Suppl. Figure 3. Bacterial taxa and feacal metabolites abundances can be used to classify non-IBD and IBD faecal samples. **A.** The ratio between the levels of lactosyl-N-palmityl-sphingosine and L-urobilin is higher in samples from patients in remission (salmon) when compared with controls (grey) **B.** Boxplot depicts the values of a potential biomarker for IBD based on microbial abundance. Y-axis represents the log-transformed values of the ratio constructed from the abundance of *F. prausnitzii* and the sum of *G. formicilis* and *M. smithii*. Boxplot in grey shows values in non-IBD controls. Boxplot in orange shows values in samples from patients with IBD. **C.** Receiver operating characteristic curve (ROC curve) of the prediction model based on patient characteristics (age, sex, BMI), the levels of faecal calprotectin (expressed as a binary trait (yes/no) if levels of this marker were >200 µg/g of faeces) and the ratio based on bacterial taxa. The prediction value, expressed as the area under the curve (AUC), reached a value of 0.86 in the test dataset. Boxplot shows the median and interquartile range (25th and 75th). Whiskers show the 1.5*IQR range. Data distribution is represented by background violin-plot.