Supp. Figure 1. Relative abundance of class and order bacterial groups change due to either anastomotic surgeries. (A) Relative abundance composition of the intestinal microbiome class or (B) order for each intestinal segment (top heading) within each surgery group (x-axis label).

Supp. Figure 2. Expression of IL-10 and IL-22 in iNKT cells after end-to-end and Roux-en-Y anastomoses. (A) Dot plots showing increased IL-10+ expression in iNKT cells after both anastomotic surgeries. (B) Normalized iNKT cells that are IL-22+. \* = p ≤ 0.05, n=5-8

Supp. Figure 3. Treg gating and expression of IL-10 and IL-22. (A) Dot plots showing Treg cells after (A) no surgery, (B) end-to-end anastomosis, and (C) Roux-en-Y anastomosis from segment A. FoxP3 vs. TCRβ dot plots (2nd column from top to bottom) back gate to either TCRβhi CD4+, TCRβhi/+ CD4+, or TCRβ+ CD4+ gates in the first dot plot. IL-22 and IL-10 plots are back gated to the TCRβhi/+ CD4+ FoxP3+ parent plot. Representative of one experiment, n=6-7.

Supp. Figure 4. Immune cell populations correlate to Bacteroidetes with distinct patterns based on either anastomotic surgery. Correlation graphs of (A) iNKT (TCRβ+ CD1dtet+) IL-22+ cells, (B) iNKT IL-10+, (C) CD11bhi CD103mid DCs (CD45+ IA-IE+ CD110+), (D) Th17 (TCRβhi CD4+ IL-17A+ IL17F+) and (E) Treg (TCRβ+ CD4+ FoxP3+) versus Bacteroidetes within surgery type.

Supp. Figure 5. Immune cell populations correlate to Proteobacteria with distinct patterns based on either anastomotic surgery. Correlation graphs of (A) iNKT (TCRβ+ CD1dtet+) IL-22+ cells, (B) iNKT IL-10+, (C) CD11bhi CD103mid DCs (CD45+ IA-IE+ CD110+), (D) Th17 (TCRβhi CD4+ IL-17A+ IL17F+) and (E) Treg (TCRβ+ CD4+ FoxP3+) versus Proteobacteria within surgery type.

Supp. Figure 6. Immune cell populations correlate to Bacteroidetes with distinct patterns based on surgical segments. Correlation graphs of (A) iNKT (TCRβ+ CD1dtet+) IL-22+ cells, (B) iNKT IL-10+, (C) CD11bhi CD103mid DCs (CD45+ IA-IE+ CD110+), (D) Th17 (TCRβhi CD4+ IL-17A+ IL17F+) and (E) Treg (TCRβ+ CD4+ FoxP3+) versus Bacteroidetes within surgical segments.

Supp. Figure 7. Immune cell populations correlate to Proteobacteria with distinct patterns based on surgical segments. Correlation graphs of (A) iNKT (TCRβ+ CD1dtet+) IL-22+ cells, (B) iNKT IL-10+, (C) CD11bhi CD103mid DCs (CD45+ IA-IE+ CD110+), (D) Th17 (TCRβhi CD4+ IL-17A+ IL17F+) and (E) Treg (TCRβ+ CD4+ FoxP3+) versus Proteobacteria within surgical segments.

Supp. Table 1. Pearson correlation coefficients (r) for immune cell population versus phylums within anastomoses segments. Bolded r value with \* have a p ≤ 0.05 and indicates a significant correlation between the immune cell population and phylum within that surgical segment.

Supp. Table 2. Pearson correlation coefficients (r) for immune cell population versus phylums within surgery types. Bolded r value with \* have a p ≤ 0.05 and indicates a significant correlation between the immune cell population and phylum within that type of surgery.