

Supplemental File

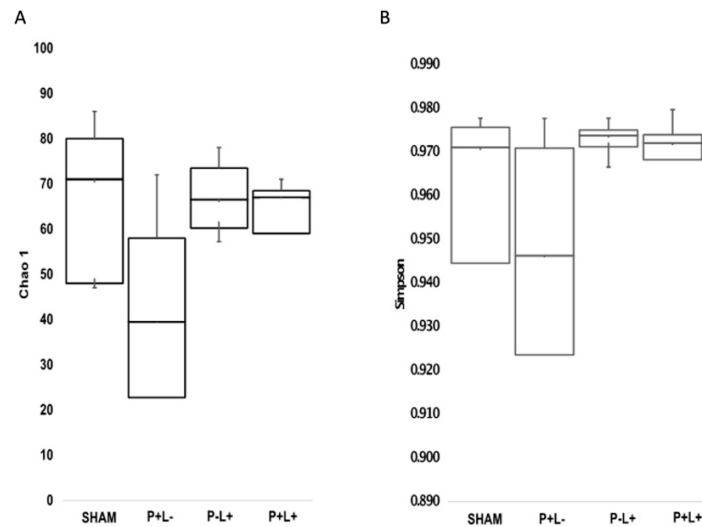


Figure S1. Phylogenetic Alpha diversity indices (Chao in A, and Simpson in B) of the gut microbial communities of C57Bl/6 mice submitted to different treatments: SHAM (negative control), P+L- (positive control, inoculated with the microbial consortium), P-L+ (*L. acidophilus* LA5), P+L+ (microbial consortium + *L. acidophilus* LA5). Kruskal Wallis with Dunn's pos hoc test. No significant differences, $p > 0.05$.

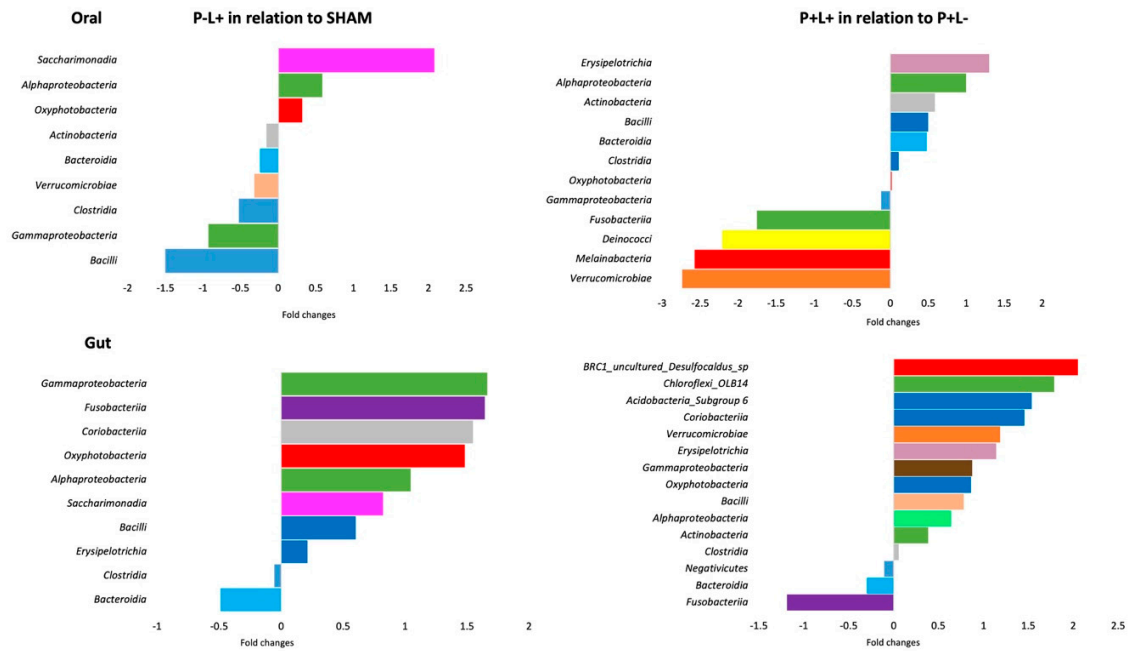


Figure S2. Fold changes of abundance at the Class taxonomic level of oral and gut microbial communities of C57Bl/6 mice submitted to different treatments: SHAM (negative control), P+L- (positive control, inoculated with the microbial consortium), P-L+ (*L. acidophilus* LA5), P+L+ (microbial consortium + *L. acidophilus* LA5). The effect of *L. acidophilus* LA5 in the oral biofilm and gut microbiomes was determined by comparing the abundance of taxons in P-L+ group and SHAM, and in P+L+ group and P+L-. Data reported as fold changes of abundance.

