**Supplemental Table 1.** Relative abundance of the major phyla in the duodenum and stool in the same subjects (Group 1, n=53)

|  |  |  |
| --- | --- | --- |
|  | Relative abundance % | |
| Phylum level | Duodenum (n=53) | Stool (n=53) | |
| Verrucomicrobia | 0 | 3 | |
| Bacteroidetes | 6 | 50 | |
| Firmicutes | 55 | 40 | |
| Fusobacteria | 5 | 1 | |
| Proteobacteria | 21 | 5-6 | |
| Actinobacteria | 11 | 1 | |
| TM7 | <2 | 0 | |

**Supplemental Table 2.** Relative abundance of the major phyla in different small intestinal segments in the same subjects (Group 2, n=23).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Relative abundance % | | |  |
| Phylum | **Duodenum** | **Jejunum** | **Farthest distance (FD)** | **FDR P-value\*** |
| Actinobacteria | 9 | 8 | 7 | 0.84 |
| Bacteroidetes | 4 | 2 | 4 | 1.13E-5 |
| Firmicutes | 47 | 47 | 52 | 0.84 |
| Fusobacteria | 7 | 4 | 5 | 1.50E-7 |
| Proteobacteria | 32 | 37 | 29 | <0.0001 |
| TM7 | <1 | <2 | <2 | 0.84 |

\* Likelihood Ratio test

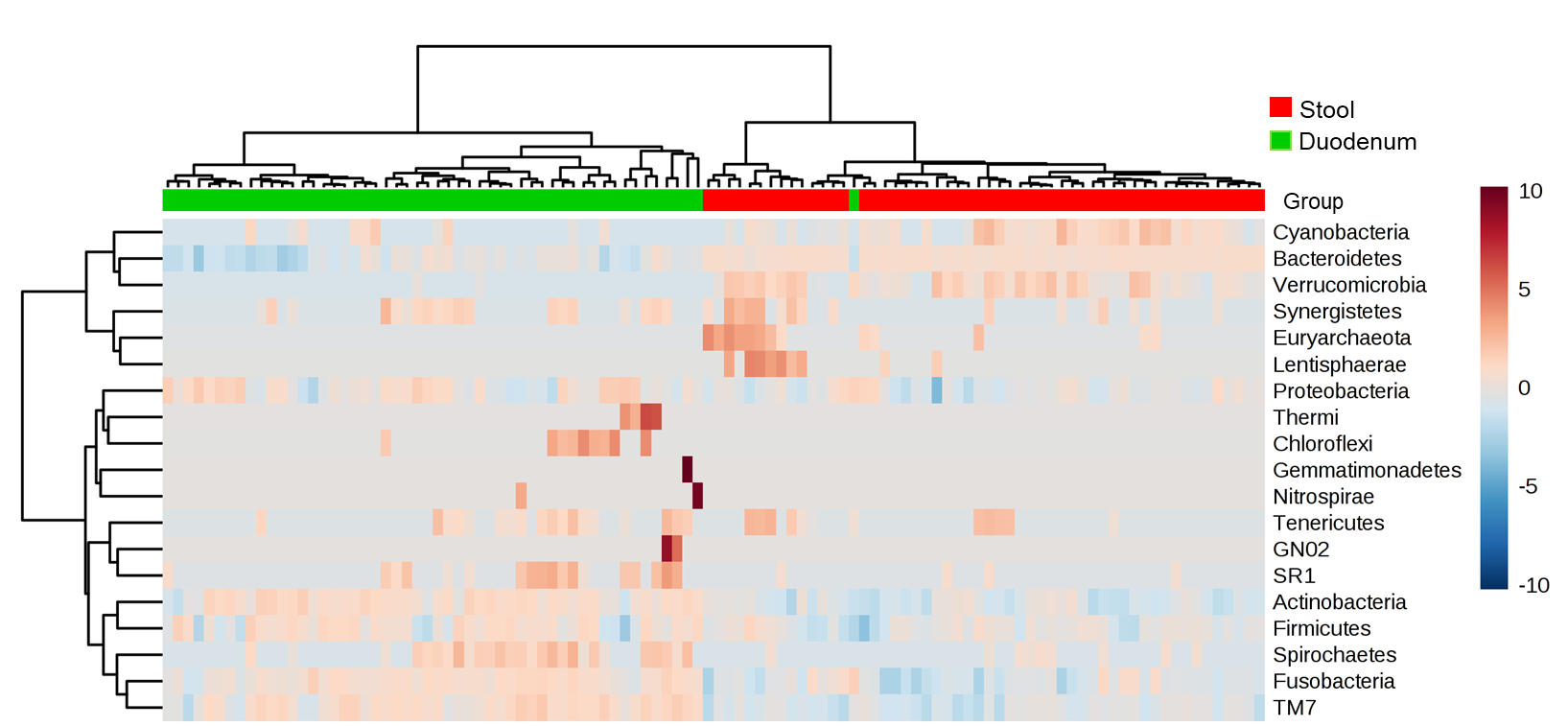
**Supplemental Table 3.** Microbial family differences between small intestinal segments in the same subjects (Group 2, n=23).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Jejunum vs. Duodenum** | | | **FD vs. Duodenum** | | | **FD vs. Jejunum** | | |
|  | Log₂ fold change | P-value | FDR P-value | Log₂ fold change | P-value | FDR P-value | Log₂ fold change | P-value | FDR P-value |
| Bradyrhizobiaceae | -4.39 | **3.30E-06** | **6.34E-04** | -2.15 | **3.77E-03** | 0.12 | 2.24 | **0.02** | 0.6 |
| Clostridiaceae | 3.39 | **9.43E-05** | **9.06E-03** | 3.67 | **2.42E-05** | **2.32E-03** | 0.28 | 0.72 | 0.95 |
| Fusobacteriaceae | -1.86 | **4.75E-03** | 0.3 | 0.98 | 0.12 | 1 | 2.84 | **1.57E-05** | **1.73E-03** |
| Peptostreptococcaceae | 1.79 | **0.03** | 0.92 | 4.46 | **4.86E-09** | **9.33E-07** | 2.67 | **1.80E-05** | **1.73E-03** |
| Bacillaceae | -0.09 | 0.87 | 0.95 | -1.92 | **2.73E-03** | 0.1 | -1.83 | **4.65E-03** | 0.18 |
| Bacteroidaceae | 0.33 | 0.79 | 0.92 | 3.08 | **0.01** | 0.23 | 2.75 | **0.02** | 0.6 |
| Enterobacteriaceae | 2.49 | **0.03** | 0.92 | 3.7 | **8.81E-04** | 0.06 | 1.21 | 0.28 | 0.95 |
| Enterococcaceae | -0.08 | 0.94 | 0.98 | 2.93 | **2.04E-03** | 0.1 | 3.02 | **2.70E-03** | 0.13 |
| Moraxellaceae | -1.05 | 0.44 | 0.98 | -1.38 | **0.035** | 0.95 | -1.31 | 0.23 | 0.98 |
| Neisseriaceae | -1.61 | 0.53 | 0.98 | -1.32 | **0.026** | 0.95 | -0.64 | 0.99 | 0.92 |
| Pasteurellaceae | -0.47 | 0.54 | 0.92 | 1.89 | **0.01** | 0.23 | 2.36 | **1.72E-03** | 0.11 |
| Prevotellaceae | -1.4 | 0.06 | 0.92 | -1.57 | **0.04** | 0.7 | -0.17 | 0.82 | 0.95 |
| Pseudomonadaceae | -0.45 | 0.58 | 0.92 | -2.37 | **5.19E-03** | 0.14 | -1.91 | **0.02** | 0.6 |

