

Table S1: Comparison of odds ratios calculated using alpha diversity community metrics associated with the presence of adenomas or carcinoma relative to those in individuals with normal colons using data collected from tissue samples.

Odds Ratio	95% CI (Lower Bound)	95% CI (Upper Bound)	P-value	Measure	Tumor	Tissue Group
1.82	0.95	3.49	0.07	OTU Richness	Adenoma	Combined
3.25	0.55	19.25	0.19	Shannon Diversity	Adenoma	Combined
3.47	0.68	17.70	0.13	Evenness	Adenoma	Combined
1.53	0.77	3.04	0.22	OTU Richness	Carcinoma	Unmatched
1.43	0.67	3.05	0.35	Shannon Diversity	Carcinoma	Unmatched
1.84	0.54	6.24	0.33	Evenness	Carcinoma	Unmatched
0.43	0.07	2.45	0.34	OTU Richness	Carcinoma	Matched
0.45	0.14	1.43	0.17	Shannon Diversity	Carcinoma	Matched
0.45	0.14	1.43	0.17	Evenness	Carcinoma	Matched

Table S2: Comparison of community dissimilarity between individuals with normal colons and those with adenomas and carcinomas as calculated using Bray-Curtis distance and tested using PERMANOVA.

Study	Tumor	Sample Type	R2	P-value
Brim	Adenoma	Feces	0.059	0.7562
Zeller	Adenoma	Feces	0.021	0.0096
Baxter	Adenoma	Feces	0.003	0.3788
Hale	Adenoma	Feces	0.001	0.3658
Wang	Carcinoma	Feces	0.034	0.0001
Weir	Carcinoma	Feces	0.107	0.3431
Ahn	Carcinoma	Feces	0.010	0.0033
Zeller	Carcinoma	Feces	0.028	0.0003
Baxter	Carcinoma	Feces	0.007	0.0024
Hale	Carcinoma	Feces	0.002	0.7163
Flemer	Carcinoma	Feces	0.016	0.0460
Lu	Adenoma	Tissue	0.144	0.0001
Flemer	Adenoma	Tissue	0.018	0.0001
Lu (Matched)	Adenoma	Tissue	0.569	0.1000
Sanapareddy	Carcinoma	Tissue	0.025	0.0069
Burns	Carcinoma	Tissue	0.051	0.0995
Flemer	Carcinoma	Tissue	0.029	0.0001
Chen	Carcinoma	Tissue	0.064	0.2691
Dejea (Matched)	Carcinoma	Tissue	0.048	0.2515
Geng (Matched)	Carcinoma	Tissue	0.030	0.9816
Burns (Matched)	Carcinoma	Tissue	0.168	1.0000

Table S3: ORs for individual taxa associated with individuals who had a normal colon or adenomas or carcinomas using data collected from stool. The listed P-values were less than 0.05 prior to using a Benjimini-Hochberg correction for multiple comparisons.

Taxon	Tumor	OR	95% CI (Lower Bound)	95% CI (Upper Bound)	P-value	BH
Clostridium_XIVb	Adenoma	1.46	1.14	1.86	2.29e-03	2.20e-01
Porphyromonas	Adenoma	1.77	1.19	2.62	4.48e-03	2.20e-01
Lachnospiraceae	Adenoma	0.71	0.56	0.91	6.40e-03	2.20e-01
Novosphingobium	Adenoma	3.33	1.27	8.72	1.41e-02	2.92e-01
Bacteroidales	Adenoma	1.35	1.06	1.72	1.63e-02	2.92e-01
Clostridium_XI	Adenoma	0.75	0.59	0.95	1.92e-02	2.92e-01
Clostridiaceae_1	Adenoma	0.71	0.54	0.95	1.99e-02	2.92e-01
Lactococcus	Adenoma	0.68	0.47	0.97	3.56e-02	4.59e-01
Porphyromonas	Carcinoma	3.20	2.26	4.54	6.73e-11	5.59e-09
Peptostreptococcus	Carcinoma	7.11	3.84	13.17	4.60e-10	1.91e-08
Parvimonas	Carcinoma	3.07	2.11	4.46	3.80e-09	1.05e-07
Fusobacterium	Carcinoma	2.74	1.95	3.85	5.54e-09	1.15e-07
Escherichia.Shigella	Carcinoma	2.15	1.57	2.95	2.20e-06	3.65e-05
Enterobacteriaceae	Carcinoma	1.79	1.33	2.41	1.30e-04	1.80e-03
Ruminococcus	Carcinoma	0.63	0.48	0.83	1.19e-03	1.41e-02
Clostridium_XI	Carcinoma	0.65	0.49	0.86	2.94e-03	3.05e-02
Roseburia	Carcinoma	0.60	0.41	0.88	8.98e-03	8.28e-02
Clostridium_XIVb	Carcinoma	1.45	1.09	1.94	1.17e-02	9.72e-02
Clostridiaceae_1	Carcinoma	0.67	0.48	0.93	1.53e-02	1.15e-01
Campylobacter	Carcinoma	1.76	1.10	2.82	1.88e-02	1.30e-01
Anaerococcus	Carcinoma	2.50	1.14	5.47	2.22e-02	1.42e-01
Desulfovibrio	Carcinoma	1.45	1.05	2.00	2.54e-02	1.50e-01
Veillonellaceae	Carcinoma	1.53	1.04	2.26	3.28e-02	1.79e-01
Lachnospiraceae	Carcinoma	0.69	0.49	0.97	3.44e-02	1.79e-01

