Supplementary Figures.

Lactobacillus rhamnosus GG modifies the metabolome of pathobionts in gnotobiotic mice

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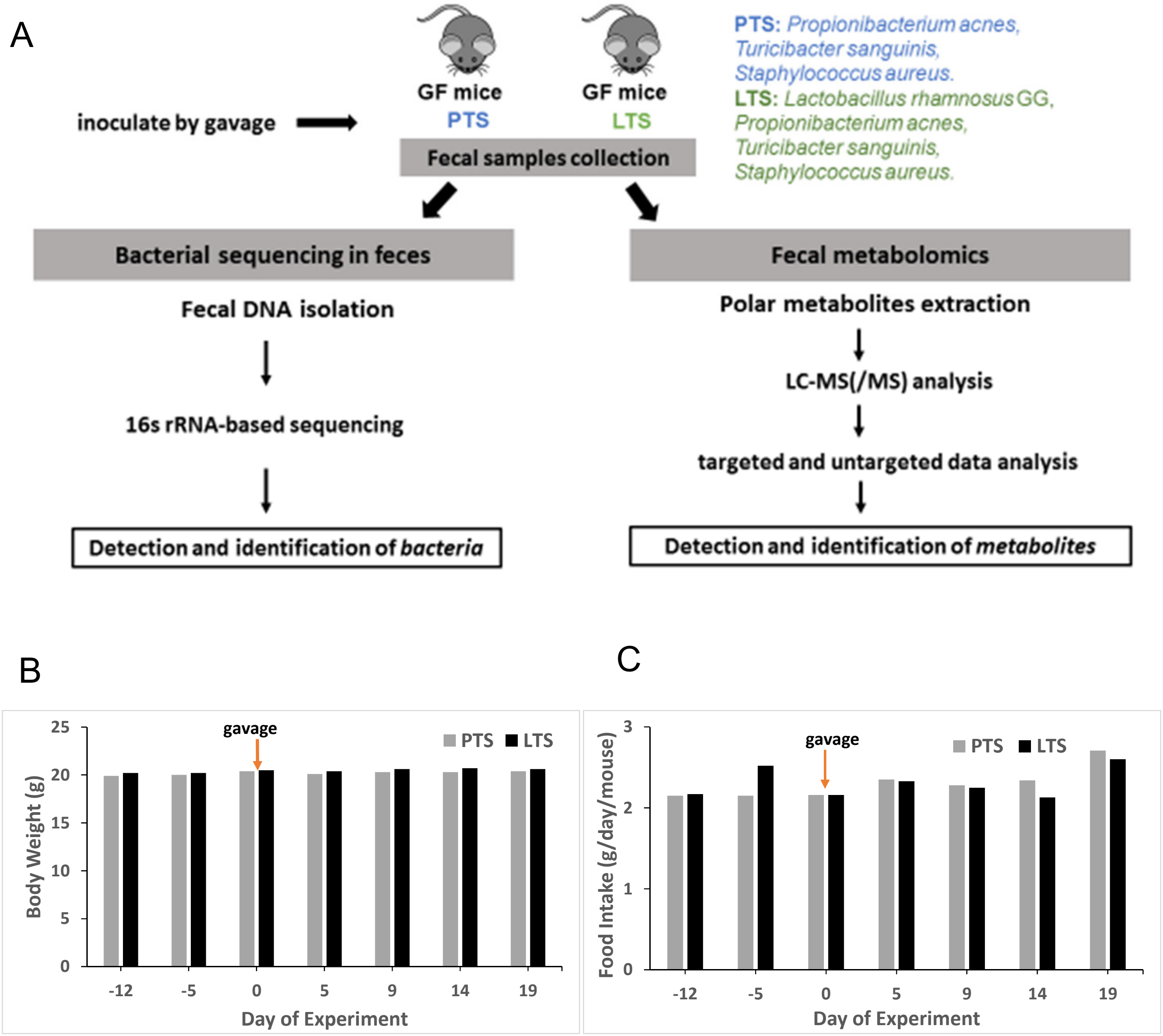
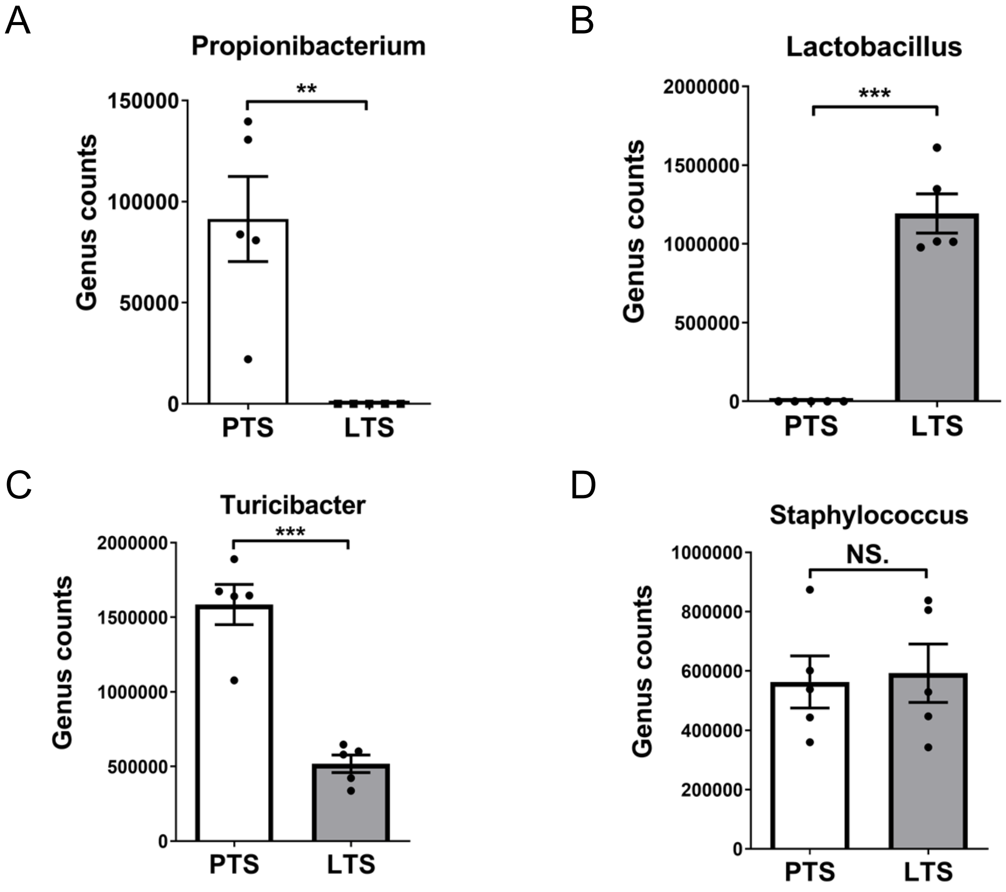
⁺, equal contribution

