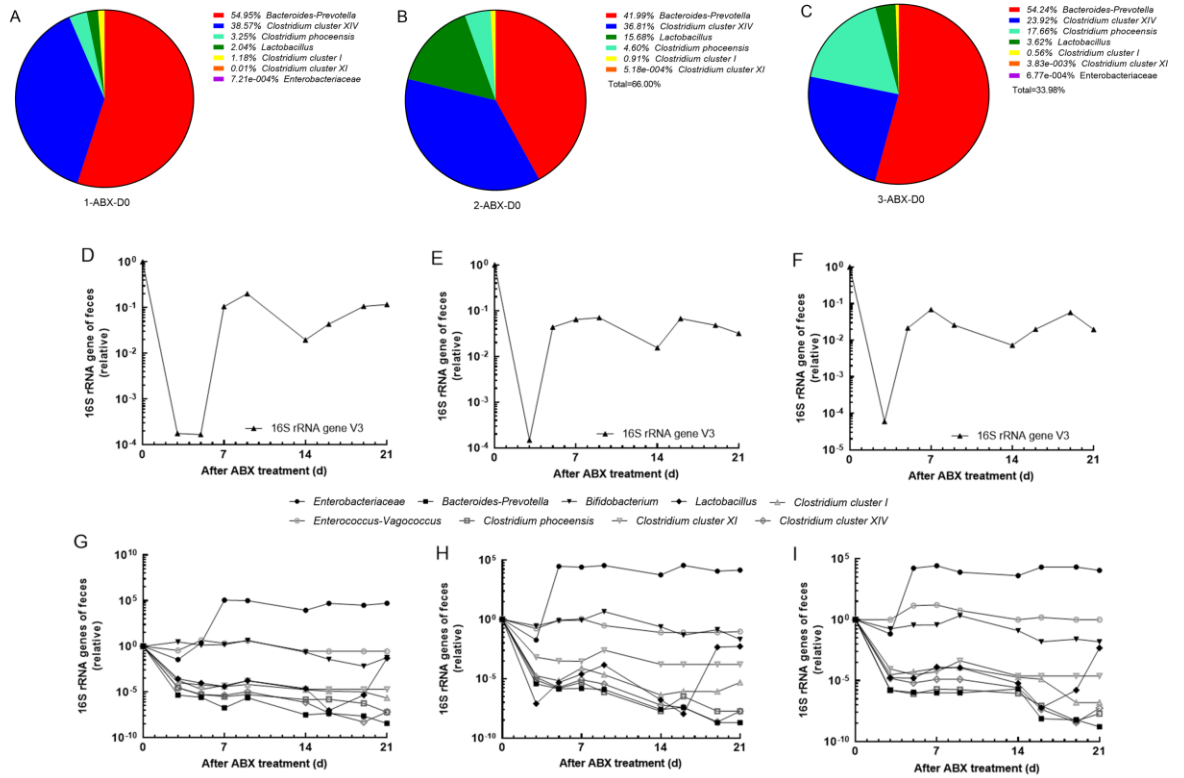
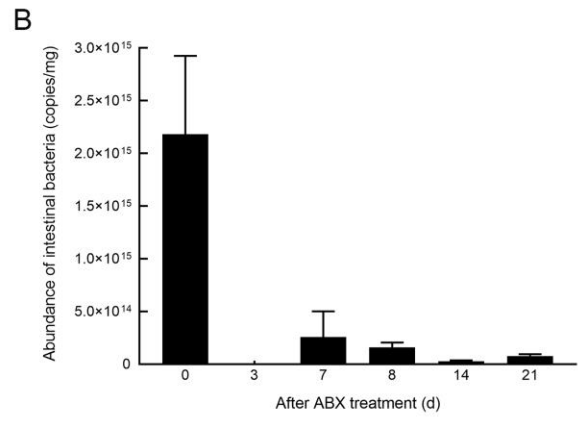
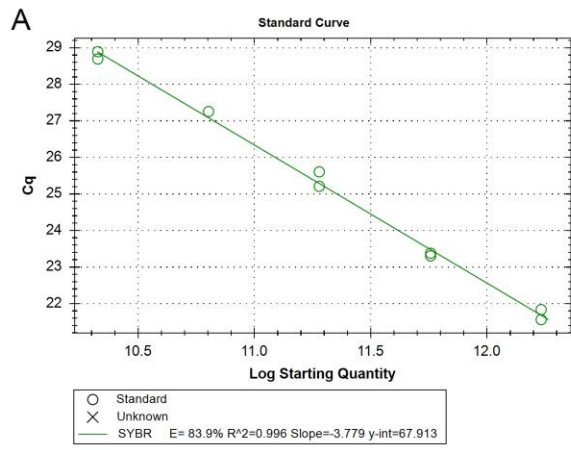


Supplementary Figures



Supplementary Figure S1 Relative quantitative RT-PCR-detected composition and abundance of intestinal bacteria

Data from three rhesus monkeys. Total 16S and taxon-specific 16S qRT-PCR for *Bacteroides*, *Prevotella*, *Lactobacillus*, *Bifidobacterium*, *Enterococcus*, *Clostridium*, and *Enterobacteriaceae* examined commensal bacteria on day 0 (A–C), with normalized to day 0 gene expression after ABX treatment (D–I).



Supplementary Figure S2 Quantitative RT-PCR-detected abundance of intestinal bacteria

Data from three rhesus monkeys. Standard curve (A) and copies of commensal bacteria per milligram of feces (B).