

Table S1: Samples used in analysis 1

Individual	Lumen	Mucosa	Mucus gel
<b>Control</b>	A	Caecum Transverse Descending Rectum	Caecum Transverse *Descending Rectum
	B	Caecum Transverse Descending Rectum	Caecum Transverse Descending *Rectum
	C	Caecum Transverse Descending Rectum	Caecum Transverse Descending Rectum
	D	Caecum Transverse Descending Rectum	Caecum Transverse Descending Rectum
<b>UC</b>	A	Caecum Transverse Descending Rectum	Caecum Transverse Descending Rectum
	B	Caecum Transverse Descending Rectum	Caecum Transverse Descending Rectum
	C	Caecum Transverse Descending Rectum	Caecum Transverse Descending Rectum
	D	Caecum Transverse Descending Rectum	Caecum Transverse Descending Rectum
	**E	Caecum Rectum	Caecum Rectum

\*Removed from pipeline prior to pyrosequencing as insufficient DNA quantity

\*\*Not included in AEM analysis

**Table S2: Abundance of bacterial families from lumen-mucosa-mucus for the entire cohort**

	Lumen		Mucosa		Mucus		*P-value
	Mean (%)	SD	Mean (%)	SD	Mean (%)	SD	
Actinomycetaceae(Actinomycetales)	0.054	0.075	0.059	0.089	0.131	0.184	0.21
Akkermansiaceae	0.898	1.636	0.857	1.796	0.713	1.504	0.52
Alcaligenaceae	2.972	2.655	2.149	1.987	1.384	1.436	<0.05*
Anaeroplasmataceae	0.156	0.488	0.215	0.645	0.136	0.359	0.85
Bacteroidaceae	22.832	18.05	19.931	17.056	10.696	12.487	<0.001***
Bifidobacteriaceae	0.556	0.713	0.847	0.87	1.72	1.622	<0.01**
Clostridiaceae	0.635	1.857	0.757	1.907	0.692	1.45	0.9
Comamonadaceae	0.008	0.022	0.008	0.018	0.045	0.101	0.08
Coriobacteriaceae	0.179	0.407	0.141	0.162	0.518	0.303	<0.001***
Desulfovibrionaceae	1.018	1.649	1.117	2.168	0.987	1.853	0.82
Enterobacteriaceae	2.727	5.345	2.26	4.064	0.93	1.844	0.3
Enterococcaceae	0.009	0.033	0.007	0.033	0.003	0.012	0.9
Erysipelotrichaceae	7.375	7.44	8.695	7.743	13.705	10.756	0.05
Family_XI_Incertae_Sedis_(Bacillales)	0.016	0.029	0.018	0.055	0.006	0.015	0.19
Family_XI_Incertae_Sedis_(Clostridiales)	1.012	2.975	0.855	2.596	0.895	2.397	0.72
Family_XIII_Incertae_Sedis	0.066	0.095	0.097	0.174	0.18	0.151	<0.001***
FJ440089	0.026	0.062	0.014	0.032	0.008	0.019	0.85
Fusobacteriaceae	0.18	0.822	0.137	0.61	0.02	0.061	0.54
Lachnospiraceae	17.25	8.536	20.998	9.093	23.852	6.481	<0.01**
Lactobacillaceae	0.008	0.016	0.01	0.033	0.05	0.149	0.56
Leptotrichiaceae	0.004	0.012	0.003	0.011	0.004	0.014	0.83
Leuconostocaceae	0.212	0.597	0.189	0.545	0.142	0.358	0.94
Micrococcaceae	0.012	0.024	0.023	0.051	0.018	0.035	0.98
Pasteurellaceae	0.994	2.029	1.235	2.931	0.589	0.913	0.95
Peptococcaceae	0.042	0.13	0.082	0.26	0.056	0.138	0.57
Peptostreptococcaceae(Clostridiales)	0.408	0.595	0.697	1.104	1.556	1.973	<0.05*
Planctomycetaceae	0	0	0.002	0.007	0.023	0.061	<0.01**
Porphyromonadaceae	2.573	1.434	2.352	1.353	1.231	0.802	<0.001***

