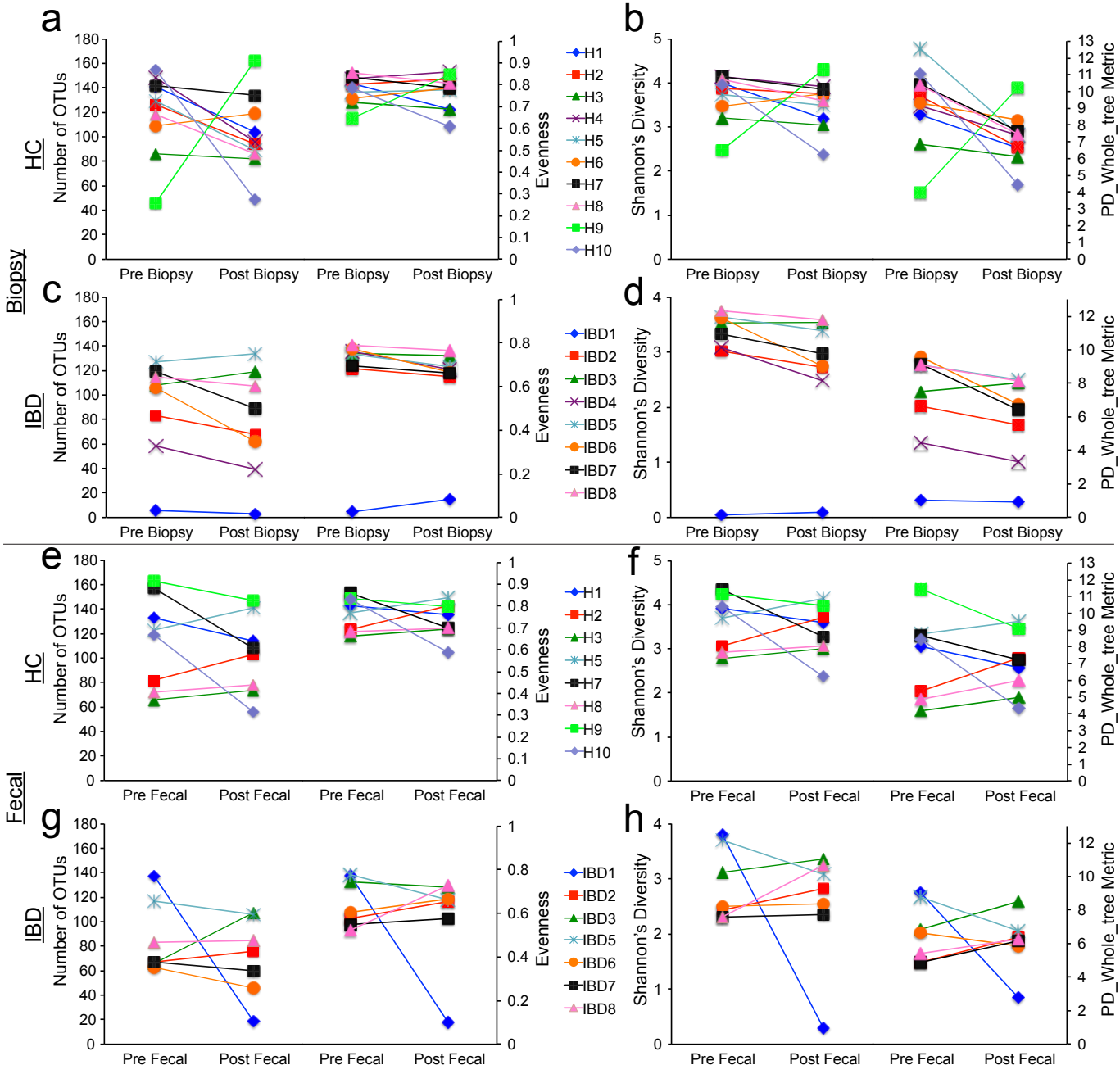

Figure S1: Diversity indices of each individual subject pre- and post-bowel prep. Each marker denotes a single sample, and each color denotes a single subject. Data is shown for 10 healthy subjects denoted H1 through H10; and for 8 IBD subjects denoted IBD1 through IBD8. The lines connect pairs of pre-bowel prep and post-bowel prep samples. Panels (a) and (b) denote diversity indices observed in the biopsies of healthy subjects. Panels (c) and (d) denote diversity indices observed in the biopsies of IBD subjects. Panels (e) and (f) denote diversity indices observed in the fecal samples of healthy subjects. Panels (g) and (h) denote diversity indices observed in the fecal samples of IBD subjects.

