

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.

Streptococcaceae

Streptococcus infantarius
18
Streptococcus pasteurianus
17
Streptococcus gallolyticus
12
Streptococcus thermophilus
25
Streptococcus oralis
15

Enterococcaceae

Enterococcus faecalis
13

Lactobacillaceae

Lactobacillus salivarius
10
Lactobacillus plantarum
5
Lactobacillus reuteri
30

Veillonellaceae

Veillonella sp.
9
Veillonella dispar
32

Clostridiaceae

Clostridium ljungdahlii
20

Eubacterium

Ruminococcus champanellensis
24

Clostridiaceae

Clostridium saccharolyticum
22

Eubacteriaceae

Eubacterium eligens
11
Eubacterium rectale
14

Lachnospiraceae

Roseburia intestinalis
16

Moraxellaceae

Acinetobacter baumannii
8

Enterobacteriaceae

Yersinia enterocolitica
26
Escherichia coli
27
Shigella boydii
28
Citrobacter rodentium
1
Enterobacter cloacae
29
Klebsiella pneumoniae
19
Erwinia billingiae
21
Raoultella ornithinolytica
23
Enterobacter sp.
31

Bacteroidaceae

Bacteroides vulgatus
2
Bacteroides thetaiotaomicron
6
Bacteroides coprosuis
7
Bacteroides helcogenes
3
Bacteroides salanitronis
4

Firmicutes

Proteobacteria

Bacteroidaceae