Supplementary Table 1:

Tukey's Multiple Comparisons Test
Adjusted P value

	Bacteroidetes	Firmicutes	Proteobacteria
Healthy vs. UC	0.563	0.897	0.639
Healthy vs. CD	0.032	0.221	0.953
CD vs. UC	0.270	0.423	0.830

Supplemental Table 2: Patient characteristics	UC n = 14	CD n = 13	VA n = 27
Age, y			
Mean (SD)	41 ± 11	38 ± 11	61 ± 7
Sex, n (%)			
Male	9 (64)	11 (84.6)	26 (96.3)
Female	5 (36)	2 (15.4)	1 (2.7)
BMI (kg/m^2)	25.3 ± 3.9	24.1 ± 4.4	29.2 ± 5.9
Ethnicity, n (%)			
Caucasian	12 (85.7)	11 (84.6)	8 (29.6)
Hispanic	2 (14.3)	--	8 (29.6)
African American	--	--	8 (29.6)
East Asian	--	1 (7.7)	--
other	1 (7.1)	1 (7.7)	3 (11.1)
Disease time, y	15.6 ± 9.2	15.8 ± 11.1	
Active Meds, n (%)			
Azathioprine	2 (14.3)	1 (7.7)	
6-MP	5 (36.0)	4 (30.8)	
Anti-TNF	2 (14.3)	4 (30.8)	
Mesalamine (5-ASA)	11 (78.6)	4 (30.8)	
Corticosteriods		3 (23.1)	
Involvement n (%)			
Colon		11 (84.6)	
Small Bowel		7 (53.8)	
Perianal		4 (30.8)	
Both small and colon		7 (53.8)	
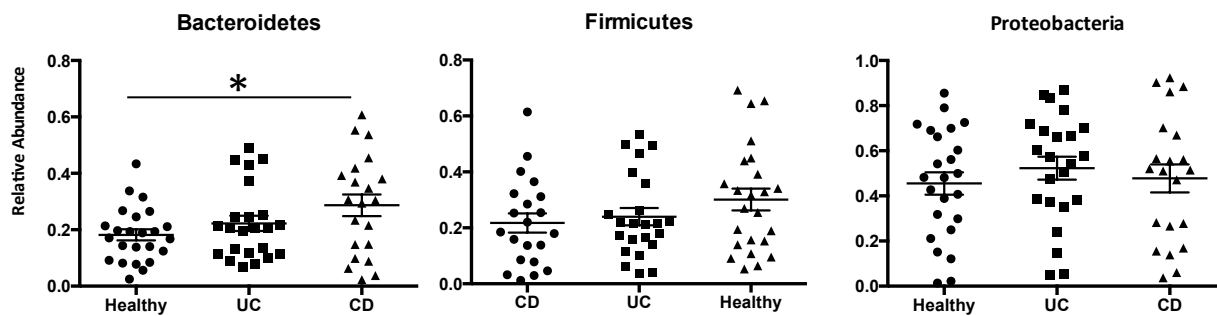
Figure S1: Taxonomic differences at the phylum level of the mucosal microbiota in IBD and healthy patients. Scatterplots showing the relative abundance of the 3 most prevalent bacterial phyla of Bacteroidetes, Firmicutes, and Proteobacteria. Samples from CD patients had a significantly higher proportion of Bacteroidetes compared with healthy control subjects. Although UC and CD biopsies showed slightly decreased abundance of Firmicutes and slightly increased abundance of Proteobacteria, these differences were not statistically significant.

