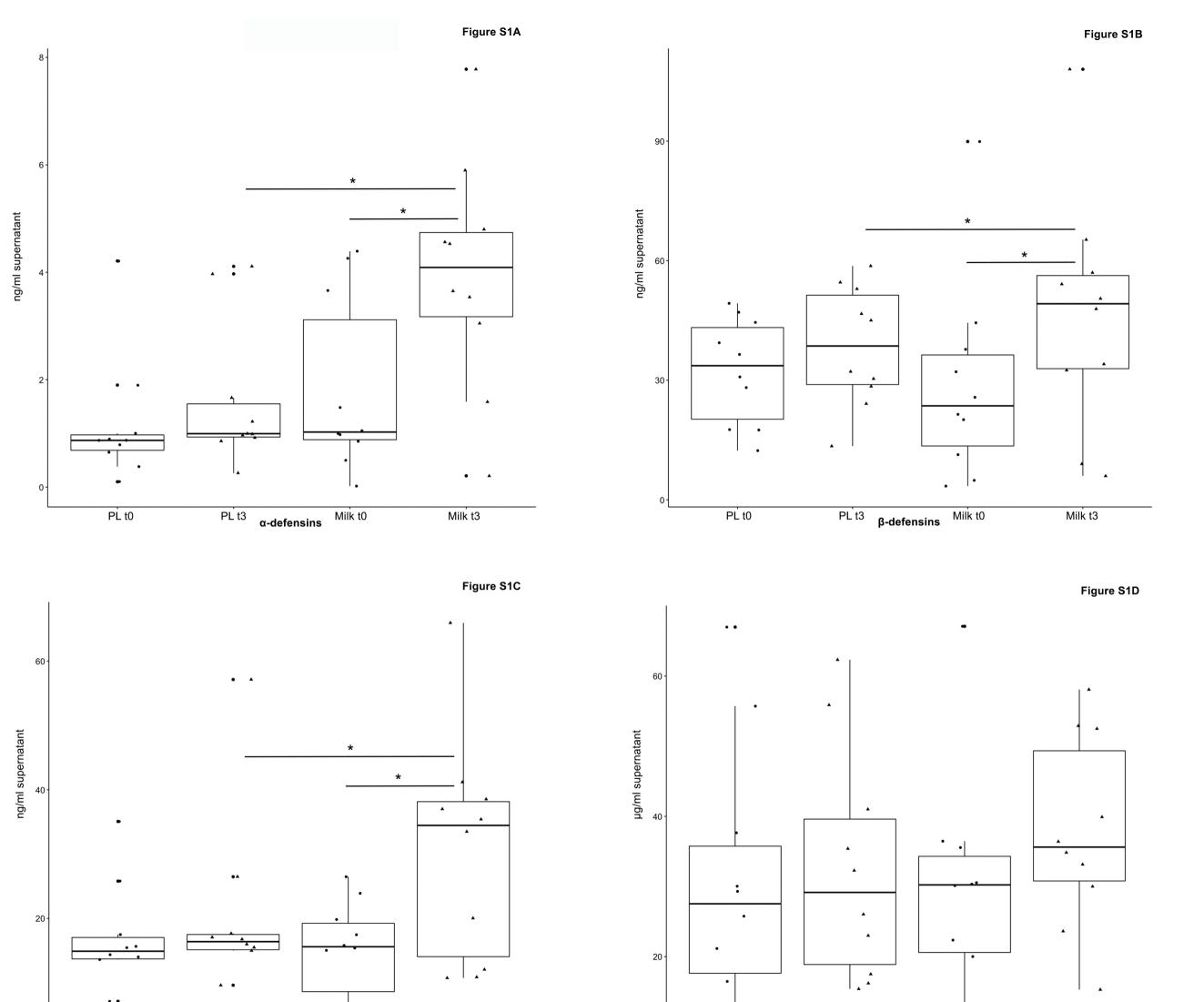
Supplementary Material

Specific signatures of the gut microbiota and increased levels of butyrate in children treated with fermented cow's milk containing heat-killed *Lactobacillus paracasei* CBA L74

