**Supplemental Table 2.** Relative abundances of the top (>1 %) bacterial genera and phyla in fecal samples from FMT recipients.

|  |  |
| --- | --- |
|  | **% of total bacteria by group (n=12 animals per group)** |
|  | **DonorCD-Veh**  | **DonorCD-DHT** | **DonorHFHS-Veh** | **DonorHFHS-DHT** | **No FMT** |
| **Top genera FMT recipients** | **med.** | **IQR** | **med.** | **IQR** | **med.** | **IQR** | **med.** | **IQR** | **med.** | **IQR** |
| †S24-7 unclass. | 59.2 | 12.48 | 60.2 | 6.92 | 36.6 | 27.10 | 53.6 | 5.55 | 34.3 | 11.43 |
| #Lachnospiraceae NK4A136 | 13.8 | 9.38 | 9.7 | 6.37 | 15.2 | 5.45 | 11.7 | 9.19 | 9.7 | 8.93 |
| §Desulfovibrio | 4.1 | 1.37 | 8.4 | 1.77 | 7.9 | 3.43 | 11.0 | 3.30 | 8.6 | 3.29 |
| †Bacteroides | 3.8 | 1.64 | 4.1 | 3.56 | 6.5 | 10.47 | 5.1 | 4.73 | 10.3 | 6.45 |
| #Lachnospiraceae unclass. | 2.4 | 2.10 | 2.1 | 0.87 | 5.5 | 7.18 | 2.8 | 1.30 | 8.0 | 8.20 |
| ‡Ackermanns | 3.8 | 5.59 | 3.8 | 6.19 | 0.9 | 2.82 | 1.1 | 1.94 | 0.0 | 0.00 |
| #Clostridiales vadinBB60 | 2.4 | 1.25 | 0.5 | 0.34 | 1.1 | 1.73 | 1.4 | 0.23 | 1.9 | 0.85 |
| †Rikenellaceae RC9 | 1.4 | 2.75 | 0.3 | 0.59 | 1.2 | 2.02 | 0.4 | 0.44 | 2.5 | 2.09 |
| §Parasutterella | 0.9 | 0.51 | 0.6 | 0.77 | 0.8 | 1.76 | 1.8 | 0.93 | 1.5 | 1.53 |
| #Ruminococcaceae unclass. | 0.9 | 0.55 | 0.7 | 0.71 | 1.4 | 1.23 | 1.0 | 0.36 | 2.1 | 1.83 |
| †Alistipes | 0.9 | 0.56 | 0.5 | 0.28 | 0.5 | 0.17 | 0.7 | 0.38 | 3.1 | 1.11 |
| †Alloprevotella | 0.8 | 0.32 | 0.5 | 0.25 | 0.5 | 0.59 | 1.0 | 0.56 | 1.3 | 3.20 |
| **Top phyla FMT recipients** | **med.** | **IQR** | **med.** | **IQR** | **med.** | **IQR** | **med.** | **IQR** | **med.** | **IQR** |
| †Bacteroidetes | 66.4 | 7.58 | 67.9 | 8.20 | 54.0 | 21.19 | 61.7 | 6.22 | 55.4 | 7.07 |
| #Firmicutes | 23.5 | 5.59 | 16.0 | 4.26 | 26.3 | 18.72 | 19.7 | 7.93 | 32.5 | 11.98 |
| §Proteobacteria | 5.4 | 1.54 | 9.2 | 2.09 | 10.7 | 5.34 | 13.3 | 3.67 | 12.7 | 3.44 |
| ‡Verrucomicrobia | 3.8 | 5.59 | 3.8 | 6.19 | 0.9 | 2.82 | 1.1 | 1.94 | 0.0 | 0.00 |

*Unclass., unclassified (the lowest classified taxonomic level is shown). #Firmicutes; †Bacteroidetes; §Proteobacteria; ‡Verrucomicrobia.*