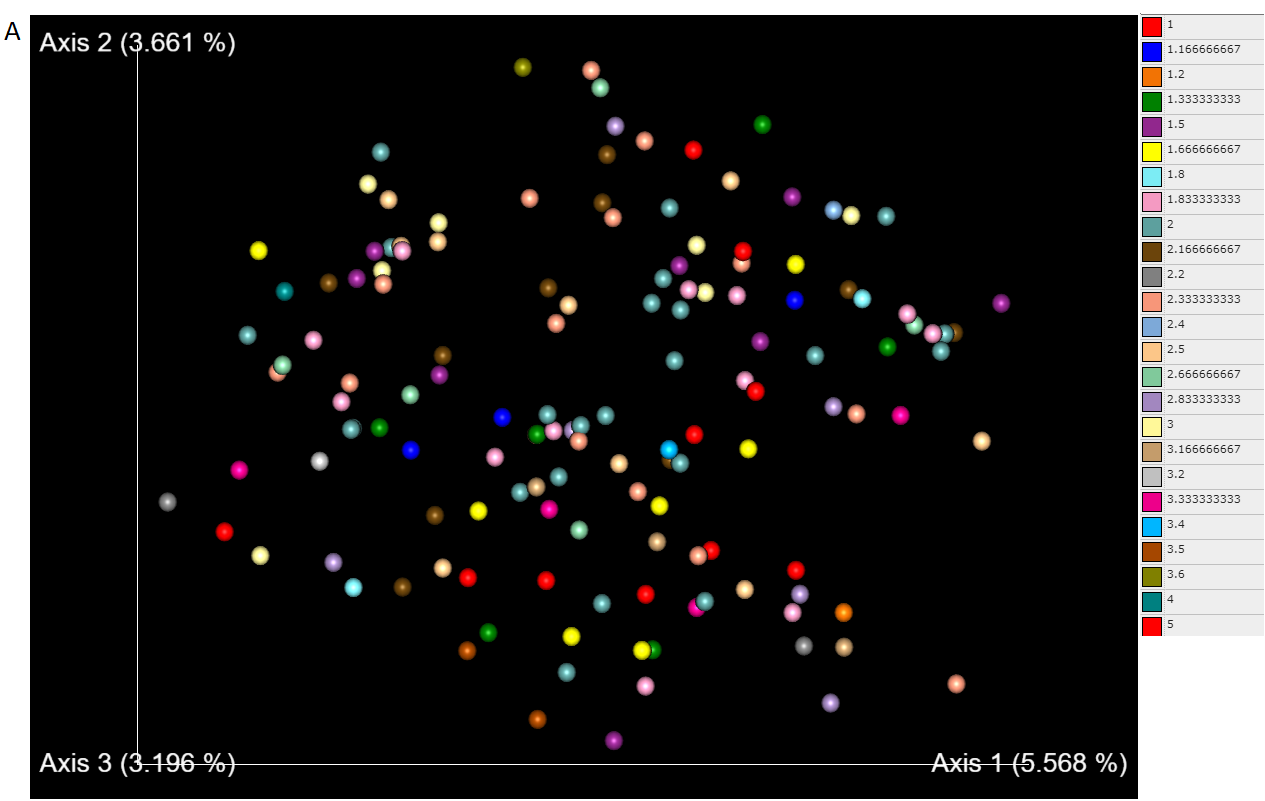
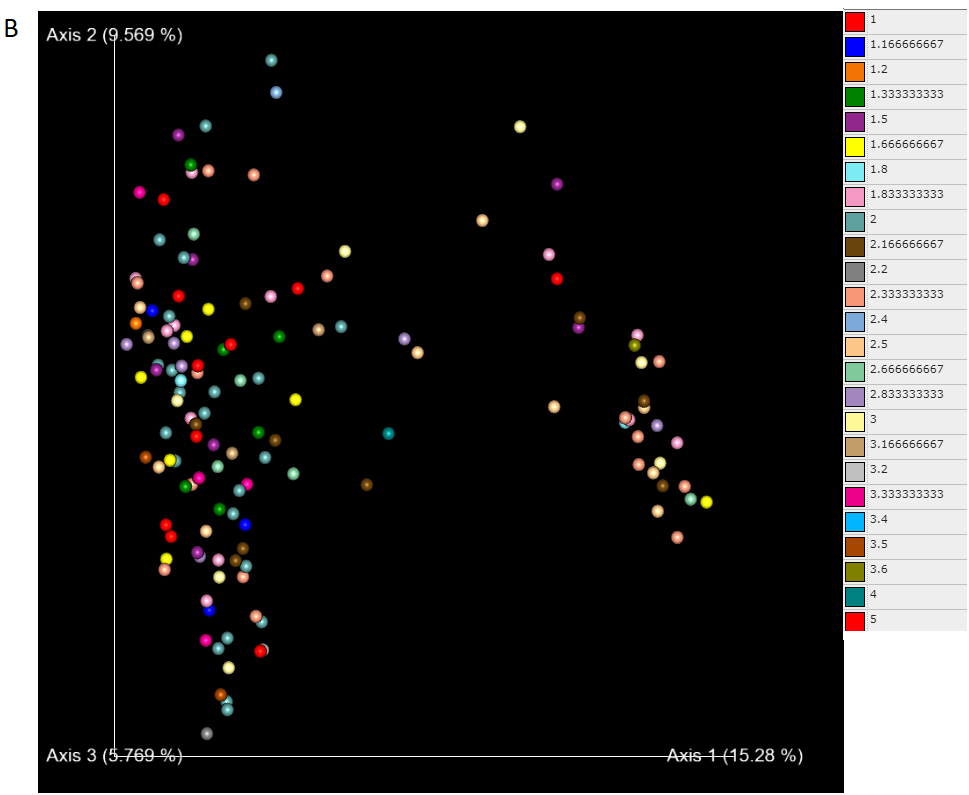
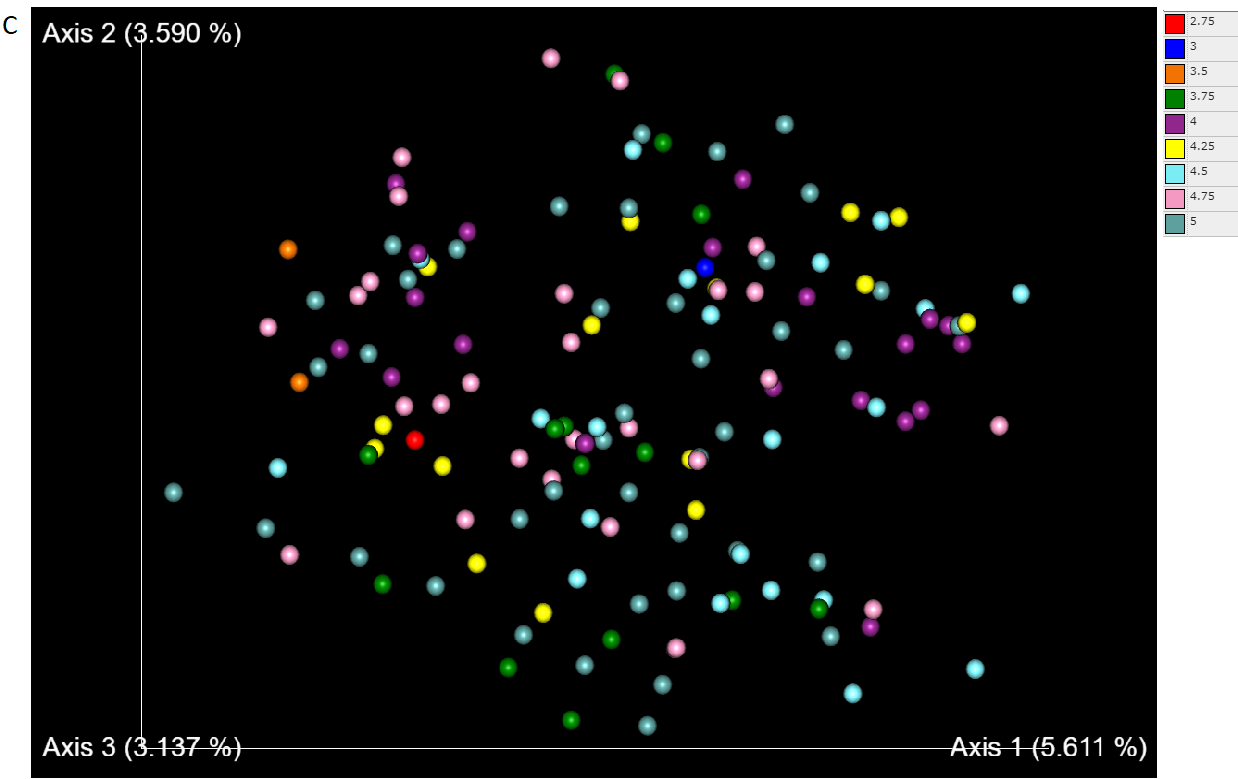
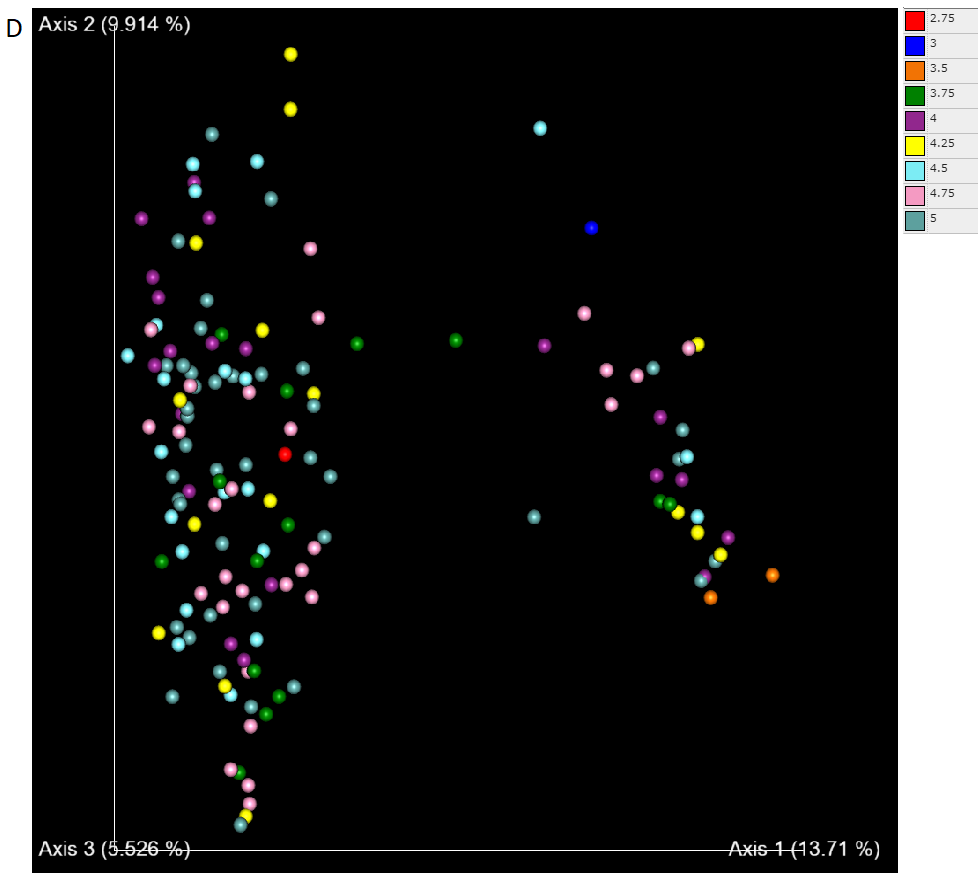
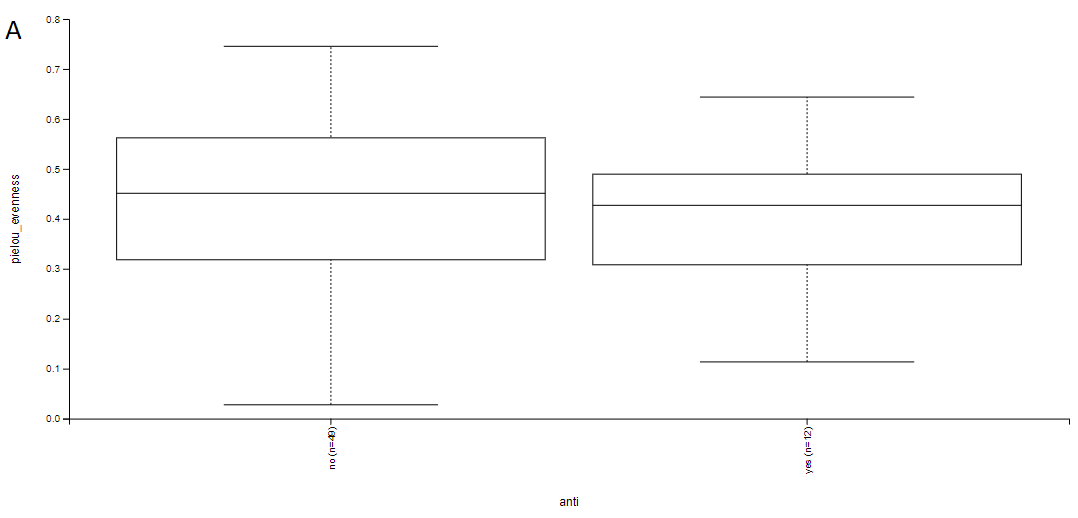
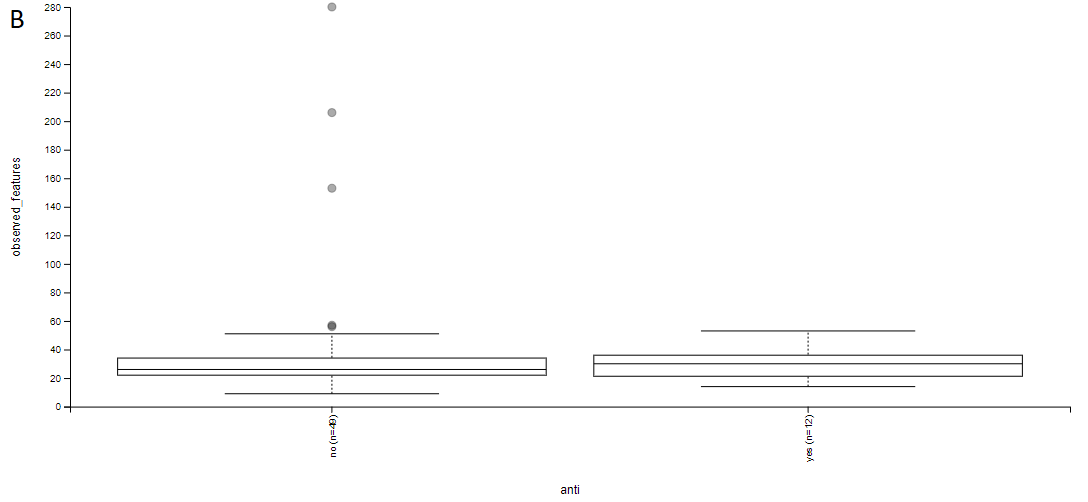
**Supplemental Figure 1. Box plots show no significant differences in alpha diversity in infant gut microbiomes based on food enjoyment/responsiveness.** Pielou’s evenness and observed features metrics are shown for (A, B) food responsiveness and (C, D) enjoyment, respectively. A 1-5 Likert scale was used for both responsiveness and enjoyment. p > 0.05 for all alpha diversity metrics (Kruskal-Wallis pairwise test).

