Supporting Information

Rea et al. 10.1073/pnas.1001224107

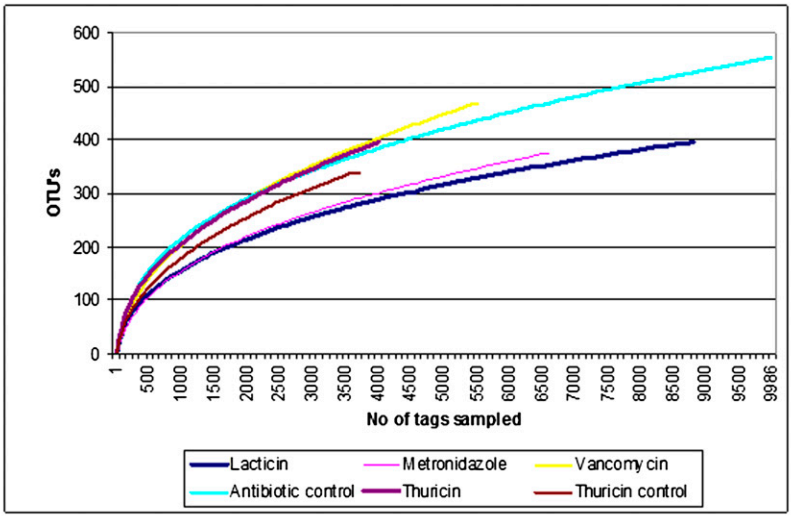

Fig. S1. Rarefaction curves at 98% similarity levels for all six datasets. Number of operational taxonomic units identified as a function of the number of sequence tags sampled.

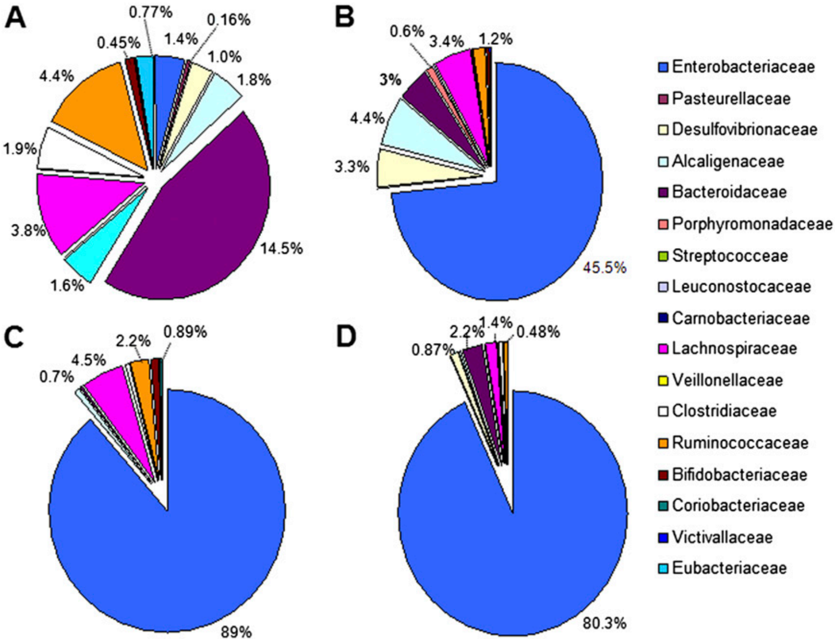

Fig. S2. Family-level diversity of gut communities in a human fecal fermentation, expressed as percentage of total population of assignable tags. *(A)* Control vessel treated with no antibiotic; *(B)* vessel treated with vancomycin (90 μM); *(C)* vessel treated with metronidazole (90 μM); *(D)* vessel treated with purified lacticin 3147 (270 μM).

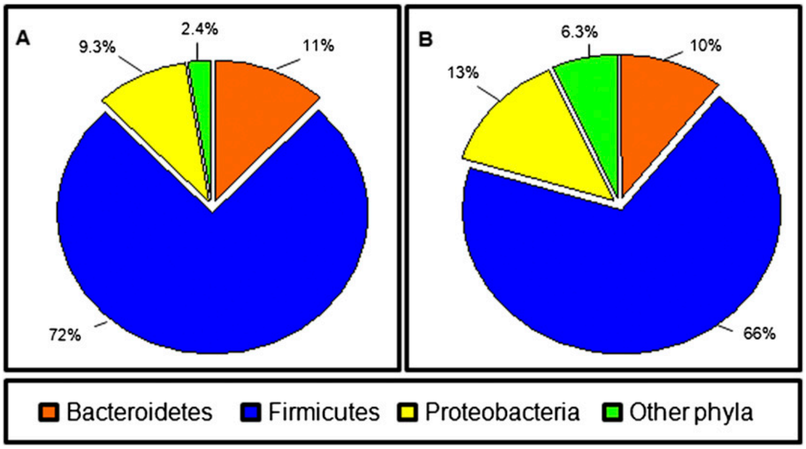

Fig. S3. Phylum-level taxonomic distribution of the microbial communities present in a human fecal fermentation, expressed as percentage of total assignable population. *(A)* Control vessel treated with no antibiotic; *(B)* vessel treated with thuricin CD (90 μM). Other phyla: Actinobacteria, Spirocaetes, Lentisphaerae, and Ternicutes.

Table S1. Pearson correlation coefficients calculated for antimicrobial treatments vs. control

Treatment	Pearson correlation coefficient
Lacticin vs. control	–002839963
Vancomycin vs. control	0.3311532
Metronidazole vs. control	0.109755048
Thuricin vs. control	0.995625797

A value of <0.5 denotes significance.