



Title	Murine fecal microRNAs alter the composition of cultured gut microbiota
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Supplementary Table 1 Primer sequences for qPCR for bacteria

Total Bacteria [1]

Eub338F ACTCCTACGGGAGGCAGCAG

Eub518R ATTACCGCGGCTGCTGG

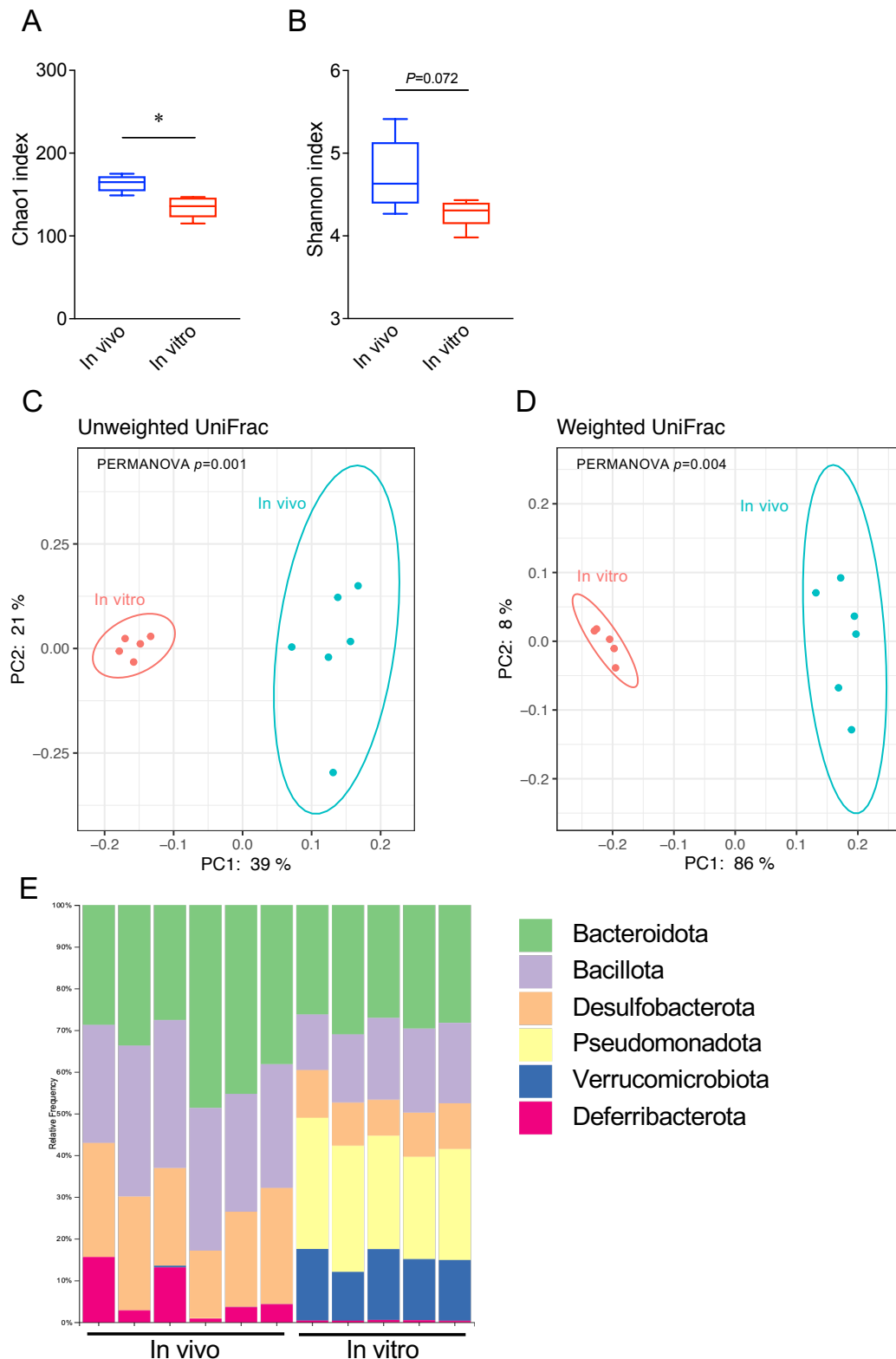
Enterococcus spp. [2]

