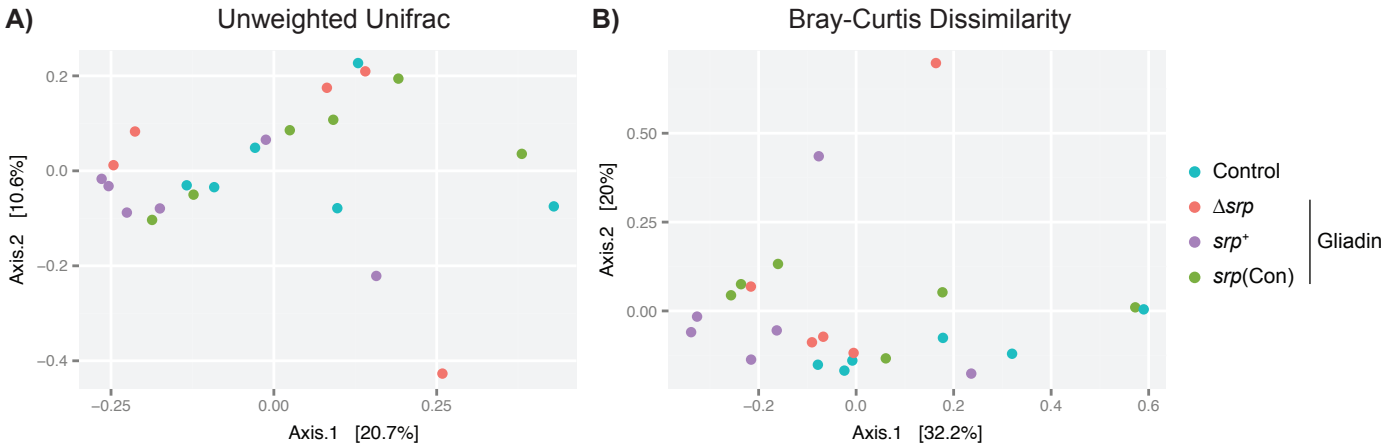
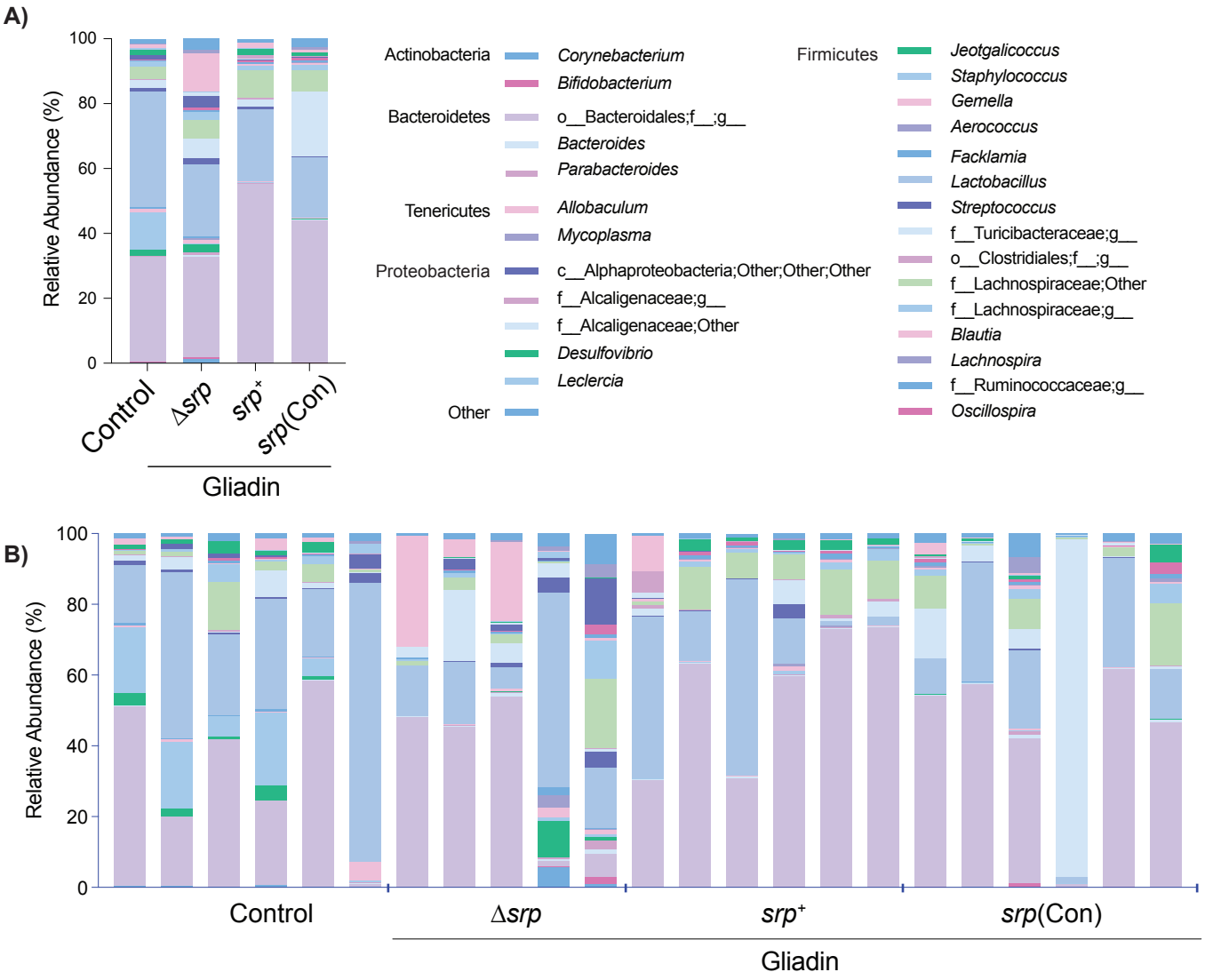
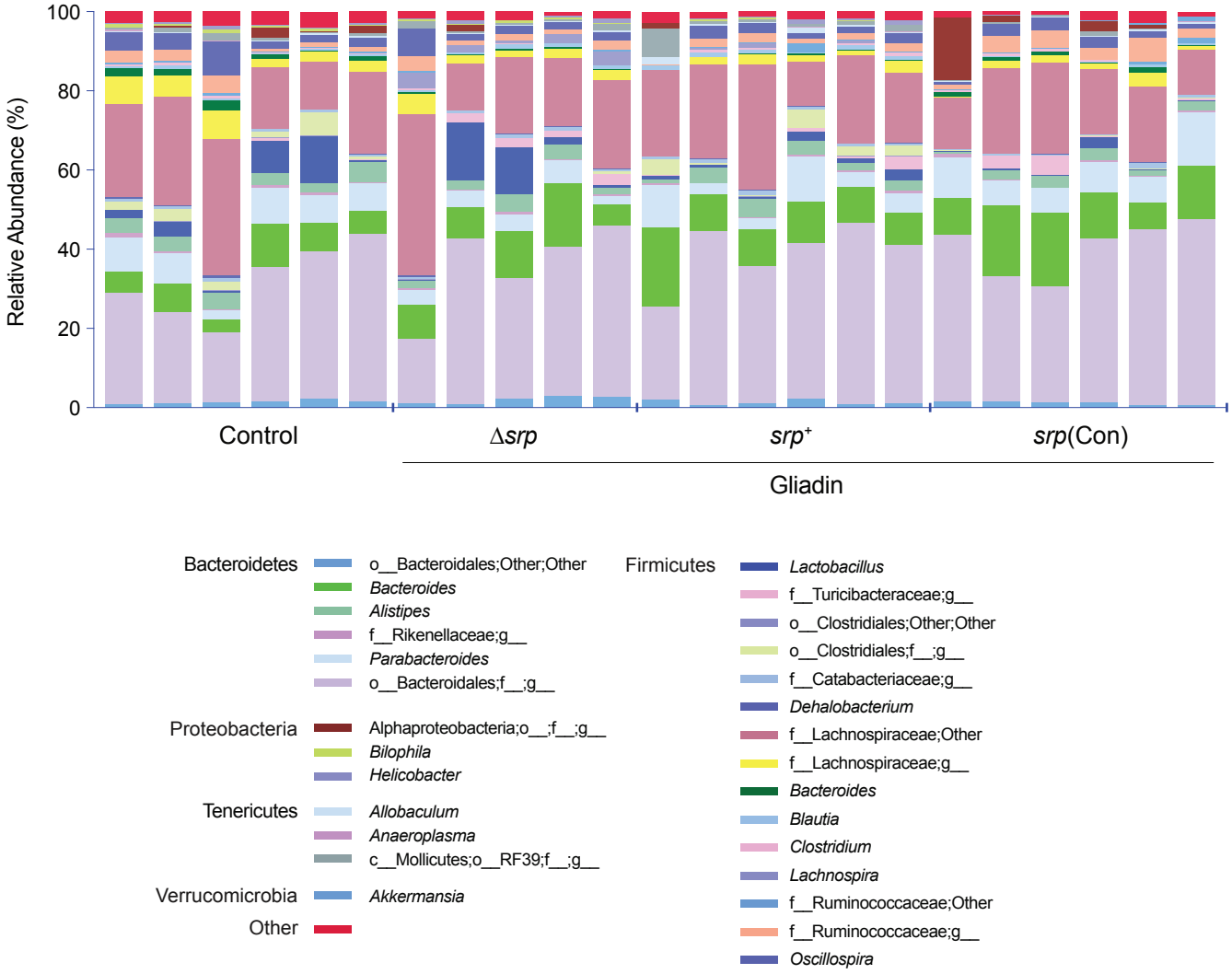