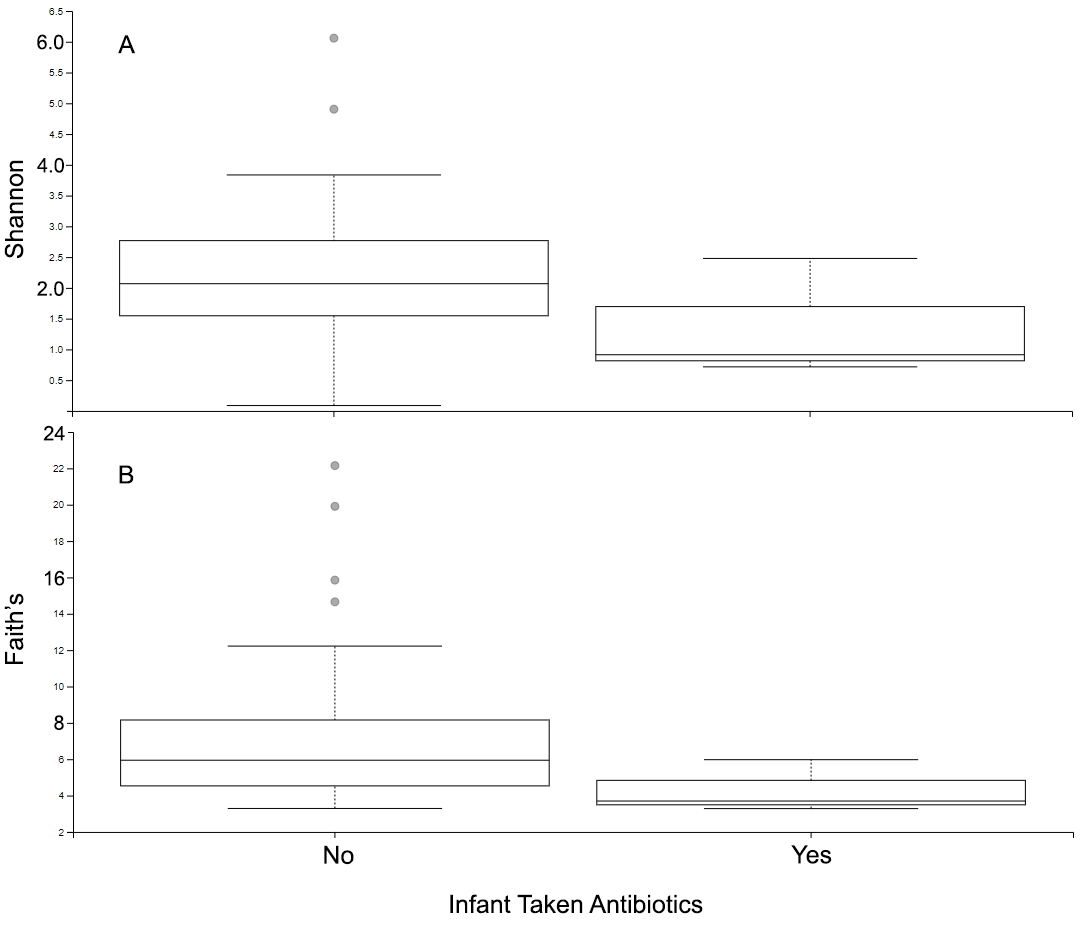




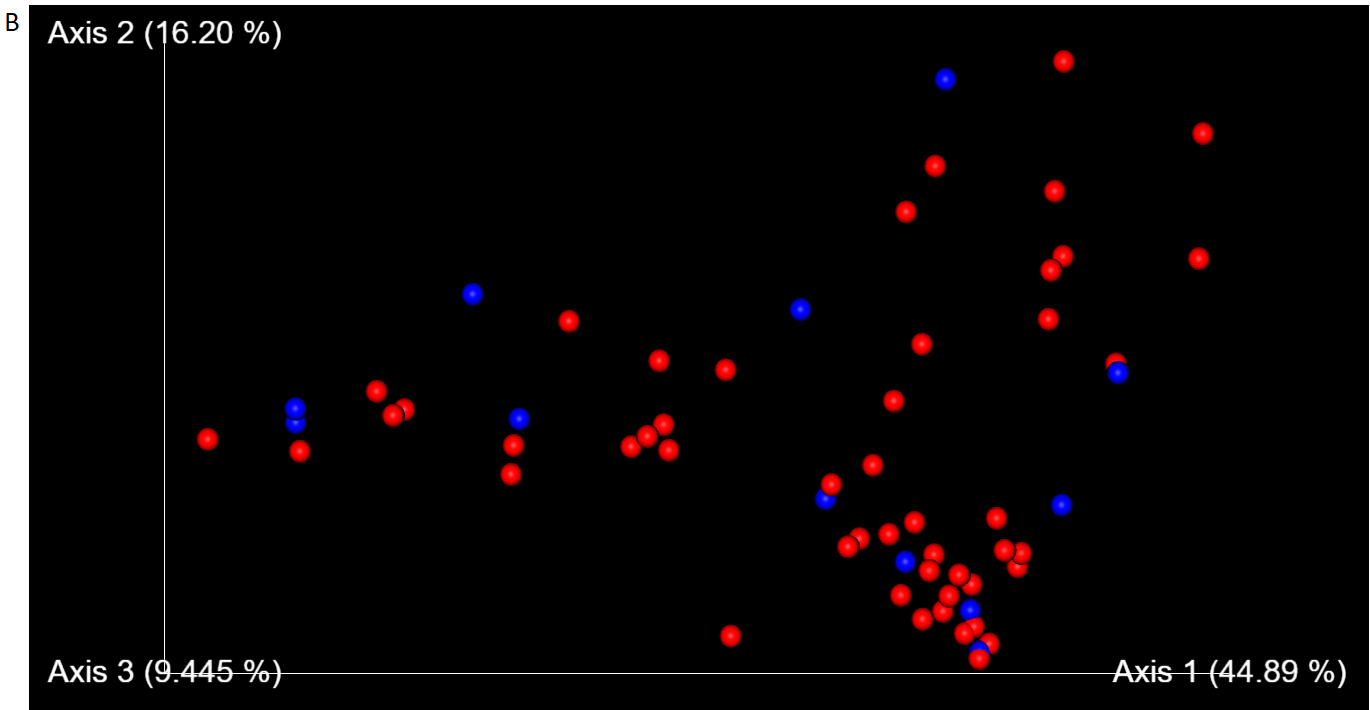
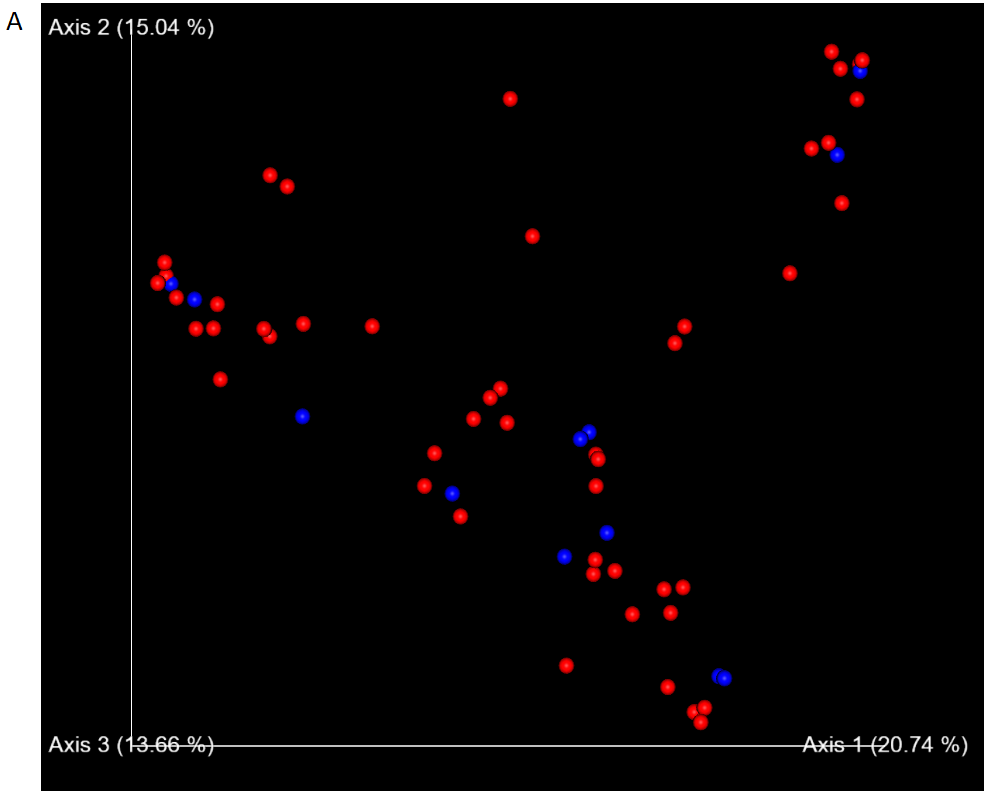
**Supplementary Figure 2. PCoA plots show no distinct microbial communities in infant gut microbiome based on food enjoyment/responsiveness.** Jaccard’s and unweighted Unifrac distance are shown for (A, B) food responsiveness and (C, D) enjoyment, respectively. A 1-5 Likert scale was used for both responsiveness and enjoyment.

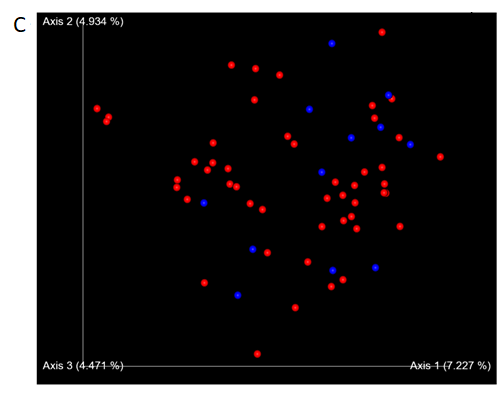


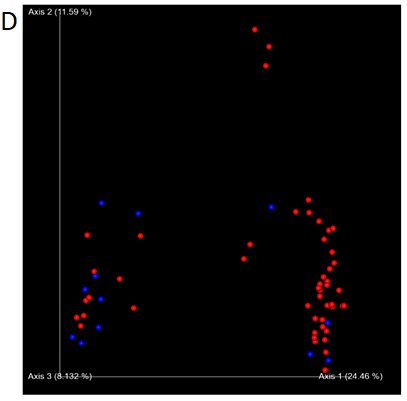
**Supplemental Figure 3. Box plots show no significant differences in alpha diversity for infant gut microbiomes based on antibiotic use.** (A) Pielou’s evenness and (B) observed features metrics are shown. N = 49 for no antibiotics and N = 12 for antibiotics used. p = 0.676 for A, p = 0.771 for B (Kruskal-Wallis pairwise test).