Prevotellaceae	4.164	4.758	3.957	4.336	2.355	2.58	0.67
RF3	0.013	0.061	0.009	0.036	0.005	0.022	0.66
Rhodospirillaceae	0.195	0.29	0.181	0.243	0.115	0.147	0.83
Rikenellaceae	6.337	7.75	4.67	4.887	3.076	2.792	0.1
Ruminococcaceae	24.688	12.133	25.068	11.524	31.954	10.527	<0.01**
Staphylococcaceae	0.003	0.014	0.011	0.027	0.019	0.044	0.19
Streptococcaceae	0.699	1.025	0.846	1.134	1.043	1.456	0.43
Synergistaceae	0.033	0.115	0.042	0.198	0.009	0.031	0.28
Veillonellaceae	1.593	1.117	1.373	0.851	0.998	0.796	0.04
Victivallaceae	0.042	0.167	0.065	0.197	0.036	0.119	0.87
4C0d_2	0.012	0.037	0.022	0.079	0.017	0.056	0.83
Xanthomonadaceae	0	0	0.001	0.005	0.084	0.393	<0.05*

\*Uncorrected p-values as determined by the Kruskal-Wallis test. Significance values: <0.05=\*, <0.01=\*\*, <0.001=\*\*\*.

Table S3: Family-level abundances between health and UC

	Health		UC		*P-value
	Mean(%)	SD	Mean(%)	SD	
Pasteurellaceae	1.22	1.88	0.73	2.38	0.42
Xanthomonadaceae	0.05	0.31	0.01	0.03	0.55
Enterobacteriaceae	2.4	4.91	1.7	3.32	<1E-5***
Rhodospirillaceae	0.12	0.17	0.21	0.28	0.29
Alcaligenaceae	1.28	0.96	3.01	2.61	<0.001***
Comamonadaceae	0.04	0.08	0	0.02	<1E-5***
Desulfovibrionaceae	1.56	2.5	0.59	0.93	<0.01**
Planctomycetaceae	0.02	0.05	0	0.01	<0.01**
X4C0d_2	0.04	0.08	0	0	<1E-4***
Bacteroidaceae	27.08	20.41	10.49	6.59	<1E-6***
Prevotellaceae	4.95	5.21	2.34	2.23	0.1
Rikenellaceae	3.42	2.77	5.95	7.23	0.2
Porphyromonadaceae	2.31	1.52	1.91	1.19	0.28
FJ440089	0	0	0.03	0.05	<1E-5***
Micrococcaceae	0.01	0.01	0.03	0.05	0.01
Bifidobacteriaceae	0.46	1.01	1.48	1.16	<1E-9***
Actinomycetaceae.Actinomycetales.	0.03	0.04	0.12	0.15	<0.001***
Coriobacteriaceae	0.18	0.23	0.34	0.41	0.02
Streptococcaceae	0.79	1.36	0.91	1.05	0.15
Enterococcaceae	0	0	0.01	0.04	0.01
Lactobacillaceae	0	0.01	0.04	0.11	0.03
Leuconostocaceae	0.39	0.7	0	0.01	0.01
Staphylococcaceae	0	0.02	0.02	0.04	<0.01**
Family_XI_Incertae_Sedis_Bacillales.	0.02	0.05	0.01	0.03	0.2
Erysipelotrichaceae	11.63	8.31	8.09	9.27	<0.01**
Lachnospiraceae	20.16	8.21	20.87	8.88	0.78
Peptostreptococcaceae.Clostridiales.	0.14	0.17	1.47	1.65	<1E-12***
Veillonellaceae	1.16	0.78	1.49	1.08	0.21
Ruminococcaceae	18.43	8.55	34.41	8.84	<1E-11***
Clostridiaceae	0	0.01	1.29	2.23	<1E-15***
Family_XIII_Incertae_Sedis	0.09	0.08	0.13	0.19	0.33
Peptococcaceae	0.12	0.26	0.01	0.02	0.06
Family_XI_Incertae_Sedis_Clostridiales.	0.09	0.3	1.64	3.47	0.16
Fusobacteriaceae	0.03	0.06	0.19	0.82	0.01
Leptotrichiaceae	0.01	0.02	0	0	<0.001***
Akkermansiaceae	1.76	2.05	0.02	0.1	<1E-14***
Anaeroplasmataceae	0	0	0.32	0.67	<0.01**
RF3	0	0	0.02	0.06	<0.01**
Victivallaceae	0	0.01	0.09	0.22	<0.01**
Synergistaceae	0.02	0.04	0.04	0.18	<0.01**

\*Uncorrected p-values as determined by the Wilcoxon rank test. Significance values: <0.05=\*, <0.01=\*\*, <0.001=\*\*\*.