Kim et al. Supplementary Figure 1



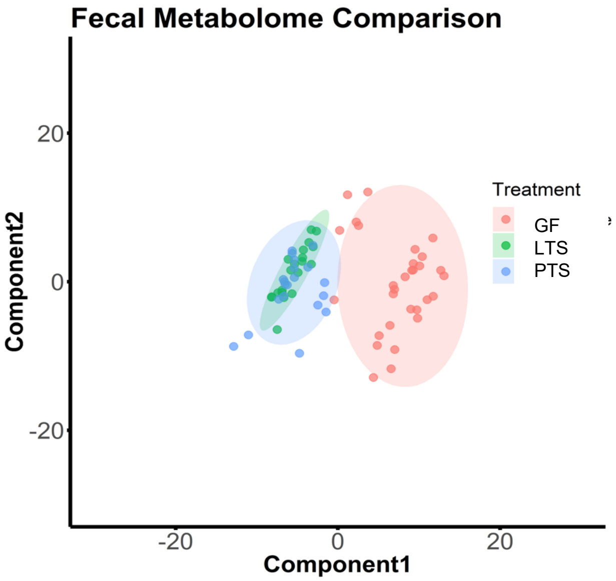
Supplementary Fig 1. Experimental design and clinical parameters (A) Schematic diagram of experimental plan (B) Body weights as a function of age of mice before and after gavage with PTS or LTS (C) Diet consumption by mice over the course of the study.