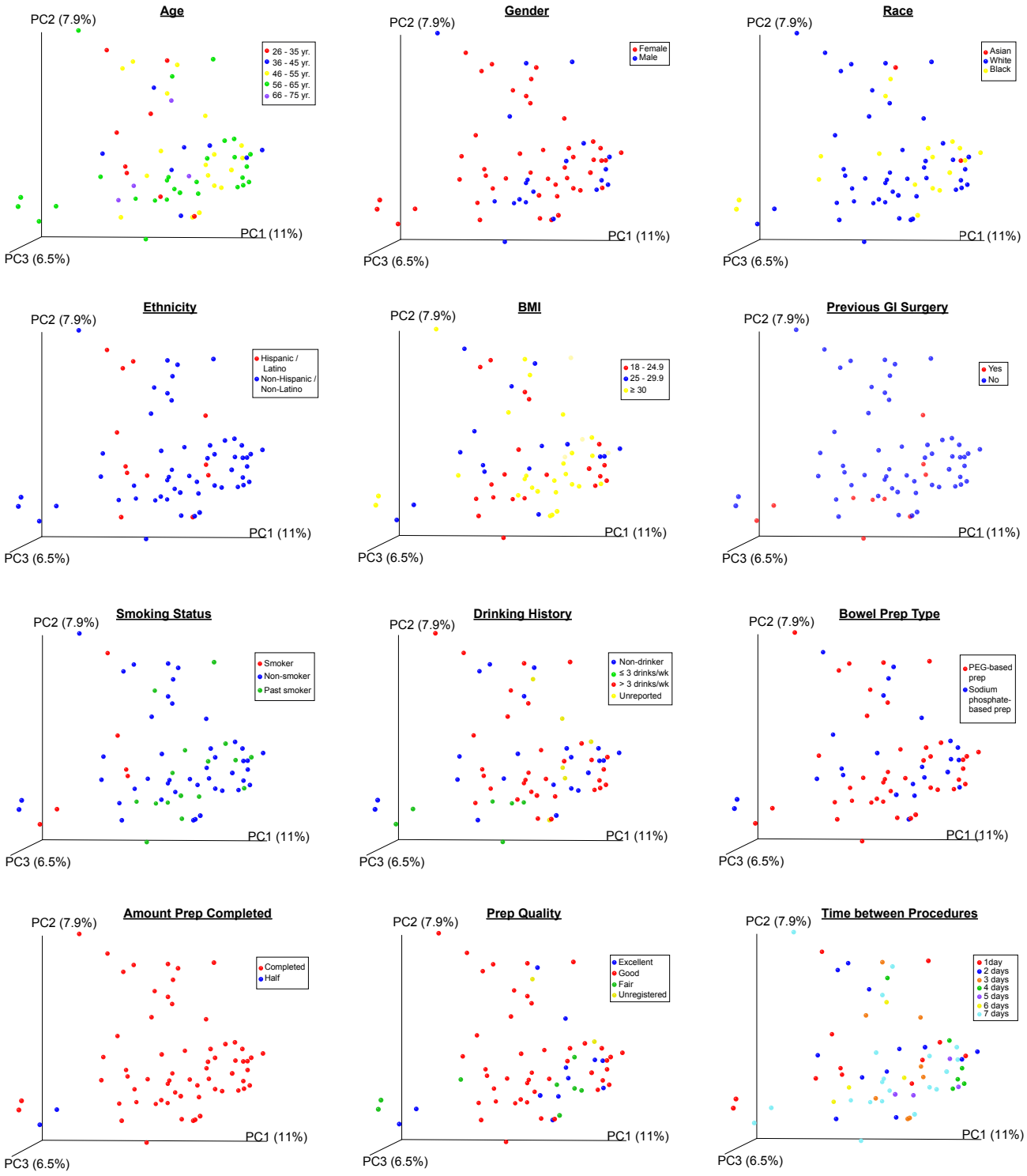

Figure S2: Principle Coordinate Analysis plots of samples using unweighted Unifrac distances by important demographic and clinical variables. Each marker denotes a single sample.

