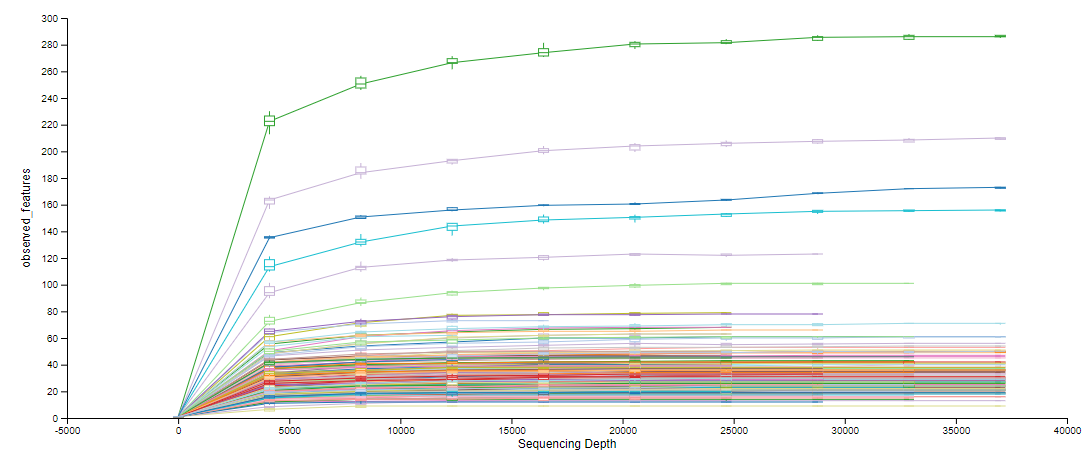
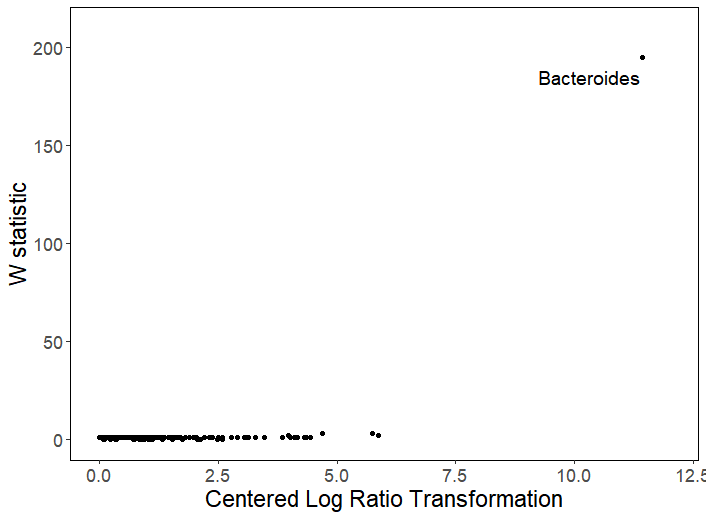
**Supplemental Material**



**Figure S1. Sampling depth was selected to be 4250 for phylogenetic analysis.** The alpha-rarefaction plot was generated using QIIME. The sequencing depth is the number of sequenced bases per sample, while the observed features represent ASV. Curves represent different wlz values.

**Table S1. *Maternal weight classification based on BMI.*** The BMI definitions used to subset data for the maternal BMI determinant.

|  |  |
| --- | --- |
| Body Mass Index (BMI) | Classification |
| Less than 18.5 | Underweight |
| Between 18.5 and 24.9 | Normal |
| Between 24.9 and 29.9 | Overweight |
| Above 30 | Obese |



**Figure S2. Only the Bacteroides genus was differentially abundant between modes of delivery.** Analysis of composition of microbiomes (ANCOM) was done at the genus level between c-section and vaginally delivered infants in QIIME. W statistic measures significance of differences while Centered Log Ratio Transformation represents the magnitude of differences. For *Bacteroides* (labelled), W=195. Data was visualized in R.