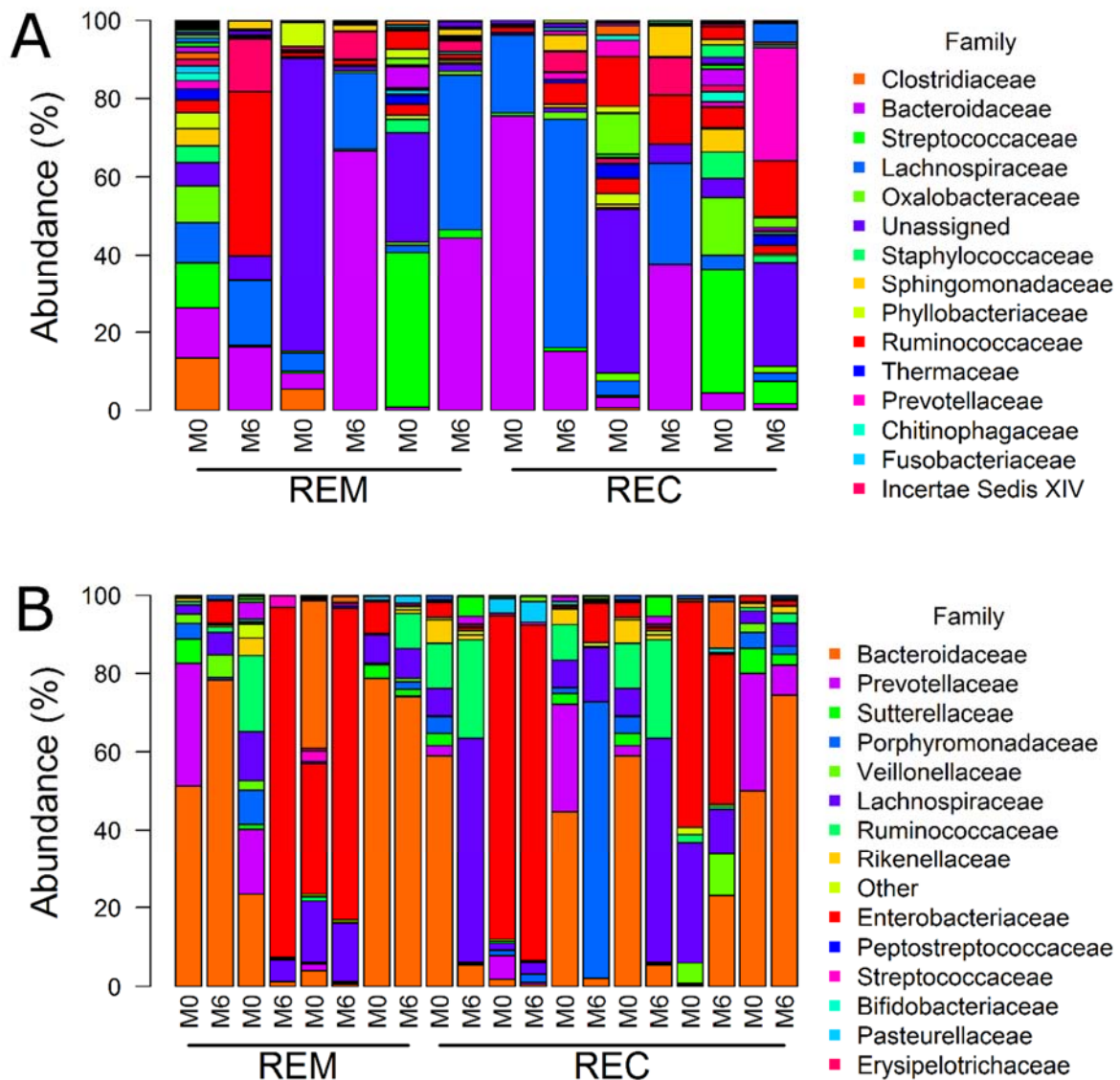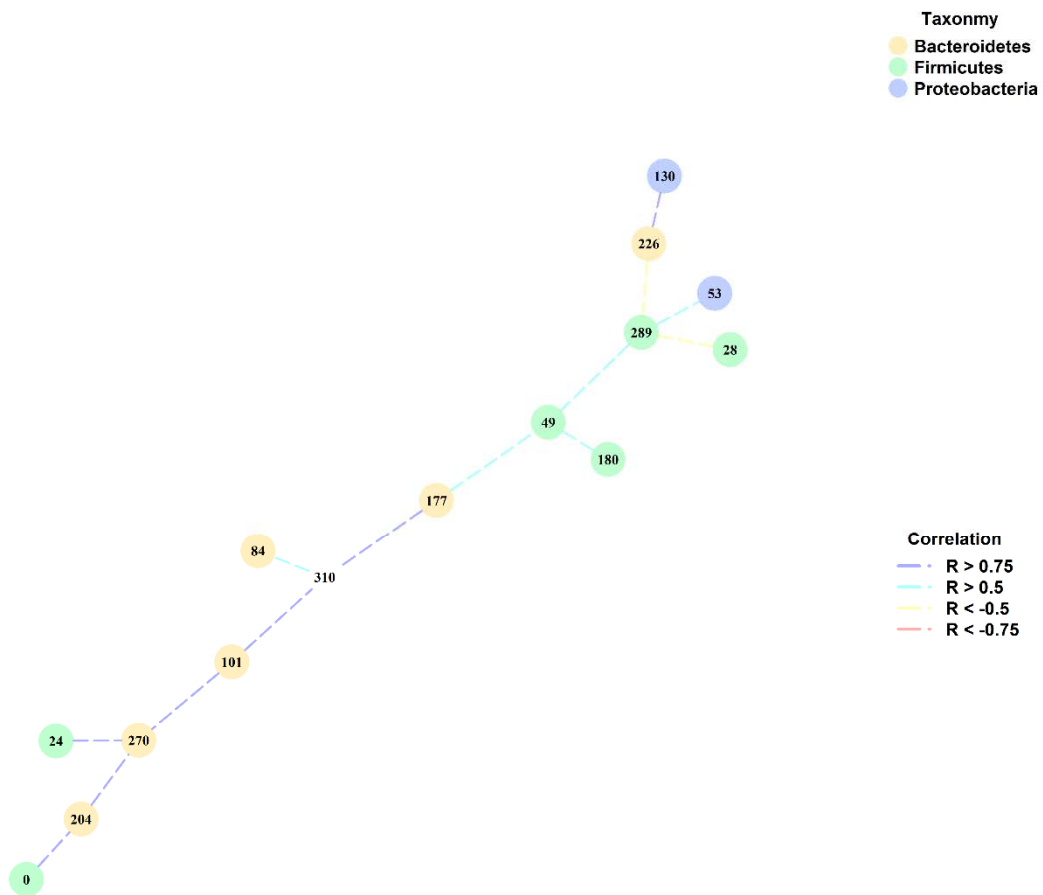**Supp. Figure 1: Distribution of bacterial families before and after ICR**

