diversity index of wild hog fecal microbiota. (A) Value close to 1 showed two sample are dissimilar in microbial diversity and value close to 0 show correlation and similarity between two samples. (B) the higher the Ward's minimum variance value between two samples, the farther the clustering compared to another one or more samples.





**Figure S10.** Predictive functional profile of wild hog microbiota in relation to certain human related diseases. Each node represents a taxon set with its color based on its p-value and its size based on the number of hits in the query. Two taxon sets are connected by an edge if the number of shared taxon hits is over 20% of the total number of their combined taxa (Chong et al., 2020).

**Table S1.** Statistically significant functional profile of coyote microbiota associated with certain human-related diseases.

Human-Related Diseases	Total	Expected	Hits	<i>p</i> -Value (Unadjusted)	* FDR-Adjusted <i>p</i> - Value	Associated Taxon Sets
Increase Susceptibility to Malaria (Increased risk)	8	0.163	5	$1.33 \times 10^{-7}$	$3.16 \times 10^{-5}$	<i>Barnesiella</i> , <i>Bacteroides</i> , <i>Odoribacter</i> , <i>Prevotella</i>
Hepatitis B (Decreased risk)	10	0.204	5	$5.81 \times 10^{-7}$	$6.91 \times 10^{-5}$	<i>Butyricimonas</i> , <i>Parabacteroides</i> ; <i>Alistipes</i> , <i>Clostridium</i> IV, <i>Bacteroides</i>
Type I Diabetes (Increased risk)	13	0.265	4	$8.80 \times 10^{-5}$	0.00698	<i>Alistipes</i> , <i>Bacteroides</i> , <i>Lactobacillus</i> , <i>Parabacteroides</i>
Autism (Decreased risk)	16	0.326	4	0.000215	0.012	<i>Prevotella</i> , <i>Treponema</i> , <i>Alloprevotella</i> , <i>Peptococcus</i>
Obese (Decreased risk)	7	0.142	3	0.000252	0.012	<i>Lactobacillus</i> , <i>Prevotella</i> , <i>Allobaculum</i>
Resistance to PD-L1 monoclonal antibodies (Increased risk)	8	0.163	3	0.000398	0.0133	<i>Bacteroides</i> , <i>Allobaculum</i> , <i>Lactobacillus</i>
Depression (Increased risk)	2	0.0407	2	0.000401	0.0133	<i>Alistipes</i> , <i>Oscillibacter</i>
Liver Cirrhosis (China, Decreased risk)	52	1.06	6	0.000446	0.0133	<i>Alistipes</i> , <i>Bacteroides</i> , <i>Lactobacillus</i> , <i>Odoribacter</i> , <i>Parabacteroides</i> , <i>Prevotella</i>

Increase Susceptibility to Malaria (Decreased risk)	10	0.204	3	0.00083	0.0198	<i>Anaeroplasma, Allobaculum, Lactobacillus</i>
Urogenital schistosomiasis (Increased risk)	10	0.204	3	0.00083	0.0198	<i>Prevotella, Alloprevotella, Peptococcus</i>
Colorectal Cancer (Tumorigenesis, Increased risk)	3	0.0611	2	0.00119	0.0257	<i>Bacteroides, Odoribacter;</i>
Resistance to Immune Checkpoint Inhibitors (Increased risk)	13	0.265	3	0.0019	0.0376	<i>Alistipes, Bacteroides, Prevotella</i>
Type 1 Diabetes (Decreased risk)	4	0.0814	2	0.00234	0.0429	<i>Prevotella, Lactobacillus</i>

\* FDR: False discovery rate.

**Table S2.** Statistically significant functional profile of wild hog microbiota associated with certain human-related diseases.

Human-Related Diseases	Total	Expected	Hits	<i>p</i> -Value (Un-adjusted)	* FDR-Adjusted <i>p</i> -Value	Associated Taxon Sets
Increase Susceptibility to Malaria (Increased risk)	8	0.179	5	$2.20 \times 10^{-7}$	$5.23 \times 10^{-5}$	<i>Barnesiella, Bacteroides, Barnesiella, Odoribacter, Prevotella</i>
Hepatitis B (Decreased risk)	10	0.224	5	$9.59 \times 10^{-7}$	$6.12 \times 10^{-5}$	<i>Bacteroides, Parabacteroides, Alistipes, Clostridium IV, Ruminococcus</i>
Urogenital schistosomiasis (Increased risk)	10	0.224	5	$9.59 \times 10^{-7}$	$6.12 \times 10^{-5}$	<i>Dialister; Acinetobacter; Prevotella, Alloprevotella, Olsenella</i>
Crohn's Disease (Decreased risk)	5	0.112	4	$1.03 \times 10^{-6}$	$6.12 \times 10^{-5}$	<i>Bacteroides, Flavobacterium, Prevotella, Faecalibacterium,</i>
Cirrhosis (China, Decreased risk)	35	0.784	7	$6.26 \times 10^{-6}$	0.000298	<i>Bacteroides, Eubacterium, Alistipes, Faecalibacterium, Parabacteroides, Odoribacter, Ruminococcus</i>
Liver Cirrhosis (China, Decreased risk)	52	1.16	8	$9.78 \times 10^{-6}$	0.000348	<i>Alistipes, Bacteroides, Eubacterium, Faecalibacterium, Odoribacter, Parabacteroides, Prevotella, Ruminococcus,</i>
Colorectal Cancer (Tumorigenesis, Increased risk)	3	0.0672	3	$1.02 \times 10^{-5}$	0.000348	<i>Bacteroides, Odoribacter, Akkermansia</i>
Autism (Decreased risk)	16	0.358	5	$1.51 \times 10^{-5}$	0.000449	<i>Prevotella, Treponema, Alloprevotella, Olsenella, Dialister</i>
Type I Diabetes (Decreased risk)	4	0.0896	3	$4.03 \times 10^{-5}$	0.00107	<i>Eubacterium, Faecalibacterium</i>
Resistance to Immune Checkpoint Inhibitors (Increased risk)	13	0.291	4	0.000129	0.0028	<i>Alistipes, Bacteroides, Prevotella</i>
Type I Diabetes (Increased risk)	13	0.291	4	0.000129	0.0028	<i>Alistipes, Bacteroides, Parabacteroides, Ruminococcus</i>
Pediatric Crohn's Disease (Increased risk)	7	0.157	3	0.000337	0.00669	<i>Bacteroides, Faecalibacterium, Ruminococcus;</i>

Depression (Increased risk)	2	0.0448	2	0.000486	0.00772	<i>Alistipes; Oscillibacter</i>
Ulcerative Colitis (Decreased risk)	2	0.0448	2	0.000486	0.00772	<i>Bacteroides, Flavobacterium</i>
Resistance to PD-L1 monoclonal antibodies (Increased risk)	8	0.179	3	0.000531	0.0079	<i>Allobaculum, Akkermansia, Bacteroides</i>
Alcoholism (Decreased risk)	3	0.0672	2	0.00144	0.0201	<i>Bacteroides; Eubacterium</i>
Colorectal Carcinoma (US and Vietnam, Decreased risk)	12	0.269	3	0.00196	0.0259	<i>Acinetobacter, Faecalibacterium, Bacteroides</i>

\* FDR: False discovery rate.