

C Diff Analysis

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Contents

Figure 1 qPCR	1
Figure 4 A	2
Figure 4 B	3
Figure 6 A	3
Figure 6 B	4
Figure 7 B	4
Supplementary Figure 3	5

Figure 1 qPCR

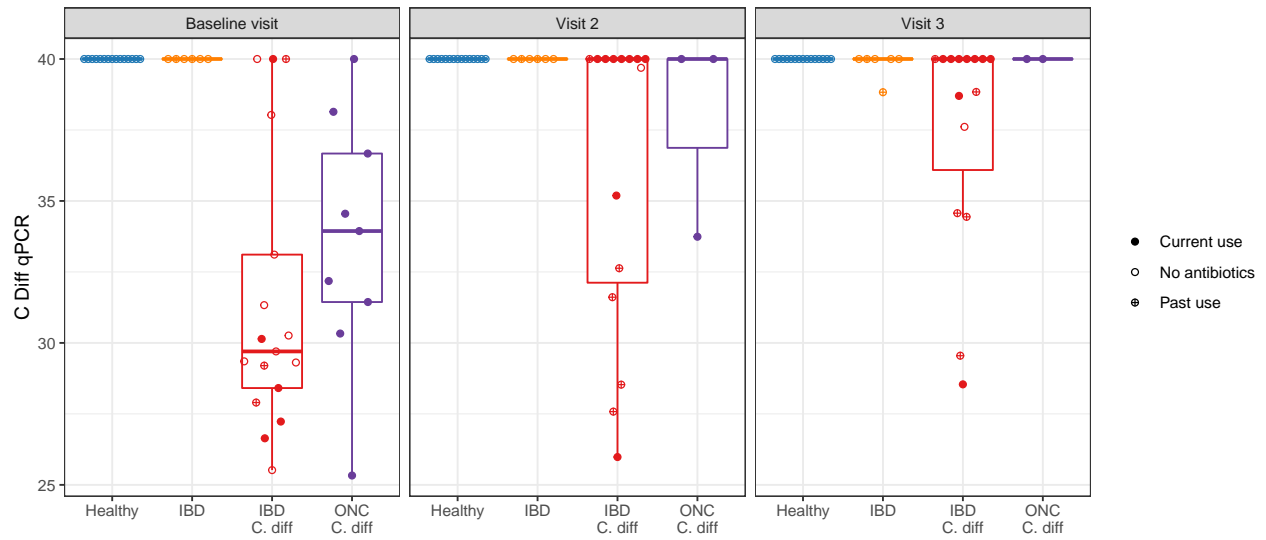
This is plot for qPCR values of fecal samples at 3 time points.

```
##  
## Fligner-Killeen test of homogeneity of variances  
##  
## data: tcdB_ct_ave by as.factor(current_antibiotics)  
## Fligner-Killeen:med chi-squared = 1.0492, df = 1, p-value = 0.3057
```

Table 1: Linear mixed-effects model fit by maximum likelihood :
tcdB_ct_ave ~ current_antibiotics + Time

	Value	Std.Error	DF	t-value	p-value
(Intercept)	30.91	1.226	25	25.22	2.682e-19
current_antibioticsYes	2.579	1.498	25	1.721	0.09755
Time	0.653	0.2269	25	2.878	0.008086

Shape by antibiotics.



Shape by response to therapy.

