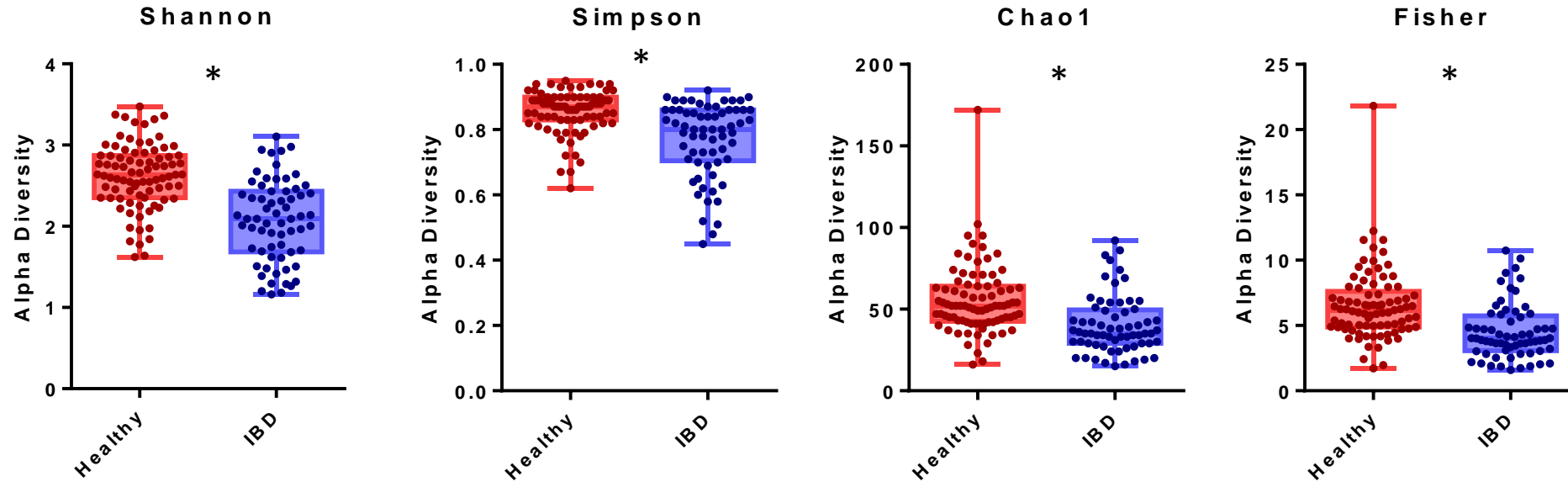
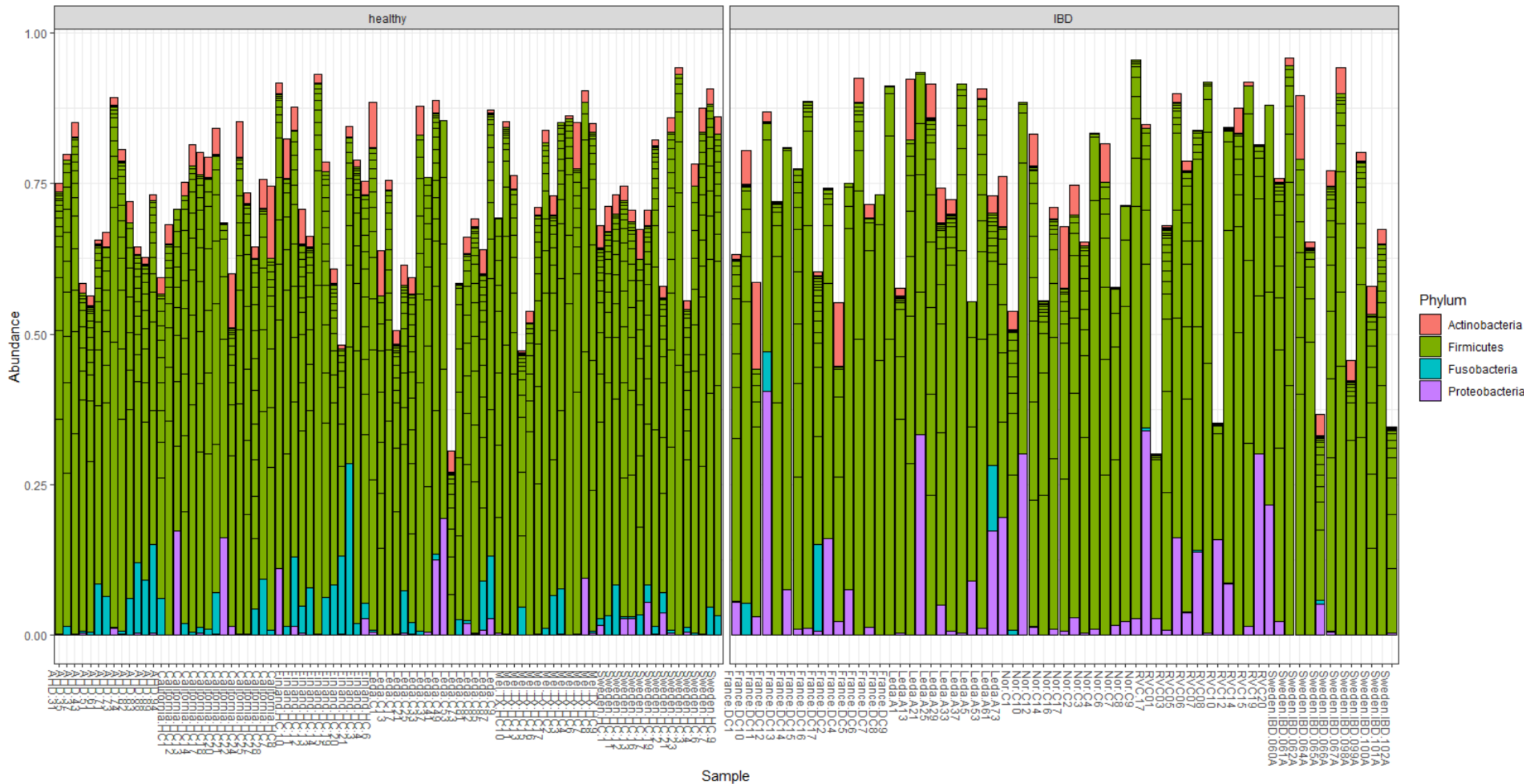


