

1 **Dog and human inflammatory bowel disease rely on overlapping yet distinct dysbiosis**
2 **networks**

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10 **Supplementary Figures and Tables**

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12 **Supplementary Table 1. List of discriminant OTUs in the random forests model.** List
13 of OTUs sorted by their scaled feature importance, only the twenty most important are
14 showed in this table.

Scaled Importance	Greengenes Taxonomy
100	Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae
92.51	Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae
89.11	Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae
88.1	Bacteria Bacteroidetes Bacteroidia Bacteroidales Bacteroidaceae <i>Bacteroides</i>
87.26	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae <i>Faecalibacterium prausnitzii</i>
87.16	Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae <i>Allobaculum</i>
85.32	Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae <i>Clostridium hiranonis</i>
83.1	Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae
82.11	Bacteria Firmicutes Clostridia Clostridiales
81.8	Bacteria Bacteroidetes Bacteroidia Bacteroidales Bacteroidaceae <i>Bacteroides</i>
80.18	Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae <i>Blautia producta</i>
79.78	Bacteria Bacteroidetes Bacteroidia Bacteroidales Bacteroidaceae <i>Bacteroides</i>
79	Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae <i>Clostridium hiranonis</i>
78.97	Bacteria Fusobacteria Fusobacteriia Fusobacteriales Fusobacteriaceae <i>Fusobacterium</i>
78.35	Bacteria Firmicutes Clostridia Clostridiales
76.76	Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae
76.16	Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae
76.08	Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae [<i>Ruminococcus</i>]
73.48	Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae
70.52	Bacteria Firmicutes Bacilli Lactobacillales Streptococcaceae <i>Streptococcus</i>

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20 **Supplementary Table 2. Dysbiosis index features.** List of Greengenes 2013 taxa found
21 in the co-occurrence network, classified by whether they are non-IBD associated or IBD
22 associated in the dog vs. the human dysbiosis index. Names enclosed by brackets are
23 known to be contested.

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Greengenes Taxonomy	Dogs	Humans
Bacteria, Actinobacteria, Coriobacteria, Coriobacteriales, Coriobacteriaceae, <i>Slackia</i>	non-IBD	NA
Bacteria, Bacteroidetes, Bacteroidia, Bacteroidales, [Paraprevotellaceae], [<i>Prevotella</i>]	non-IBD	NA
Bacteria, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, <i>Bacteroides</i>	non-IBD	non-IBD
Bacteria, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, <i>Prevotella</i>	non-IBD	NA
Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, <i>Bacillus</i>	IBD	NA
Bacteria, Firmicutes, Bacilli, Bacillales, Planococcaceae	IBD	NA
Bacteria, Firmicutes, Bacilli, Lactobacillales, Carnobacteriaceae, <i>Granulicatella</i>	IBD	NA
Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, <i>Enterococcus</i>	IBD	NA
Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, <i>Lactobacillus</i>	IBD	NA
Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, <i>Streptococcus</i>	IBD	NA
Bacteria, Firmicutes, Clostridia, Clostridiales, [Mogibacteriaceae]	IBD	NA
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, <i>Clostridium</i>	non-IBD	NA
Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae	non-IBD	non-IBD
Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, <i>Dorea</i>	non-IBD	non-IBD
Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae	non-IBD	non-IBD
Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, <i>Butyrivibrio</i>	non-IBD	NA
Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, <i>Faecalibacterium</i>	non-IBD	non-IBD
Bacteria, Firmicutes, Clostridia, Clostridiales, Veillonellaceae, <i>Megamonas</i>	non-IBD	NA
Bacteria, Firmicutes, Erysipelotrichi, Erysipelotrichales, Erysipelotrichaceae, [Eubacterium]	non-IBD	NA
Bacteria, Firmicutes, Erysipelotrichi, Erysipelotrichales, Erysipelotrichaceae, <i>Allobaculum</i>	non-IBD	NA
Bacteria, Firmicutes, Erysipelotrichi, Erysipelotrichales, Erysipelotrichaceae, <i>Catenibacterium</i>	non-IBD	NA
Bacteria, Fusobacteria, Fusobacteria, Fusobacteriales, Fusobacteriaceae, <i>Fusobacterium</i>	non-IBD	IBD
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, <i>Sutterella</i>	non-IBD	non-IBD
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae,	IBD	NA
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, <i>Serratia</i>	IBD	NA
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, <i>Pseudomonas</i>	IBD	NA
Bacteria, Proteobacteria, Gammaproteobacteria, Thiohalorhabdales	IBD	NA