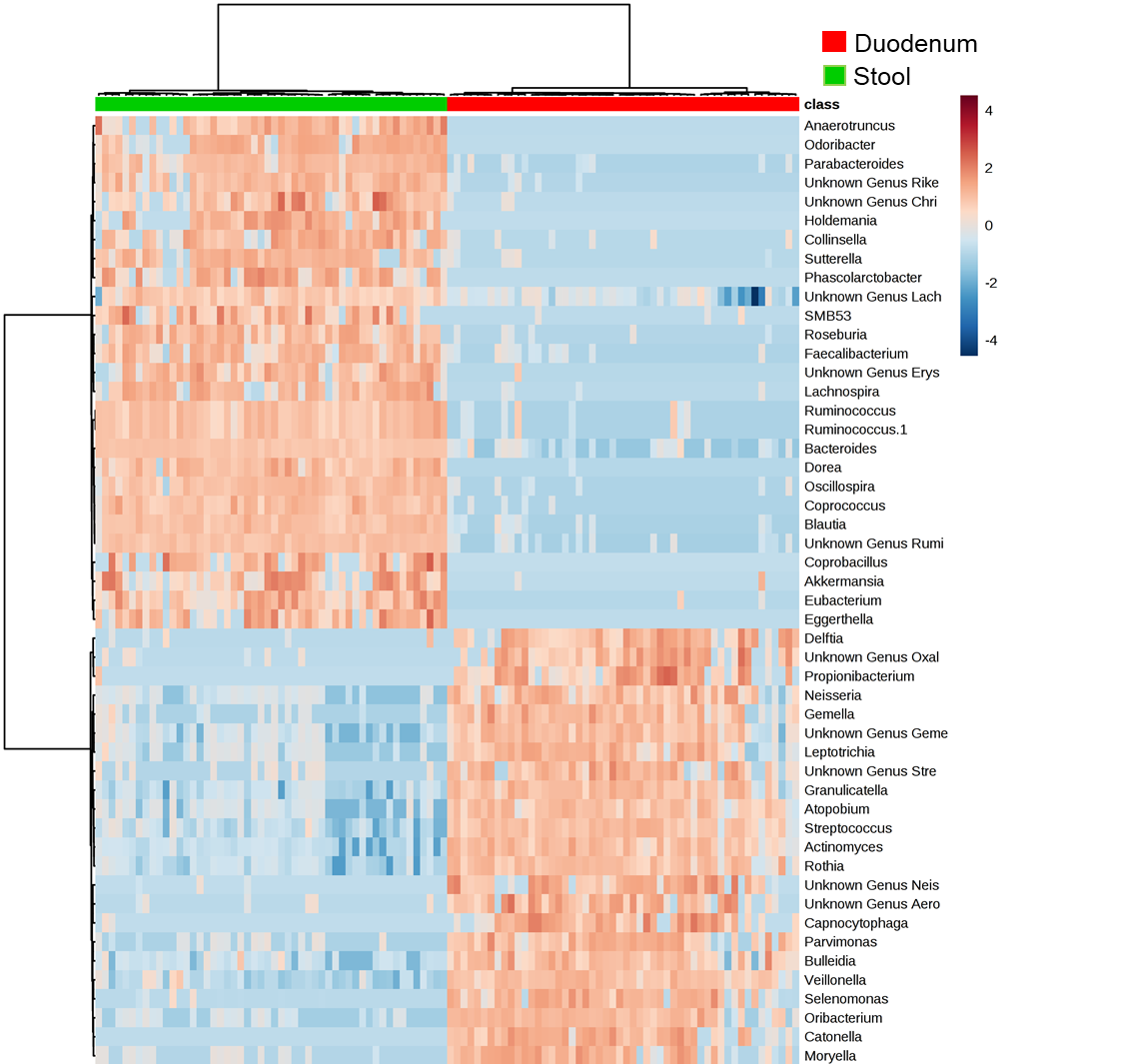
P-value and FDR P-value < 0.05 are in bold.