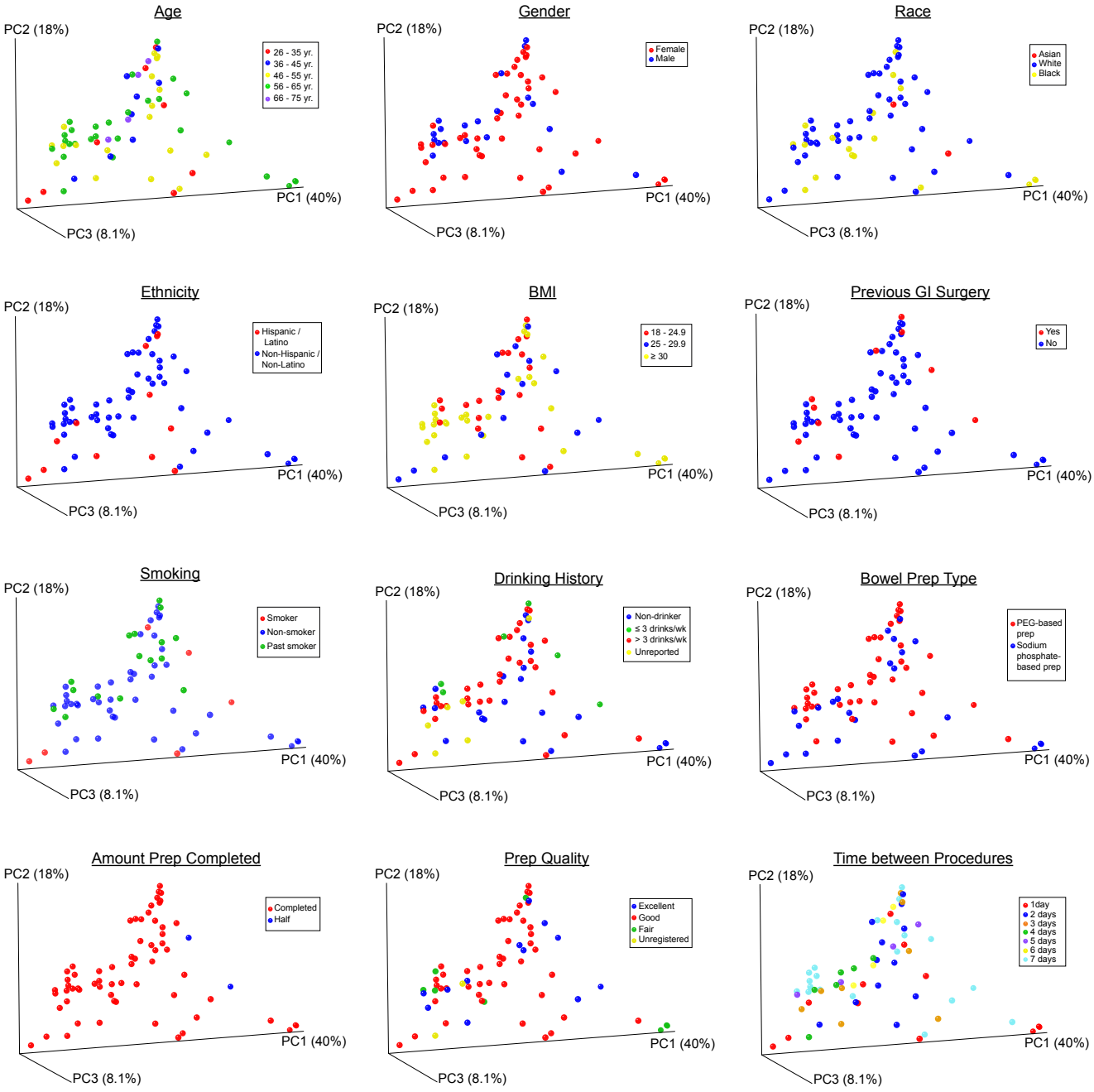

Figure S3: Principle Coordinate Analysis plots of samples using weighted Unifrac distances by important demographic and clinical variables. Each marker denotes a single sample.

