Text, Supplemental Digital Content 3

Analysis 2: Serial evaluation of MR infants. Seventeen MR infants were sampled at all 3 age points permitting a serial analysis of developmental change within each infant. Linear mixed effect modeling revealed that community richness was characterized by an increase in diversity that stabilized at 8 weeks (F(2,16)=3.175, *p*=0.055). However, there was no difference in beta diversity over time. Despite the relative stability of these diversity indices, the relative abundance of genera did change. *Prevotella*, the most common genera, increased to 22.8% (F(2,32)=3.29; *p*=0.05), with higher levels at 8 weeks than at 2 and 4 weeks (*p*=0.053; *p*=0.011, respectively). *Bifidobacteria* were second most abundant, comprising an average 15.5% of identified taxa, and the levels were stable during active nursing. *Lactobacillus* abundance diverged, increasing to 6.7% by 4 weeks of age, but decreased by nearly half as other taxa became prominent at 8 weeks (F(2,32)=5.82, *p=0*.007). KEGG orthologs analyses did not identify any age-related predictions in microbial gene function that survived correction for FDR in this smaller subset of MR infants.