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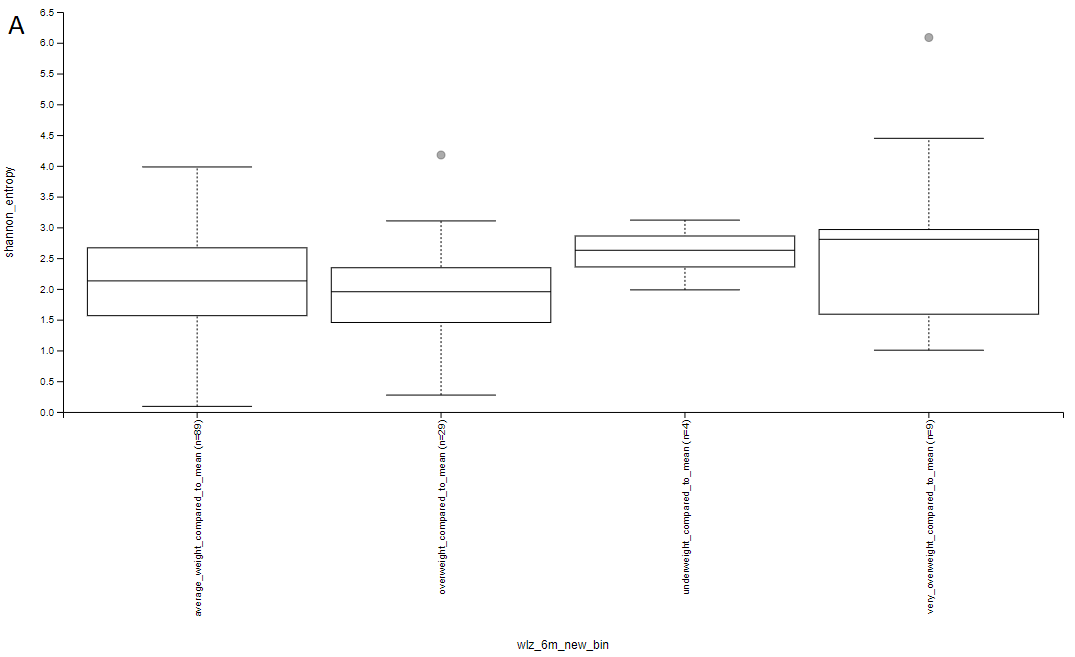
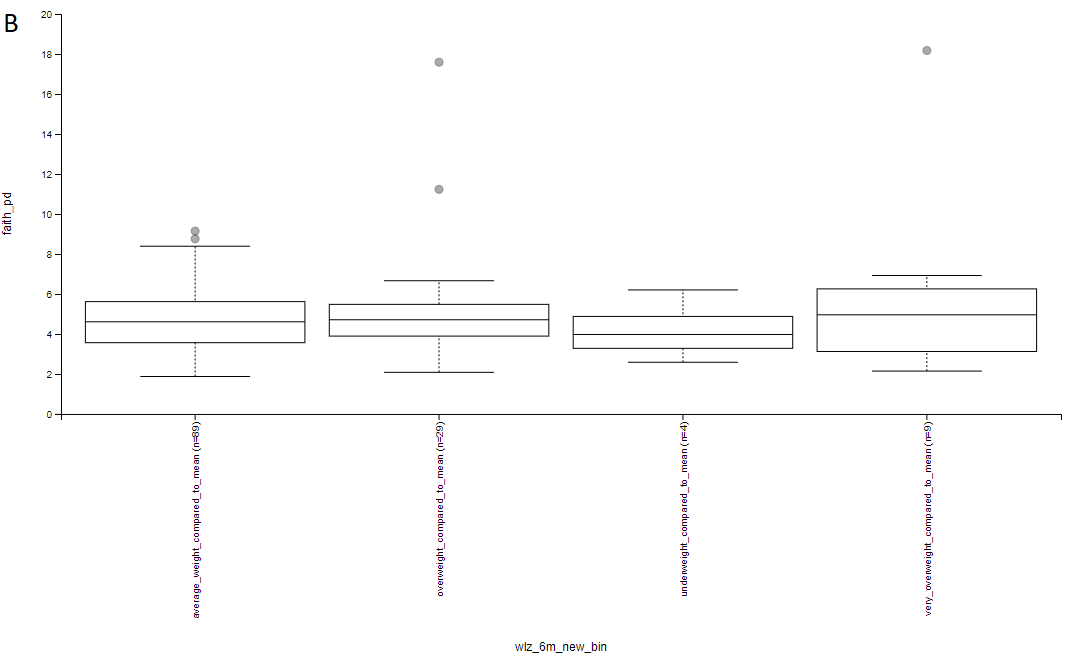
**Supplemental Figure 4. Boxplots showing no significant difference in alpha diversity for infant gut microbiomes based on antibiotic use.** (A) Shannon’s and (B) Faith’s phylogenetic diversity metrics are shown for food enjoyment. p = 0.430 for A, p = 0.929 for B (Kruskal-Wallis pairwise test).