**Supplemental Table 4.** Fold change in the relative abundance of major families from phylum Firmicutes in different small intestinal segments compared to stool, in the same subjects (Group 3, n=8).

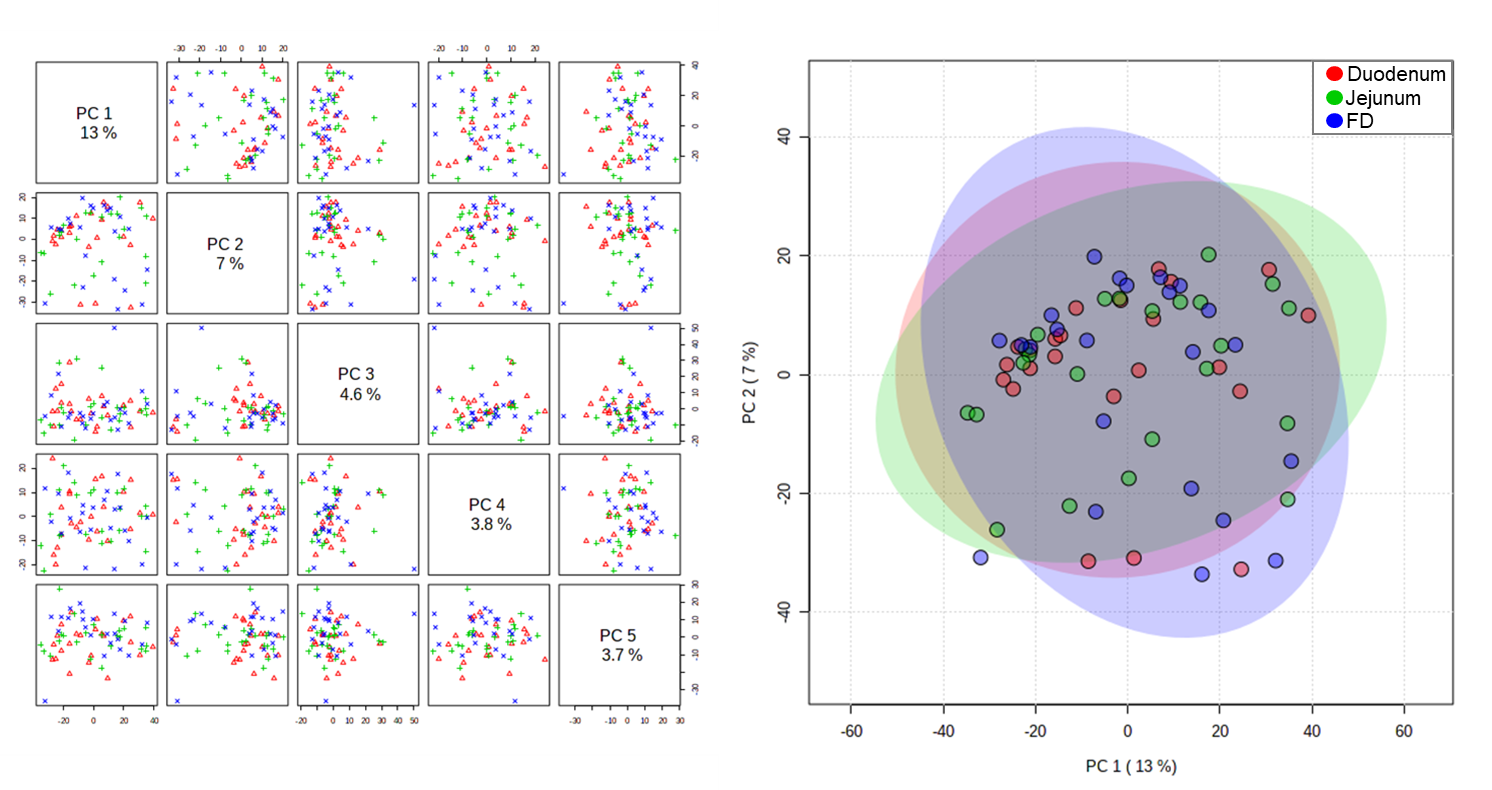
|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Stool vs. Duodenum | | Stool vs. Jejunum | | Stool vs. Farthest Distance | |
| Families from Firmicutes phylum | Fold change | FDR P-value | Fold change | FDR P-value | Fold change | FDR P-value |
| Ruminococcaceae | 21.64 | 1.58E-07 | 675.86 | 0 | 351.21 | 1.56E-11 |
| Lachnospiraceae | 5.29 | 9.21E-11 | 4.5 | 1.99E-05 | 2.68 | 0.01 |
| Christensenellaceae | 277 | 0 | 665.94 | 0 | 698.11 | 0 |
| Veillonellaceae | -7.95 | 0 | -6.07 | 1.28E-08 | -3.82 | 1.62E-04 |
| Lactobacillaceae | -18.7 | 5.85E-09 | -4.51 | 0.04 | 2.79 | 0.27 |
| Clostridiaceae | -20.33 | 4.88E-09 | -27.71 | 2.08E-06 | -15.69 | 4.45E-04 |
| Streptococcaceae | -45.86 | 0 | -41.4 | 0 | -43.46 | 0 |
| Carnobacteriaceae | -950.62 | 0 | -814.67 | 0 | -862.95 | 0 |