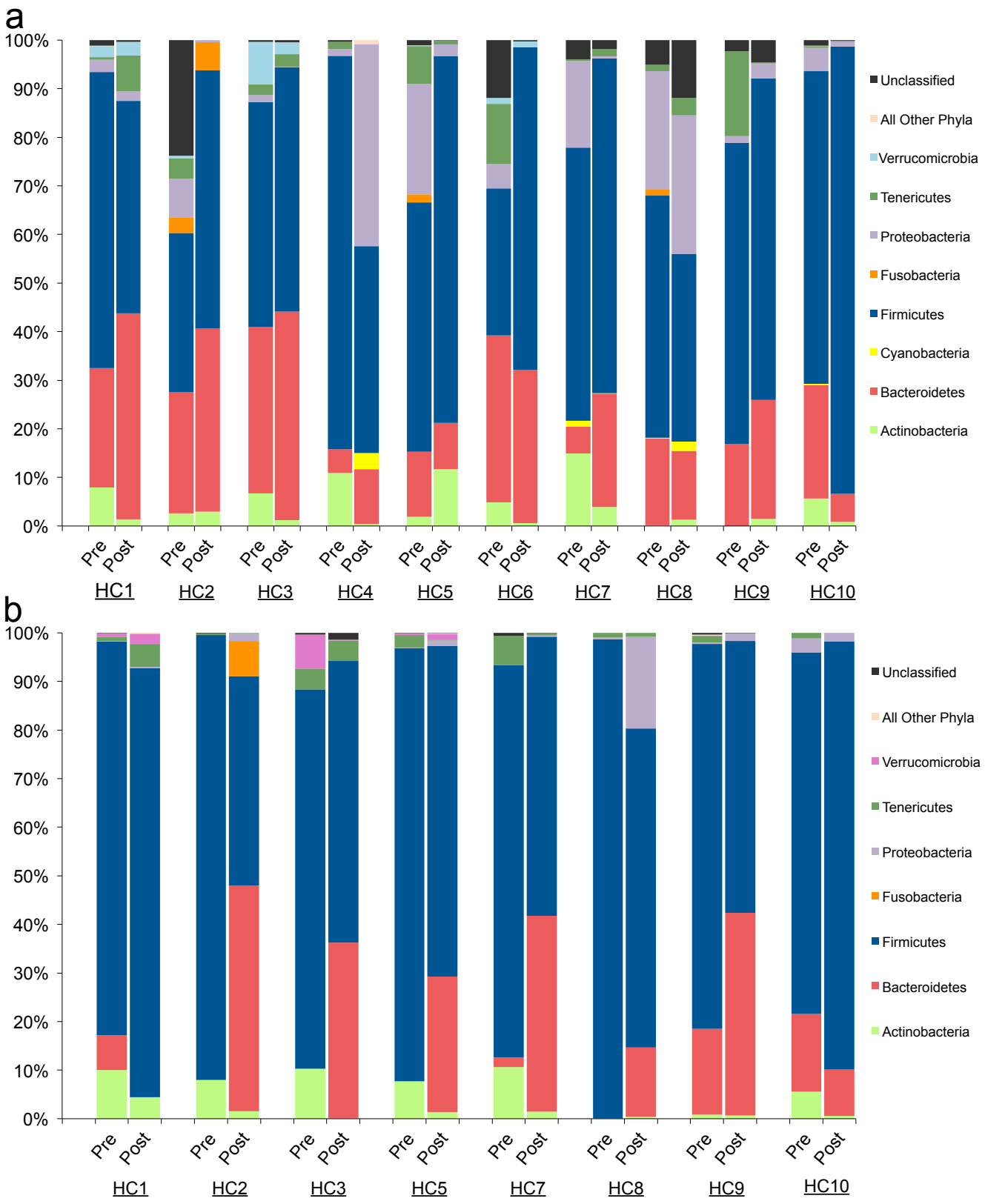

Figure S4: Relative phyla composition in individual pre- and post-bowel prep samples of healthy subjects. Data is shown for 10 healthy subjects, denoted H1 through H10. "Pre" indicates the samples collected at the time of un-prepped sigmoidoscopy i.e. before the bowel prep. "Post" indicates samples collected at the time of prepped colonoscopy i.e. after the bowel prep. The phyla that were present in low abundance (< 1 %) were combined under "all other phyla". Unclassified microbial phyla were combined under "Unclassified". Panel (a) shows the relative abundance of bacterial phyla in the biopsy samples collected from the healthy subjects. Panel (b) shows the relative abundance of bacterial phyla in the fecal samples collected from the healthy subjects.

