SUPPLEMENTARY MATERIAL

TABLE. S1 Indicator species analysis of disease states between humans vs. dogs resolved to genus level. Only significant indicator values (*p < 0.05*) are shown. Stat values closer to one are likely more indicative of a stronger indicator taxa for the respective disease state. No indicator species were identified for dog disease states including IBD, or healthy dogs. Indicator species belonging to numerous human IBD disease states (CD, UC, healthy) have been excluded. Indicator species for the dog disease state, acute hemorrhagic diarrhea, have been excluded. (**p < 0.05; **p < 0.01; ***p < 0.001*)

Organism	Disease State	Family	Genus	stat	p
Dog	**IBD**	N/A	N/A	N/A	N/A
	Healthy	N/A	N/A	N/A	N/A
Human	**Control**	*Lachnospiraceae*	*Lachnospira*	0.769	**
		Lachnospiraceae	*[Eubacterium] oxidoreducens group*	0.699	**
		Morganellaceae	*Proteus*	0.577	**
		Akkermansiaceae	*Akkermansia*	0.565	**
		Barnesiellaceae	*Coprobacter*	0.474	**
		Ruminococcaceae	*Phocea*	0.4714	**
		Oscillospiraceae	*UCG-007*	0.471	**
		Eggerthellaceae	-	0.471	**
		Veillonellaceae	*Megasphaera*	0.471	**
		Lachnospiraceae	*Butyrivibrio*	0.471	**
		Oscillospiraceae	*Intestinimonas*	0.471	**
		Resolved to Order *Rhodospirillales*	-	0.470	**
		Lachnospiraceae	*Anaerostignum*	0.438	**
		Lachnospiraceae	*Howardella*	0.387	*
		Peptococcaceae	*Peptococcus*	0.333	*
		Butyricicoccaceae	*UCG-009*	0.333	*
		Lachnospiraceae	*Lachnospiraceae_UCG-003*	0.333	*
		Eggerthellaceae	*CHKCI002*	0.333	*
		Eggerthellaceae	*Eggerthella*	0.333	*
		Porphyromonadaceae	*Porphyromonas*	0.333	*
		Lachnospiraceae	*GCA-900066575*	0.333	*

	Lachnospiraceae	*GCA-900066755*	0.333	*
	Lachnospiraceae	*Frisingicoccus*	0.333	*
	Oscillospirales	*Hydrogenoanaerobacterium*	0.333	*
Crohn's Disease	*Sutterellaceae*	*Sutterella*	0.512	**
	Erysipelotrichaceae	*Merdibacter*	0.447	**
	Ruminococcaceae	*Anaerotruncus*	0.447	**
	Erysipelotrichaceae	*N/A*	0.447	**
	Gastranaerophilales	*Gastranaerophilales*	0.427	*
	Lachnospiraceae	*Lactonifactor*	0.420	*
	Eggerthellaceae	*Senegalimassilia*	0.407	*
	Anaerovoracaceae	*Family_XIII_UCG-001*	0.405	*
	Desulfovibrionaceae	*Desulfovibrio*	0.395	*
Ulcerative Colitis	*Lachnospiraceae*	*Lachnospiraceae_UCG-004*	0.757	**
	Erysipelotrichaceae	*Turicibacter*	0.590	**
	Oxalobacteraceae	*Herbaspirillum*	0.522	**
	Lachnospiraceae	*Faecalimonas umbilicata*	0.522	**
	Peptostreptococcaceae	*Romboutsia*	0.512	**
	Erysipelotrichaceae	*N/A*	0.426	**
	Prevotellaceae	*Alloprevotella*	0.426	**
	Lachnospiraceae	*Hungatella*	0.426	*
	Lachnospiraceae	*Lachnospiraceae_FCS020_group*	0.426	**
	Lachnospiraceae	*Lachnospiraceae_UCG-001*	0.426	**
	Selenomonadaceae	*N/A*	0.409	*