Human Diseases;Infectious Diseases
Environmental Information Processing;Signaling Molecules and Interaction
Cellular Processes;Transport and Catabolism
Human Diseases;Immune System Diseases
Unclassified;Cellular Processes and Signaling
Metabolism;Amino Acid Metabolism
Cellular Processes;Cell Motility
Human Diseases;Cardiovascular Diseases
Environmental Information Processing;Signal Transduction
Human Diseases;Neurodegenerative Diseases
Organismal Systems;Circulatory System
Metabolism;Lipid Metabolism
Metabolism;Xenobiotics Biodegradation and Metabolism
Metabolism;Metabolism of Other Amino Acids
Metabolism;Metabolism of Terpenoids and Polyketides
Human Diseases;Cancers
Organismal Systems;Endocrine System
Organismal Systems;Excretory System
Unclassified;Poorly Characterized
Cellular Processes;Cell Growth and Death
Metabolism;Metabolism of Cofactors and Vitamins
Environmental Information Processing;Membrane Transport
Genetic Information Processing;Folding, Sorting and Degradation
Metabolism;Carbohydrate Metabolism
Genetic Information Processing;Transcription
Genetic Information Processing;Replication and Repair
Genetic Information Processing;Translation
Metabolism;Enzyme Families
Metabolism;Nucleotide Metabolism
Human Diseases;Metabolic Diseases
Organismal Systems;Nervous System
Organismal Systems;Immune System
Metabolism;Biosynthesis of Other Secondary Metabolites
Metabolism;Energy Metabolism
Organismal Systems;Environmental Adaptation
Unclassified;Genetic Information Processing
Metabolism;Glycan Biosynthesis and Metabolism
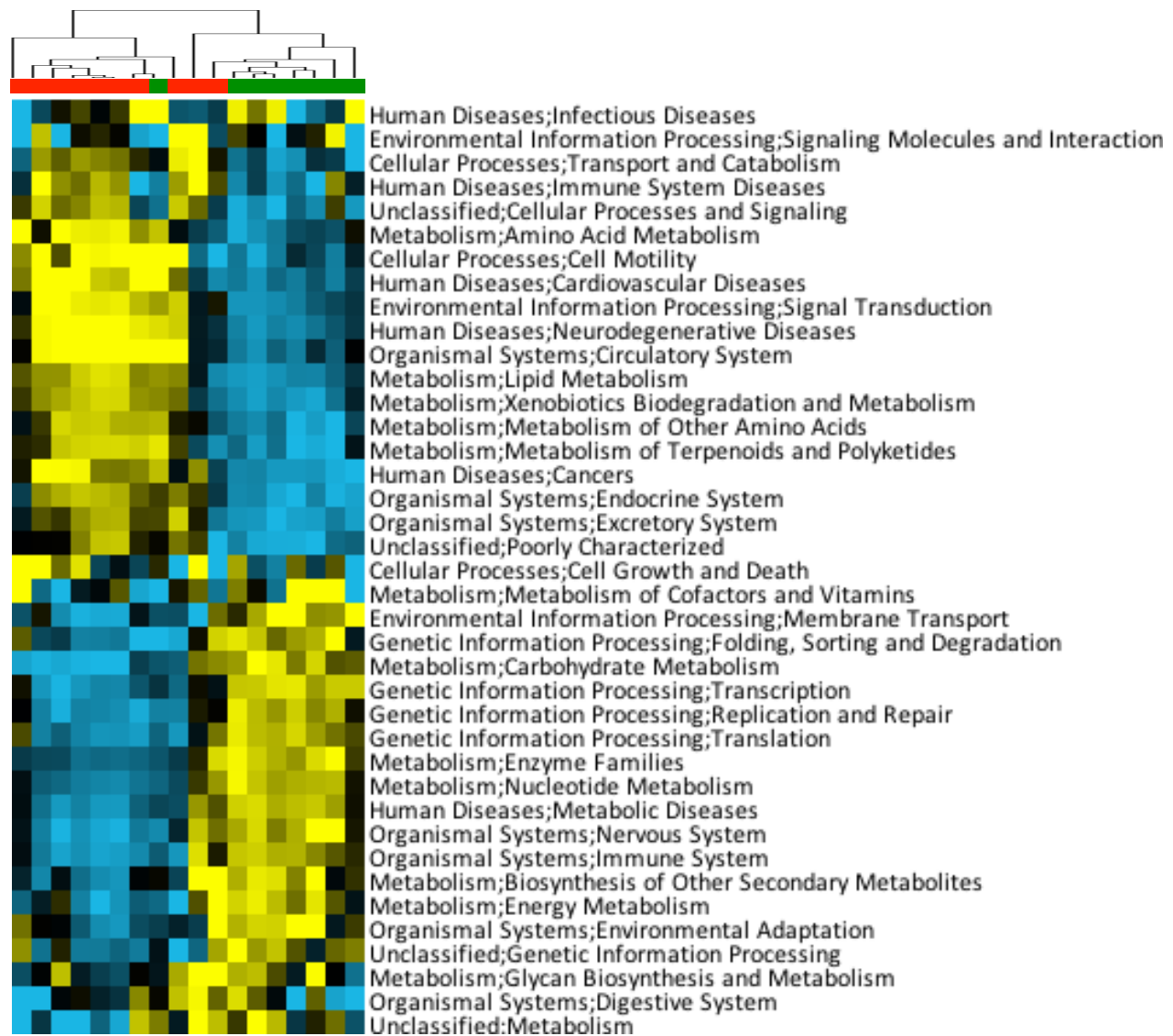Organismal Systems;Digestive System
Unclassified:Metabolism

