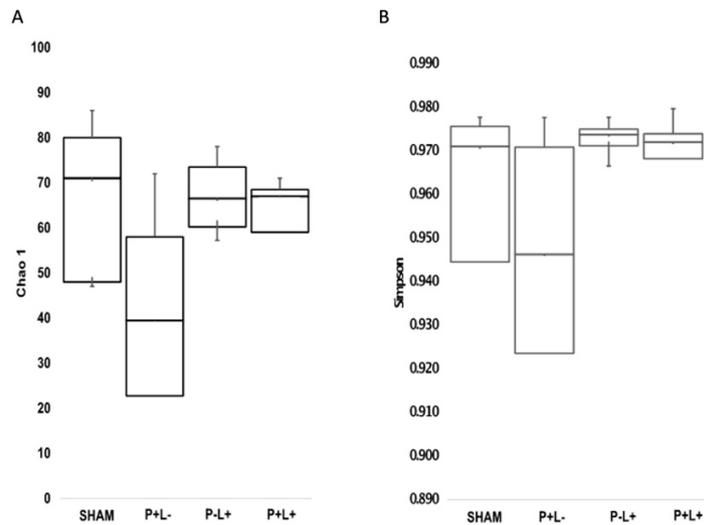
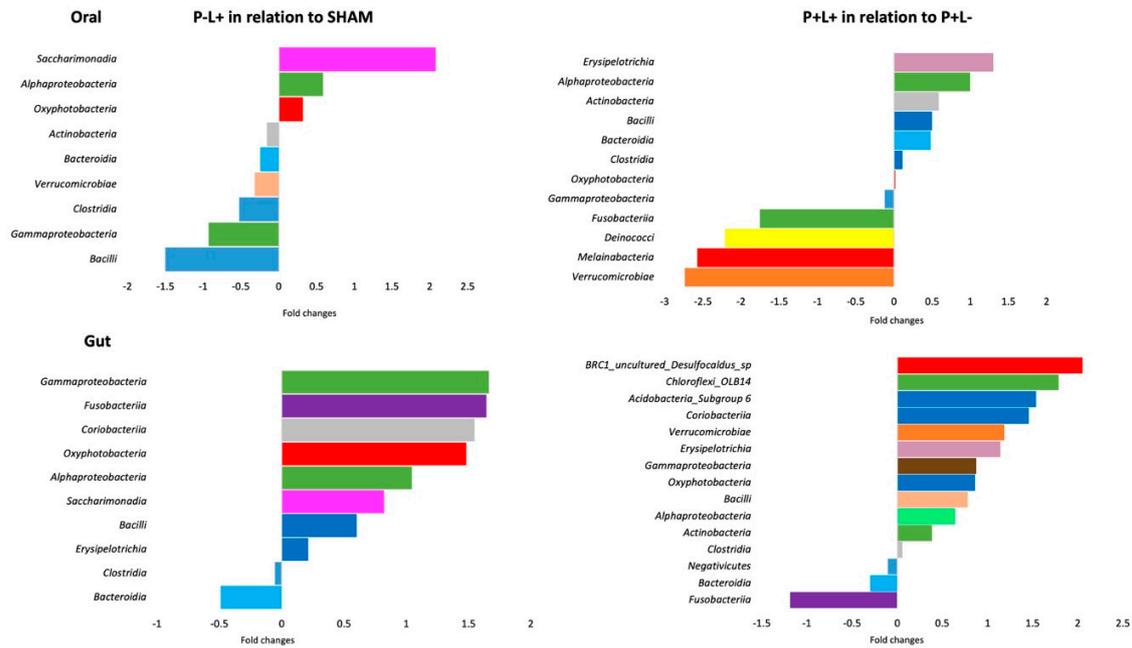


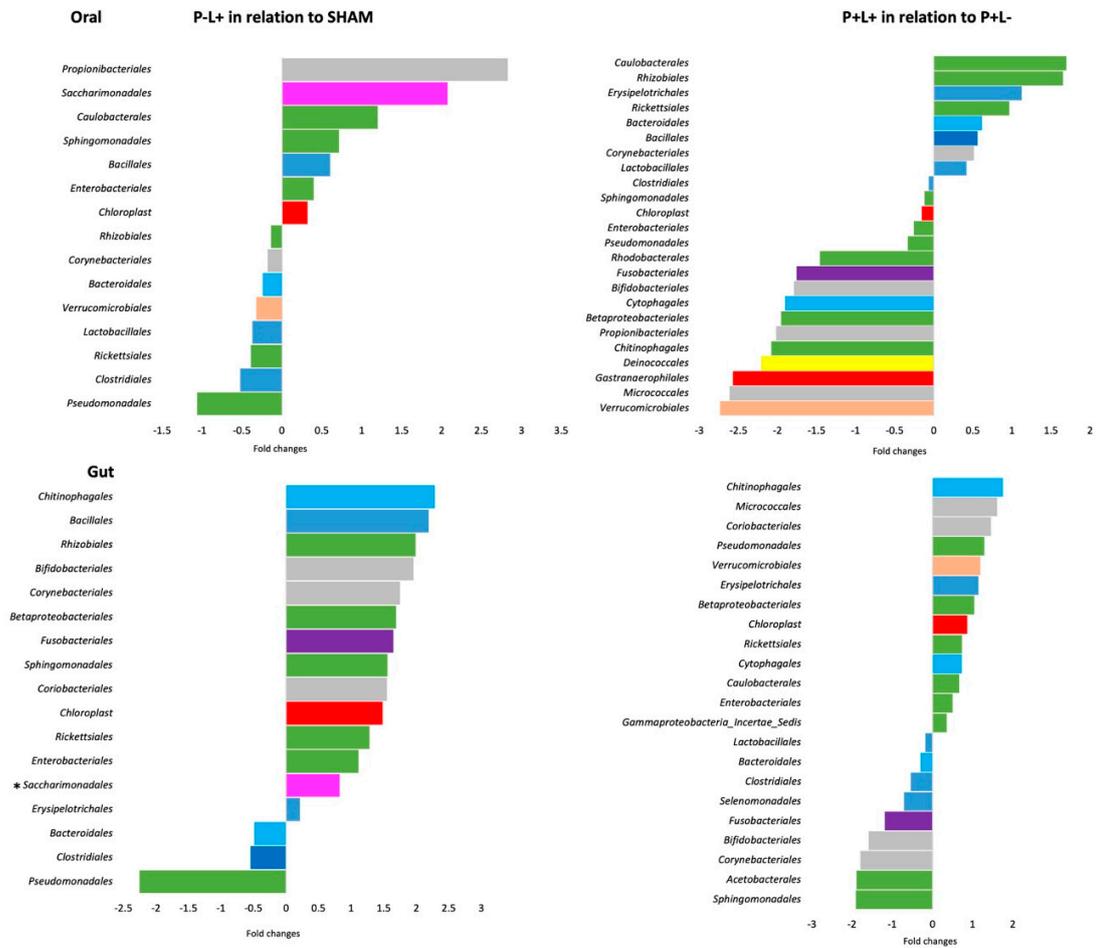
## Supplemental File



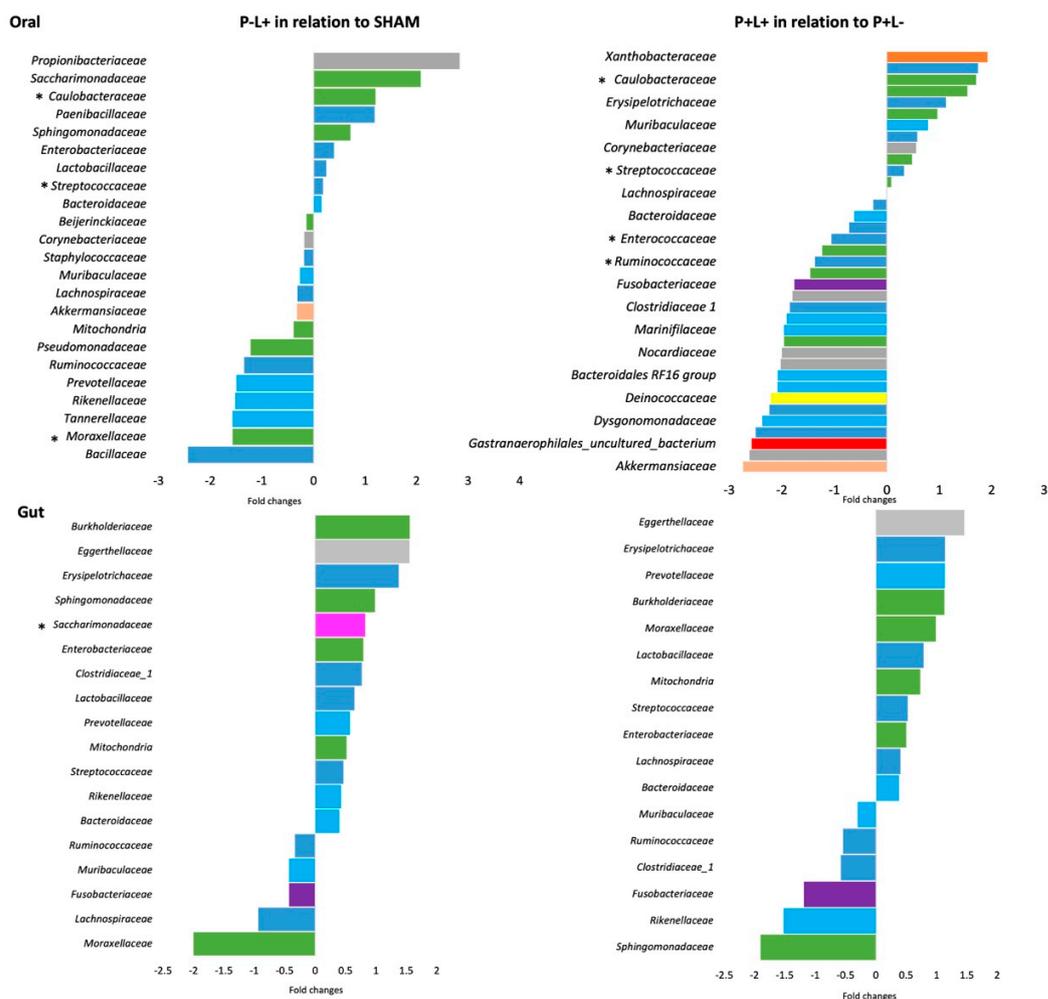
**Figure S1.** Phylogenetic Alpha diversity indices (Chao in A, and Simpson in B) of the gut microbial communities of C57Bl/6 mice submitted to