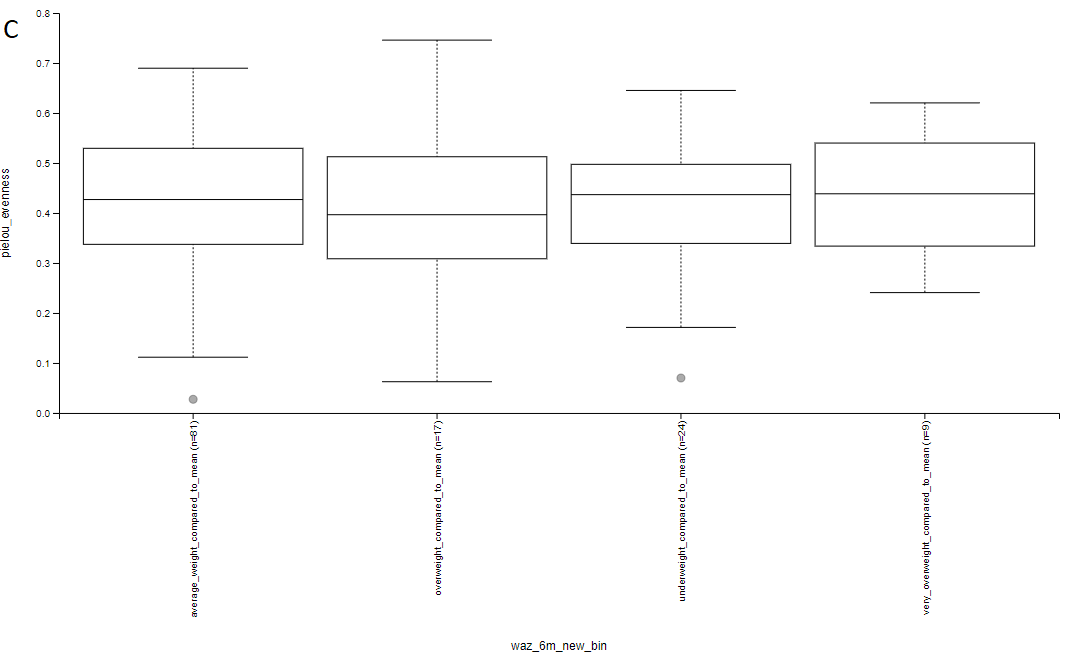


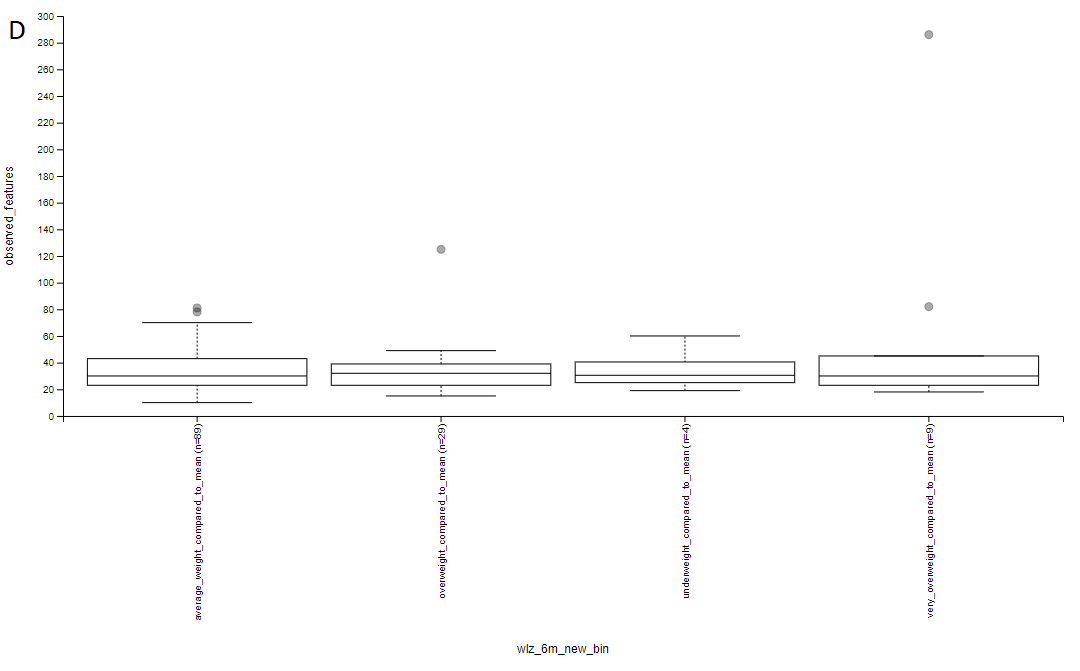


