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SUPPLEMENTARY INFORMATION

Lactoferrin modulates gut microbiota and Toll-like receptors (TLRs) in mice with dysbiosis induced by antibiotics

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3. Results

3.1. Raw sequence processing to obtain the ASVs



Figure S1. Rarefaction curves showing the observed ASVs in each sample of experiment 1 (A) and experiment 2 (B).

3.2. Bacterial composition



Figura S2. Bacterial relative abundances at order level in each sample of vehicle (Control, labeled with SS), clin (labeled with CLI), nLf (labeled with LFN), sLf (labeled with LFS), nLf_Clin (labeled with LFNCL) and sLf_Clin (labeled with LFSCL) groups.



Figura S3. Bacterial relative abundances at family level in each sample of vehicle (Control, labeled with SS), clin (labeled with CLI), nLf (labeled with LFN), sLf (labeled with LFS), nLf_Clin (labeled with LFNCL) and sLf_Clin (labeled with LFSCL) groups.

3.3. Alpha and Beta diversity

Figure S4. NMDS showing the Bray-Curtis distances between the different microbial populations of the groups Vehicle (Control), Clin, nLf, sLf, nLf_Clin and sLf_Clin in Experiment 1 and Experiment 2.

3.7. Histopathological analysis

Figure S5. Histopathological images of colon sections corresponding to mice from the six experimental groups. A: Vehicle (Control), B: Clin, C: nLf, D: sLf, E: nLf_Clin, F: sLf_Clin. Representative sections from six different animals. Hematoxylin eosin stain, 400x.