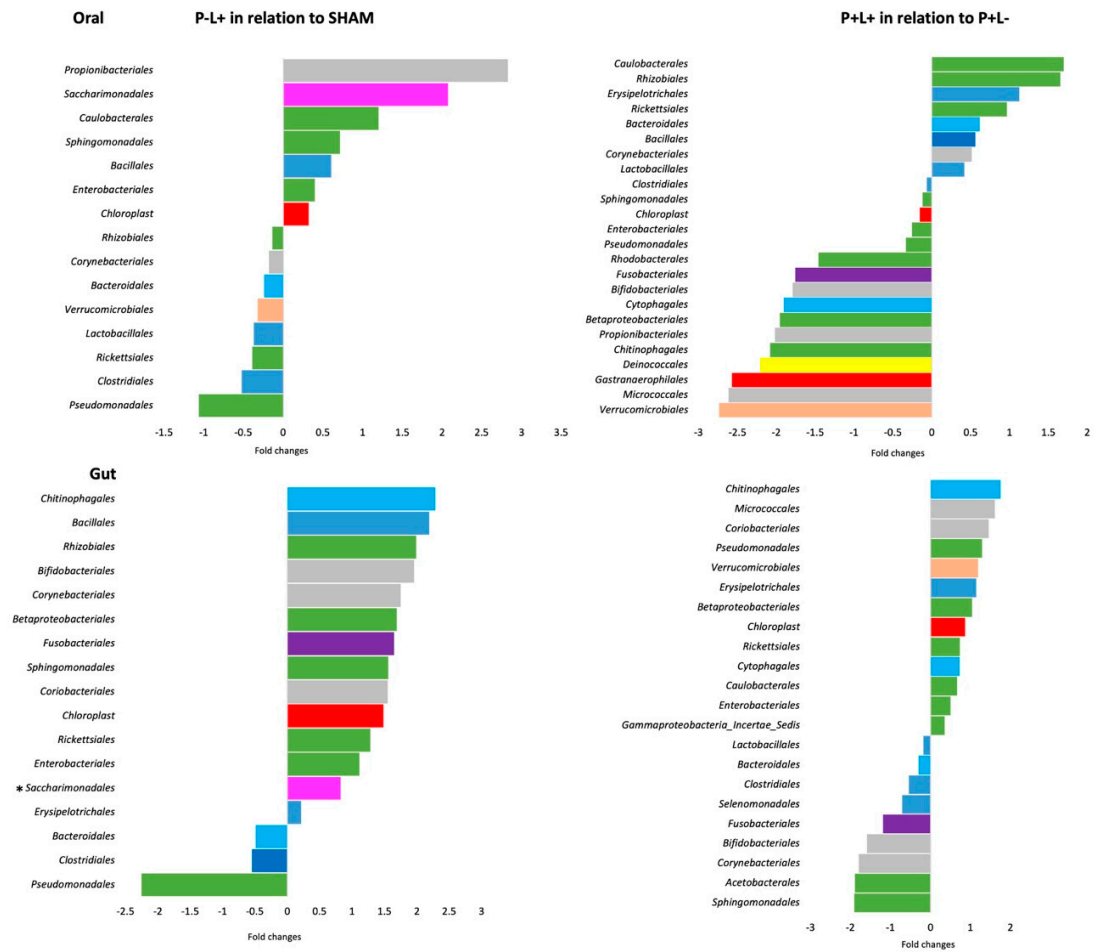


Figure S3. Fold changes of abundance at the Order taxonomic level of oral and gut microbial communities of C57Bl/6 mice submitted to different treatments: SHAM (negative control), P+L- (positive control, inoculated with the microbial consortium), P-L+ (*L. acidophilus* LA5), P+L+ (microbial consortium + *L. acidophilus* LA5). The effect of *L. acidophilus* LA5 in the oral biofilm and gut microbiomes was determined by comparing the abundance of taxons in P-L+ group and SHAM, and in P+L+ group and P+L-. Data reported as fold changes of abundance.