different treatments: SHAM (negative control), P+L- (positive control, inoculated with the microbial consortium), P-L+ (*L. acidophilus* LA5), P+L+ (microbial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



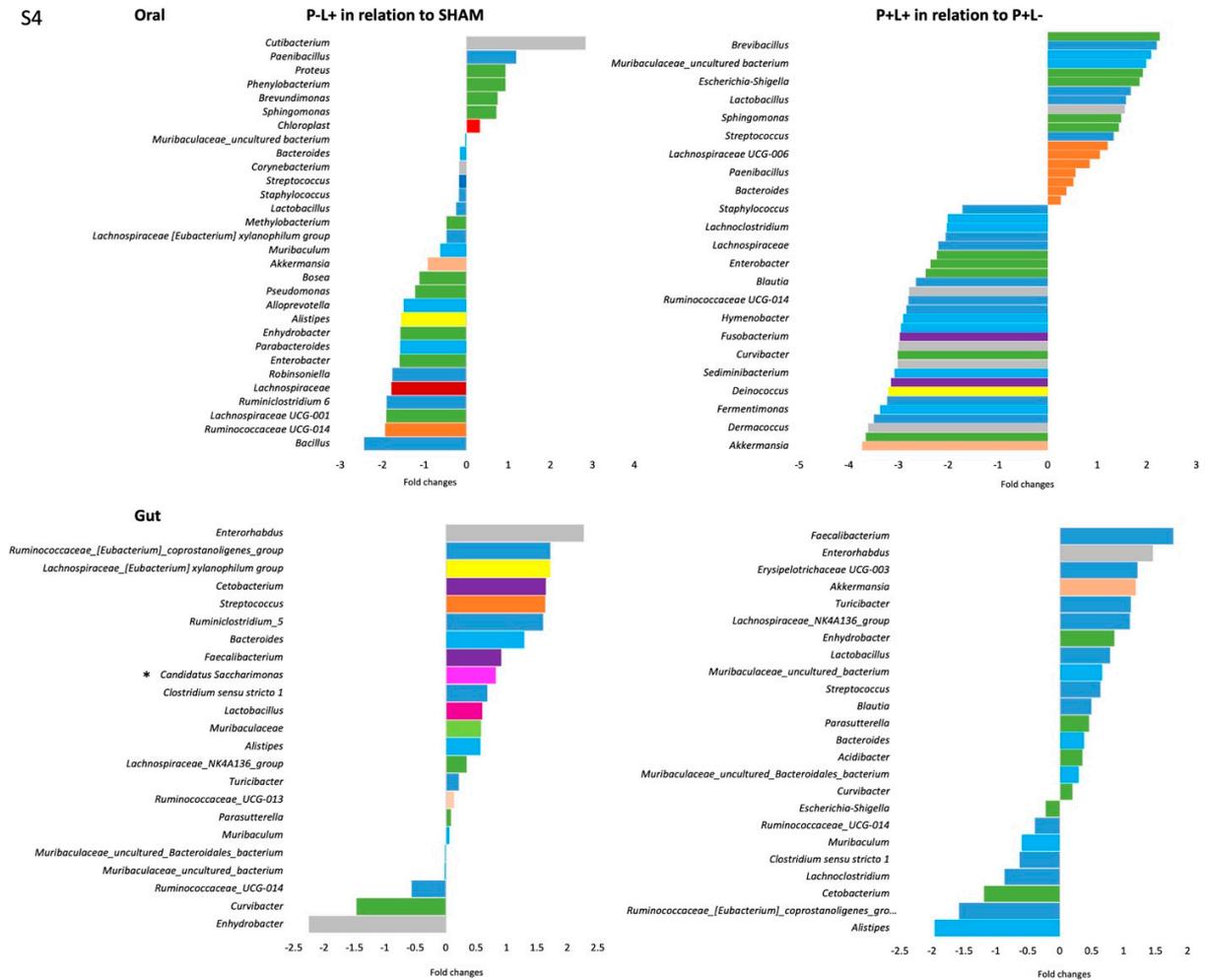
**Figure S2.** Fold changes of abundance at the Class taxonomic level of oral and gut microbial communities of C57Bl/6 mice submitted to different treatments: SHAM (negative control), P+L- (positive control, inoculated with the microbial consortium), P-L+ (*L. acidophilus* LA5), P+L+ (microbial consortium + *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.



**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.