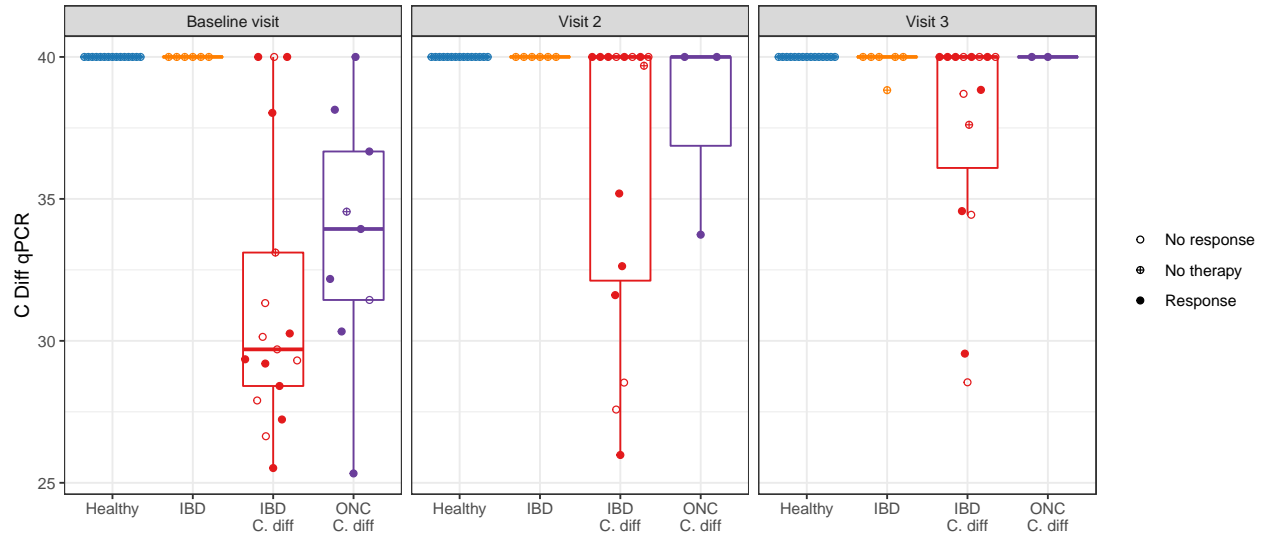


Figure 4 A

This is the heatmap of the top 30 important features from the randomForest model when comparing IBD_C.Diff and Healthy using the Kraken result at the Baseline Visit.

The data is arc sin transformed before making the heatmap.

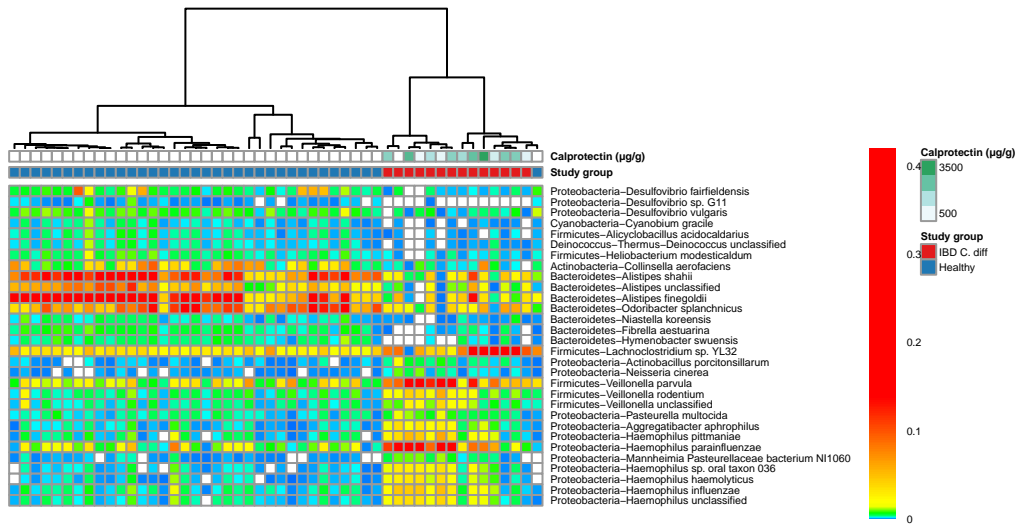


Figure 4 B

This is the heatmap of the top 30 important features from the randomForest model when comparing IBD C.Diff and IBD using the Kraken result at the Baseline Visit.

The data is arc sin transformed before making the heatmap.

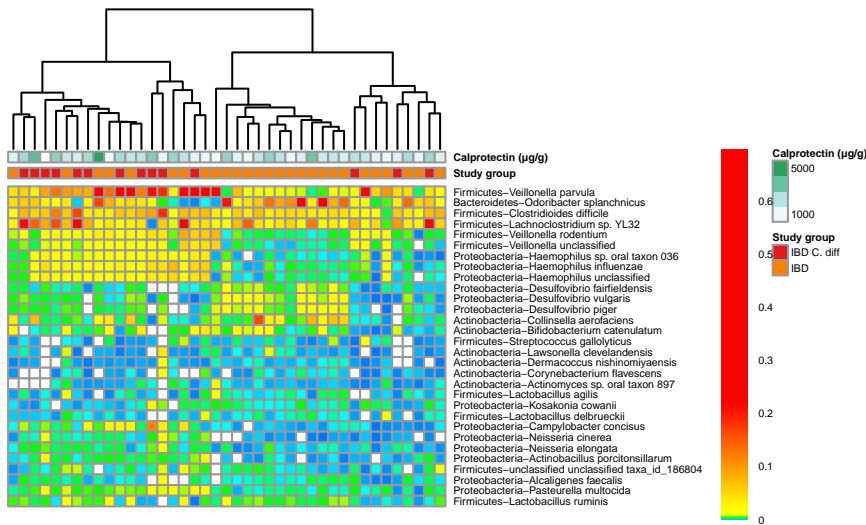


Figure 6 A

This is the heatmap of the top 30 important features from the randomForest model when comparing IBD C.Diff and Healthy using the metabolomics data at the Baseline Visit.