Only 15 main bacterial families are represented in the figures. Data are shown as Abundance (percent of total reads) for each family in A) Mucosal samples and B) Fecal samples.

M0: Month 0, time of surgery; M6: Month 6 after surgery; REM: Remission at M6; REC: Endoscopic recurrence at M6.

Supp. Figure 2: Structural analysis of the microbial communities detected in patients at time of surgery

The correlation network analysis depicts the structure inferred from the mucosal microbiota composition of CD patients at ICR. Each number relates to OTU indexes. OTU phylogeny at phylum level is described by colors filling each OTU dot. Correlation scores are indicated by the color of the edges linking OTU pairs.

Supp. Figure 3: Venn diagram describing similarities between microbiota structures at OTU level
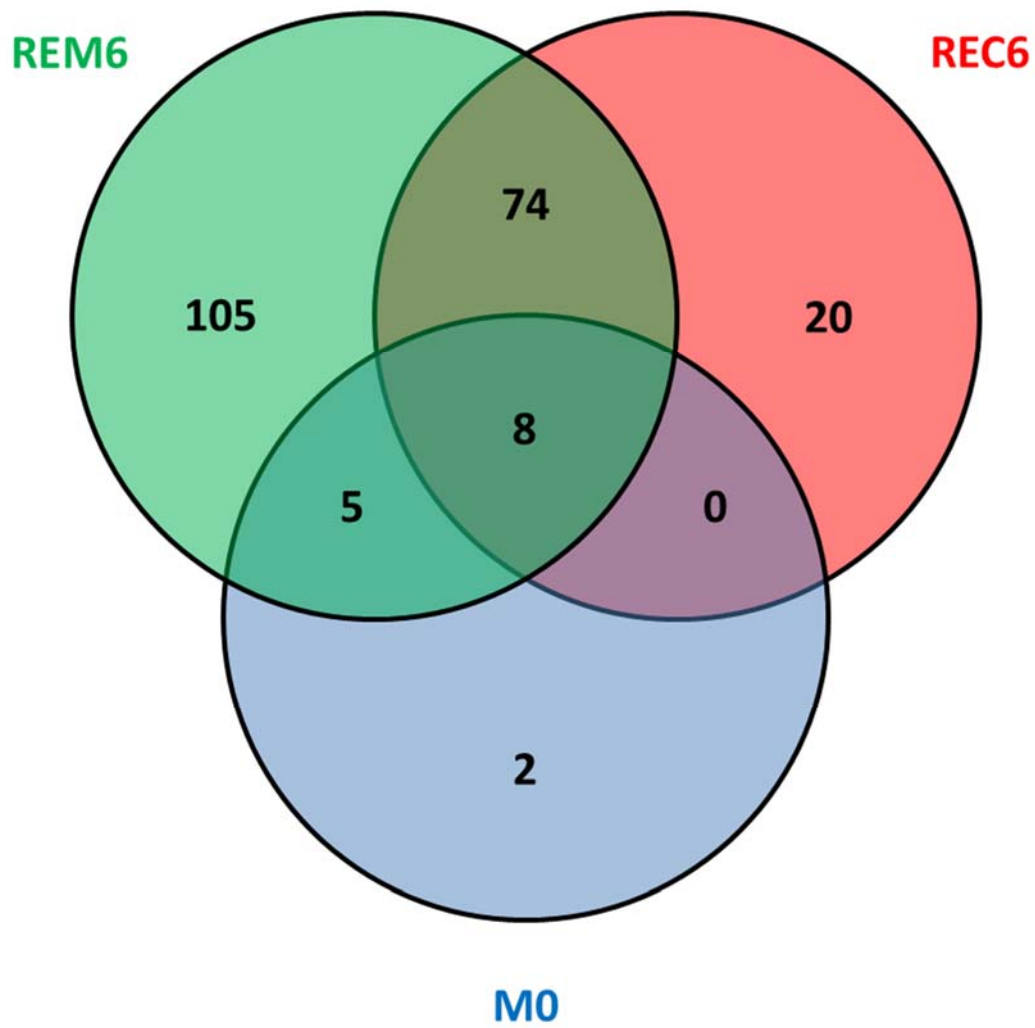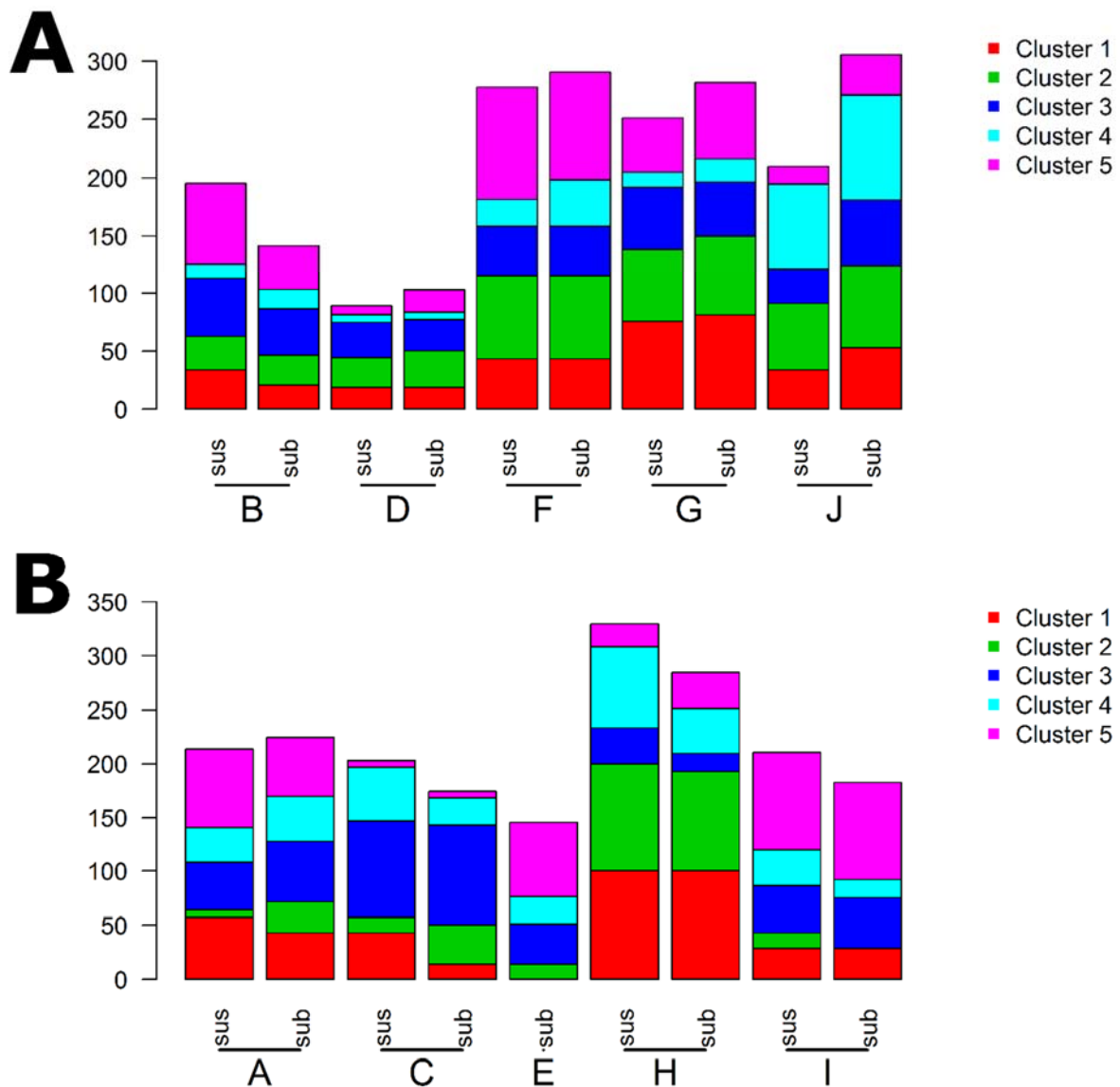

Diagram displaying the number of OTUs that are common or specific to microbiota structures inferred before and after surgery. M0: Samples at time of surgery; REC6: samples from patients with recurrence at 6 months; REM6: samples from patients in remission at 6 months.

Supp. Figure 4: Bacterial clusters distribution within each patient's microbiota 6 months after ICR in neoterminal ileum and subanastomotic colon.

The clusters abundance across samples was assessed using the occurrence of cluster specific OTUs. For each sample, the sum of OTUs occurrences found for a cluster was computed and then divided by the total number of OTUs identified in the cluster. Then, the relative clusters abundance (varying from 0 to 100%) was displayed as a cumulative bar plot.

A. Clusters distribution in the microbiota of patients in remission 6 months after ICR in both neoterminal ileum (sus) and subanastomotic colon (sub).

B. Clusters distribution in the microbiota of patients with endoscopic recurrence 6 months after ICR in both neoterminal ileum (sus) and subanastomotic colon (sub).