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PL t0

PL t3

slgA

Milk t0

Milk t3

PL t0

PL t3

LL-37

Milk t0

Milk t3

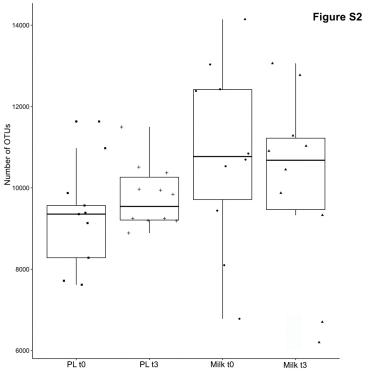
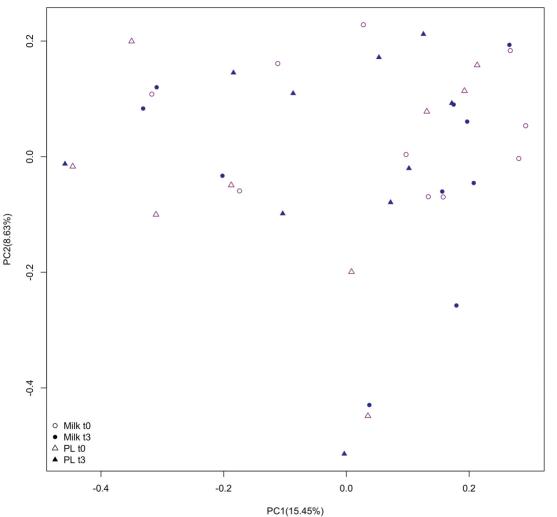