Table S4: ORs for individual taxa associated with individuals who had a normal colon or adenomas or carcinomas using data collected from tissue samples. The listed P-values were less than 0.05 prior to using a Benjamini-Hochberg correction for multiple comparisons.

Taxon	Tumor	Tissue Group	OR	95% CI (Lower Bound)	95% CI (Upper Bound)	P-value	BH
Lachnospiraceae	Adenoma	Combined	0.27	0.14	0.56	3.23e-04	7.17e-02
Pseudomonas	Adenoma	Combined	3.73	1.73	8.05	8.13e-04	7.17e-02
Howardella	Adenoma	Combined	3.69	1.72	7.95	8.30e-04	7.17e-02
Rothia	Adenoma	Combined	2.87	1.48	5.58	1.82e-03	1.18e-01
Blautia	Adenoma	Combined	0.39	0.20	0.77	6.96e-03	3.61e-01
Enterobacter	Adenoma	Combined	3.42	1.28	9.12	1.42e-02	4.65e-01
Puniceicoccaceae	Adenoma	Combined	2.94	1.22	7.10	1.61e-02	4.65e-01
Erysipelotrichaceae	Adenoma	Combined	2.27	1.16	4.42	1.62e-02	4.65e-01
Streptococcus	Adenoma	Combined	2.27	1.16	4.42	1.62e-02	4.65e-01
Lactococcus	Adenoma	Combined	3.24	1.17	9.00	2.37e-02	6.15e-01
Micrococcaceae	Adenoma	Combined	3.91	1.17	13.06	2.65e-02	6.24e-01
Shewanella	Adenoma	Combined	2.05	1.05	3.98	3.46e-02	6.66e-01
Phascolarctobacterium	Adenoma	Combined	2.03	1.05	3.93	3.57e-02	6.66e-01
Achromobacter	Adenoma	Combined	7.10	1.14	44.44	3.61e-02	6.66e-01
Anaerostipes	Adenoma	Combined	0.10	0.01	0.89	3.96e-02	6.66e-01
Neisseria	Adenoma	Combined	2.09	1.00	4.35	4.88e-02	6.66e-01
Fusobacterium	Adenoma	Combined	2.85	1.00	8.12	4.94e-02	6.66e-01
Dorea	Carcinoma	Unmatched	0.35	0.22	0.55	3.96e-06	4.40e-04
Weissella	Carcinoma	Unmatched	5.15	2.02	13.14	5.96e-04	2.88e-02
Blautia	Carcinoma	Unmatched	0.47	0.30	0.73	7.79e-04	2.88e-02
Campylobacter	Carcinoma	Unmatched	2.13	1.23	3.67	6.57e-03	1.80e-01
Leptotrichia	Carcinoma	Unmatched	2.71	1.30	5.67	8.10e-03	1.80e-01
Parvimonas	Carcinoma	Unmatched	1.94	1.17	3.21	1.05e-02	1.95e-01
Clostridiaceae_1	Carcinoma	Unmatched	1.99	1.15	3.45	1.40e-02	2.15e-01
Flavobacteriaceae	Carcinoma	Unmatched	2.34	1.17	4.69	1.64e-02	2.15e-01
Ruminococcus2	Carcinoma	Unmatched	0.28	0.10	0.81	1.81e-02	2.15e-01
Clostridium_XIVb	Carcinoma	Unmatched	0.60	0.39	0.92	1.95e-02	2.15e-01
Corynebacterium	Carcinoma	Unmatched	0.52	0.29	0.92	2.41e-02	2.15e-01
Finegoldia	Carcinoma	Unmatched	0.43	0.21	0.90	2.45e-02	2.15e-01
Lachnospiraceae	Carcinoma	Unmatched	0.43	0.21	0.90	2.52e-02	2.15e-01
Bacteroides	Carcinoma	Unmatched	0.48	0.26	0.92	2.71e-02	2.15e-01
Clostridium_sensu_stricto	Carcinoma	Unmatched	1.89	1.04	3.43	3.79e-02	2.80e-01
Barnesiella	Carcinoma	Unmatched	0.64	0.41	0.98	4.16e-02	2.89e-01
Fusobacterium	Carcinoma	Matched	3.98	1.19	13.24	2.45e-02	9.26e-01
Campylobacter	Carcinoma	Matched	7.80	1.20	50.88	3.18e-02	9.26e-01