Table S4: Genus-level abundances between health and UC

	Health		UC		*P-values
	Mean(%)	SD	Mean(%)	SD	
0319-6G20	0.03	0.11	0	0	0.06
4C0d-2	0.05	0.11	0	0	<1E-4***
Acidaminococcus	0.09	0.17	0	0	<1E-4***
Actinomyces	0.04	0.06	0.16	0.21	<0.001***
Akkermansia	2.19	2.53	0.02	0.11	<1E-14***
Alistipes	2.9	1.82	4.62	4.22	0.16
Anaerococcus	0.07	0.36	0.24	0.61	0.11
Anaeroplasma	0	0	0.46	0.99	<0.01**
Anaerostipes	0.25	0.34	0.44	0.81	0.3
Anaerotruncus	0.05	0.07	0.12	0.18	0.04
Asteroleplasma	0.08	0.16	0.11	0.25	0.93
Atopobium	0	0	0	0.01	0.63
Bacteroides	32.59	22.2	13.71	8.36	<1E-6***
Barnesiella	0.07	0.08	0.09	0.14	0.62
Bifidobacterium	0.58	1.28	1.94	1.48	<1E-9***
Bilophila	0.26	0.29	0.21	0.31	0.11
Blautia	3.06	2.76	2.5	2.72	0.38
Butyricimonas	0.12	0.16	0.02	0.05	<1E-4***
Campylobacter	0	0.02	0	0	0.07
Catabacter	0.02	0.03	0.02	0.03	0.38
Catenibacterium	0	0	0.24	0.58	<0.01**
Chryseobacterium	0	0.02	0.01	0.05	0.14
Cloacibacillus	0.02	0.04	0	0	<1E-4***
Clostridium_(Clostridiaceae)	0	0.01	1.53	2.6	<1E-14***
Collinsella	0.11	0.17	0.3	0.46	<0.001***
Comamonas	0.01	0.03	0	0	<0.001***
Coprococcus	0.24	0.27	0.1	0.2	<0.001***
Coriobacteriaceae_bacterium	0.03	0.05	0	0.01	<0.001***
Desulfovibrio	1.82	3.22	0.62	1.12	0.02
Dialister	0.12	0.16	0.11	0.15	0.6
Dorea	0.79	0.61	0.45	0.5	<0.01**
DQ804406	0	0	0	0.01	0.06
Eggerthella	0.02	0.08	0.04	0.09	0.17
Enterococcus	0	0	0.01	0.05	0.01
Enterorhabdus	0	0.01	0	0.01	0.65
Erysipelotrichaceae_I_S	11.99	8.72	8.28	10.6	<0.01**
Escherichia_Shigella	2.66	5.42	2.13	3.83	<1E-5***
Faecalibacterium	10.19	5.86	17.95	6.7	<1E-7***
FJ440089	0	0	0.04	0.09	<1E-5***
Flavobacterium	0.03	0.11	0	0	0.01
Fusobacterium	0.04	0.09	0.01	0.04	<0.01**
Gemella	0.02	0.05	0.01	0.03	0.2
GQ079293	0.01	0.03	0	0.01	0.5

