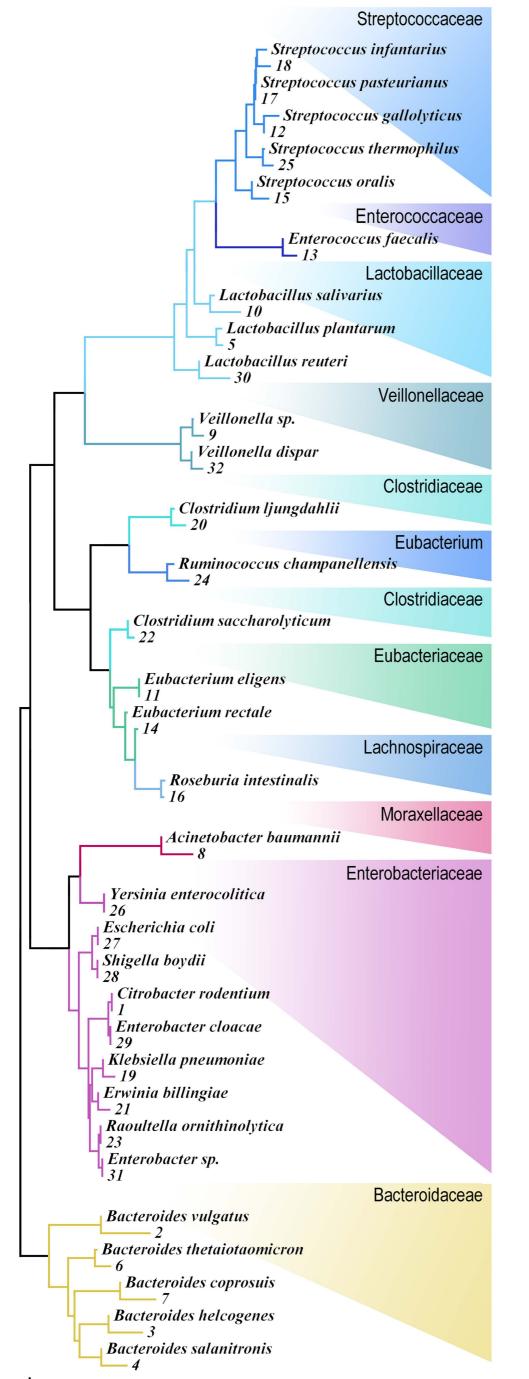
Additional file 3 Phylogenetic tree generated from the partial 16S rDNA sequences obtained from the fecal microbiotas. The sequences were aligned with closely related 16S rDNA sequences retrieved from GenBank database using the Basic Local Alignment Search Tool. The tree was conducted by the sequences of the predominant species in the feces through the *MEGA* software. The scale bar represents the genetic distance.



Firmicutes

Proteobacteria

Bacteroidaceae

0.05