Figure S2: Unsupervised hierarchical clustering analysis on the relative abundance values of KEGG pathways represented from the mucosal microbiota of UC patients. Red = Inflamed. Green = Non-inflamed
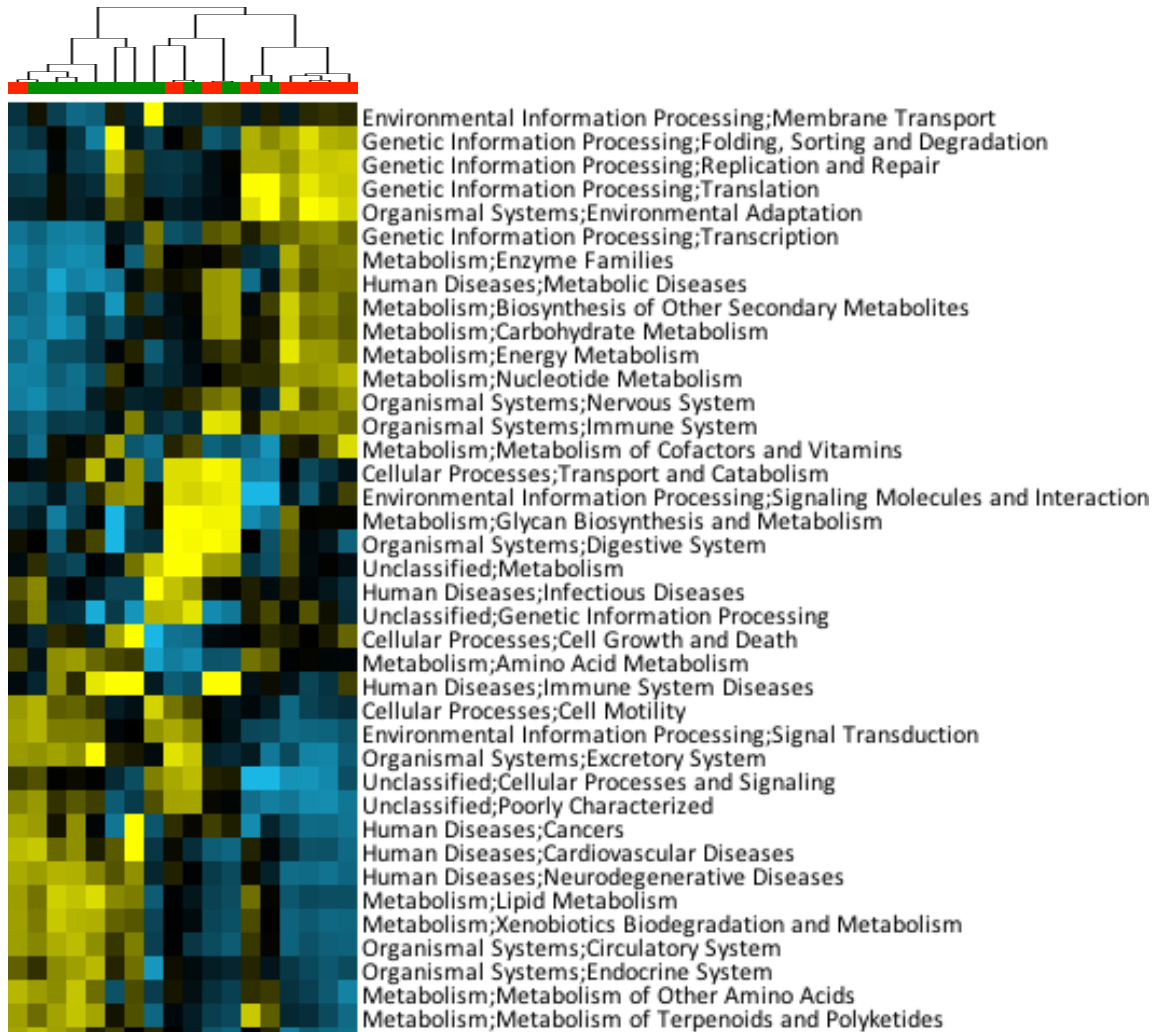
Figure S3: Unsupervised hierarchical clustering analysis on the relative abundance values of KEGG pathways represented from the mucosal microbiota of CD patients. Red = Inflamed. Green = Non-inflamed