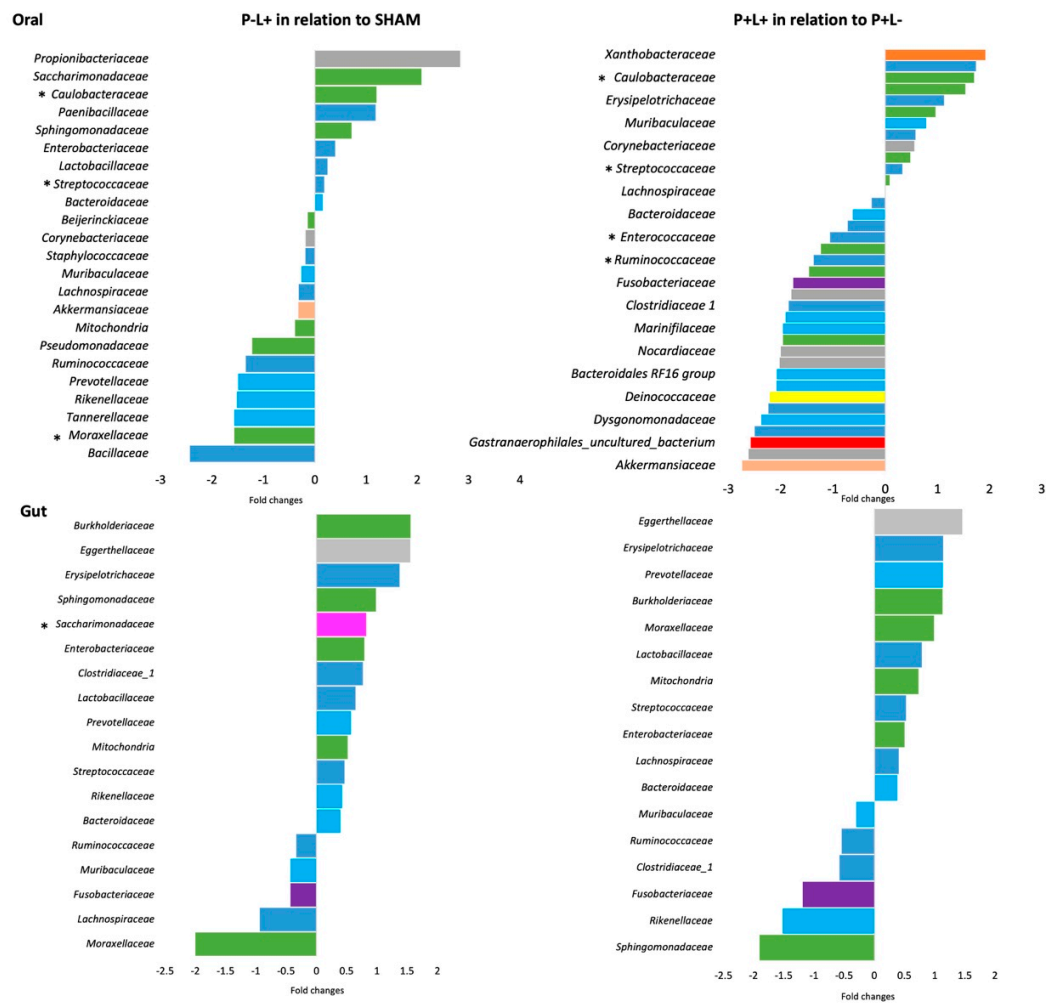


Figure S4. Fold changes of abundance at the family taxonomic level of oral and gut microbial communities of C57Bl/6 mice submitted to different treatments: SHAM (negative control), P+L- (positive control, inoculated with the microbial consortium), P-L+ (*L. acidophilus* LA5), P+L+ (microbial consortium + *L. acidophilus* LA5). The effect of *L. acidophilus* LA5 in the oral biofilm and gut microbiomes was determined by comparing the abundance of taxons in P-L+ group and SHAM, and in P+L+ group and P+L-. Data reported as fold changes of abundance. * ANCOM, significant differences.

