Supplementary Figure 1

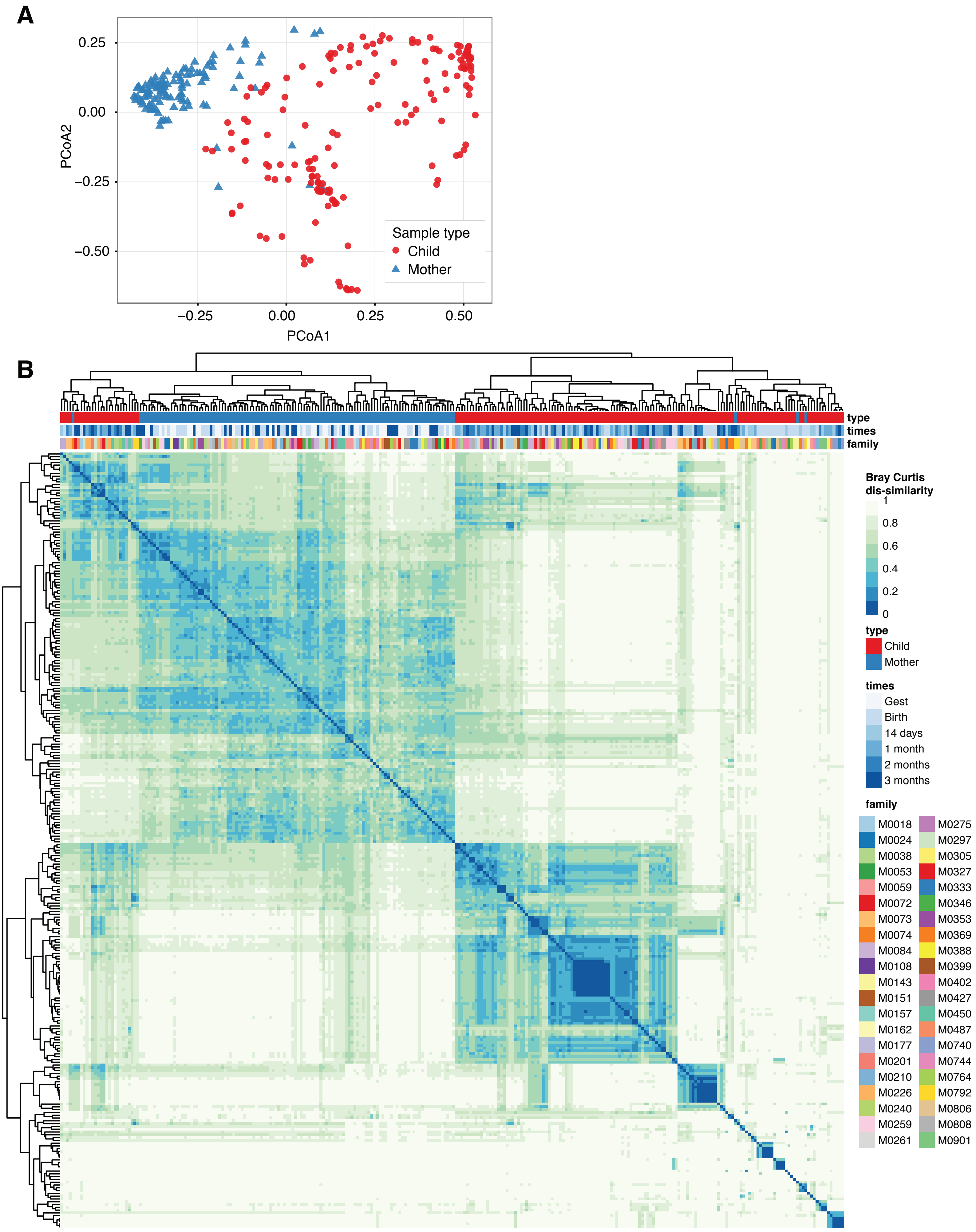

Figure S1 (related to Figure 1): (A) Genus-level clustering based on first two components of principle coordinate analysis (PCoA). The PCoA results based on genus relative abundance profiles for each sample in the cohort, using Bray-Curtis dissimilarity. Mother and child samples show distinct patterns after dimensionality reduction with PCoA. The two types of samples are statistically different (p<0.001, with the PERMANOVA analysis, using the adonis R function). **(B) Clustering of pairwise comparisons using species-level community profiles**
The Bray-Curtis dissimilarity of the MetaPhlan community profiles for all samples appearing in the cohort. Clustering was performed with the *complete linkage* method using euclidean distance.