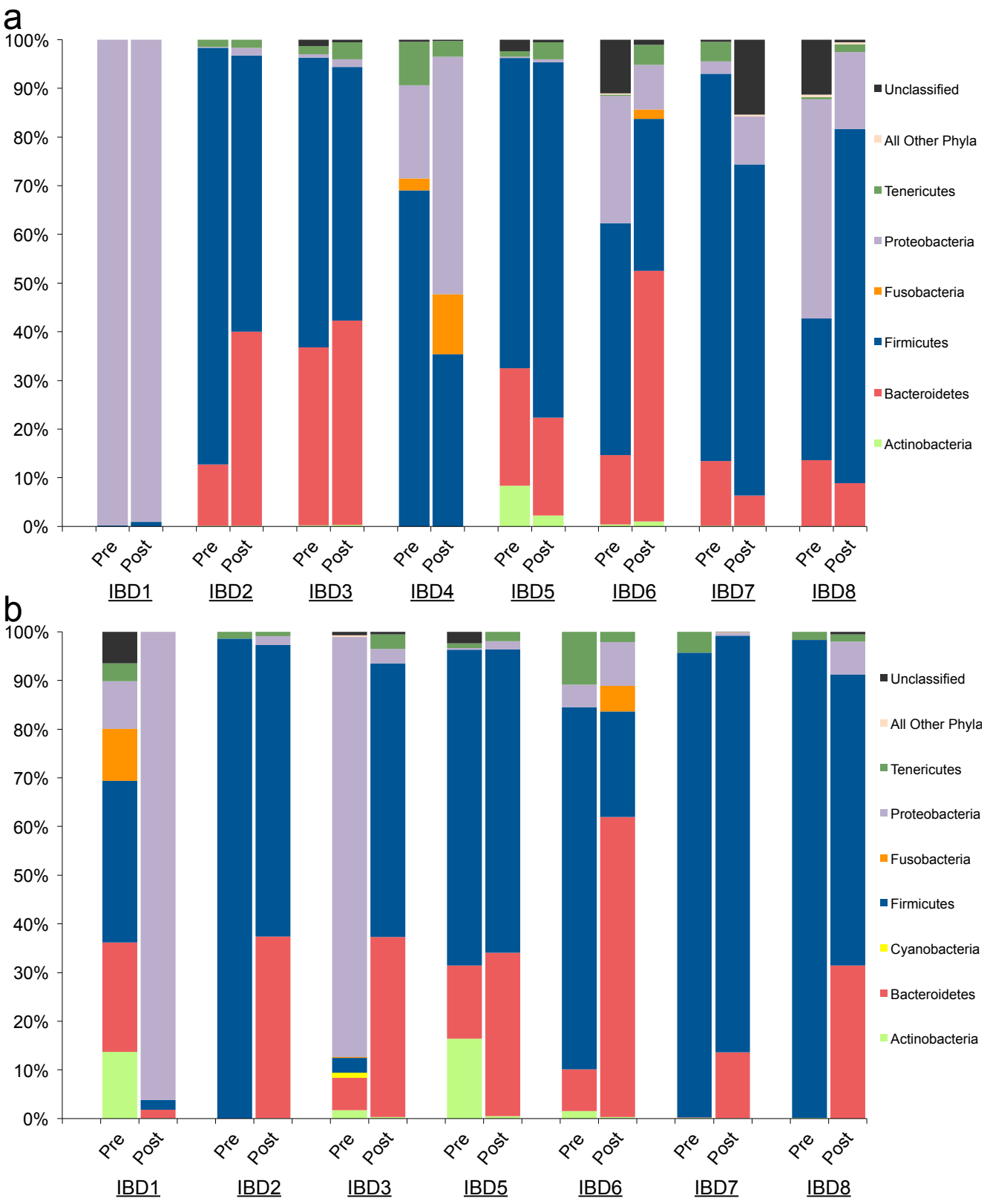

Figure S5: Relative phyla composition in individual pre- and post-bowel prep samples of IBD subjects. Data is shown for 8 IBD subjects, denoted IBD1 through IBD8. "Pre" indicates the samples collected at the time of un-prepped sigmoidoscopy i.e. before the bowel prep. "Post" indicates the samples collected at the time of prepped colonoscopy i.e. after the bowel prep. The phyla that were present in low abundance (< 1 %) were combined under "all other phyla". Unclassified microbial phyla were combined under "Unclassified". Panel (a) shows the relative abundance of bacterial phyla in the biopsy samples collected from the IBD subjects. Panel (b) shows the relative abundance of bacterial phyla in the fecal samples collected from the IBD subjects. It appears that subject IBD1 might have been having an asymptomatic infection since the phylum Proteobacteria was noted to be the major phylum in the microbial composition of the mucosal sample from IBD1 with high abundance of an unclassified genus belonging to the family Enterobacteriaceae.

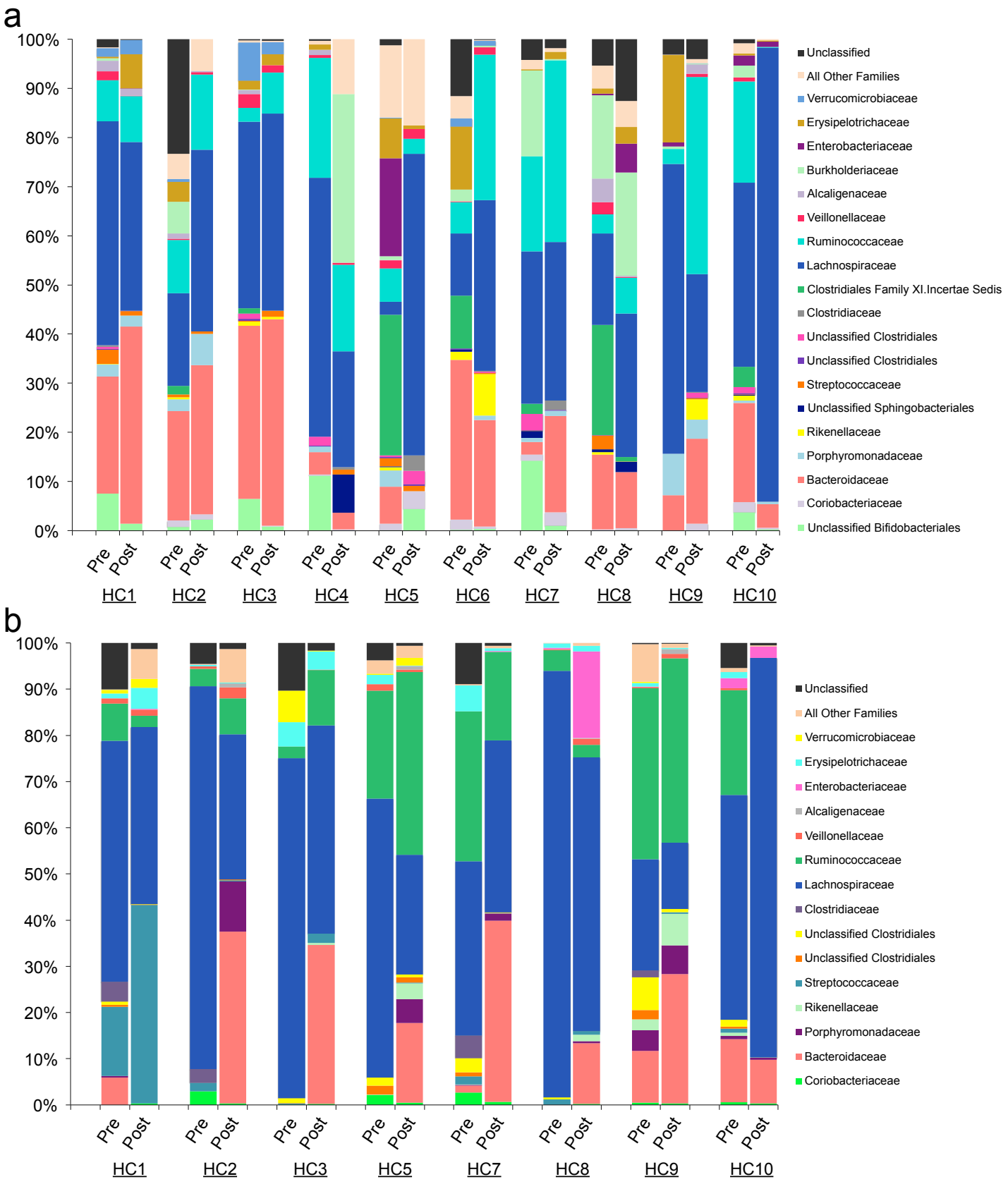

Figure S6: Relative family composition in individual pre- and post-bowel prep samples of healthy subjects. Data is shown for 10 healthy subjects, denoted H1 through H10. "Pre" indicates the samples collected at the time of un-prepped sigmoidoscopy i.e. before the bowel prep. "Post" indicates the samples collected at the time of prepped colonoscopy i.e. after the bowel prep. The families that were present in low abundance (< 1 %) were combined under "all other families". Unclassified microbial families were combined under "Unclassified". Panel (a) shows the relative abundance of bacterial families in the biopsy samples collected from healthy subjects. Panel (b) shows the relative abundance of bacterial families in the fecal samples collected from healthy subjects.

