|  |  |
| --- | --- |
|  | Higher proportion of taxa |
|  | Lesser proportion of taxa |

All zeros in this data were replaced using multiplicative replacement, followed by calculating the centered-log ratio for each data point. Taxonomy was taken from Megan program.

|  |  |  |  |
| --- | --- | --- | --- |
| **Phylum Bacteroidetes** | |  |  |
|  | **Family Bacteriaceae** | **Chick 1** | **Chick 2** |
|  | *Bacteroides fragilis* | 3.41529 | 0.87924 |
|  | *Bacteroides thetaiotaomicron* | 1.61005 | -3.0468 |
|  | *Bacteroides plebeius* | -1.9444 | -0.2165 |
|  | uncultured Bacteroides sp. | -1.9444 | -0.3395 |
|  | **Family Chitinophagaceae** |  |  |
|  | *Sediminibacterium goheungense* | -1.9444 | 0.31862 |
|  | **Family Cytophagaceae** |  |  |
|  | *Arcicella aurantiaca* | -1.9444 | -0.381 |
|  | **Family Flavobacteriaceae** |  |  |
|  | *Cloacibacterium normanense* | -1.9444 | 0.58874 |
|  | Unclassified Bacteroidetes (Bacteroidetes bacterium) | -1.9444 | -0.0659 |
|  |  |  |  |
| **Phylum Fusobacteria** | |  |  |
|  | **Family Fusobacteriaceae** |  |  |
|  | *Fusobacterium mortiferum* | 3.65663 | 2.30135 |
|  | *Fusobacterium ulcerans* | 3.32175 | -3.0468 |
|  | *Fusobacterium varium* | 5.11311 | -3.0468 |
|  | *Fusobacterium sp. HMSC073F01* | 2.20051 | -3.0468 |
| **Phylum Proteobacteria** | |  |  |
|  | **Family Caulobacteraceae** |  |  |
|  | *Asticcacaulis excentricus* | -1.9444 | 0.12591 |
|  | *Caulobacter vibrioides* | -1.9444 | -0.0667 |
|  | **Family Burkholderiaceae** |  |  |
|  | *Cupriavidus pauculus* | -1.9444 | -0.3757 |
|  | **Burkholderiales genera incertae sedis** |  |  |
|  | **Aquabacterium olei** | -1.9444 | 0.33155 |
|  | *Aquincola tertiaricarbonis* | 1.53837 | 1.81564 |
|  | *Tepidicella xavieri* | 1.14398 | -3.0468 |
|  | **Family Comamonadaceae** |  |  |
|  | Curvibacter sp. PAE-UM | -1.9444 | -0.3011 |
|  | Kinneretia asaccharophila | -1.9444 | -0.2401 |
|  | **Unclassified Burkholderiales** |  |  |
|  | *Burkholderiales bacterium* | -1.9444 | 0.28994 |
|  | **Family Campylobacteriaceae** |  |  |
|  | *Campylobacter coli* | 0.96424 | -0.1487 |
|  | **Family Helicobacteraceae** |  |  |
|  | *Helicobacter pullorum* | -0.5493 | 0.54931 |
|  | **Family Enterobacteriaceae** |  |  |
|  | *Escherichia coli* | 4.05823 | 1.41547 |
|  | *Salmonella enterica* | 0.86779 | -3.0468 |
|  | *Proteus mirabilis* | 1.47047 | -3.0468 |
|  | **Family Bdellovibrionaceae** |  |  |
|  | *Bdellovibrio* sp. 28-41-41 | -1.9444 | 0.06767 |
| **Phylum Actinobacteria** | |  |  |
|  | **Family Bifidobacteriaceae** |  |  |
|  | *Bifidobacterium pseudolongum* | -1.9444 | -0.0713 |
|  | **Family Lawsonellaceae** |  |  |
|  | *Lawsonella clevelandensis* | -1.9444 | 0.9708 |
|  | **Family Propionibacteriaceae** |  |  |
|  | *Cutibacterium acnes* | -1.9444 | 1.44372 |
| **Phylum Deinococcus-Thermus** | |  |  |
|  | **Family Thermaceae** |  |  |
|  | *Thermus scotoductus* | -1.9444 | -0.341 |
| **Phylum Firmicutes** | |  |  |
|  | **Family Bacillaceae** |  |  |
|  | *Bacillus marisflavi* | -1.9444 | -0.341 |
|  | *Pseudogracilibacillus auburnensis* | 2.62966 | -0.0652 |
|  | **Family Enterococcaceaa** |  |  |
