|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Rank** | **Indicator Taxa Value** | **Phylum** | **Class** | **Order** | **Family** | **Genus** |
| #1 | 0.9486617 | Bacteroidota | Bacteroidia | Bacteroidales | *Prevotellaceae* | *Prevotellaceae NK3B31 group* |
| #2 | 0.9481380 | Spirochaetota | Spirochaetia | Spirochaetales | *Spirochaetaceae* | *Treponema* |
| #3 | 0.9336436 | Bacteroidota | Bacteroidia | Bacteroidales | *Rikenellaceae* | *Rikenellaceae RC9 gut group* |
| #4 | 0.9156844 | Bacteroidota | Bacteroidia | Bacteroidales | *Prevotellaceae* | *Alloprevotella* |
| #5 | 0.8802860 | Bacteroidota | Bacteroidia | Bacteroidales | *Prevotellaceae* | *Prevotellaceae UCG-003* |
| #6 | 0.8774668 | Firmicutes | Clostridia | Lachnospirales | *Lachnospiraceae* | *Marvinbryantia* |
| #7 | 0.8767199 | Bacteroidota | Bacteroidia | Bacteroidales | *Prevotellaceae* | *Genus uncultured* |
| #8 | 0.8692888 | Firmicutes | Clostridia | Lachnospirales | *Lachnospiraceae* | *Eubacterium hallii group* |
| #9 | 0.8635102 | Proteobacteria | Gammaproteobacteria | Aeromonadales | *Succinivibrionaceae* | *Succinivibrio* |
| #10 | 0.8338405 | Firmicutes | Clostridia | Lachnospirales | *Lachnospiraceae* | *Lachnospiraceae ND3007 group* |
| #11 | 0.8328376 | Bacteroidota | Bacteroidia | Bacteroidales | *Prevotellaceae* | *Prevotellaceae\_UCG-001* |

**Table 1.** **Tanzanian gut microbiome greatly associated with taxa from the family *Lachnospiraceae* and *Prevotellacoccae*:** Indicator taxa analysis was carried out upon Tanzanian Data set. Significance was set at a P value of <0.05

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Rank** | **Indicator Taxa Value** | **Phylum** | **Class** | **Order** | **Family** | **Genus** |
| #1 | 0.9520242 | Actinobacteriota | Coriobacteriia | Coriobacteriales | *Coriobacteriaceae* | *Collinsella* |
| #2 | 0.9496711 | Verrucomicrobiota | Verrucomicrobiae | Verrucomicrobiales | *Akkermansiaceae* | *Akkermansia* |
| #3 | 0.9396726 | Bacteroidota | Bacteroidia | Bacteroidales | *Rikenellaceae* | *Alistipes* |
| #4 | 0.9385316 | Actinobacteriota | Actinobacteria | Bifidobacteriales | *Bifidobacteriaceae* | *Bifidobacterium* |
| #5 | 0.9364858 | Proteobacteria | Gammaproteobacteria | Enterobacterales | *Enterobacteriaceae* | *Escherichia-Shigella* |
| #6 | 0.9163843 | Firmicutes | Bacilli | Lactobacillales | *Streptococcaceae* | *Streptococcus* |
| #7 | 0.8946547 | Firmicutes | Clostridia | Oscillospirales | *Ruminococcaceae* | *UBA1819* |
| #8 | 0.8925271 | Actinobacteriota | Actinobacteria | Actinomycetales | *Actinomycetaceae* | *Actinomyces* |
| #9 | 0.8748514 | Proteobacteria | Gammaproteobacteria | Enterobacterales | *Ruminococcaceae* | *Incertae\_Sedis* |
| #10 | 0.8715185 | Actinobacteriota | Coriobacteriia | Coriobacteriales | *Enterobacteriaceae* | *N/A* |
| #11 | 0.8462536 | Actinobacteriota | Coriobacteriia | Coriobacteriales | *Eggerthellaceae* | *Slackia* |
| #12 | 0.7886247 | Actinobacteriota | Actinobacteria | Micrococcales | *Eggerthellaceae* | *Senegalimassilia* |

**Table 2.** **Columbian gut microbiome greatly associated with taxa from the phylum Actinobacteriota:** Indicator taxa analysis was carried out upon the Columbian Data set. Significance was set at a P value of <0.05