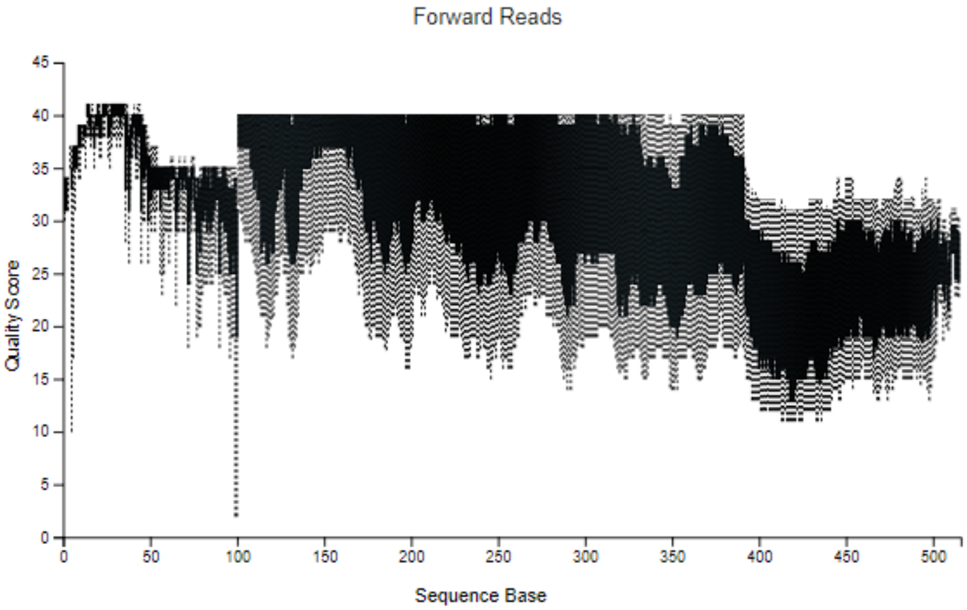

FIG. S1 QIIME2 View read-quality plot of all sequences after demultiplexing the raw data. A noticeable drop in read quality can be observed at 100 base lengths due to the inherent differences between the human and dog datasets. As the latter dataset has a maximum read length of 100 bases, the quality scores beyond only assess the reads from the human dataset. At 100 bases, the media quality score is 27, which has an inferred error rate of under 1%.

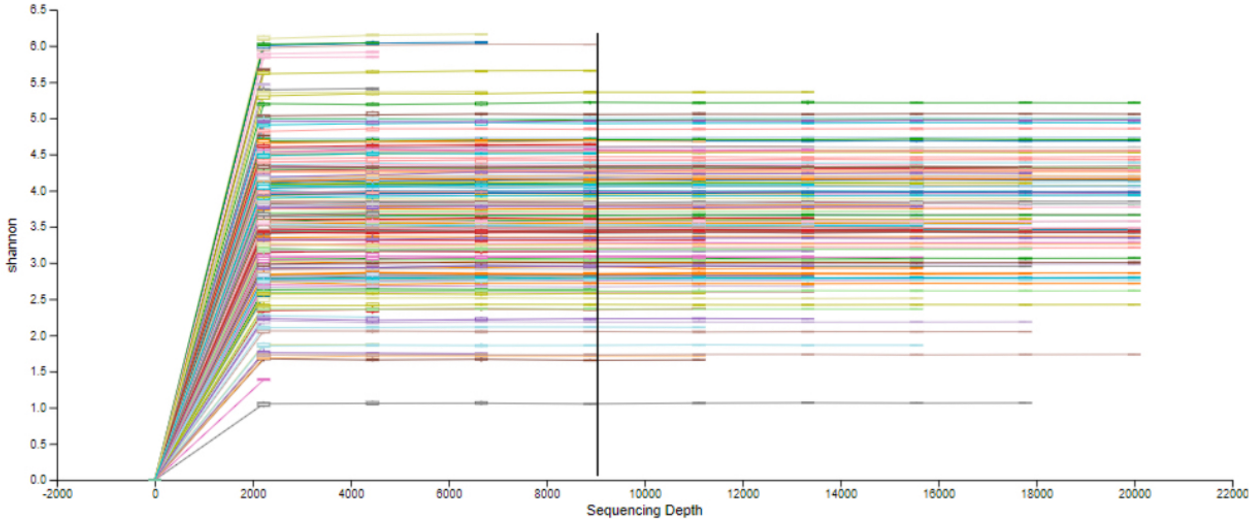

FIG. S2 Alpha rarefaction curve of the Shannon index of each sample, with maximum sequencing depth set to 20000. The black vertical line shows that many different samples are cut off at a sequencing depth of 8564, indicating that depth to be the optimal rarefaction threshold to maximize sample retention.