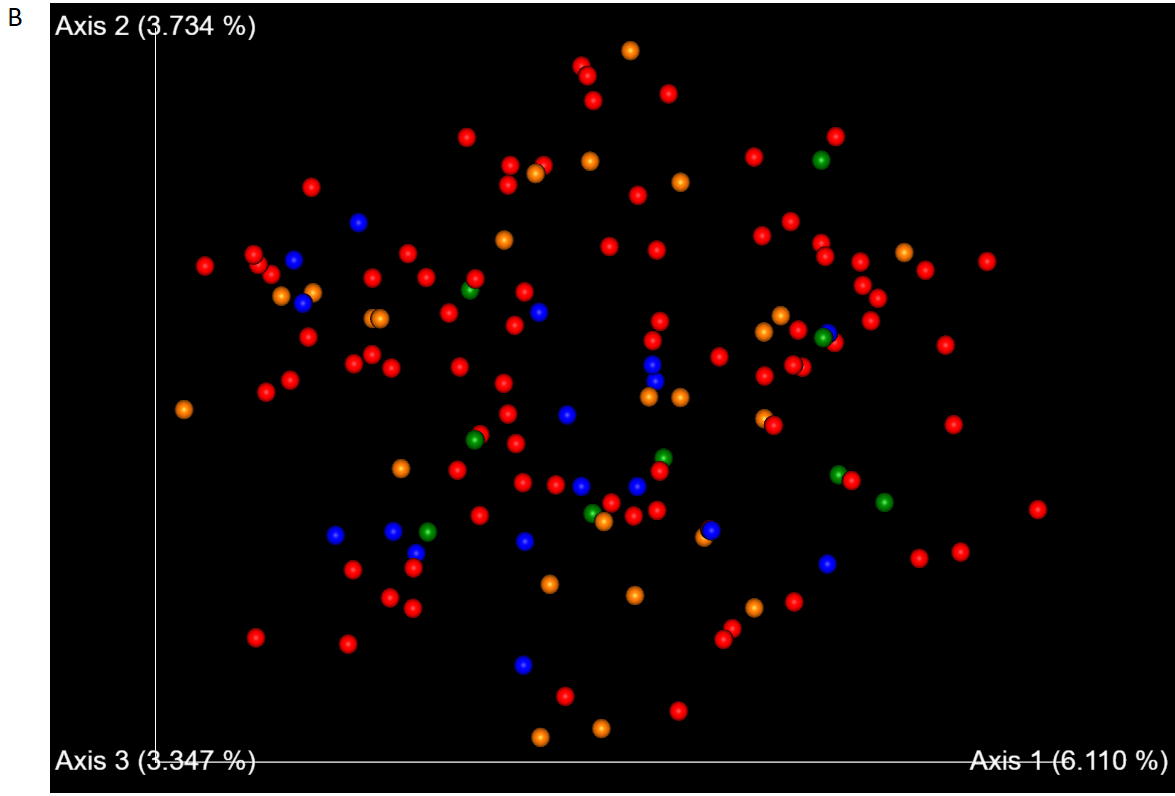
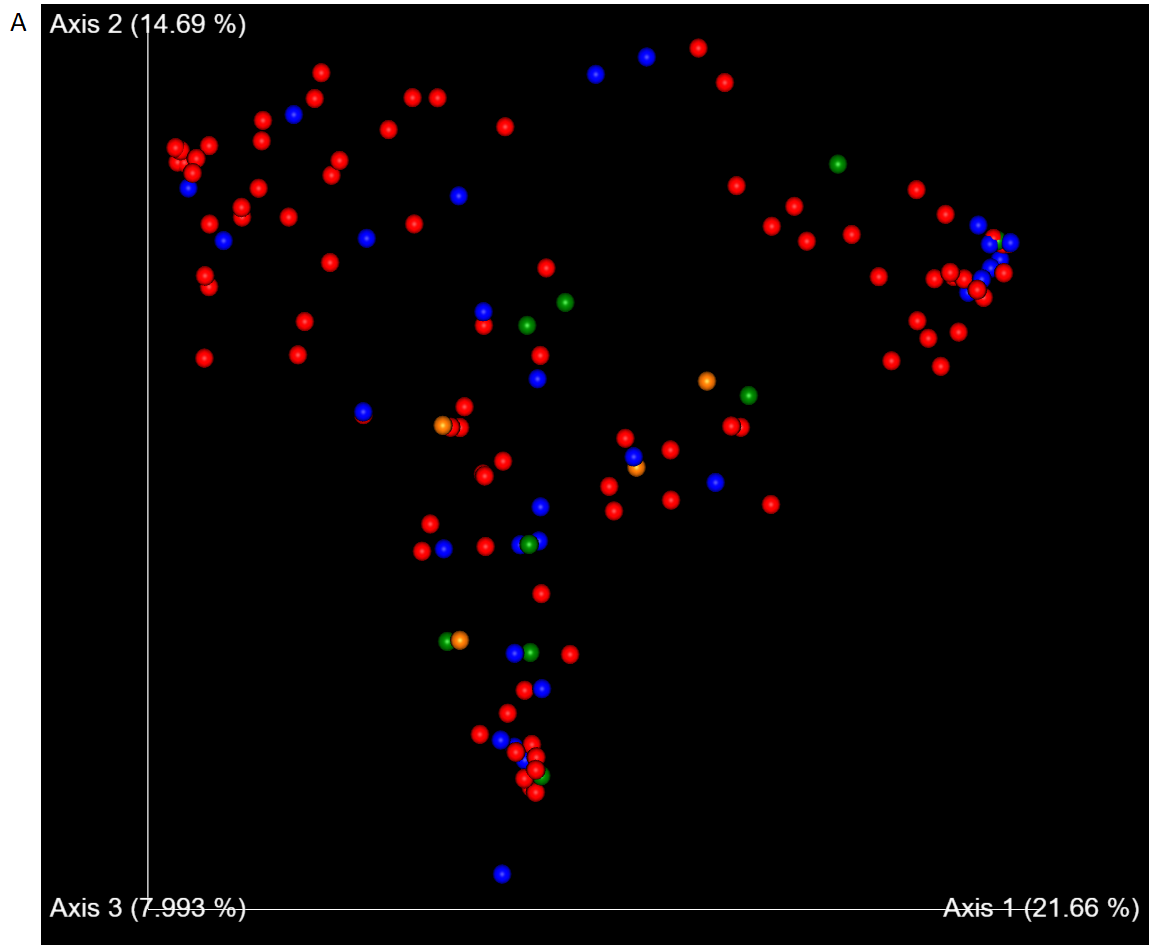