Kim et al. Supplementary Figure 2



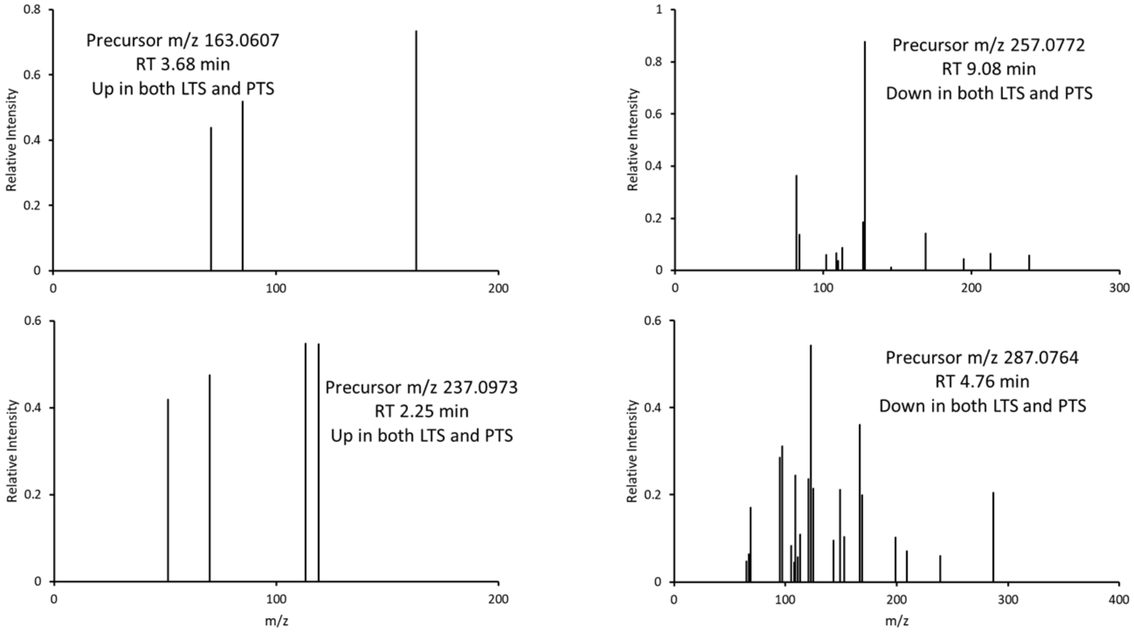
Supplementary Fig 2. Abundance of pathobionts when coassociated with LGG. Propionibacterium (A), Lactobacillus (B), Turicibacter (C), and Staphylococcus (D) abundance was determined in the feces from PTS (n=5) and LTS (n=5) mice by 16S amplicon profiling.

Kim et al. Supplementary Figure 3



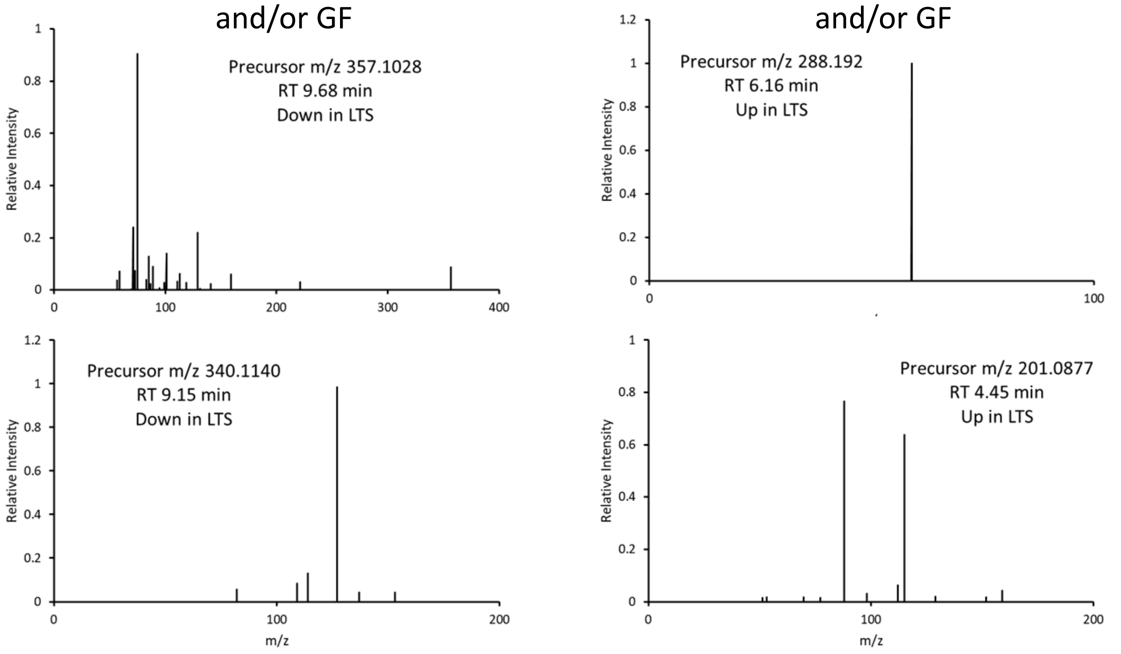
Supplementary Fig 3. Unsupervised principal component analysis (PCA) of fecal metabolites from GF, PTS, and LTS mice.