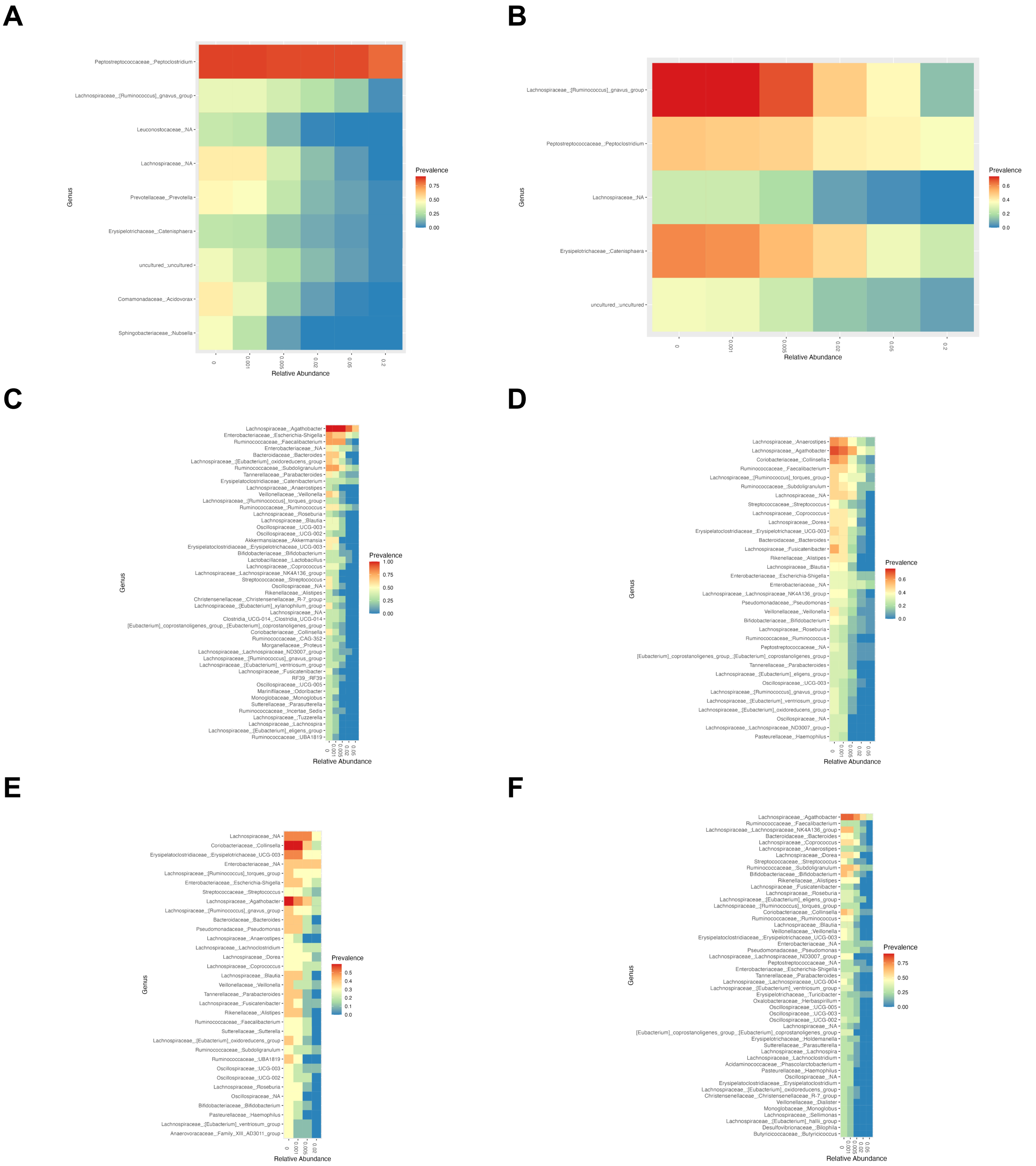

FIG. S3 Heatmaps of core microbiotas that are retained in permutations of minimum relative abundances (0.000-0.200) and minimum prevalences (0.00-1.00) for different groups. The samples were filtered to only include (A) healthy dogs, (B) IBD dogs, (C) healthy humans, (D) IBD humans, (E) CD humans, and (F) UC humans. Heatmaps were used to visualize the number of core taxa that will be accounted for in each set of parameters. Core microbiota used in this study was characterized using 0.000% minimum abundance and 0.25% minimum prevalence. Heatmap ASVs were renamed with taxonomy resolved at the genus level.

