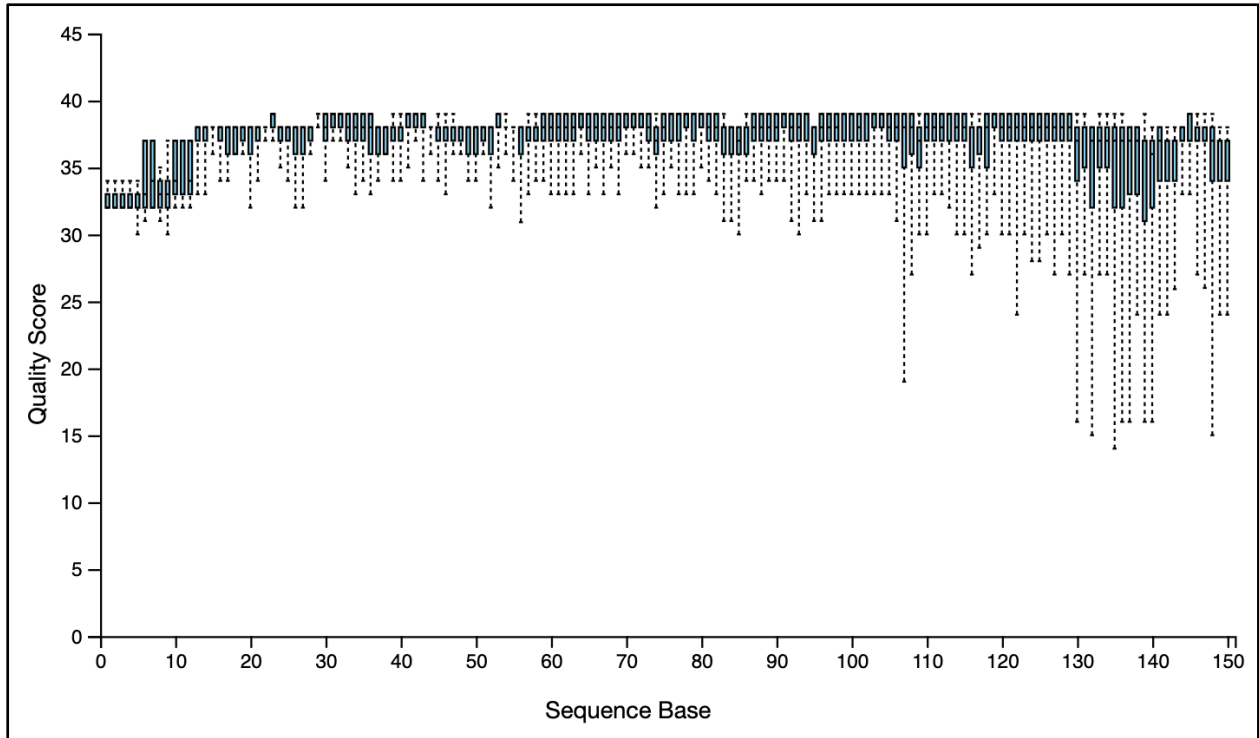## Supplement materials

Figure S1. Quality scores for demultiplexed sequence reads. The x-axis represents position of the sequence base, from 0 to 150. The y-axis represents the quality score (Phred score) of each base.
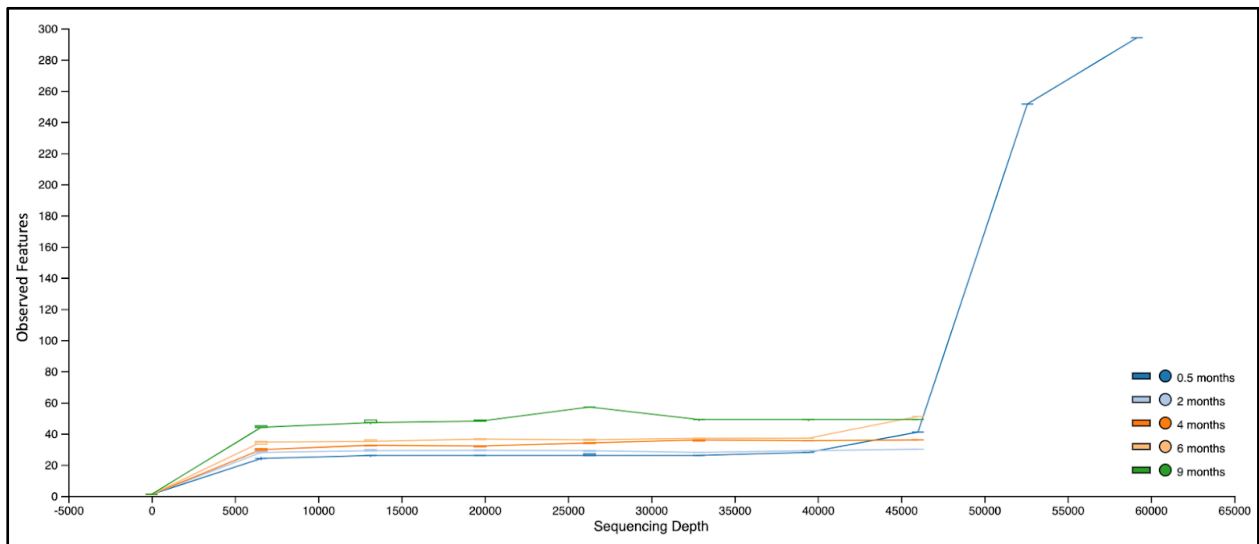
Figure S2. Alpha rarefaction curves of all infants samples based on time of collections. The x-axis represents the sequencing depth (the number of reads in each sample). The y-axis represents the Shannon diversity/richness at each sequencing depth.

Supplemental Scripts

Supplementary scripts can be found at: https://github.com/Mellaw/MICB447T4