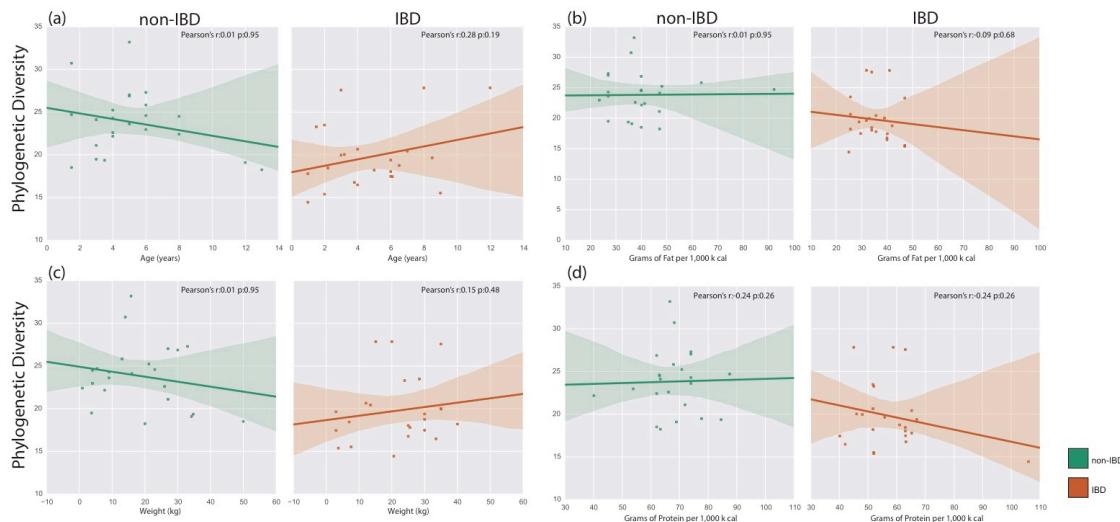
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Supplementary Table 3. **Summary of statistically significant metagenome predictions.** Mean abundance of predicted metagenomes that show a significant difference between healthy and diseased dogs.

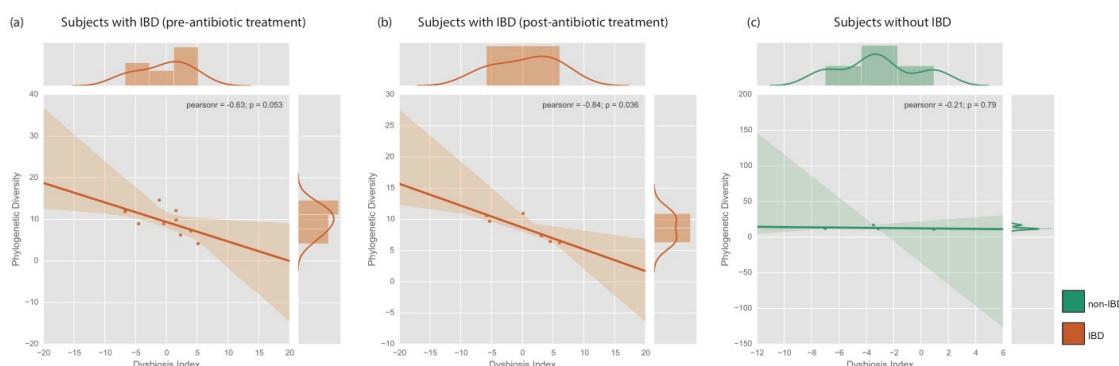
Healthy vs. IBD, Dogs				
Pathway Functional Category	FDR corrected p-value	Bonferroni corrected p-value	non-IBD mean	IBD Mean
<i>Staph aureus</i> infection	3.00e-11	3.00e-11	65.03	313.19
Ion channels	2.90e-12	5.69e-10	43.65	149.44
Tetracycline biosynthesis	6.75e-8	6.96e-7	915.54	984.81
Carbon fixation pathways in prokaryotes	1.54e-7	1.26e-6	4560.91	4253.41
Bacterial chemotaxis	0.004	0.334	1884.65	1667.17