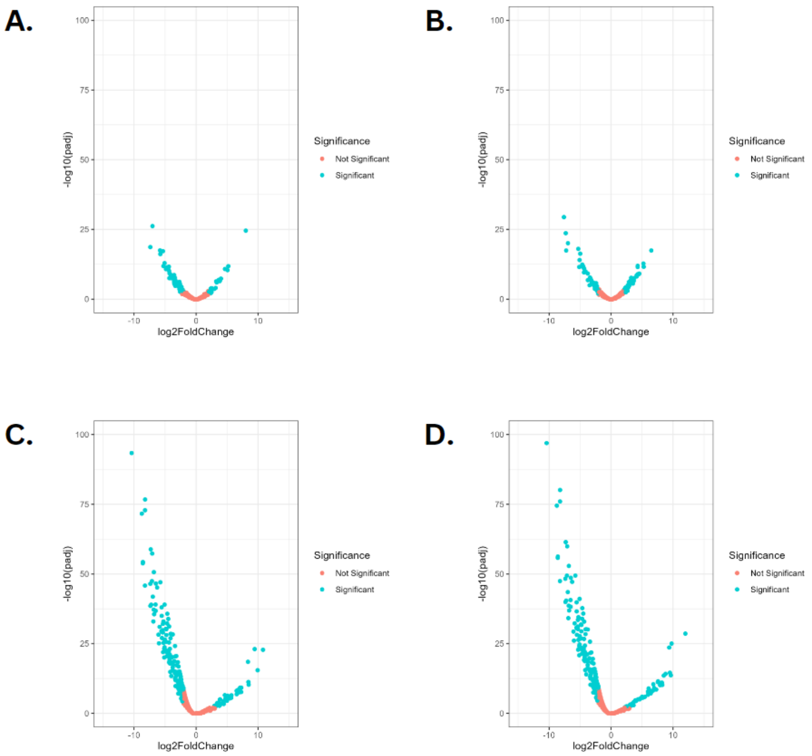

FIG. S4 The dog microbiota contains differentially abundant taxa from the human microbiota, regardless of disease state. Results of differential abundance analyses showing significant differential abundance in terms of the magnitude of fold changes (|log2FoldChange| > 2) and high statistical significance (padj < 0.01), highlighted by volcano plots. Using healthy humans as the reference group, magnitude of differential abundance was evaluated in **(A)** CD humans, **(B)** UC humans, **(C)** IBD dogs, and **(D)** healthy dogs.

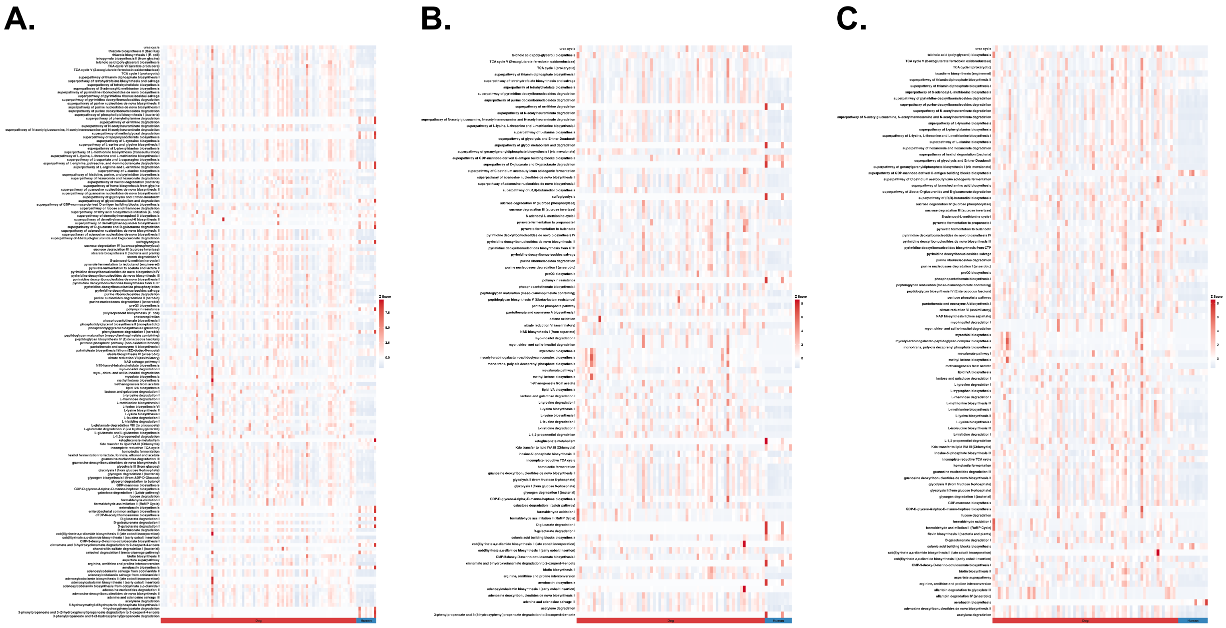

FIG. S5 Predicted functional pathways are significantly up and downregulated in different groups. The samples were filtered to only include (A) healthy humans and healthy dogs, (B) dogs with IBD and humans with Crohn’s disease, and (C) dogs with IBD and humans with Ulcerative Colitis. Heatmaps were used to visualize differential abundance. Only significantly differentially expressed enzymatic pathways (p_{adj} <0.01) were shown along the Y axis. Legend shows the coloring scheme based on the Z scores.