**Supplementary Table 2: Differential abundance of duodenal MAM taxa between CLD and control subjects. Median and mean abundance (%) are shown.**

1. Phyla, DESeq2

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Taxa (phylum)** | **p (DESeq2)** | **FDRq** | **CLD mean** | **Control mean** | **CLD median** | **Control median** |
| Firmicutes | 0.00023 | 0.0011 | 73.1 | 56.54 | 71.59 | 59.35 |
| Actinobacteria | 0.034 | 0.085 | 5.4 | 10.48 | 4.48 | 10.25 |
| Bacteroidetes | 0.54 | 0.68 | 15.4 | 23.08 | 13.32 | 23.68 |
| Proteobacteria | 0.58 | 0.68 | 5.29 | 8.74 | 3.42 | 2.95 |
| Fusobacteria | 0.68 | 0.68 | 0.81 | 1.16 | 0.14 | 0.83 |

1. Genera, DESeq2

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Taxa (genus)** | **p (DESeq2)** | **FDRq** | **CLD mean** | **Control mean** | **CLD median** | **Control median** |
| Moryella | 0.00045 | 0.011 | 0.27 | 0.86 | 0.16 | 0.83 |
| Veillonella | 0.0021 | 0.026 | 8.04 | 13.09 | 6.05 | 8.98 |
| Porphyromonas | 0.0039 | 0.033 | 0.91 | 3.76 | 0.004 | 0.7 |
| Prevotella | 0.054 | 0.25 | 14.45 | 19.29 | 12.79 | 15.73 |
| Atopobium | 0.057 | 0.25 | 0.65 | 1.69 | 0.1 | 0.76 |
| Streptococcus | 0.06 | 0.25 | 60.34 | 39.24 | 58.02 | 49.25 |
| Gemella | 0.079 | 0.28 | 1.4 | 1.38 | 0.92 | 0.76 |
| Actinomyces | 0.12 | 0.36 | 3.4 | 7.14 | 2.4 | 4.5 |
| Rothia | 0.16 | 0.44 | 1.34 | 1.65 | 0.92 | 0.53 |
| Fusobacterium | 0.33 | 0.82 | 0.36 | 0.94 | 0.09 | 0.59 |
| f\_Enterobacteriaceae | 0.42 | 0.86 | 0.0042 | 0.044 | 0 | 0 |
| f\_Lachnospiraceae | 0.42 | 0.86 | 0.0024 | 0 | 0 | 0 |
| Neisseria | 0.45 | 0.86 | 2.68 | 6.13 | 0.31 | 1.14 |
| Collinsella | 0.53 | 0.91 | 0.008 | 0.0013 | 0 | 0 |
| Actinobacillus | 0.57 | 0.91 | 0.9 | 0.39 | 0 | 0.085 |
| Ruminococcus | 0.64 | 0.91 | 0.00087 | 0 | 0 | 0 |
| Bacteroides | 0.69 | 0.91 | 0.044 | 0.024 | 0 | 0.015 |
| Haemophilus | 0.72 | 0.91 | 1.37 | 1.82 | 0.68 | 0.87 |
| Parabacteroides | 0.73 | 0.91 | 0.00064 | 0 | 0 | 0 |
| Granulicatella | 0.76 | 0.91 | 1.05 | 1.09 | 0.99 | 0.77 |
| Leptotrichia | 0.76 | 0.91 | 0.45 | 0.22 | 0 | 0.12 |
| f\_Erysipelotrichaceae | 0.81 | 0.92 | 0.0003 | 0 | 0 | 0 |
| Megasphaera | 0.99 | 1 | 0.44 | 0.87 | 0.15 | 0.5 |
| Kingella | 1 | 1 | 0.34 | 0.36 | 0.063 | 0.18 |
| Lactobacillus | 1 | 1 | 1.56 | 0 | 0 | 0 |

1. Phyla, ANCOM

No significant features found

1. Genera, ANCOM

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Selected Taxa (genus)** | **CLD mean** | **Control mean** | **CLD median** | **Control median** |
| Actinomyces | 3.4 | 7.14 | 2.4 | 4.5 |
| Moryella | 0.27 | 0.86 | 0.16 | 0.83 |
| Porphyromonas | 0.91 | 3.76 | 0.004 | 0.7 |

**Abbreviations:** CLD, chronic liver disease; DESeq2, Differential expression analysis based on the negative binomial distribution; ANCOM, analysis of composition of microbiomes; FDRq, false discovery rate q value.

Significance defined as p<0.05 and FDRq<0.1 for DESeq2; ANCOM only lists significantly different taxa.