# Alpha Diversity by Various Measures

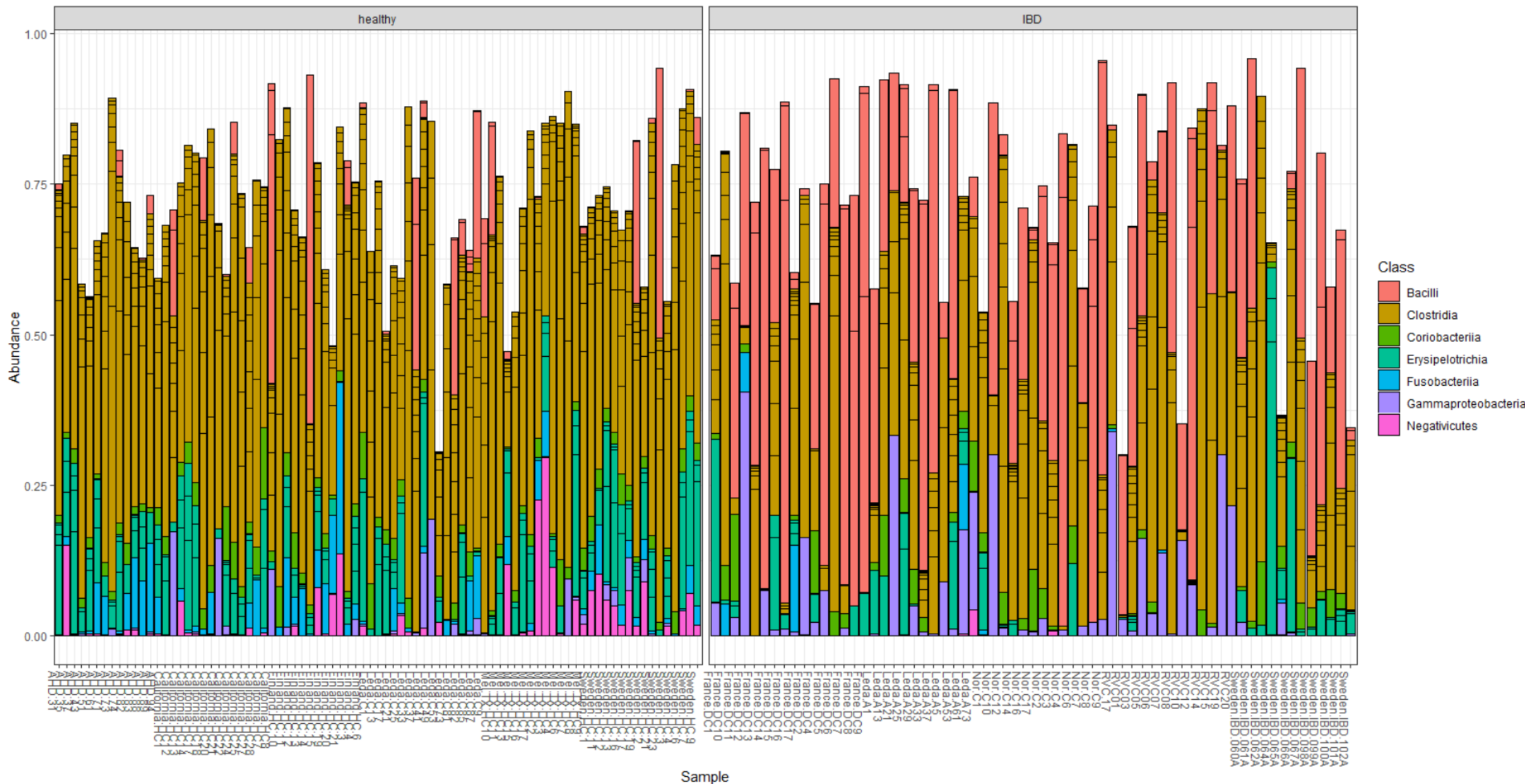


**Figure 1. Dogs with inflammatory bowel disease (IBD) have lower alpha diversity than healthy dogs.** Alpha diversity was calculated vis the Shannon, Simpson, Chao1, and Fisher methods. Points represent individual dogs overlaid