patients studied off PPI (p=0.97 figure 1). There was no difference in MNBI between the 10 patients with persistent (>3 cm) Barrett’s who had attempts at therapy (ablation, mucosal resection) compared to the 27 who had not received therapy (p=0.96).

There was a moderately inverse correlation between Barrett’s segment length (median 5 cm (3 cm,9 cm) and MNBI (r = -0.436; p=0.038).

Conclusion This study suggests that the impact of reflux disease on mucosal permeability (MNBI) may have an influence on symptom perception. Both MNBI and symptom perception were significantly reduced in Barrett’s compared to NERD. Furthermore, neither MNBI nor symptom perception are affected by use of acid reducing medication despite the difference in AET. This study provides further validation to the Lyon consensus definition of MNBI as a measure of reflux disease severity.

**Abstract P326 Figure 1** MNBI is reduced in Barrett’s (regardless of PPI use) compared to NERD and FH. Median and IQR for the MNBI of: patients with Barrett’s off PPIs 4065Ω (3680Ω, 1111.5Ω); Barrett’s on PPIs 4533Ω (261.5Ω, 10000Ω); NERD 1160Ω (964.5Ω, 2764Ω) and FH 3355Ω (2866.5Ω, 3809.25Ω)

**P325** AN EXPANDED INTESTINAL INTRAEPITHELIAL LYMPHOCYTE COMPARTMENT IS LINKED TO SHIFTS IN COMPOSITION OF MUCOSAL MICROBIOTA


**P326** IDENTIFICATION OF NOVEL SUBGROUPS IN IRRITABLE BOWEL SYNDROME USING LATENT CLASS ANALYSIS: BEYOND STOOL FORM

**Introduction** The composition of bacteria colonising the gastrointestinal tract shapes mucosal and systemic immune responses and impacts susceptibility to different diseases. However, a consistent microbiome signature of Irritable Bowel Syndrome (IBS) has yet to be established, and the microbiome was not altered in a large, population-based study of IBS.

Since it has been proposed that immune activation and subtle intestinal inflammation may be present in a subset of IBS, we hypothesised that alterations in the gut microbiome may underpin changes in gut immune phenotype.

**Methods** The study population comprised IBS cases and controls (defined by modified Rome III criteria) from the PopCol study. All participants had a normal colonoscopy. Biopsies were taken from the terminal ileum (TI), caecum, transverse colon (TC), sigmoid and rectum (Re). Assessment of histology was blinded and dual read, and disagreement was resolved by consensus. Intraepithelial lymphocyte (IEL) counts were dichotomised: high IEL count was defined as >15 per 100 enterocytes in TI and >8 per 100 colonocytes in the colon. Colonic mucosa-associated microbiota (MaM) and faecal microbiota (FM) were characterised by 16S rRNA sequencing on Illumina MiSeq. Data were processed and analysed in R, Graphpad & STAMP, with p value correction for multiple testing.

**Results** 76 participants (including 30 with IBS) were analysed, in whom IEL and microbiome data were available. The median age was 50 years (range 23–69) and 40 (53%) were women. 55% of TI samples and between 39% (Re) and 51% (TC) of samples from colonic sites had a high IEL count. No difference was observed in alpha diversity of MaM or FM based on IEL count. There were trends towards differences in beta diversity of the MaM according to IEL count in the TI and TC (p=0.079 & 0.072). No difference in FM beta diversity was observed. In the MaM, the genus Blautia and unclassified Clostridiales were associated with high IEL count in the TI (p=0.024 & 0.036). Alloprevotella was associated with low IEL count in the sigmoid (p=0.035).

**Conclusions** In this nested analysis of participants in the PopCol study, modest but discernible differences in the mucosa-associated microbiota were seen according to IEL count.

**REFERENCES**