Figure S3



Roseburia oligotypes

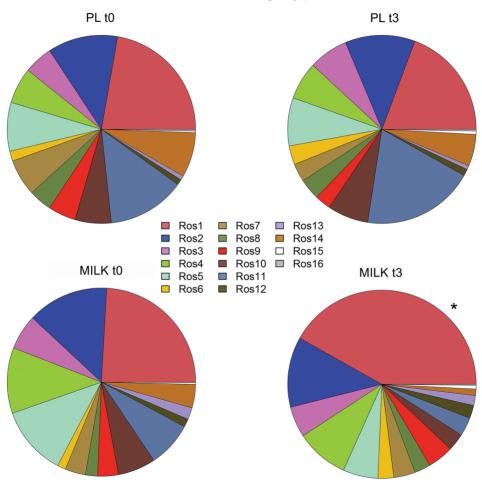


Figure S4A

Blautia oligotypes

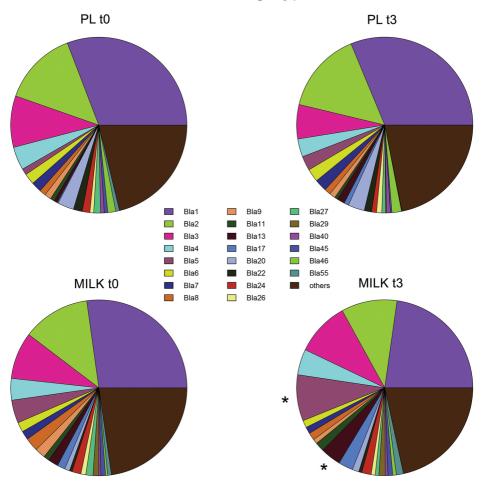


Figure S4B

Bacteroides oligotypes

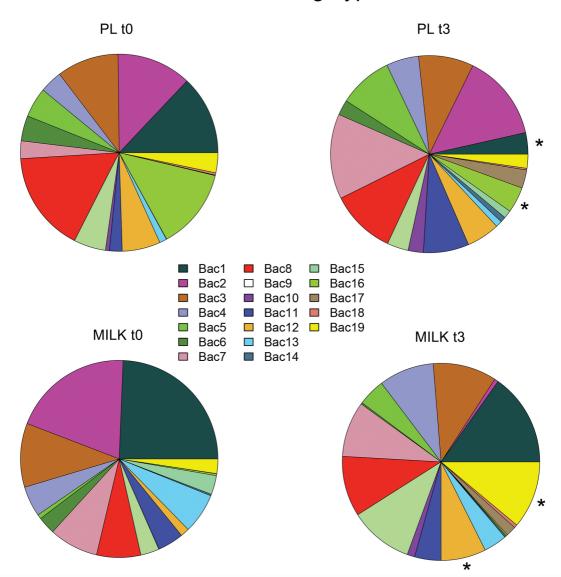
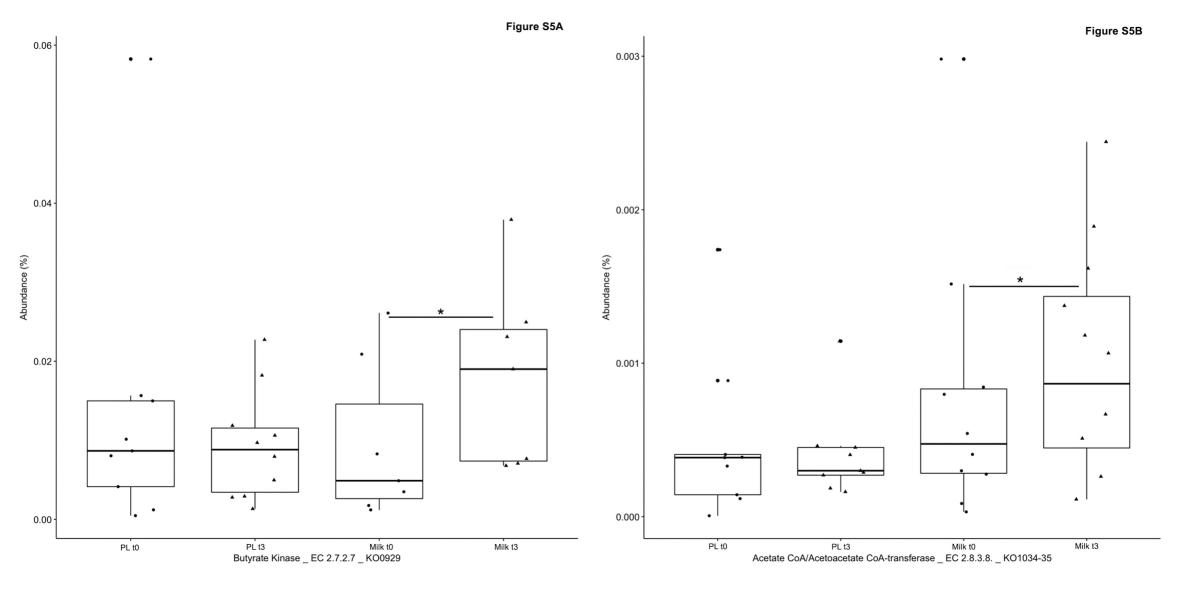


Figure S4C



Supplementary Figure Legends

Figure S1. Innate and acquired immunity biomarkers levels. Box plots showing levels of α-defensin, β-defensin 2, cathelicidin and sIgA in the study population at baseline (t0) and after 3 months of treatment (t3) with fermented milk (Milk) and placebo (PL). Boxes represent the interquartile range (IQR) between the first and third quartiles, and the line inside represents the median (2nd quartile). Whiskers denote the lowest and the highest values within 1.5 x IQR from the first and third quartiles, respectively. Asterisks indicate a significant difference as obtained by pairwise Wilcoxon test (P<0.05). **Figure S2. Alpha-diversity.** Box plots showing the number of observed OTUs in the study population at baseline (t0) and after 3 months of treatment (t3) with fermented milk (Milk) and placebo (PL). See Figure 1 legend for a description of the box plots.

Figure S3. Principal Coordinates Analysis. PCoA of Bray Curtis distances. Different colors indicate samples before (t0, blue) and after 3 months of treatment (t3, purple) with fermented milk (Milk) and placebo (PL).

Figure S4. *Roseburia*, *Blautia* and *Bacteroides* oligotype patterns. Pie charts showing the abundance of *Roseburia* (A), *Blautia* (B) and *Bacteroides* (C) oligotypes in the different subject categories.

Figure S5. Predicted abundance of key genes involved in butyrate production. Box plots showing the abundance of genes encoding for butyryl CoA: acetate CoA transferase and butyrate kinase in the study population at baseline (t0) and after 3 months of treatment (t3) with fermented milk (Milk) and placebo (PL). Gene abundance was predicted by PICRUSt. See Figure 1 legend for a description of the box plots.