on a min-to-max box and whisker plot. Dogs with IBD have significantly lower alpha diversity than healthy dogs for all measures as calculated by a Mann-Whitney test ( $p < 0.001$  denoted by \*). N=85 (healthy) and N=65 (IBD).

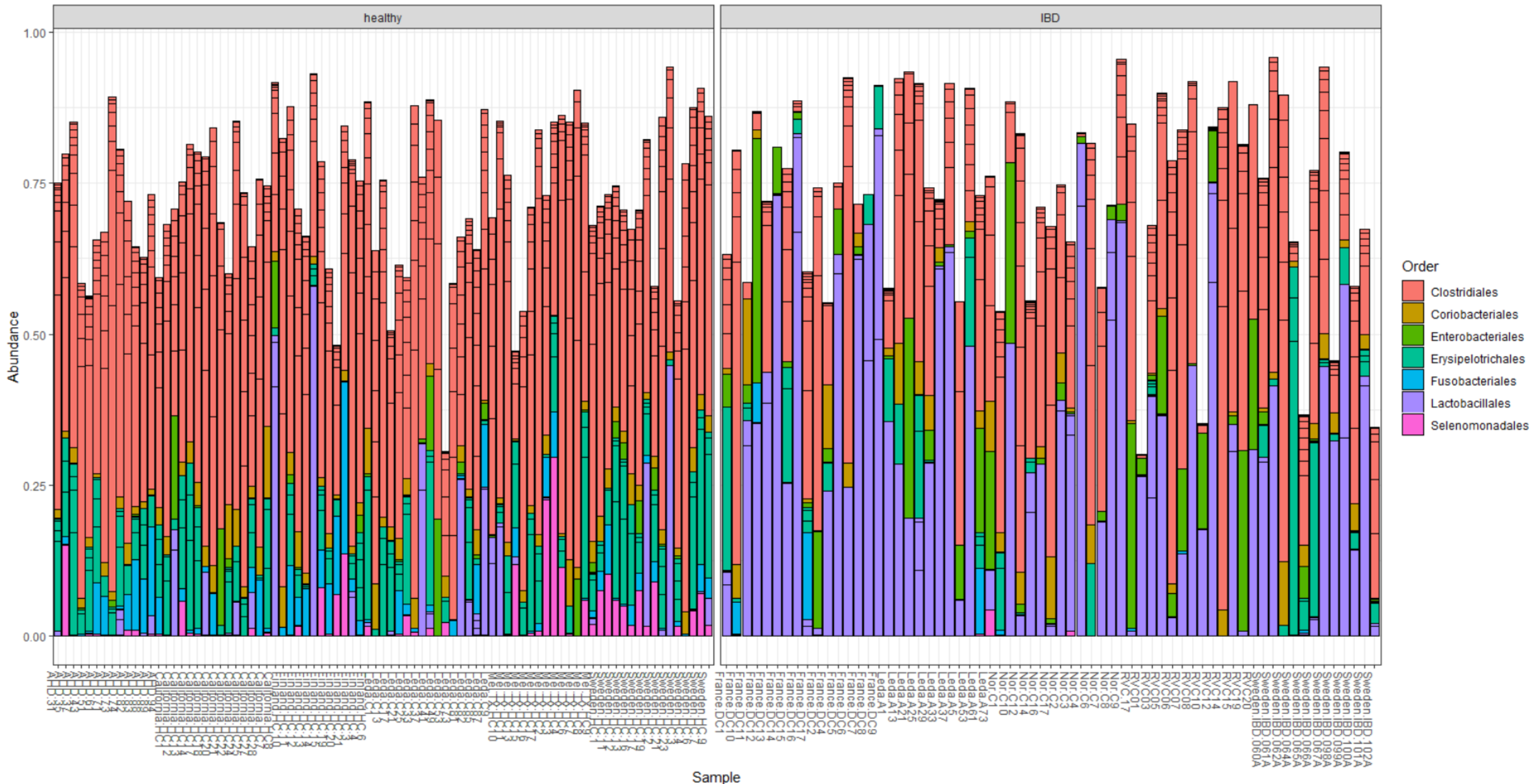
Proportions of top 20 sequences - Phylum



