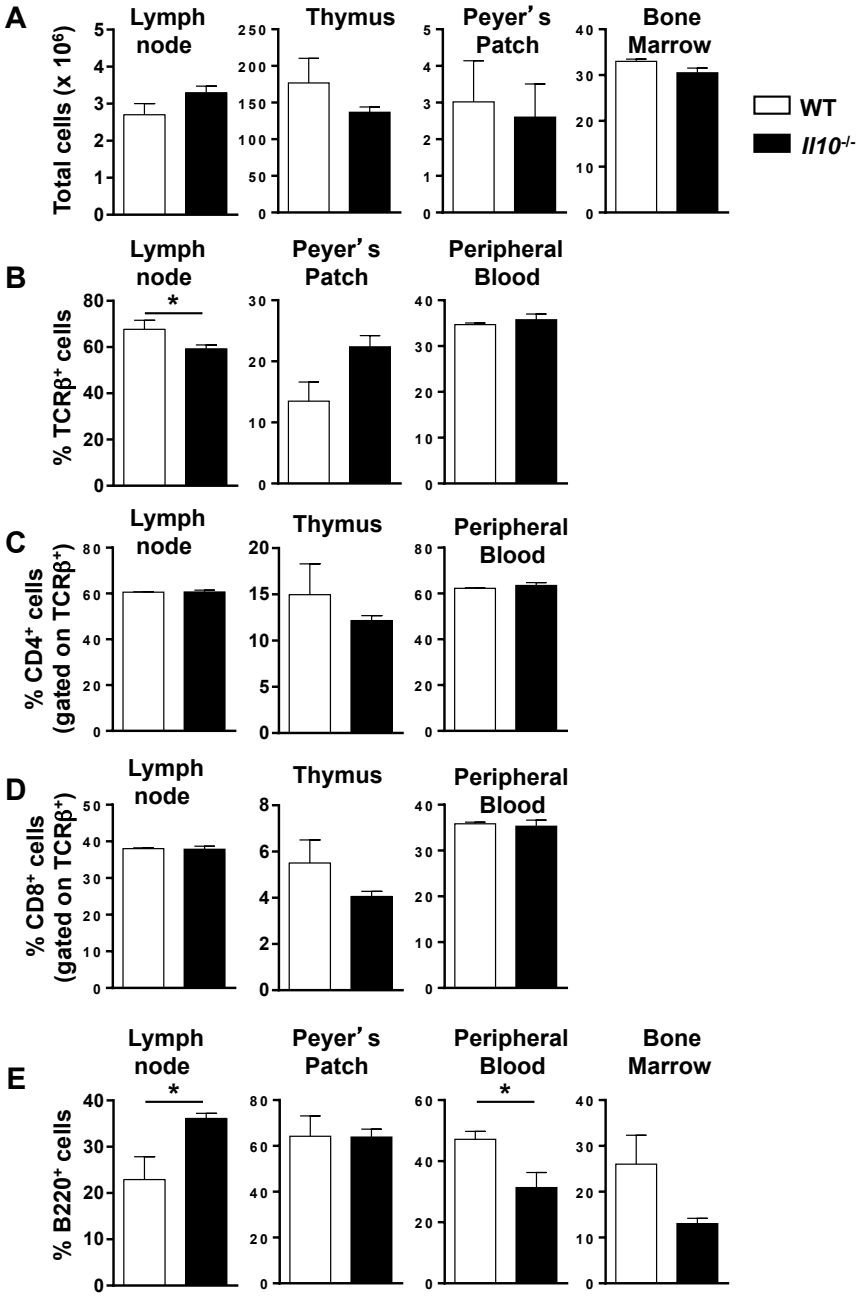
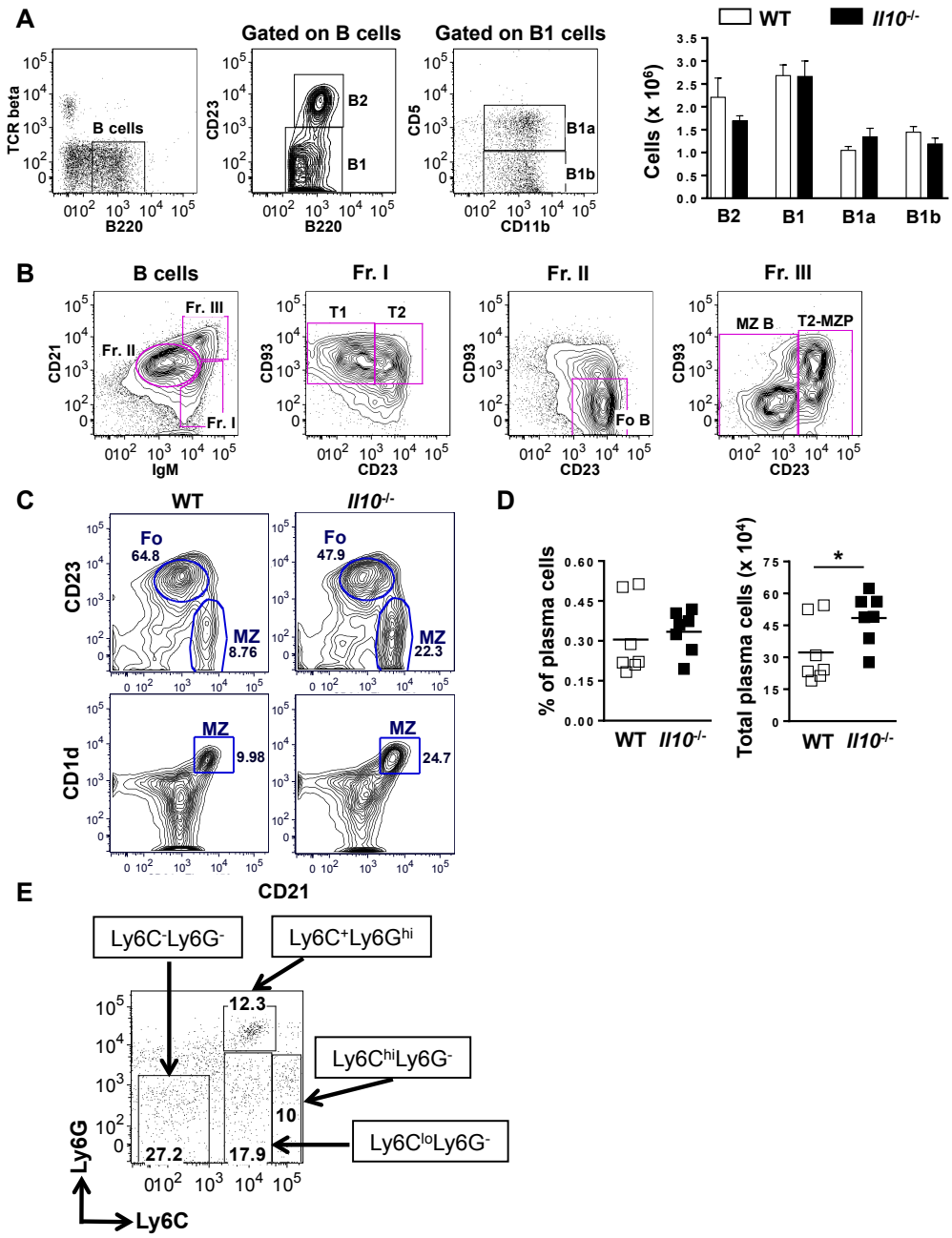
Supplemental Figure 1