Ent151F ACACTTGGAAACAGGTGC

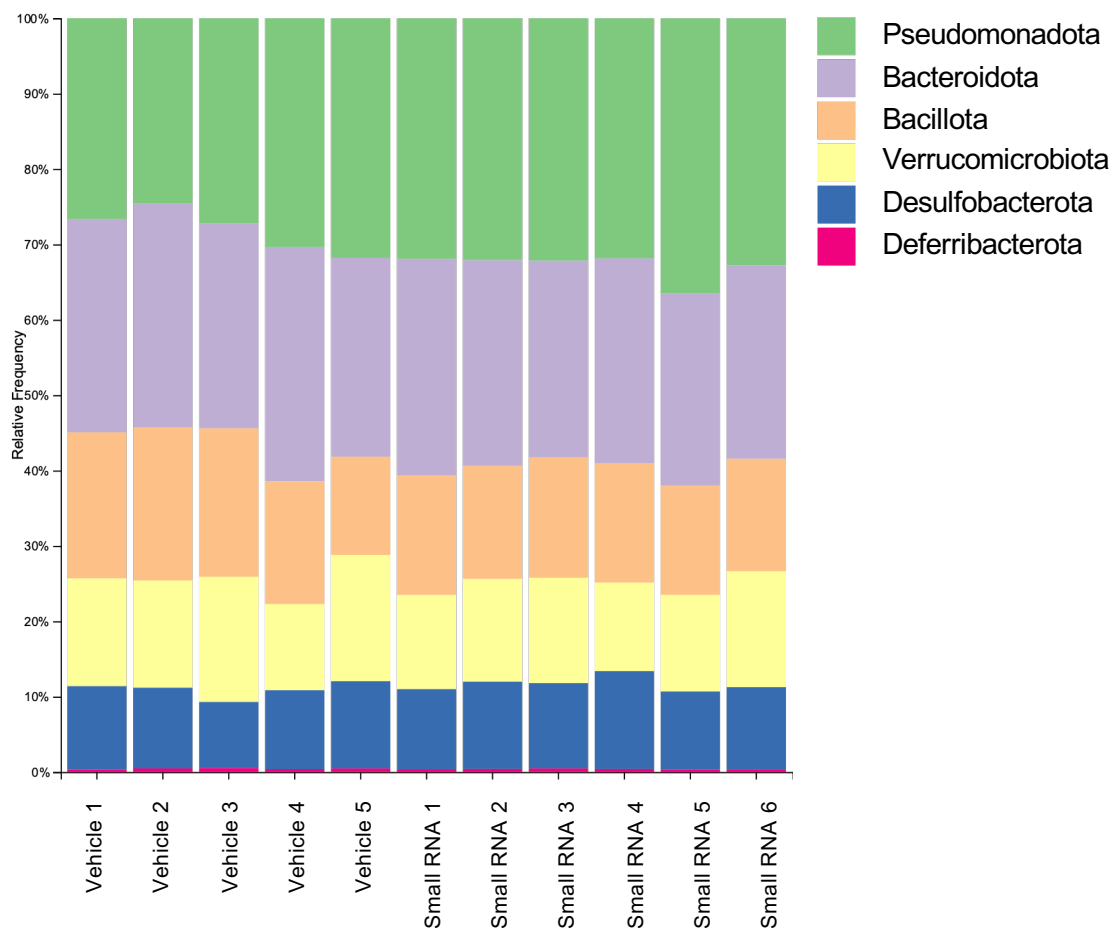
Ent376R TCGGTCAGACTTKCGTCC

[1] N. Fierer, J.A. Jackson, R. Vilgalys, *et al.*, Assessment of soil microbial community structure by use of taxon-specific quantitative PCR assays, *Appl. Environ. Microbiol.* 71 (2005) 4117-4120. <https://doi.org/10.1128/AEM.71.7.4117-4120.2005>.

[2] H. Ryu, M. Henson, M. Elk, *et al.*, Development of quantitative PCR assays targeting the 16S rRNA genes of *Enterococcus* spp. and their application to the identification of *Enterococcus* species in environmental samples, *Appl. Environ. Microbiol.* 79 (2013) 196-204. <https://doi.org/10.1128/AEM.02802-12>.



Supplementary Fig. 1 Comparison of the structure of microbiota in the cecal contents (In vivo) and cultured fecal bacteria (In vitro). Graphs A and B show the Chao1 and Shannon α -diversity indexes, respectively. C and D show PCoA plots of the β -diversity computed based on the unweighted and weighted UniFrac distances, respectively. E shows the ratio of bacterial taxa at the phylum level. In graphs A and B, results are presented as standard box plots composed of medians and interquartile ranges with minima and maxima, $n=6$ and 5 in the cecal contents and cultured fecal bacteria, respectively. Mean values between groups were compared using Welch's t -test ($P < 0.05$).



Supplementary Fig. 2 Comparison of microbiota structure between the cultured fecal bacteria supplemented with vehicle and small RNAs. The ratio of bacterial taxa at the phylum level was shown.