**Figure Captions**

DESeq2 Volcano plot:

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| Figure x. Volcano plot showing differentially expressed genes between IBD and control patients. The vertical axis corresponds to the log10-transformed mean expression values, and the horizontal axis corresponds to the log2-transformed fold changes. Magenta dots indicate significantly up-regulated genes, while teal dots indicate significantly down-regulated genes. Blue and yellow dots indicate negligible and insignificant differences in gene expression, respectively. Values were obtained by running DESeq2 analysis on transcript-level estimates obtained from Kallisto. |

DESeq2 PCA plot:

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| Figure x. PCA plot showing variances in gene expression across control and IBD patients. Control patients are labeled red and IBD patients are labeled blue. Gene expression between the patient two groups differ notably along PC1 while differences along PC2 are negligible. PC1 and PC2 cover 39% and 7% of the total variance, respectively. Principal component values were obtained by performing log2 transforms on the transcript count data obtained from DEseq2 and Kallisto analysis. |

PERMAOVA Bar plot:

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| Figure x. Bar plot showing linear coefficients for the most differentially expressed genes between control and IBD patients. Multivariate results indicate differences in several mitochondrial and immunoglobulin genes, suggesting a correlation between IBD presence and metabolic and immune dysregulation. Linear coefficients were obtained by performing the PERMANOVA test on gene-aggregated TPM values obtained from Kallisto. Each coefficient represents a fit of gene abundance to the PERMANOVA linear model. |

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| Figure x. PCA plot showing variances in metabolic flux across control and IBD patients. Control patients are labeled red and IBD patients are labeled blue. Several distinct groups of patients can be identified across PC1 and PC2, suggesting the presence of several factors that affect patient metabolism. PC1 and PC2 represent 40.21% and 23.76% of total variance, respectively. |