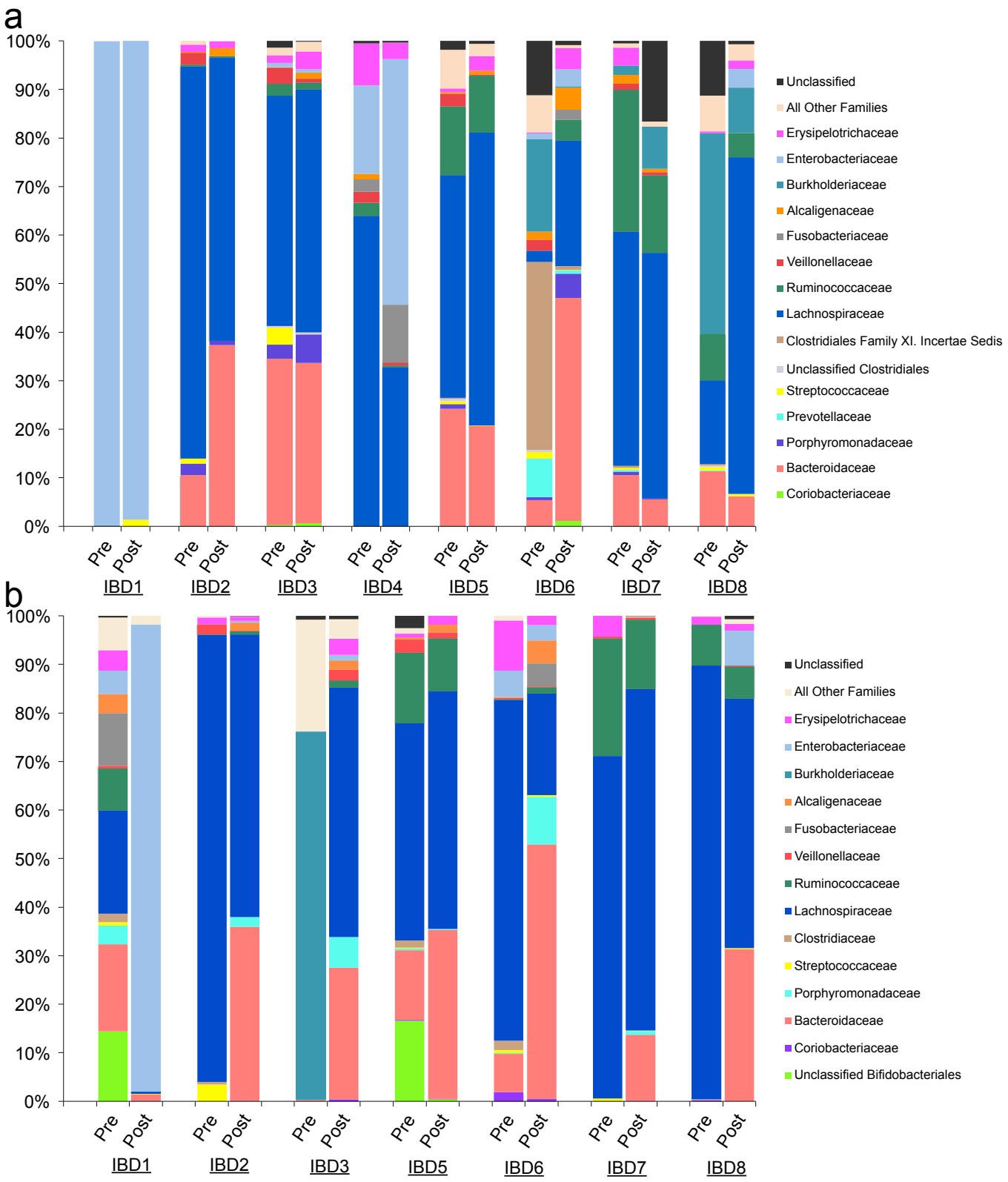

Figure S7: Relative family composition in individual pre- and post-bowel prep samples of IBD subjects. Data is shown for 8 IBD subjects denoted IBD1 through IBD8. "Pre" indicates the samples collected at the time of un-prepped sigmoidoscopy i.e. before the bowel prep. "Post" indicates the samples collected at the time of prepped colonoscopy i.e. after the bowel prep. The families that were present in low abundance (< 1 %) were combined under "all other families". Unclassified microbial families were combined under "Unclassified". Panel (a) shows the relative abundance of bacterial families in the biopsy samples collected from IBD subjects. Panel (b) shows the relative abundance of bacterial families in the fecal samples collected from IBD subjects. It appears that subject IBD1 might have been having an asymptomatic infection.