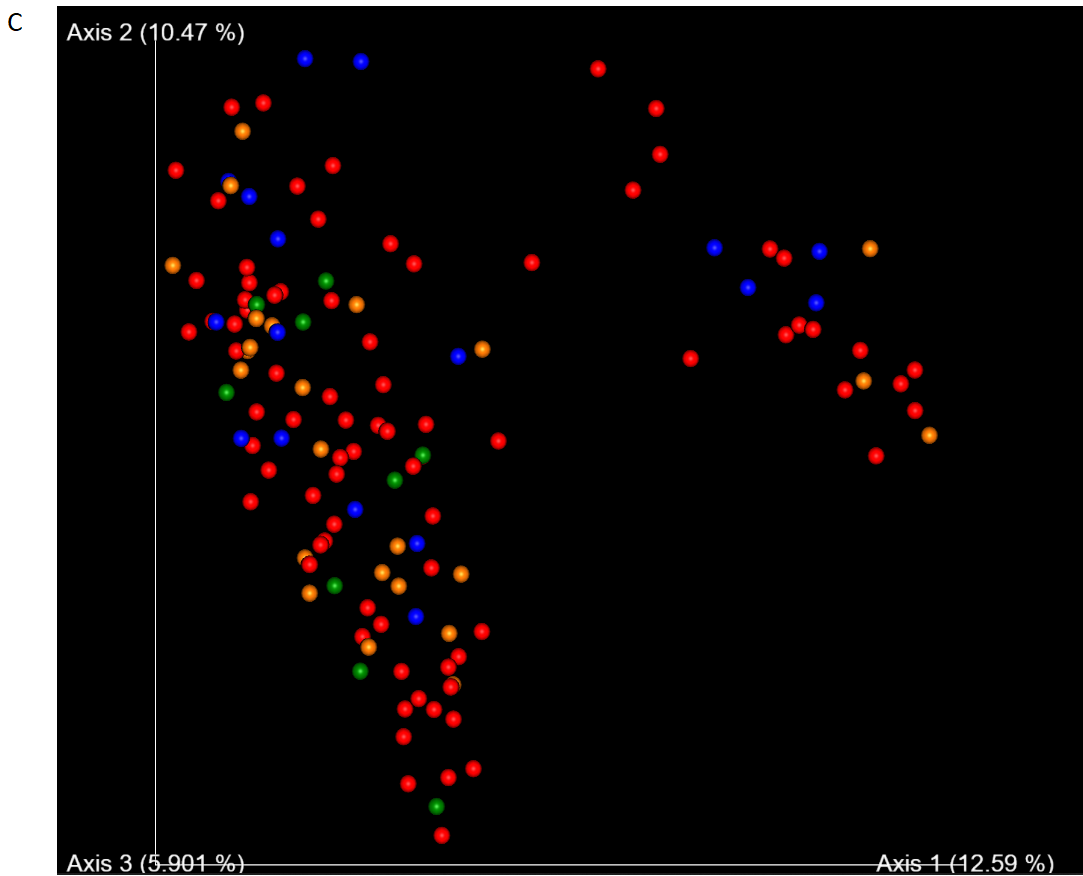
**Supplemental Figure 5. PCoA plots showing that there are no distinct microbial communities in infant gut microbiomes based on antibiotic use.** (A) Bray-Curtis, (B) weighted UniFrac, (C) Jaccard’s and (D) unweighted UniFrac distances are shown between infants who used antibiotics (blue) and did not use antibiotics (red). N = 49 for no antibiotics and N = 12 for antibiotics used.