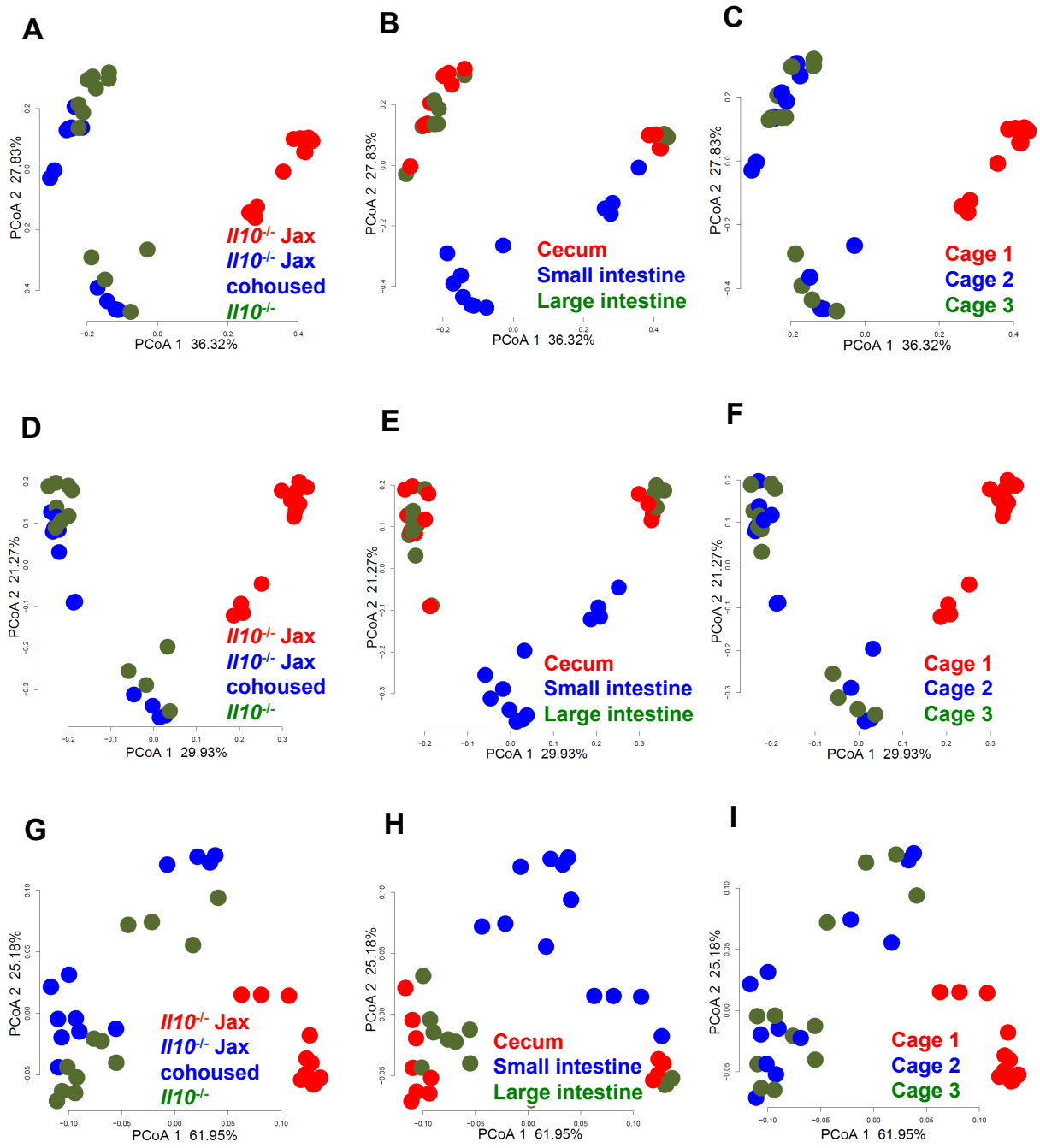
Supplemental Figure 1. Characterization of immune cells in the inguinal lymph node, thymus, Peyer's patch, peripheral blood and bone marrow of WT and *Il10*$^{-/-}$ mice. (A) The cellularity in the lymph node, thymus, Peyer's patch and bone marrow were determined in WT and *Il10*$^{-/-}$ mice. Data are shown as the mean ± SE (n = 3). (B) In the same mice as (A) the percentage of TCRβ^{+} cells was determined by flow cytometry in the inguinal lymph node, Peyer's patch, and peripheral blood. (C) In the same mice as (A) the percentage of CD4^{+} among TCRβ^{+}-gated cells was determined by flow cytometry in the inguinal lymph node, thymus, and peripheral blood. (D) In the same mice as (A) the percentage of CD8^{+} among TCRβ^{+}-gated cells was determined by flow cytometry in the inguinal lymph node, thymus, and peripheral blood. (E) In the same mice as (A) the percentage of B220^{+} cells was determined by flow cytometry in the inguinal lymph node, Peyer's patch, peripheral blood and bone marrow. *p<0.05.