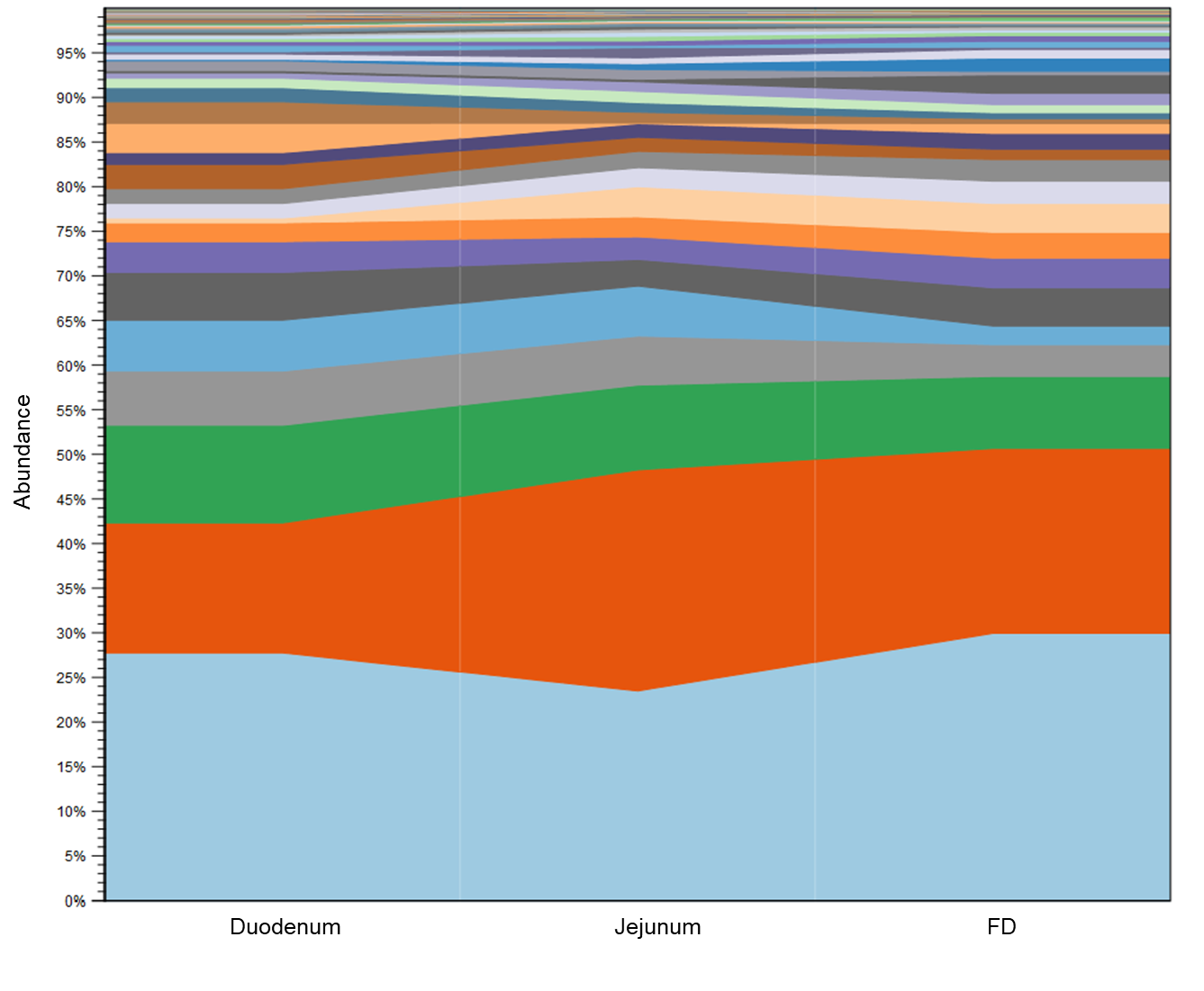
**Supplemental Figure 1.** Heatmap of the Euclidean Ward clustering analysis of all phyla in the duodenum and stool in the same subjects (Group 1, n=53). Each colored cell corresponds to the relative abundance value of each normalized microbial phylum included in this analysis.