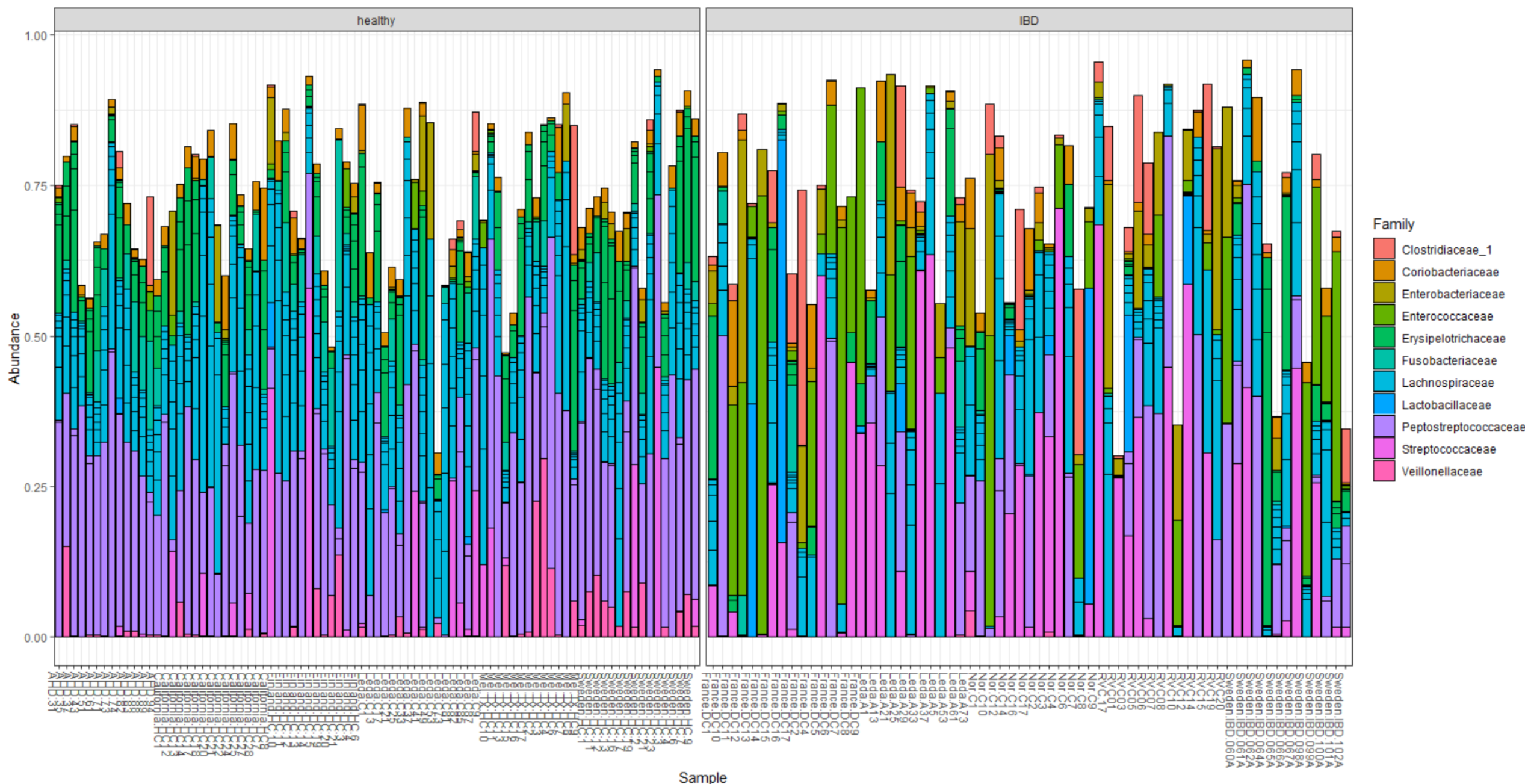
# Proportions of top 20 sequences - Class