Cellular Processes;Cell Growth and Death
Environmental Information Processing;Membrane Transport
Metabolism;Energy Metabolism
Genetic Information Processing;Replication and Repair
Genetic Information Processing;Translation
Metabolism;Nucleotide Metabolism
Organismal Systems;Environmental Adaptation
Genetic Information Processing;Transcription
Organismal Systems;Immune System
Human Diseases;Metabolic Diseases
Metabolism;Enzyme Families
Metabolism;Carbohydrate Metabolism
Metabolism;Biosynthesis of Other Secondary Metabolites
Organismal Systems;Nervous System
Genetic Information Processing;Folding, Sorting and Degradation
Unclassified;Genetic Information Processing
Metabolism;Metabolism of Cofactors and Vitamins
Environmental Information Processing;Signaling Molecules and Interaction
Metabolism;Glycan Biosynthesis and Metabolism
Unclassified;Metabolism
Cellular Processes;Cell Motility
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Metabolism;Metabolism of Terpenoids and Polyketides
Organismal Systems;Endocrine System
Organismal Systems;Excretory System
Unclassified;Poorly Characterized
Human Diseases;Immune System Diseases
Unclassified;Cellular Processes and Signaling
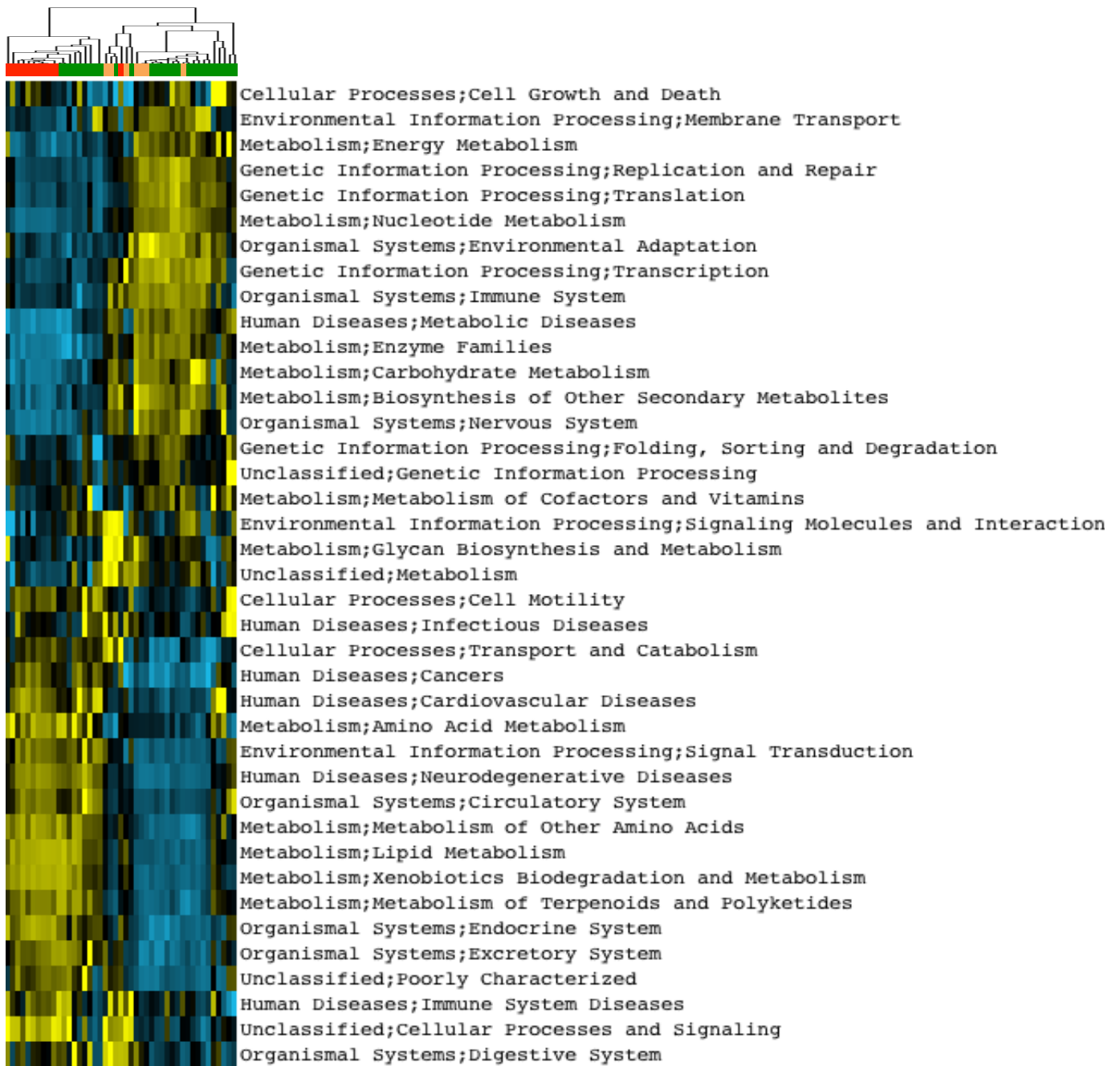Organismal Systems;Digestive System

Figure S4: Unsupervised hierarchical clustering analysis on the relative abundance values of KEGG pathways represented from the inflamed mucosal microbiota of UC and CD patients, as well as healthy controls. Red = Inflamed UC. Orange = Inflamed CD. Green = Healthy Subjects.