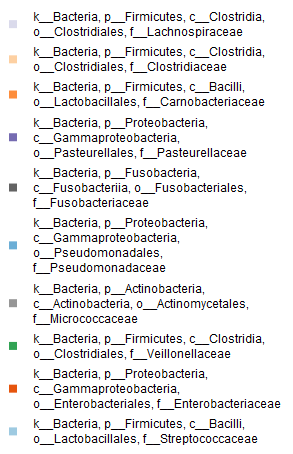
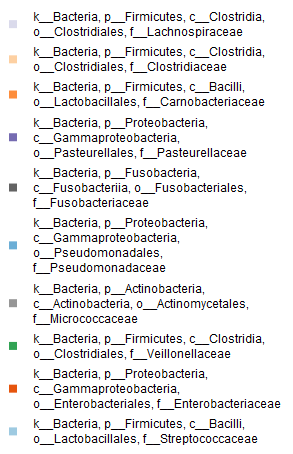
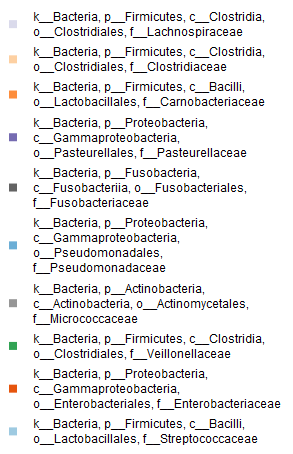


**Supplemental Figure 2.** Heatmap of the Euclidean Ward clustering analysis of the top 50 statistically significant microbial genera in the duodenum and stool (Group 1, n=53). Each colored cell corresponds to the relative abundance value of each normalized microbial genus included in this analysis.

