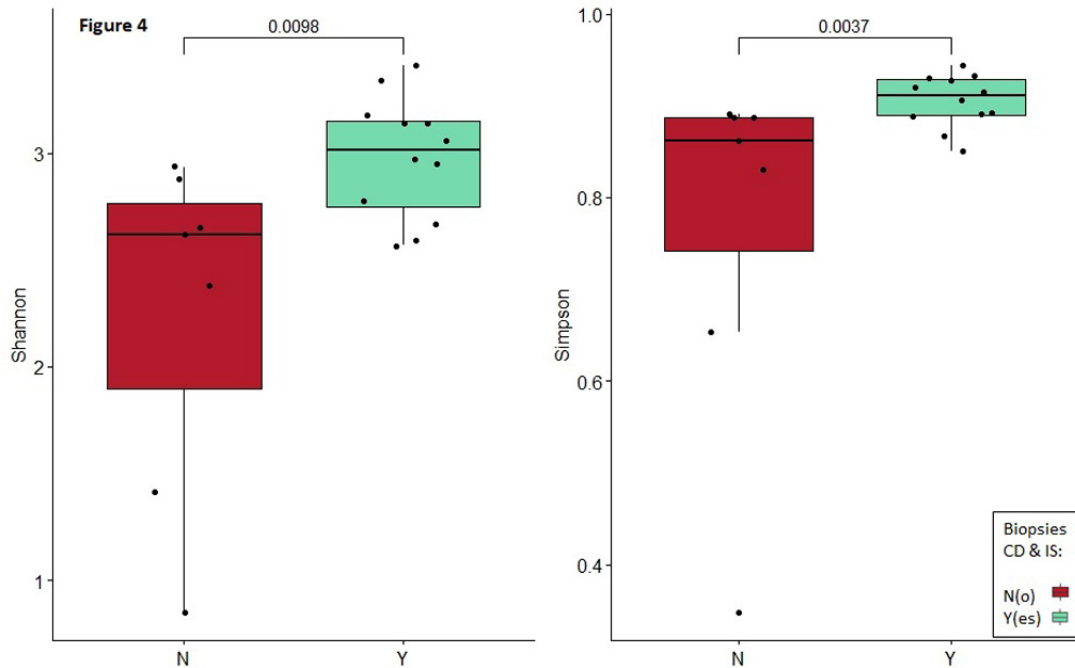


Abstract P676



UCsr patients (median $5.60E-07$, FDR $p=0.0072$), there were no differences between UClr and UCsr patients.

Conclusion: Fungal abundance was increased in UC flare patients compared to UC patients in long remission, while there were no differences in bacterial abundance. This high number of fungi could be involved in the inflammatory response of UC patients.

P678

Definition of a microbial signature as a predictor of post-surgical recurrence in patients with Crohn's disease

L. Oliver¹, J. Amoedo¹, D. Julià², B. Camps^{*3}, S. Ramió-Pujol¹, M. Malagón¹, P. Torres⁴, E. Domènech⁴, J. Guardiola³, M. Serra-Pagès¹, J. Garcia-Gil⁵, X. Aldeguer²

¹GoodGut, Laboratory, Girona, Spain, ²Hospital Universitari Doctor Josep Trueta, General and digestive surgery, Girona, Spain, ³Hospital Universitari de Bellvitge, Gastroenterology, Hospitalet de Llobregat, Spain, ⁴Hospital Germans Trias i Pujol, Gastroenterology, Badalona, Spain, ⁵Universitat de Girona, Biology, Girona, Spain

Background: Although there are several effective drugs for the treatment of Crohn's disease (CD), almost 80% of patients will end up needing a surgical resection throughout their lives. This procedure is not always curative, as the disease often reappears in the intestine. Endoscopic recurrence occurs in 65%-90% of patients after one year from surgery. The aetiology of the recurrence is unknown; however, several studies have shown how the resident microbiota is modified after surgery.

The aim of this study is to evaluate samples from patients with CD before and after an intestinal resection to determine if at baseline there are differences in the abundance of different microbial markers, which could be capable of predicting endoscopic recurrences.

Methods: In this observational study, a stool sample was obtained from 20 patients with CD before undergoing surgery, recruited at Hospital Universitari Dr. Josep Trueta, Hospital Universitari de Bellvitge, and the Hospital Universitari Germans Trias i Pujol. From each sample, DNA was purified and the relative abundance of the following microbial markers was quantified using qPCR: *E. prausnitzii* (Fpra) and its phylogroups (PHG-I and PHG-II), *E. coli* (Eco), *A. muciniphila* (Akk), *Ruminococcus* sp. (Rum), Bacteroidetes (Bac), *M. smithii* (Msm), and total bacterial load (Eub).

Results: Individually, none of the biomarkers demonstrated the ability to differentiate patients who will develop post-surgical recurrence from those who will not. In contrast, the combination of 4 microbial markers (Eco, PHGI, Bac, and Eub) showed a high capacity of discrimination between the 2 groups. The algorithm that incorporates these three markers shows a sensitivity and specificity of 100% and 90.91%, respectively, and a positive and negative predictive value of 90.00% and 100%, respectively.

Conclusion: A microbial signature to determine patients who will have post-surgical recurrence has been identified. This tool can be very useful in daily clinical practice allowing to schedule a personalized therapy, enabling preventive treatment only in that subgroup of patients who really require it. A broader prospective study will be needed to validate these results.