S4

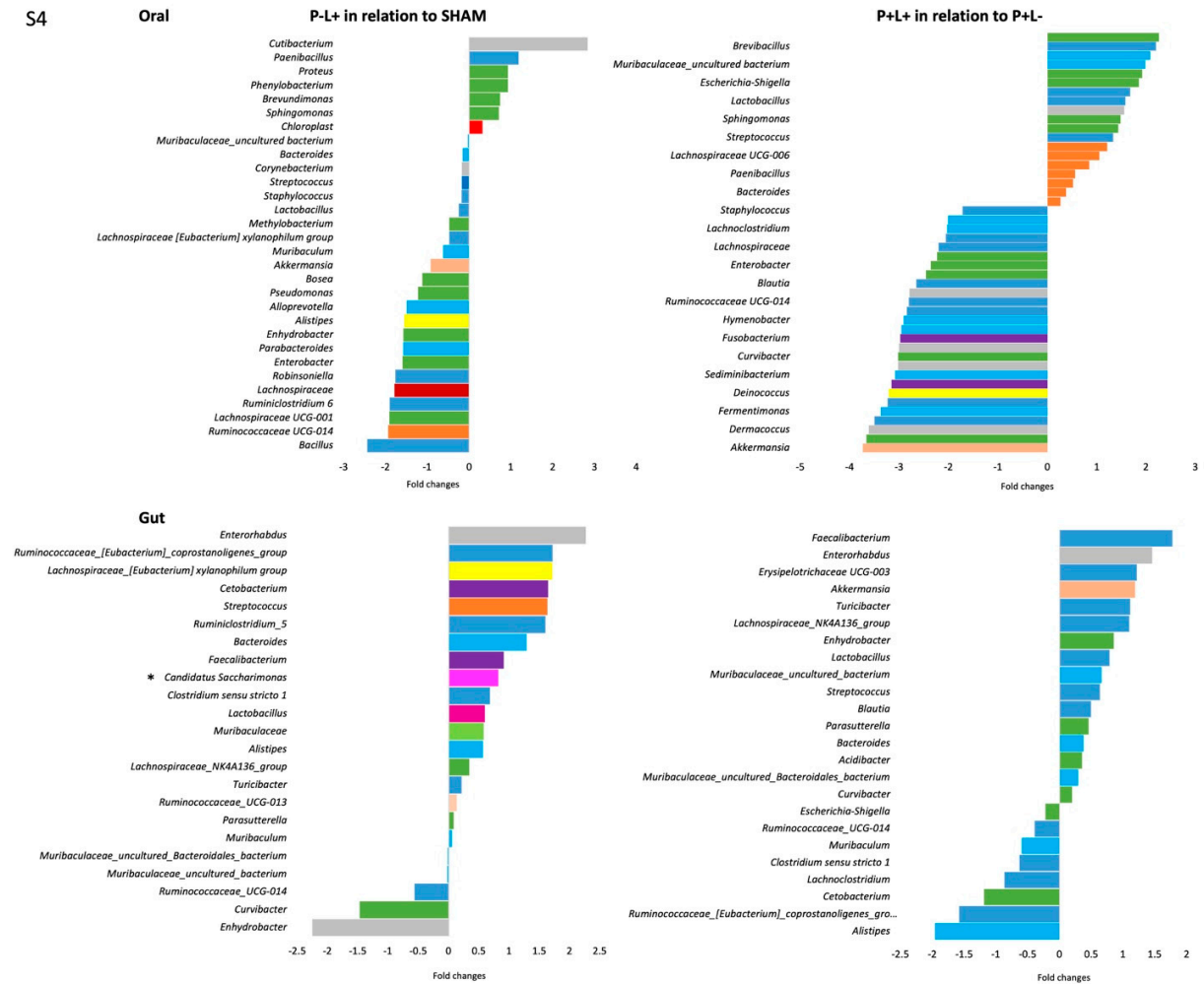


Figure S5. Fold changes of abundance at the genus taxonomic level of oral and gut microbial communities of C57Bl/6 mice submitted to different treatments: SHAM (negative control), P+L- (positive control, inoculated with the microbial consortium), P-L+ (*L. acidophilus* LA5), P+L+ (microbial consortium + *L. acidophilus* LA5). The effect of *L. acidophilus* LA5 in the oral biofilm and gut microbiomes was determined by comparing the abundance of taxons in P-L+ group and SHAM, and in P+L+ group and P+L-. Data reported as fold changes of abundance.