Supplementary Figure 2

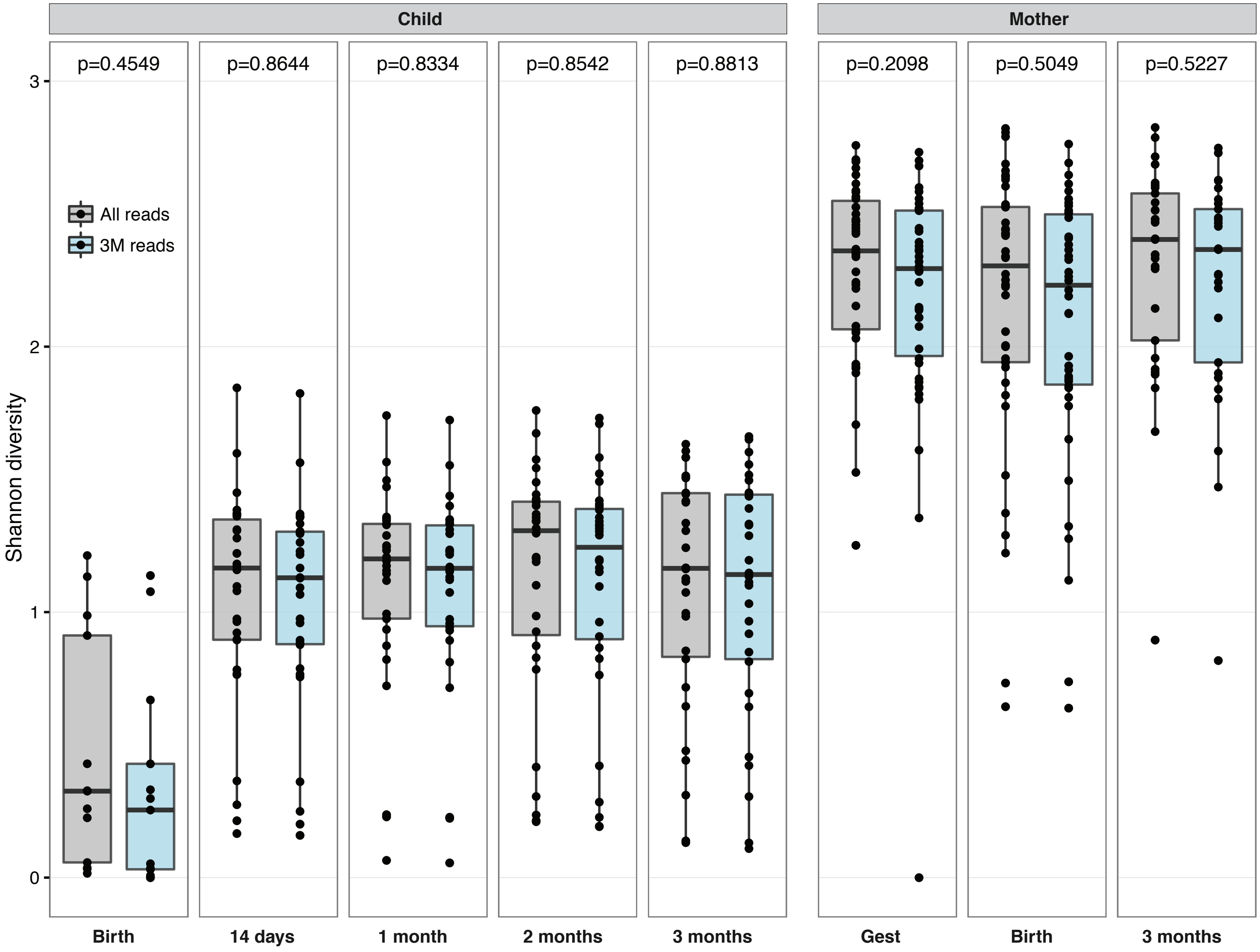

Figure S2 (related to Figure 1): Alpha-diversity of mother and child samples are robust to read downsampling
Shannon diversity calculated for each time point using all reads (above) and a subset of 3 million of the reads (below). Inputs were the species-level relative abundance profiles for each sample as reported by MetaPhlan, and p-values were calculated by t-test.

