|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Location:** | Tanzania |  |  |  |  |  |
| **Rank** | **Indicator Value** | **Phylum** | **Class** | **Order** | **Family** | **Genus** |
| #1 | 0.949 | Bacteroidota | Bacteroidia | Bacteroidales | *Prevotellaceae* | *Prevotellaceae NK3B31 group* |
| #2 | 0.948 | Spirochaetota | Spirochaetia | Spirochaetales | *Spirochaetaceae* | *Treponema* |
| #3 | 0.934 | Bacteroidota | Bacteroidia | Bacteroidales | *Rikenellaceae* | *Rikenellaceae RC9 gut group* |
| #4 | 0.916 | Bacteroidota | Bacteroidia | Bacteroidales | *Prevotellaceae* | *Alloprevotella* |
| #5 | 0.880 | Bacteroidota | Bacteroidia | Bacteroidales | *Prevotellaceae* | *Prevotellaceae UCG-003* |
| #6 | 0.877 | Firmicutes | Clostridia | Lachnospirales | *Lachnospiraceae* | *Marvinbryantia* |
| #7 | 0.876 | Bacteroidota | Bacteroidia | Bacteroidales | *Prevotellaceae* | *Genus uncultured* |
| #8 | 0.869 | Firmicutes | Clostridia | Lachnospirales | *Lachnospiraceae* | *Eubacterium hallii group* |
| #9 | 0.863 | Proteobacteria | Gammaproteobacteria | Aeromonadales | *Succinivibrionaceae* | *Succinivibrio* |
| #10 | 0.834 | Firmicutes | Clostridia | Lachnospirales | *Lachnospiraceae* | *Lachnospiraceae ND3007 group* |
| #11 | 0.833 | 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* |

**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

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Tanzania** | |  | |  |  |  | |  | |  | |  |
| **Rank** | **Indicator Value** | | **P-Value** | **Phylum** | **Class** | | **Order** | | **Family** | | **Genus** | | |
| #1 | 0.949 | | 0.005 | Bacteroidota | Bacteroidia | | Bacteroidales | | *Prevotellaceae* | | *Prevotellaceae NK3B31 group* | | |
| #2 | 0.948 | | 0.005 | Spirochaetota | Spirochaetia | | Spirochaetales | | *Spirochaetaceae* | | *Treponema* | | |
| #3 | 0.934 | | 0.005 | Bacteroidota | Bacteroidia | | Bacteroidales | | *Rikenellaceae* | | *Rikenellaceae RC9 gut group* | | |
| #4 | 0.916 | | 0.005 | Bacteroidota | Bacteroidia | | Bacteroidales | | *Prevotellaceae* | | *Alloprevotella* | | |
| #5 | 0.880 | | 0.005 | Bacteroidota | Bacteroidia | | Bacteroidales | | *Prevotellaceae* | | *Prevotellaceae UCG-003* | | |
| #6 | 0.877 | | 0.005 | Firmicutes | Clostridia | | Lachnospirales | | *Lachnospiraceae* | | *Marvinbryantia* | | |
| #7 | 0.876 | | 0.005 | Bacteroidota | Bacteroidia | | Bacteroidales | | *Prevotellaceae* | | *Genus uncultured* | | |
| #8 | 0.869 | | 0.005 | Firmicutes | Clostridia | | Lachnospirales | | *Lachnospiraceae* | | *Eubacterium hallii group* | | |
| #9 | 0.863 | | 0.005 | Proteobacteria | Gammaproteobacteria | | Aeromonadales | | *Succinivibrionaceae* | | *Succinivibrio* | | |
| #10 | 0.834 | | 0.005 | Firmicutes | Clostridia | | Lachnospirales | | *Lachnospiraceae* | | *Lachnospiraceae ND3007 group* | | |
|  |  | | **Colombia** |  |  | |  | |  | |  | | |
| #1 | 0.952 | | 0.005 | Actinobacteriota | Coriobacteriia | | Coriobacteriales | | *Coriobacteriaceae* | | *Collinsella* | | |
| #2 | 0.950 | | 0.005 | Verrucomicrobiota | Verrucomicrobiae | | Verrucomicrobi-ales | | *Akkermansiaceae* | | *Akkermansia* | | |
| #3 | 0.940 | | 0.005 | Bacteroidota | Bacteroidia | | Bacteroidales | | *Rikenellaceae* | | *Alistipes* | | |
| #4 | 0.939 | | 0.005 | Actinobacteriota | Actinobacteria | | Bifidobacteriales | | *Bifidobacteriaceae* | | *Bifidobacterium* | | |
| #5 | 0.936 | | 0.005 | Proteobacteria | Gammaproteobacteria | | Enterobacterales | | *Enterobacteriaceae* | | *Escherichia-Shigella* | | |
| #6 | 0.916 | | 0.005 | Firmicutes | Bacilli | | Lactobacillales | | *Streptococcaceae* | | *Streptococcus* | | |
| #7 | 0.895 | | 0.005 | Firmicutes | Clostridia | | Oscillospirales | | *Ruminococcaceae* | | *UBA1819* | | |
| #8 | 0.893 | | 0.005 | Actinobacteriota | Actinobacteria | | Actinomycetales | | *Actinomycetaceae* | | *Actinomyces* | | |
| #9 | 0.875 | | 0.005 | Proteobacteria | Gammaproteobacteria | | Enterobacterales | | *Ruminococcaceae* | | *Incertae\_Sedis* | | |
| #10 | 0.872 | | 0.005 | Actinobacteriota | Coriobacteriia | | Coriobacteriales | | *Enterobacteriaceae* | | *N/A* | | |

**Table 1. Top 10 indicator taxa within Tanzanian and Colombian gut microbiome:** Indicator taxa analysis was carried out. Significance was set at a P value of <0.05.