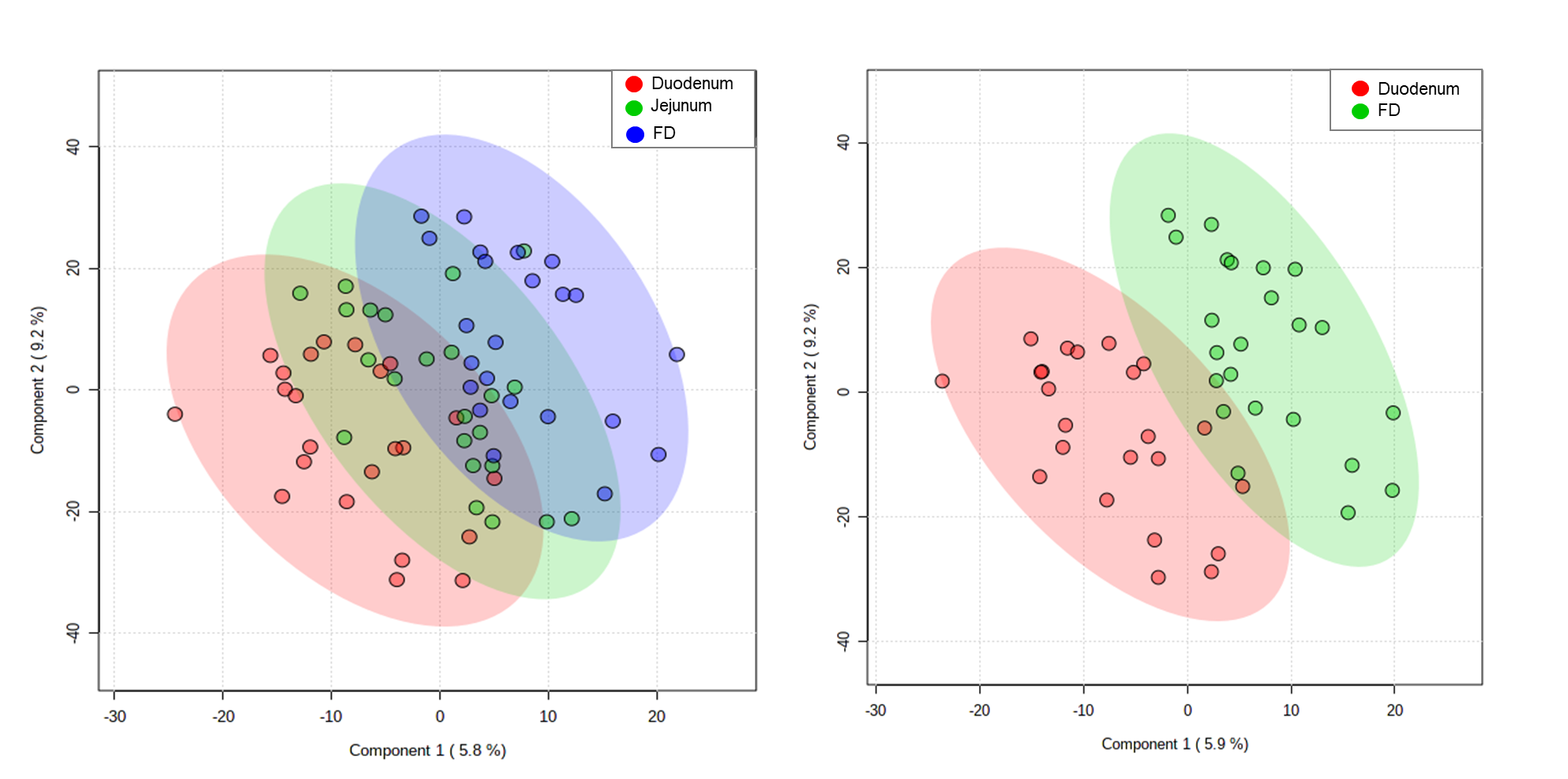


**Supplemental Figure 3.** PCoA plot of the microbial profiles in different small intestinal segments in the same subjects (Group 2, n=23). Duodenum - red, jejunum - green and farthest distance reached during DBE (FD) - blue. Transparent circles indicate the 95% confidence region.

