Segmented filamentous bacteria are a major group in terminal ileum of piglets

Metabolically active microbiota of the porcine terminal ileum mucosa was analyzed by RT-PCR of 16S rRNAs. The majority of 1951 sequences retrieved (24.8%) displayed the closest similarity to segmented filamentous bacteria (SFB). Phylogenetic analysis inferred the host-specific clusters of SFB sequences suggesting the host-specific selection of this group of bacteria.

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