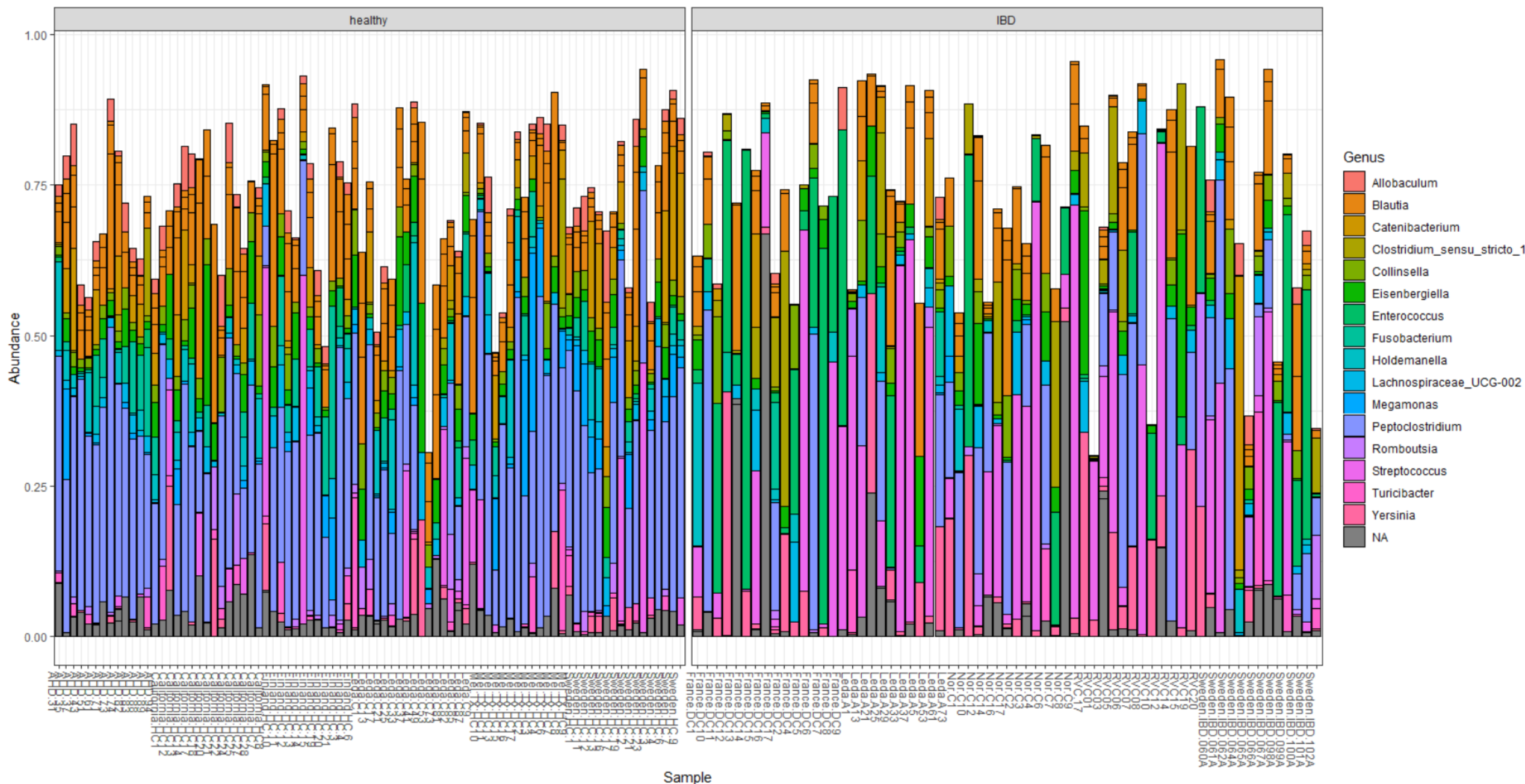
Proportions of top 20 sequences - Order