Supplemental Figure 2



Supplemental Figure 2. Flow cytometry gating strategies and plasma cell quantitation. (A) A representative flow cytometry gating strategy for the analysis of peritoneal cavity B cell subsets is shown. The percentage of B2, B1, B1a and B1b peritoneal cavity B cell subsets was determined by flow cytometry in WT and *Il10*$^{-/-}$ mice. Data are shown as the mean ± SE (n = 3). (B) A representative flow cytometry gating strategy for the analysis of the T1, T2, T2-MZP, MZ and Fo splenic B cell subset is shown. (C) A representative flow cytometry alternative gating strategy for the analysis of splenic MZ and Fo B cells is shown for WT and *Il10*$^{-/-}$ mice. (D) WT and *Il10*$^{-/-}$ mice were immunized with NP-ficoll and 14 days later the percentage (left panel) and absolute number (right panel) of B220^{+}IgM^{-}IgD^{-}CD138^{+} plasma cells was determined in the spleen. Each data point represents one mouse. (E) A representative flow cytometry gating strategy for the analysis of splenic CD11b^{+}-gated cells expressing the Ly6C^{-}Ly6G^{-}, Ly6C^{+}Ly6G^{hi}, Ly6C^{hi}Ly6G^{-} or Ly6C^{lo}Ly6G^{-} phenotypes is shown. *p<0.05.

Supplemental Figure 3



Supplemental Figure 3. Change in microbial community composition analyzed using the QIIME open-reference OTU picking approach. Plots representing Bray Curtis PCoA (A-C), unweighted-Unifrac PCoA (D-F) and weighted-Unifrac PCoA (G-I) are shown with each PCoA colored by either origin (A, D, G), tissue source (B, E, H), or cage (C, F, I).