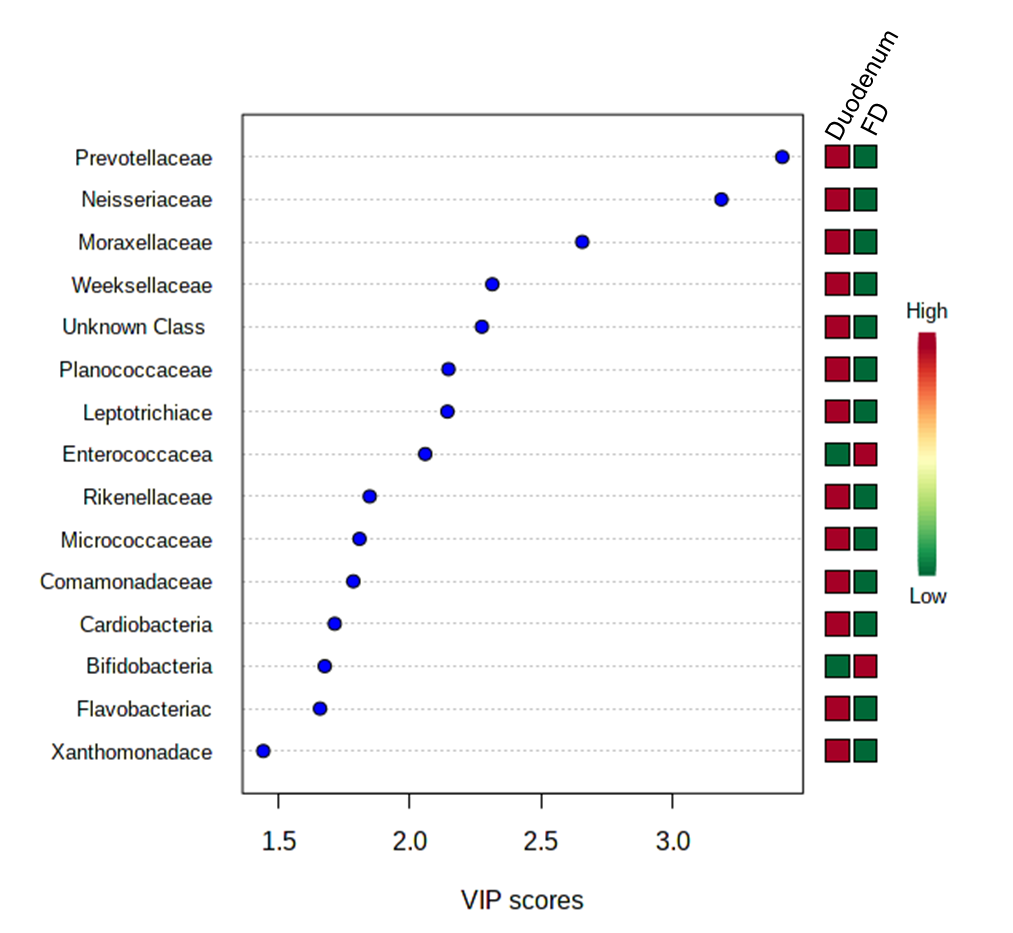




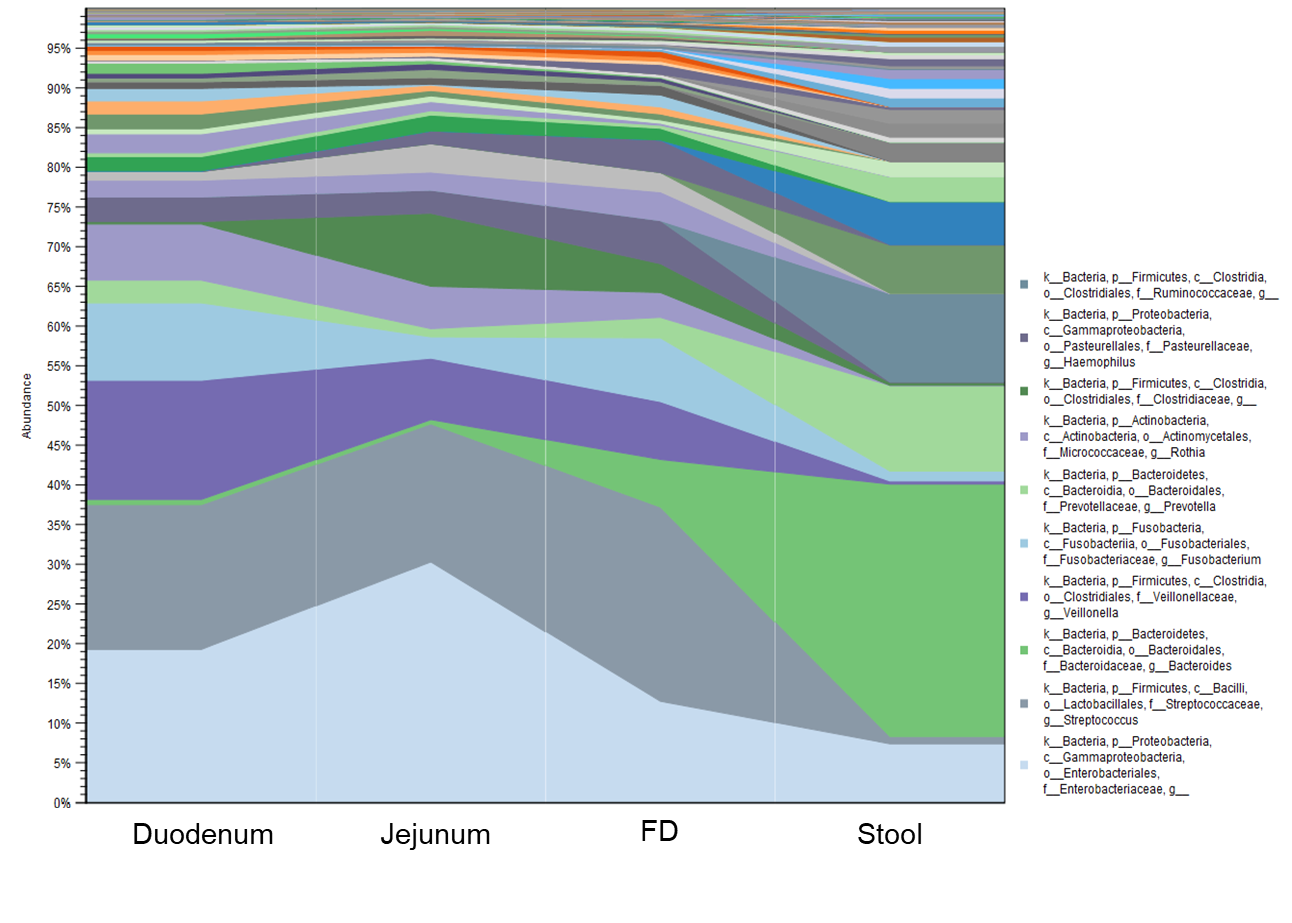
**Supplemental Figure 4.** Relative abundance of microbial populations at the family level in the duodenum, jejunum and FD, in the same subjects (Group 2, n=23).