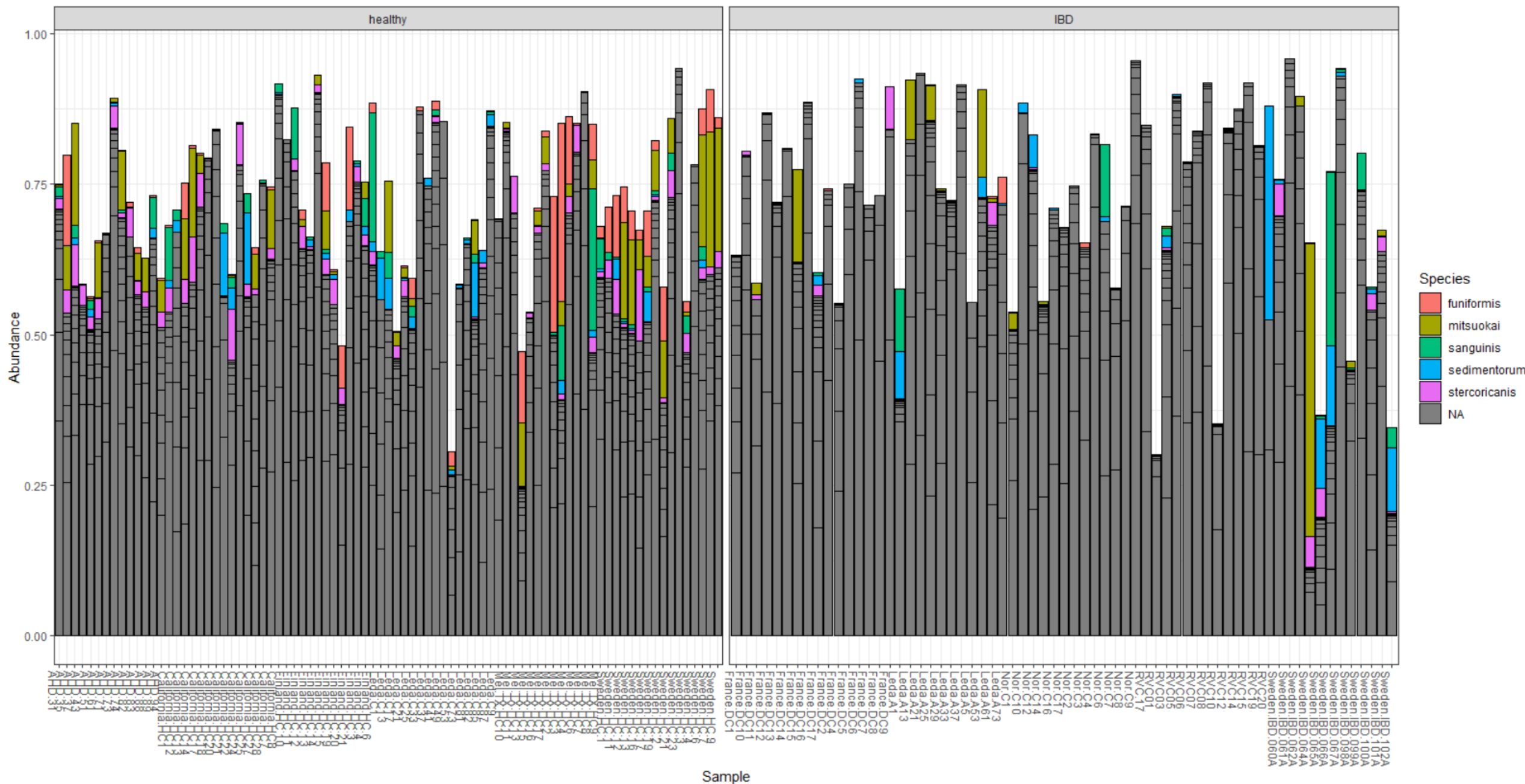
# Proportions of top 20 sequences - Family



