(a) Taxonomic distribution of organisms associated with disease

1: Escherichia/Shigella
2: Enterobacteriaceae (unclassified)
3: Clostridiaceae (unclassified)
4: Clostridium
5: Faecalibacterium
6: Ruminococcaceae (unclassified)
7: Phascolarctobacterium
8: Veillonellaceae (unclassified)
9: Clostridiaceae
10: Ruminococcaceae

(b) Association of community ecology with IBD and environmental factors

- Diversity
- Evenness
- Richness

Phyla:
- Firmicutes
- Bacteroidetes
- Actinobacteria
- Proteobacteria
- Erysipelotrichi
- Alphaproteobacteria
- Gammaproteobacteria
- Betaproteobacteria

Families:
- Enterobacteriaceae
- Bacteroidaceae
- Ruminococcaceae
- Clostridiaceae
- Lachnospiraceae

Genera:
- Faecalibacterium
- Roseburia
- Blautia
- Eubacterium
- Odoribacter

- FDR(q) < 0.25

- UC
- CD
- Pancolonic
- Ileal

- Antibiotics
- Immunosuppression
- Mesalamine
- Smoking
- Steroids
- Stool

Diversity: 1.20, 0.90, 0.60, 0.30
Evenness: 1.20, 0.90, 0.60, 0.30
Richness: 1.20, 0.90, 0.60, 0.30