Supplementary Figure 3

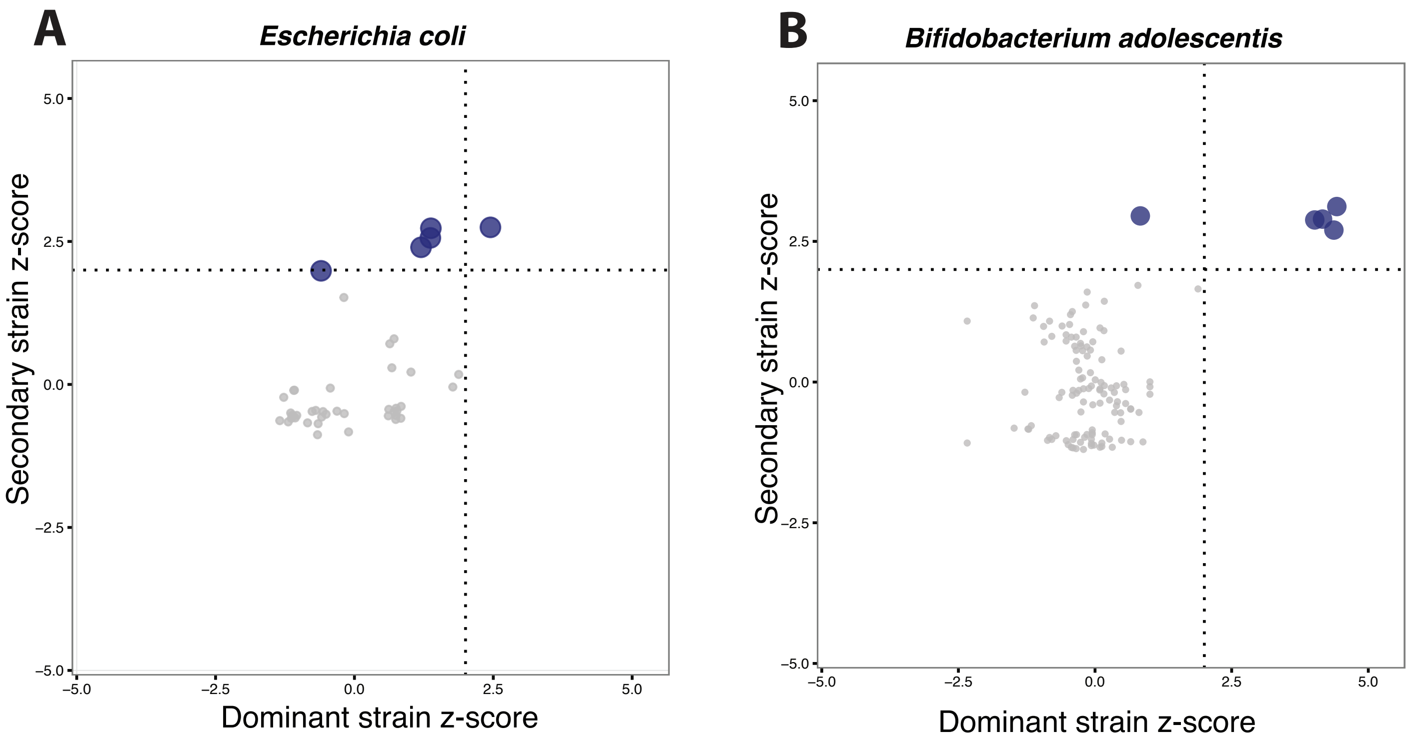

Figure S3 (related to Figure 2): Strain transmission analysis for *B. adolescentis* and *E. coli*.
Distributions of dominant- and secondary-strain z-scores for **(A)** *E. coli*. and **(B)** *B. adolescentis*, calculated as in **Figure 2C-F**.