|  | *Enterococcus avium* | 3.57304 | -3.0468 |
|  | *Enterococcus casseliflavus* | 2.64082 | -3.0468 |
|  | *Enterococcus cecorum* | 4.38633 | 4.46866 |
|  | *Enterococcus columbae* | -1.9444 | -0.1836 |
|  | *Enterococcus faecalis* | 4.68838 | 0.1517 |
|  | *Enterococcus faecium* | 2.80619 | 2.18622 |
|  | *Enterococcus gallinarum* | 5.15766 | 1.48358 |
|  | *Enterococcus hirae* | 1.97218 | 1.1602 |
|  | *Enterococcus saccharolyticus* | 1.50539 | -3.0468 |
|  | *Enterococcus sp. HSIEG1* | 2.40582 | -3.0468 |
|  | **Family Lactobacillaceae** |  |  |
|  | *Lactobacillus agilis* | 2.44768 | 0.70906 |
|  | *Lactobacillus amylovorus* | 2.02538 | 0.89265 |
|  | *Lactobacillus aviarius* | 2.77953 | 1.90761 |
|  | *Lactobacillus crispatus* | 1.30216 | 1.69791 |
|  | *Lactobacillus delbrueckii* | 1.34992 | -0.2718 |
|  | *Lactobacillus gigeriorum* | 3.31376 | -3.0468 |
|  | *Lactobacillus ingluviei* | 2.25662 | -3.0468 |
|  | *Lactobacillus johnsonii* | 1.69472 | -0.3667 |
|  | *Lactobacillus kitasatonis* | 2.9594 | 1.67903 |
|  | *Lactobacillus saerimneri* | 1.61885 | -3.0468 |
|  | *Lactobacillus salivarius* | 2.86708 | 1.44778 |
|  | ***Family Clostridiaceae*** |  |  |
|  | *Clostridium cadaveris* | -1.9444 | 0.44324 |
|  | *Clostridium cuniculi* | -1.9444 | -0.3516 |
|  | *Clostridium nigeriense* | -1.9444 | 0.13296 |
|  | *Clostridium paraputrificum* | -1.9444 | 0.26536 |
|  | *Clostridium perfringens* | -1.9444 | 3.96393 |
|  | *Clostridium sp. CL-6* | -1.9444 | 0.11366 |
|  | **Unclassified Clostridiaceae** |  |  |
|  | *Clostridiaceae bacterium* | -1.9444 | 0.09631 |
|  | *Clostridiaceae bacterium 14S0207* | -1.9444 | 0.98121 |
|  | **Clostridiales incertae sedis** |  |  |
|  | *[Eubacterium] brachy* | -1.9444 | -0.0902 |
|  | **Family Lachnospiraceae** |  |  |
|  | *Merdimonas faecis* | -1.9444 | 1.31594 |
|  | *Niameybacter massiliensis* | -1.9444 | 2.31353 |
|  | *Tyzzerella sp. An114* | -1.9444 | -0.0448 |
|  | **Family Peptostreptococcaceae** |  |  |
|  | Clostridioides difficile | -1.9444 | 3.0602 |
|  | Paraclostridium bifermentans | -1.9444 | -0.2505 |
|  | Romboutsia timonensis | -1.9444 | -0.076 |
|  | Terrisporobacter glycolicus | -1.9444 | 1.5089 |
|  | Terrisporobacter othiniensis | -1.9444 | 1.24492 |
|  | **Unclassified Peptostreptococcaceae** |  |  |
|  | Peptostreptococcaceae bacterium | -1.9444 | 1.90332 |
|  | **Famliy Ruminococcaceae** |  |  |
|  | Pseudoflavonifractor sp. An85 | -1.9444 | -0.2321 |
|  | **Family Eryspelotrichaceae** |  |  |
|  | *[Clostridium] spiroforme* | 1.07541 | 1.86321 |
|  | *Faecalicoccus pleomorphus* | 1.49514 | 0.24341 |
|  | *Faecalitalea cylindroides* | -1.9444 | 0.5714 |
|  | *Massilimicrobiota timonensis* | -1.9444 | -0.3906 |
|  | *Traorella massiliensis* | -1.9444 | -0.0235 |
|  | **Family Acidaminococcaceae** |  |  |
|  | *Phascolarctobacterium* sp. CAG:266 | -1.9444 | 0.16485 |
|  | **Family Selenomonadaceae** |  |  |
|  | *Megamonas rupellensis* | -1.9444 | -0.2375 |
|  | **Family Veillonellaceae** |  |  |
|  | *Veillonella magna* | 1.13222 | -3.0468 |
|  | **Not classified** |  |  |
|  | uncultured bacterium | -1.9444 | -0.0061 |