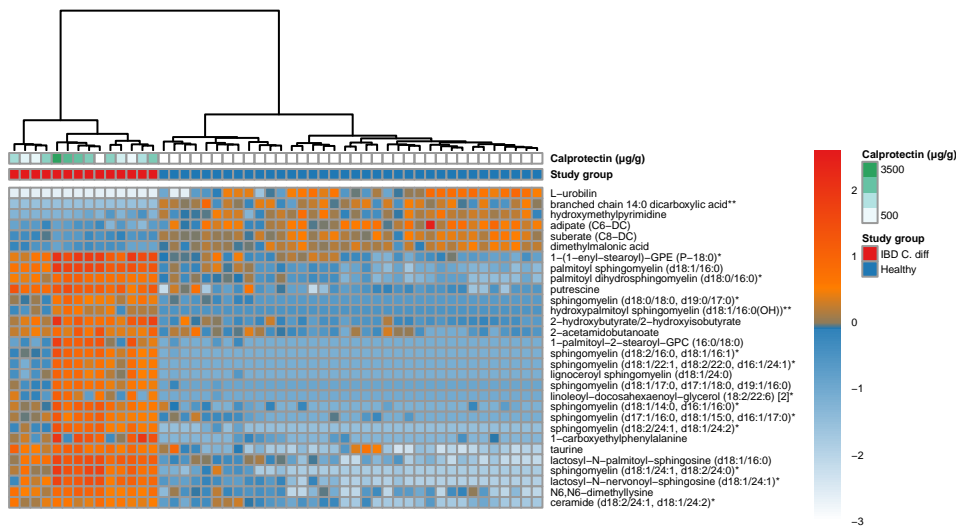


Figure 6 B

This is the heatmap of the top 30 important features from the randomForest model when comparing IBD C.Diff and IBD using the metabolomics data at the Baseline Visit.

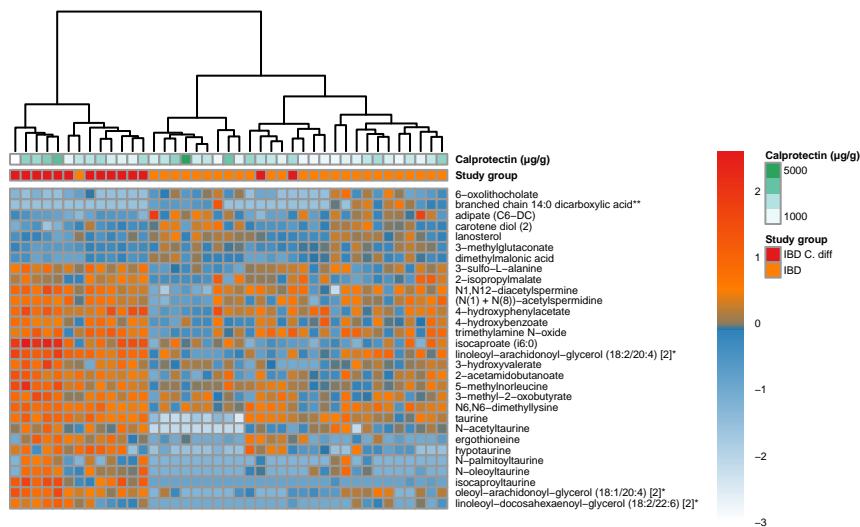
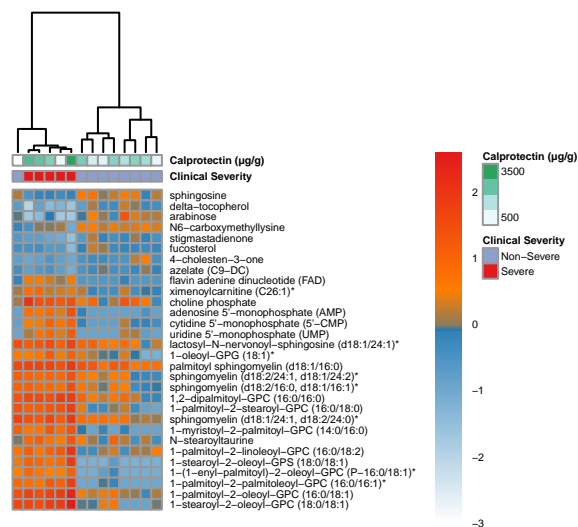


Figure 7 B

This is the heatmap of the top 30 important features from the randomForest model when comparing severe IBD C.Diff and non-severe IBD C.Diff using the metabolomics data at the Baseline Visit.



Supplementary Figure 3

This is a plot to summarise the antibiotics information for oncology C.Diff and IBD C.Diff patients.