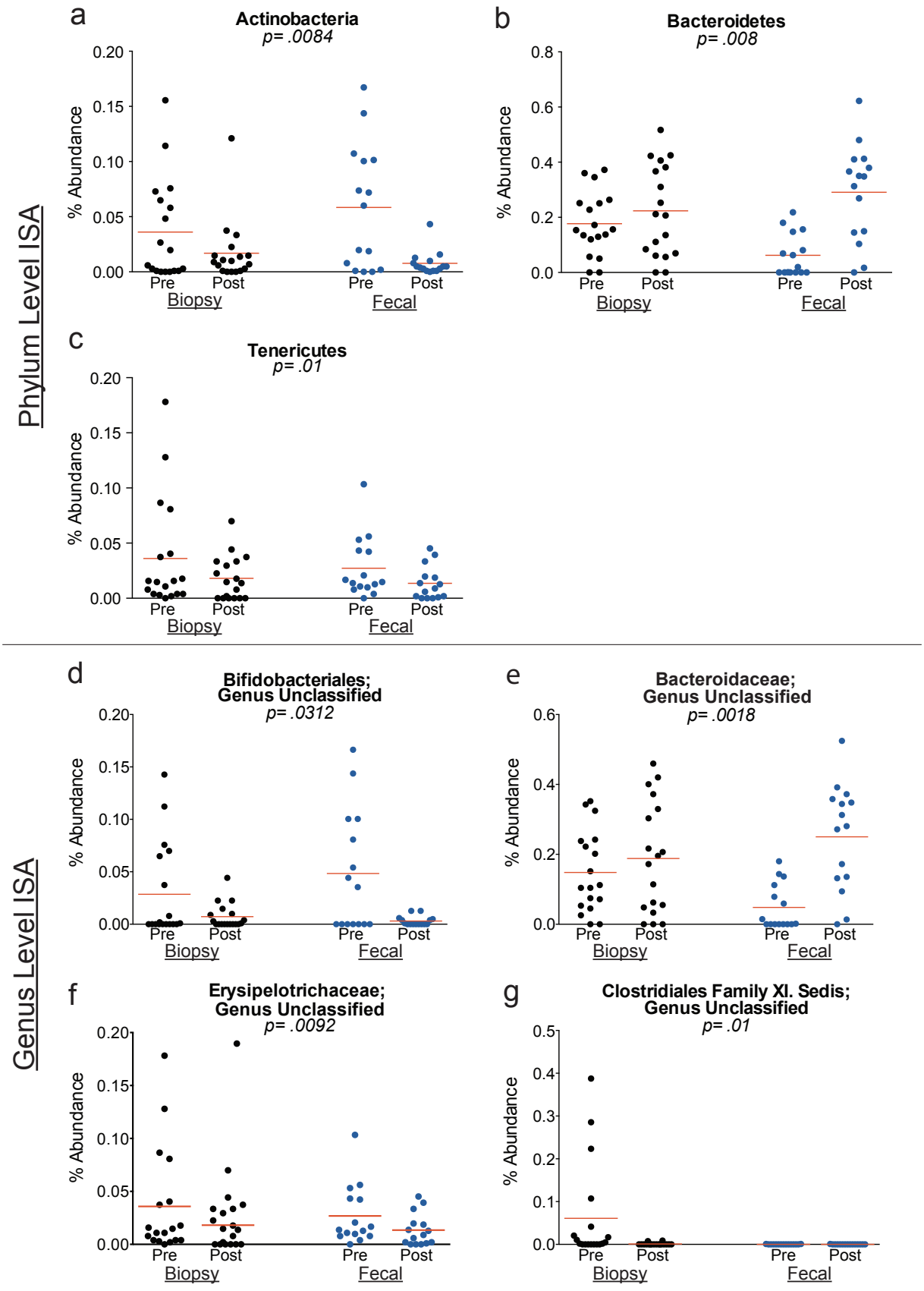

Figure S8: Relative abundances of significant indicator phyla and genera in samples of all subjects. Each marker represents the relative (%) abundance of the denoted phylum in one sample. Each panel shows the relative (%) abundance in the pre- and post-bowel prep samples collected from all subjects. The lines represent the mean relative abundance. Black circles represent the biopsy samples and blue circles represent the fecal samples. Graph (a) shows the relative abundance of the phylum Actinobacteria (an indicator of the pre-bowel prep state). Graph (b) shows the relative abundance of the phylum Bacteroidetes (an indicator of

the post-bowel prep state). Graph (c) shows the relative abundance of the phylum Tenericutes (an indicator of the pre-bowel state). Panel (d) shows the relative abundance of an unclassified genus within the Bifidobacteriales order (an indicator of the pre-bowel prep state). Panel (e) shows the relative abundance an unclassified genus within the Bacteroidaceae family (an indicator of the post-bowel prep state). Panel (f) shows the relative abundance of an unclassified genus within the family Erysipelotrichaceae (an indicator of the pre-bowel state). Panel (g) shows the relative abundance of an unclassified genus within the family Clostridiales Family XI. Insertae Sedis (an ndicator of the pre-bowel prep state).