Supplementary Figure 4

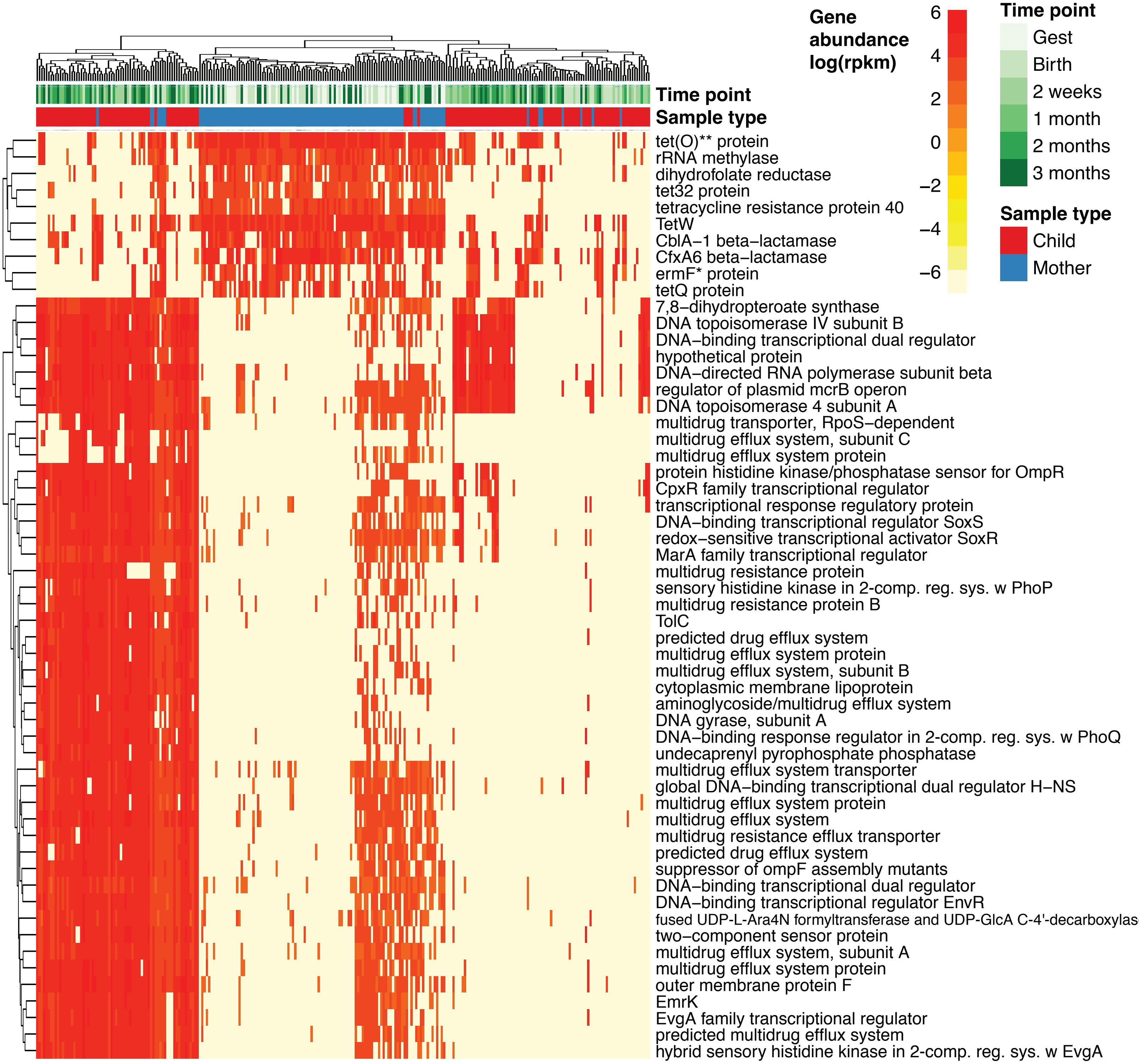

Figure S4 (related to STAR Methods and Measuring antibiotic resistance genes): Clustering of antibiotic resistance genes as measured by ShortBRED

Clustering of high abundance antibiotic resistance genes based on sequences belonging to the Comprehensive Antibiotic Resistance Database. Genes with low abundance across the cohort were not included. Entries are reported as log(rpkm).