Supporting Information

Koenig et al. 10.1073/pnas.1000081107

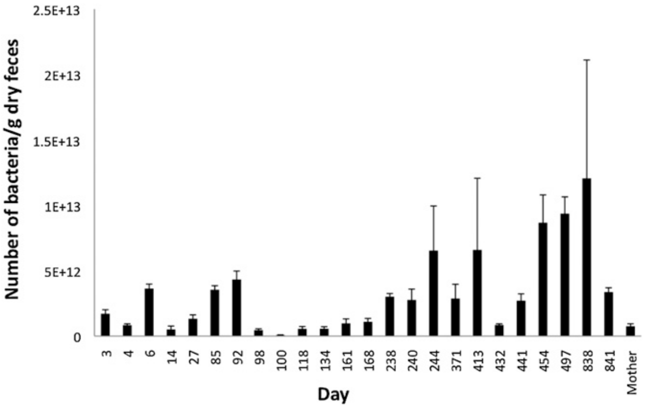

Fig. S1. Bacterial load in fecal samples determined by quantitative PCR. Means of five replicates per sample are plotted. Error bars are SDs.

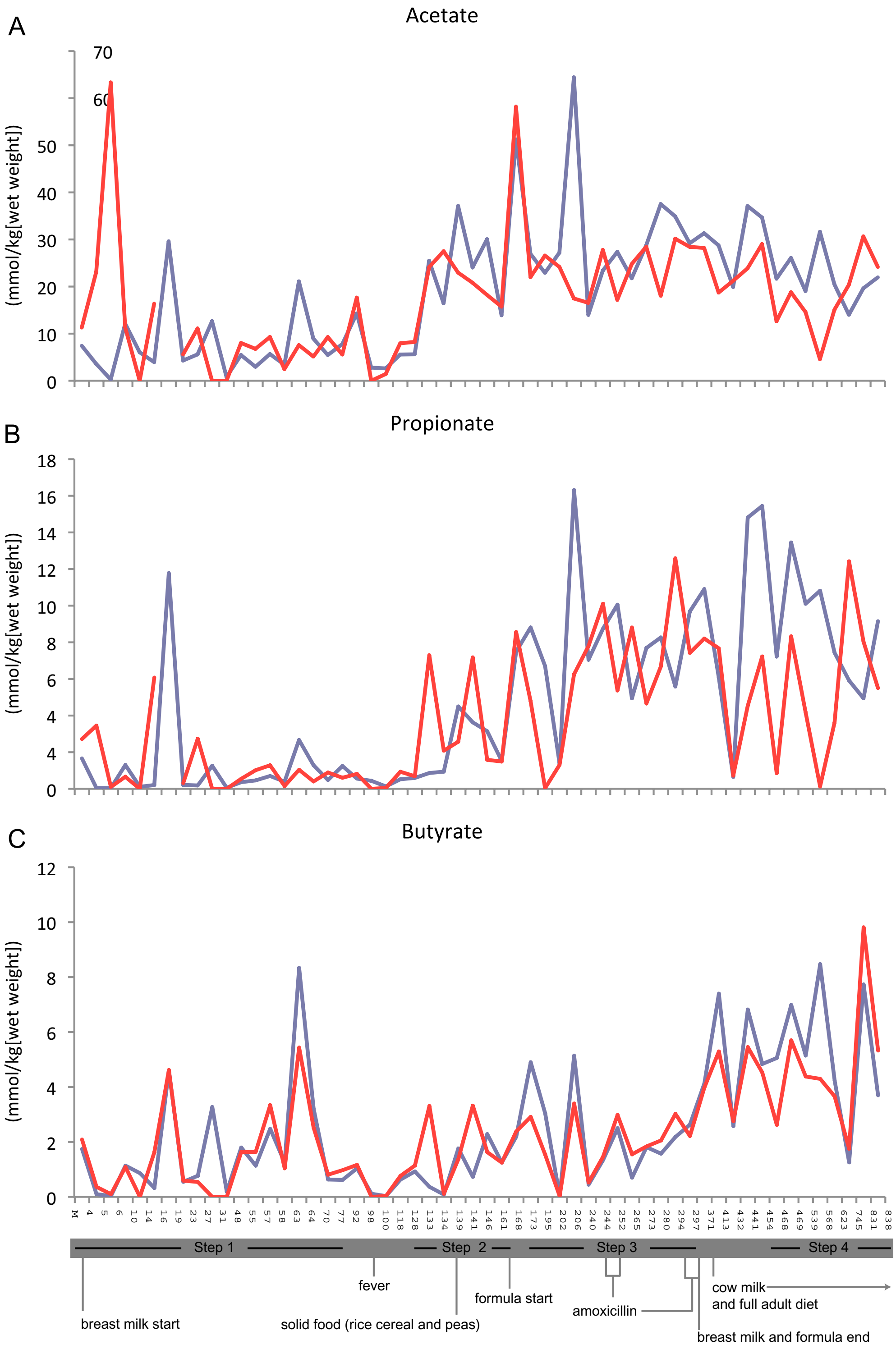

Fig. S2. Short chain fatty acid concentrations in fecal samples. (*A*) Acetate. (*B*) Propionate. (*C*) Butyrate. Blue and red lines show two measurements made from separate fecal extractions for each sample assayed.