Supplementary figure 1. Small intestinal microbiota profiles. Principal coordinate analysis plots representing β-diversity using both **A)** Bray-Curtis Dissimilarity and **B)** Unifrac Unweighted parameters revealed no significant differences in small intestinal microbiota (n=5-6/group). Non-sensitized, no treatment (Control); *B. longum srp*$^{+}$ (*srp*$^{+}$); *B. longum* Δ*srp* (Δ*srp*); *B. longum srp*(Con) (*srp*(Con)). Statistics were performed via PERMANOVA in QIIME. Plots were constructed in R.



Supplementary figure 2. Relative abundances in small intestinal microbiota profiles at genus level. Small intestinal microbiota was sequenced via 16s miSeq Illumina technology. Operational taxonomic units at relative abundances ≥ 1% are presented as **A**) average of each group and **B**) per mouse (n=5-6/group). No changes in relative abundances were found. Non-sensitized, no treatment (Control); *B. longum srp*$^{+}$ (*srp*$^{+}$); *B. longum* Δ*srp* (Δ*srp*); *B. longum srp*(Con) (*srp*(Con)). Statistics were performed via Kruskal-Wallis followed by FDR ($q<0.05$).



Supplementary figure 3. Relative abundances of fecal microbiota for individual mice at genus level. Fecal microbiota was sequenced via 16s miSeq illumina technology by amplification of the 16S rRNA gene, and relative abundances are represented at a genus level in stacked column charts (n=5-6/group). Non-sensitized, no treatment (Control); *B. longum srp*$^{+}$ (*srp*$^{+}$); *B. longum* Δ*srp* (Δ*srp*); *B. longum srp*(Con) (*srp*(Con)). Statistics were performed via Kruskal-Wallis followed by FDR ($q<0.05$).