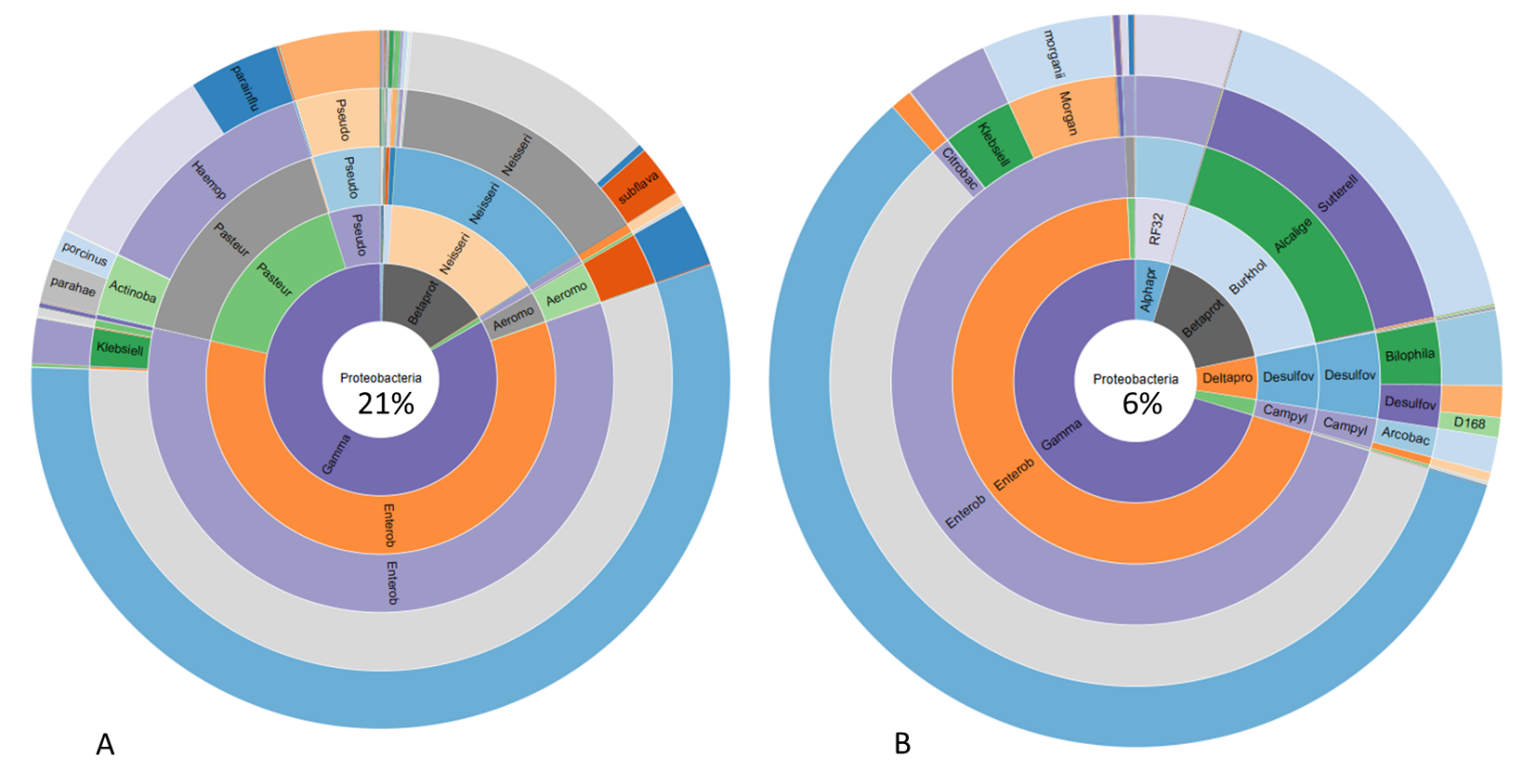
**Supplemental Figure 5.** **A** - PLS-DA plot of the microbial populations at the family level in different segments of the small intestine (duodenum - red, jejunum - green and farthest distance reached during DBE (FD) - blue) in the same subjects (Group 2, n=23). Transparent circles indicate the 95% confidence region. **B -** PLS-DA plot of the microbial populations at the family level in the duodenal and FD in the same subjects (Group 2, n=23). Duodenum – red, FD - green. Transparent circles indicate the 95% confidence region.



**Supplemental Figure 6.** Variable importance in projection (VIP) selected during PLS-DA analysis of families identified in duodenum and farthest distance (FD) in the same subjects (Group 2, n=23). Each colored cell on the right side corresponds to the relative abundance value of each normalized microbial family included in this analysis.



**Supplemental Figure 7.** Relative abundance of microbial populations at the genus level in the duodenum, jejunum, FD and stool in the same subjects (Group 3, n=8).



**Supplemental Figure 8.** Composition of phylum Proteobacteria in the small intestine (A) and stool (B).