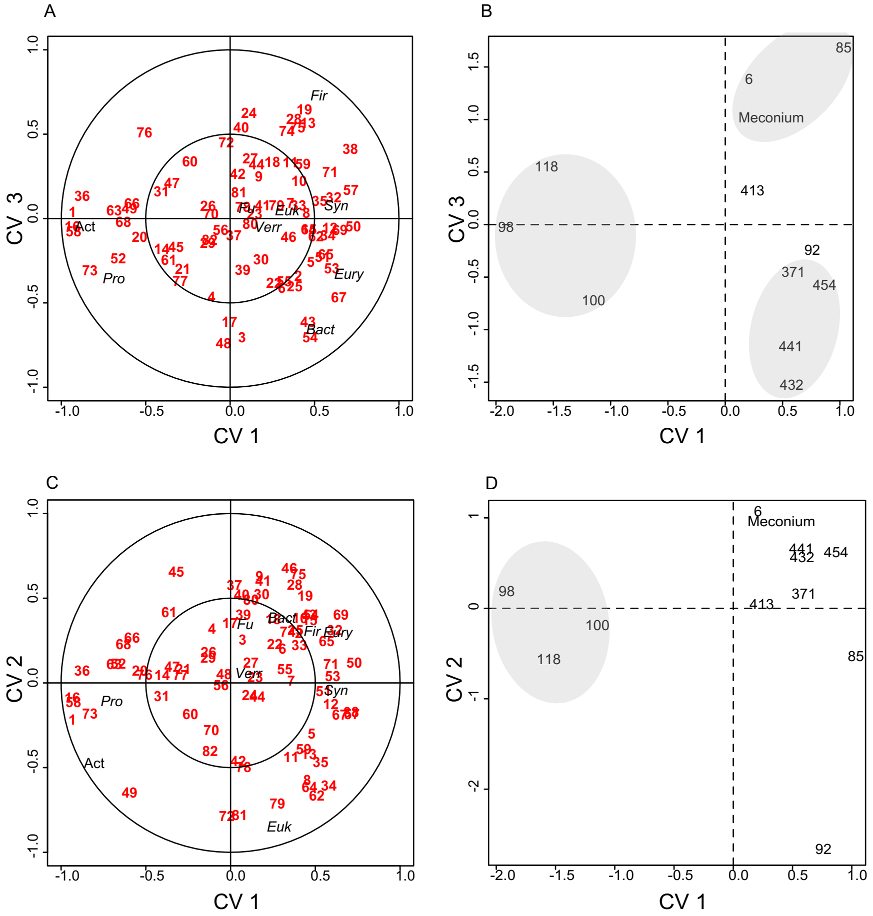

Fig. S3. Correlations between phylogenetic and functional gene contents, and clustering of samples based on their phylogenetic and functional gene contents. Results for canonical variates (CV) 1 and 3 are shown in *A* and *B*, and for CVs 1 and 2 are shown in *C* and *D*. Canonical variates of the RCCA are plotted in *A* and *C* and show correlation values for phylum abundances and gene functions: those that are projected in the same direction from the origin have a positive relationship; conversely, those projected in opposite directions from the origin have a negative relationship. The stronger the relationship, the further they fall from the center. Phyla are indicated as follows: Fir, Firmicutes; Act, Actinobacteria; Pro, Proteobacteria; Bact, Bacteroidetes; Syn, Synergistes; Verr, Verrucomicrobia; Eury, Euryarchaeota; and Euk, Eukaryotes. Red numbers refer to gene functions listed in Table S6. *Right:* Units plots: coordinates of the units on the canonical variates axis are plotted. Numbers refer to sample collection days. The clustering of samples in the right-hand side plots can be explained by the gene and phyla abundance data that are in the same quadrant in the left-hand plots.

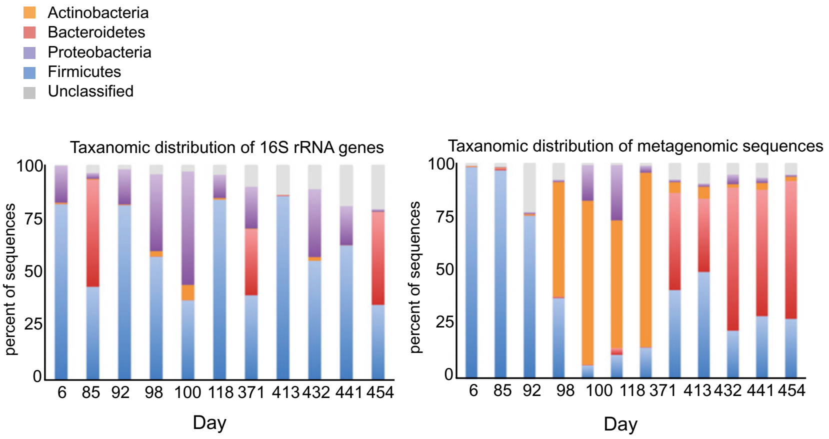

Fig. S4. Comparison of the taxonomic distributions of 16S rRNA gene sequences (*Left*) and metagenomic sequences (*Right*). Percentage of sequences assigned to each phylum are shown for the 12 samples selected for metagenomic analysis.

Table S1. Distribution of 16S rRNA genes amplified from samples associated with the infant time series

Table S1 (DOC)

Table S2. Metagenomic sequencing statistics

Table S2 (DOC)

Table S3. Pairwise analysis summarizing the posterior probability of being assigned to one of four defined steps within the infant gut microbial succession

Table S3 (DOC)

Table S4. Microbial subsystem genes that are overrepresented in whole-community DNA extracted from the infant meconium sample ($P < 0.05$)

Table S4

Table S5. Key for metagenomic functions illustrated in Fig. 6 (main text)

Table S5 (DOC)

Table S6. Summary of the regularized canonical correlation analysis for metagenomic function and bacterial phyla

Table S6 (DOC)