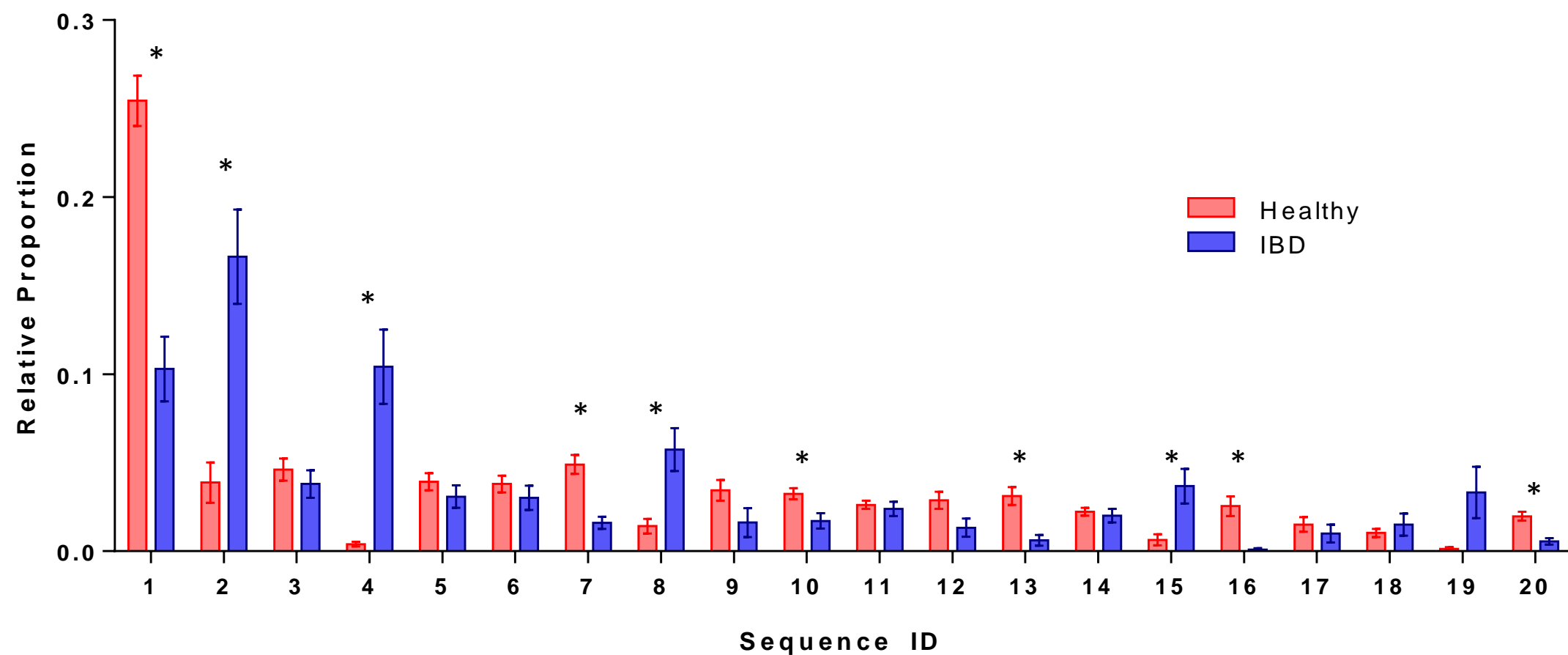
# Proportions of top 20 sequences - Genus



# Proportions of top 20 sequences - Species



# Proportions of top 20 sequences



**Figure 2. Healthy dogs and dogs with inflammatory bowel disease (IBD) have differences in their microbiome.** Proportions of the top 20 abundant sequences were compared between healthy dogs and dogs with IBD. For statistical analysis, comparisons were made using multiple unpaired t-tests using the Holm-Sidak method (\*,  $P < 0.05$ ). Data are mean $\pm$ SEM, N=85 (healthy) and N=65 (IBD).