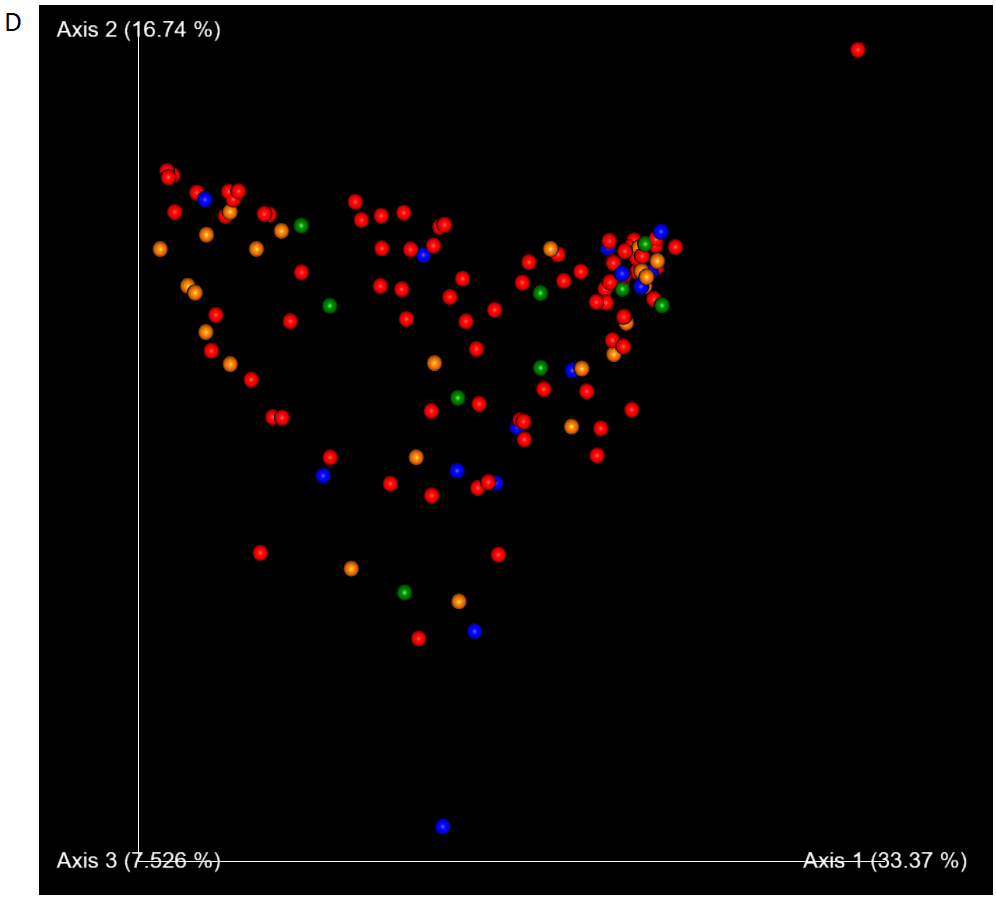




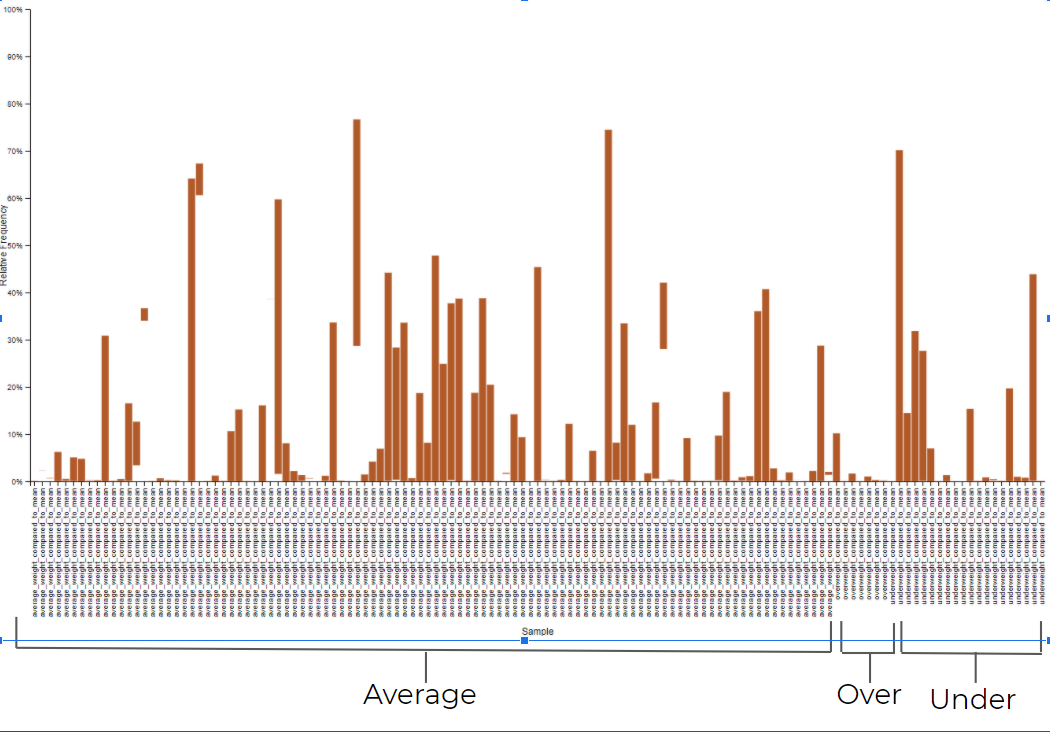
**Supplemental Figure 6. Boxplots show no significant differences in alpha diversity for infant gut microbiomes based on weight compared to mean weight-to-length at 6 months**. (A) Shannon’s, (B) Faith’s, (C) Pielou’s evenness and (D) observed features distances are shown between infants who are underweight, average weight, overweight and very overweight. There are no significant differences among all the groups as p > 0.05.







**Supplemental Figure 7. PCoA plots show no distinct microbial communities in infant gut microbiomes based on weight compared to mean weight-to-length at 6 months**. (A) Bray-Curtis, (B) Jaccard’s, (C) unweighted UniFrac and (D) weighted UniFrac distances are shown between infants who are underweight (orange), average weight (red), overweight (blue) and very overweight (green).



**Supplemental Figure 8: Taxonomic bar graph showing relative frequency of Bacteroidetes phyla present in infants sorted by weight for lengths at 6 months.** Taxonomic level 2 (phyla) was used.

**Table S1. Kruskal-Wallis analysis of food responsiveness on microbial composition.** There is no significant difference between infant gut microbial communities and infants who responded to food differently.

|  |  |
| --- | --- |
| Shannon Diversity | 0.774 |
| Observed Features | 0.859 |
| Faith’s Phylogenetic Diversity | 0.417 |
| Pielou’s Evenness | 0.755 |

**Table S2. Kruskal-Wallis analysis of food enjoyment on microbial composition.** There is no significant difference between infant gut microbial communities and infants who enjoyed food differently.

|  |  |
| --- | --- |
| Shannon Diversity | 0.834 |
| Observed Features | 0.452 |
| Faith’s Phylogenetic Diversity | 0.670 |
| Pielou’s Evenness | 0.760 |

**Table S3. Kruskal-Wallis analysis for infants with and without antibiotic usage.** There is no significant difference between infant gut microbial communities with and without antibiotic usage.

|  |  |
| --- | --- |
| Shannon Diversity | p = 0.430 |
| Observed Features | p = 0.771 |
| Faith’s Phylogenetic Diversity | p = 0.929 |
| Pielou’s Evenness | p = 0.676 |

**Table S4. Kruskal-Wallis analysis for obese, healthy weight and underweight infants.** There is no significant difference in infant gut microbial diversity between the three groups for all alpha diversity metrics

|  |  |
| --- | --- |
| Shannon Diversity | p = 0.430 |
| Observed Features | p = 0.771 |
| Faith’s Phylogenetic Diversity | p = 0.929 |
| Pielou’s Evenness | p = 0.676 |

**Table S5. PERMANOVA analysis for infants and food responsiveness**. There is no significant difference between infant gut microbial communities and infants who responded to food differently.

|  |  |
| --- | --- |
| Bray-Curtis | p = 0.987 |
| Weighted UniFrac | p = 0.996 |
| Jaccard | p = 0.461 |
| Unweighted UniFrac | p = 0.381 |

**Table S6. PERMANOVA analysis for infants and food enjoyment**. There is no significant difference between infant gut microbial communities and infants who enjoyed food differently.

|  |  |
| --- | --- |
| Bray-Curtis | p = 0.075 |
| Weighted UniFrac | p = 0.091 |
| Jaccard | p = 0.582 |
| Unweighted UniFrac | p = 0.351 |

**Table S7. PERMANOVA analysis for infants with and without antibiotic usage**. There is no significant difference between infant gut microbial communities with and without antibiotic usage.

|  |  |
| --- | --- |
| Bray-Curtis | p = 0.913 |
| Weighted UniFrac | p = 0.428 |
| Jaccard | p = 0.711 |
| Unweighted UniFrac | p = 0.188 |