Table S1:

Exclusion Criteria
1) A bleeding disorder or a tendency to bleed with a platelet count <50 or INR >1.4
2) Extensive colonic or ileocolonic resection
3) An ileostomy or colostomy
4) Current or past use of an antibiotic within the 30 days prior to sampling
5) Use of a specific dietary therapy or diet change during the study
6) Symptomatic organic GI disease other than hemorrhoids, hiatus hernia or GERD for the healthy control group or symptomatic organic GI disease other than hemorrhoids, hiatus hernia, GERD, UC or CD for the IBD group
7) Pre-existent organ failure or clinically significant co-morbidities as these conditions may change the microbiota: a) Liver disease (known cirrhosis or persistently abnormal AST or ALT that are 2x > normal); b) Clinically significant kidney disease (creatinine > 2 mg/dl); c) Clinically important lung disease or heart failure; d) HIV or AIDS; e) Alcoholism; f) Transplant recipients; g) Diabetes Mellitus; h) Uncontrolled psychiatric illness
8) Short bowel syndrome or severe malnutrition with ideal body weight ≤ 90 %
9) Estimated survival < 1 year and a Karnofsky performance status < 50 %
10) Pregnant and nursing patients or patients who have the desire to get pregnant
11) Endoscopic or histologic evidence of severely active disease or infection
12) Lack of decisional capacity
13) A desire to start smoking or change smoking habits and those who have changed their smoking habits within the month prior to the study
14) IBD complications with anticipation of an imminent surgical intervention
15) Poor or inadequate bowel prep at the time of colonoscopy

Table S2: Histopathology of mucosal specimens taken during colonoscopy for IBD subjects (n= 8).

Intestinal area	Histopathology Involvement (mild/moderate/severe/ no histology)
Ileum	1 / 1 / 0 / 1
Right Colon	2 / 0 / 0 / 0
Transverse colon	1 / 0 / 0 / 0
Left Colon	1 / 0 / 0 / 0
Rectosigmoid	2 / 0 / 0 / 0
Rectum	0 / 0 / 0 / 0

Table S3: Number and percentage of shared OTUs between samples across time and across sample types of same visit.

Subject ID	Number (%) of shared OTUs between pre and post bowel prep biopsy samples	Number (%) of shared OTUs between pre and post bowel prep stool samples	Number (%) of shared OTUs between sample types prior to bowel prep	Number (%) of shared OTUs between sample types after bowel prep
H1	65 (36.11%)	64 (34.97%)	88 (47.31%)	54 (32.93%)
H2	55 (33.33%)	41 (28.47%)	33 (18.86%)	70 (55.12%)
H3	48 (40%)	33 (30.84%)	39 (34.51%)	55 (54.45%)
H4	38 (18.45%)	/	/	/
H5	9 (4.31%)	54 (25.71%)	37 (17.21%)	17 (7.98%)
H6	38 (20 %)	/	/	/
H7	59 (27.19%)	64 (31.84%)	74 (32.89%)	67 (38.29%)
H8	48 (30.77%)	39 (35.14%)	31 (19.50%)	28 (20.59%)
H9	16 (8.3%)	68 (28.10%)	25 (13.59%)	97 (45.75%)
H10	33 (19.30%)	40 (29.63%)	80 (41.24%)	36 (52.17%)
IBD1	1 (12.50%)	9 (6.12%)	4 (2.88%)	2 (10.00%)
IBD2	42 (38.53%)	29 (25.44%)	41 (37.61%)	48 (50.00%)
IBD3	52 (29.71%)	2 (1.17%)	1 (0.58%)	62 (37.80%)
BPD4	31 (46.90%)	/	/	/
IBD5	73 (38.83%)	62 (38.51%)	82 (50.62%)	73 (43.71%)
IBD6	31 (22.63%)	30 (37.97%)	21 (14.19%)	36 (50.00%)
IBD7	39 (23.08%)	21 (19.81%)	38 (25.68%)	29 (24.17%)
IBD8	45 (25.42%)	34 (25.37%)	29 (17.16%)	47 (32.41%)

Table S4: Significant indicator species for sampling time (pre vs. post bowel prep) controlled for sample type in both subject groups (HC and IBD) analyzed collectively:

Phylum	Class	Order	Family	Genus	Observed Indicator Value	p-value	Effect of Bowel Prep
Actinobacteria*					66.3	0.008	decreased
	Actinobacteria				66.3	0.008	decreased
		Bifidobacteriales			44.8	0.025	decreased
				Unclassified Bifidobacteriales	44.8	0.031	decreased
Bacteroidetes*					63.1	0.008	increased
	Bacteroidia				63.4	0.002	increased
		Bacteriodales			63.5	0.002	increased
				Unclassified Bacteroidaceae	61.8	0.002	increased
Tenericutes*					63.0	0.010	decreased
	Erysipelotrichi				62.7	0.011	decreased
		Erysipelotrichales			62.7	0.010	decreased
				Unclassified Erysipelotrichaceae	62.7	0.009	decreased
			Clostridiales Family XI. Incertae Sedis*		33.9	0.008	decreased
				Unclassified Clostridiales FamilyXI. Incertae Sedis	32.5	0.010	decreased
			Burkholderiaceae*		44.8	0.004	decreased
				Unclassified Clostridiales*	47.8	0.005	decreased

*Denotes the highest level of taxonomy at which changes occur