## Sequence taxological information for Figure 2

Sequence ID	Sequence	Kingdom	Phylum	Class	Order	Family	Genus	Species
1	TACGTAGGGGGCTAGCGTTATCCGGATTTACTGGGCGTAAAGGGTGCGTAGGCGGTCTTTCAAGTCAGGAGTTAA	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptoclostridium	NA
2	TACGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTAATAAGTCTGAAGTTAA	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	NA
3	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGAAGAGCAAGTCTGATGTGAA	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	NA
4	TACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAA	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	NA
5	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGAGCAGCAAGTCTGATGTGAA	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	NA
6	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCATGGCAAGCCAGATGTGAA	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Eisenbergiella	NA
7	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGTGCAAGTCTGATGTGAA	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	NA
8	TACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTTTGTTAAGTCAGATGTGAA	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Yersinia	NA
9	TACGTAGGTGGCGAGCGTTATCCGGAATCATTGGGCGTAAAGAGGGAGCAGGCGGCCGCAAGGGTCTGTGGTGAA	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Catenibacterium	mitsuokai
10	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGACGGGCAAGTCTGAAGTGAA	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA	NA
11	TACGTAGGGGGCGAGCGTTATCCGGATTCATTGGGCGTAAAGCGCGCGTAGGCGGCCCGGCAGGCAGGGGGTCAA	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	NA
12	TACGTAGGTGGCGAGCGTTATCCGGAATGATTGGGCGTAAAGGGTGCGTAGGTGGCAGATCAAGTCTGGAGTAAA	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Holdemanella	NA
13	TACGTATGTCGCAAGCGTTATCCGGATTTATTGGGCGTAAAGCGCGTCTAGGCGGTTTGTTAAGTCTGATGTGAA	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Fusobacterium	NA
14	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGTGCAAGTCTGAAGTGAA	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_UCG-002	NA
15	TACGTAGGTGGCGAGCGTTATCCGGATTTACTGGGCGTAAAGGGAGCGTAGGCGGATGATTAAGTGGGATGTGAA	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto_1	NA
16	TACGTAGGCGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGGGAGCGCAGGCGGGAACTAAGCGGATCTTAAA	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megamonas	funiformis
17	TACGTAGGTGGCGAGCGTTATCCGGAATTATTGGGCGTAAAGAGCGCGCAGGTGGTTGATTAAGTCTGATGTGAA	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter	sanguinis
18	TACGTAGGGGGCTAGCGTTATCCGGAATTACTGGGCGTAAAGGGTGCGTAGGTGGTTTCTTAAGTCAGAGGTGAA	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia	sedimentorum
19	TACGTAGGTGGCAAGCGTTATCCGGATTTATTGGGCGTAAAGGGAACGCAGGCGGTCTTTAAGTCTGATGTGAA	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	NA	NA
20	TACGTAGGTGGCGAGCGTTATCCGGAATGATTGGGCGTAAAGGGTGCGCAGGCGGCATATCAAGTCTGAAGTGAA	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Allobaculum	stercoricanis

## Conclusions

- Overall
  - Given that this is my first time, there are likely errors, as well as areas for improvement, and optimization/testing of different parameters in the code
- Alpha diversity (Fig 1)
  - Diversity is lower in dogs with IBD compared to healthy dogs by all measures, similar to what was reported
  - There is 1 outlier in the healthy group – investigate further to see if it can be excluded
- Bar plots per sample
  - Phylum – appears most similar between the groups
  - Class – more Clostridia in healthy, more Bacili in IBD
  - Order – more Clostradiales in healthy, more Lactobacillales in IBD
  - Family – more Peptostreptococcaceae in healthy, more Streptococcaceae in IBD
  - Genus – more Peptoclastridium in healthy, more Streptococcus in IBD
  - Species – The majority were undetermined, perhaps a higher proportion of named species in healthy, particularly funiformus
- Bar plots of sequences (Fig 2)
  - Matches the bar plot (more Peptoclastridium in healthy, more Streptococcus in IBD)
  - Other differences between groups observed as well