Kim et al. Supplementary Figure 4



A. Upregulated in both LTS and PTS

B. Downregulated in both LTS and PTS

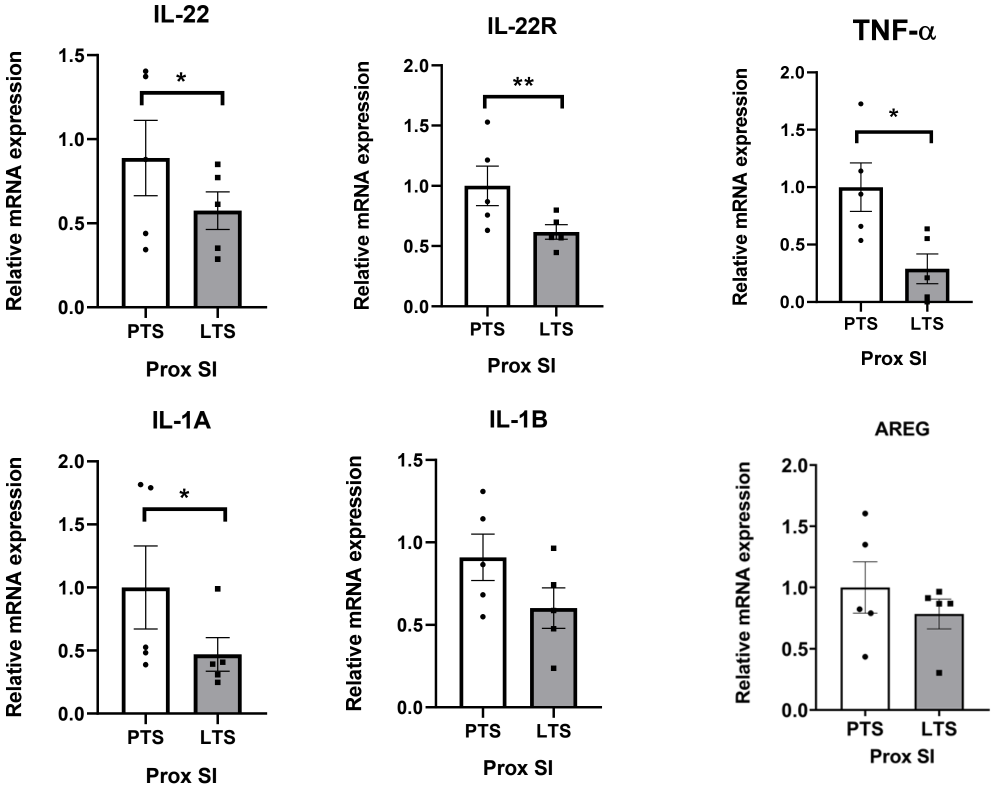


C. Downregulated LTS compared to PTS and/or GF

D. Upregulated LTS compared to PTS and/or GF

Supplementary Fig. 4. Accurate mass and MS^2 spectra of unidentified metabolites

Kim et al. Supplementary Figure 5



Supplementary Figure 5. Relative mRNA expression of intestinal immune-related genes in mucosa of proximal small intestine in GF mice associated PTS or LTS