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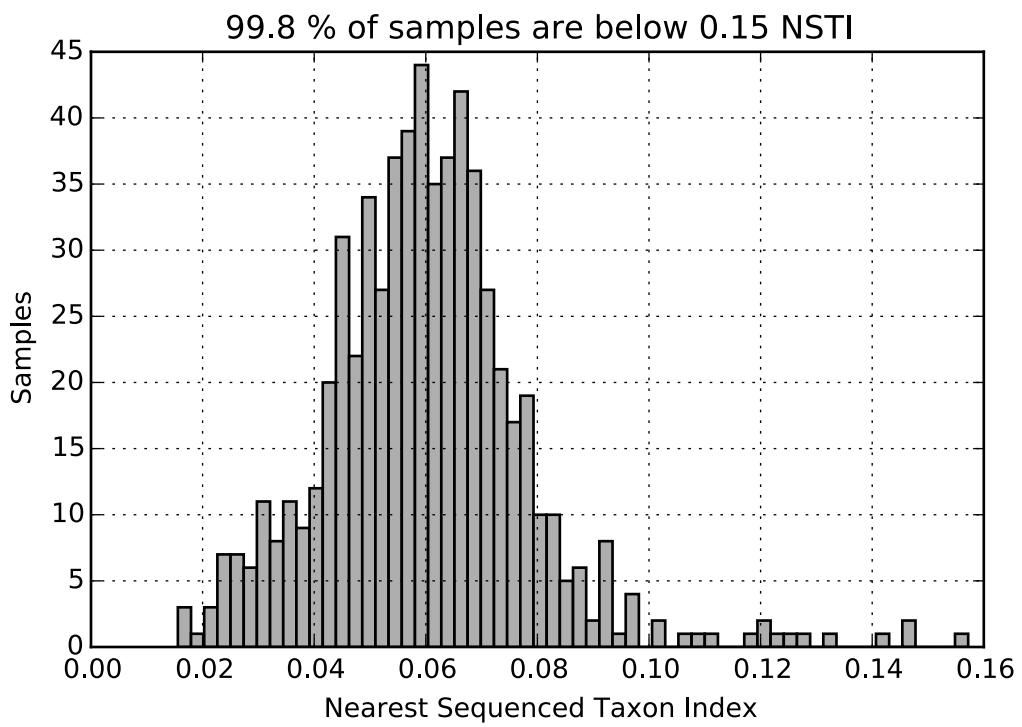
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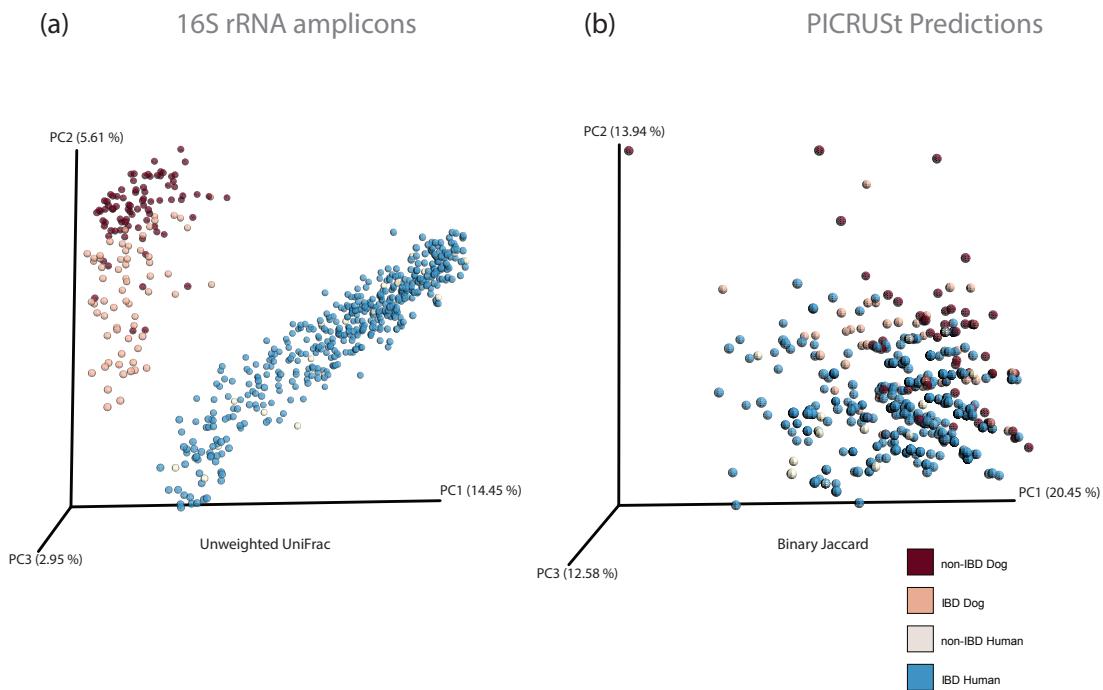
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35 **Supplementary Figure 1. Alpha diversity relationships.** Linear regressions of Faith's
36 phylogenetic diversity and (A) age in years, (B) grams of fat per 1,000 kilocalorie,
37 (C) weight in kilograms, and grams of protein per 1,000 kilocalorie (D), for all figures
38 samples used are: non-IBD=23 and IBD=23. The plot displays 95% confidence
39 intervals.
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42 **Supplementary Figure 2. Dysbiosis Index visualized in an external dataset.**
43 Phylogenetic diversity and dysbiosis are negatively correlated in diseased subjects.
44 (A) Subjects with IBD before antibiotic treatment n=9, (B) subjects with IBD after
45 antibiotic treatment n=6 and (C) non-IBD subjects n=4. The plot displays 95%
46 confidence intervals.
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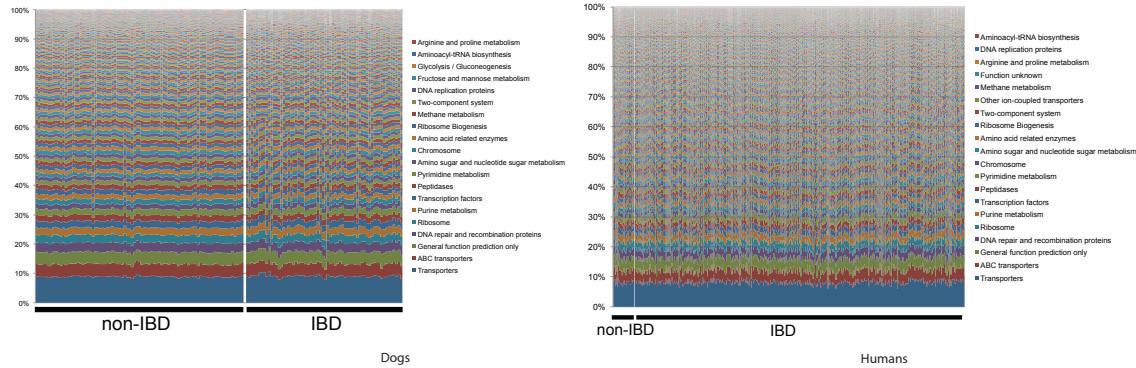
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49 **Supplementary Figure 3. Nearest Sequenced Taxon Index (NSTI).** Histogram of
50 the NSTIs for the samples in our study, 99.8% of our samples have a score below
51 0.15 (the recommended minimum).
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54 **Supplementary Figure 4. Meta-analysis of human and dog samples.** Principal
55 coordinates analysis plot of the meta-analysis of human and dog samples using the 16S

56 Data (A) and the PICRUSt predicted metagenomes (B), colored by disease status and
57 host species (see supplemental methods). The number of samples are as follows non-
58 IBD Dogs=85, IBD Dogs=64, non-IBD Humans=29 and IBD Human=450.

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61 **Supplementary Figure 5. Feature summary of the predicted metagenomes.** Summary
62 of the PICRUSt predicted metagenomes from the microbial communities of dogs and
63 humans, grouped by disease state. The number of samples are as follows non-IBD
64 Dogs=85, IBD Dogs=64, non-IBD Humans=29 and IBD Human=450.