<b>GQ897367</b>	0.05	0.09	0	0.01	<0.01**
<b>Haemophilus</b>	1.46	2.24	0.51	1.55	0.25
<b>Holdemania</b>	0.11	0.15	0.06	0.07	0.07
<b>Jonquetella</b>	0	0	0.04	0.21	0.06
<b>Lachnospira</b>	0.18	0.21	0.92	3.15	0.11
<b>Lachnospiraceae_I_S</b>	2.48	0.79	2.42	1.5	0.16
<b>Lactobacillus</b>	0	0.01	0.05	0.15	0.03
<b>Lactococcus</b>	0	0.01	0	0.01	0.13
<b>Leptotrichia</b>	0.01	0.02	0	0	<0.01**
<b>Leuconostoc</b>	0	0	0	0.01	0.06
<b>Marvinbryantia</b>	0.01	0.03	0	0	<0.001***
<b>Megasphaera</b>	0	0	0.47	0.97	0.02
<b>Mogibacterium</b>	0.02	0.09	0.03	0.11	0.64
<b>Moryella</b>	0	0	0.03	0.15	0.06
<b>Neisseria</b>	0	0.02	0	0	0.03
<b>Odoribacter</b>	0.75	0.44	0.59	0.49	0.03
<b>Oribacterium</b>	0	0.01	0	0.01	0.57
<b>Oxalobacteraceae</b>	0.01	0.02	0	0	0.01
<b>Parabacteroides</b>	1.9	1.56	1.64	1.29	0.61
<b>Paraprevotella</b>	0	0.01	0.28	0.44	<1E-9***
<b>Parasutterella</b>	0.04	0.08	2.24	3.42	<1E-13***
<b>Parvimonas</b>	0.02	0.04	1.65	3.5	0.04
<b>Peptoniphilus</b>	0.01	0.03	0.3	0.72	0.02
<b>Peptostreptococcaceae_I_S</b>	0.15	0.2	1.87	2.11	<1E-12***
<b>Peptostreptococcus</b>	0.01	0.02	0.02	0.1	0.05
<b>Phascolarctobacterium</b>	0.78	0.97	0.83	0.8	0.45
<b>Porphyromonas</b>	0.01	0.02	0.19	0.38	0.11
<b>Prevotella</b>	6.45	6.91	2.78	2.6	0.08
<b>Propionibacterium</b>	0.08	0.22	0.03	0.2	0.04
<b>Pseudobutyrvibrio</b>	1.03	0.82	3.73	3.9	0.01
<b>RC9_gut_group</b>	1.43	2.89	3.66	9.76	0.32
<b>RF3</b>	0	0	0.02	0.08	0
<b>RF9</b>	0	0.02	0.02	0.06	0.03
<b>Roseburia</b>	0.95	0.65	0.79	0.68	0.12
<b>Rothia</b>	0	0.01	0.03	0.05	<0.01**
<b>Ruminococcaceae_I_S</b>	1.19	0.71	3	2.07	<1E-7***
<b>Ruminococcus</b>	3.74	4.22	7.85	4.95	<1E-5***
<b>Schlesneria</b>	0.01	0.03	0	0	0.01
<b>Staphylococcus</b>	0	0.02	0.02	0.05	<0.01**
<b>Streptococcus</b>	1.08	1.86	1.2	1.41	0.16
<b>Subdoligranulum</b>	2.86	2.11	3.48	3.05	0.68
<b>Succiniclasticum</b>	0	0	0.48	1.01	<0.01**
<b>Sutterella</b>	1.53	1.06	1.67	2.32	0.02
<b>Thalassospira</b>	0.16	0.23	0.28	0.37	0.29
<b>Turicibacter</b>	0	0	0.03	0.04	<1E-6***
<b>Veillonella</b>	0.38	0.63	0.09	0.2	0.03
<b>Victivallis</b>	0	0.01	0.13	0.3	0.01
<b>Weissella</b>	0.54	0.95	0	0.01	<0.01**

\*Uncorrected p-values as determined by the Wilcoxon rank test. Significance values:  
<math><0.05=^\*</math>, <math><0.01=^{\*\*}</math>, <math><0.001=^{\*\*\*}</math>.

Table S5a: Family-level abundances between luminal and mucosal samples in health

	Lumen (health)		Mucosa (health)		Mucus gel (health)		*P-value
	Mean	SD	Mean	SD	Mean	SD	
Actinomycetaceae.Actinomycetales.	0.022	0.027	0.019	0.029	0.048	0.067	0.55
Akkermansiaceae	1.861	1.999	1.807	2.297	1.59	1.942	0.55
Alcaligenaceae	1.746	1.216	1.176	0.797	0.841	0.448	0.03
Anaeroplasmataceae	0	0	0	0	0.002	0.006	0.27
Bacteroidaceae	33.307	20.983	29.367	20.388	16.609	16.725	<0.01**
Bifidobacteriaceae	0.168	0.216	0.229	0.263	1.101	1.718	0.12
Clostridiaceae	0.004	0.006	0.001	0.004	0.005	0.013	0.5
Comamonadaceae	0.017	0.031	0.018	0.023	0.09	0.138	<0.05*
Coriobacteriaceae	0.042	0.035	0.103	0.12	0.461	0.236	<1E-5***
Desulfovibrionaceae	1.448	2.115	1.54	2.935	1.737	2.545	0.86
Enterobacteriaceae	2.945	5.736	3.142	5.629	0.819	1.985	0.61
Erysipelotrichaceae	8.638	6.737	10.567	7.369	16.612	9.403	0.05
Family_XI_Incertae_Sedis_.Bacillales.	0.017	0.024	0.025	0.075	0.007	0.015	0.23
Family_XI_Incertae_Sedis_.Clostridiales.	0.06	0.116	0.037	0.056	0.188	0.545	0.93
Family_XIII_Incertae_Sedis	0.061	0.035	0.058	0.044	0.148	0.109	<0.05*
Fusobacteriaceae	0.037	0.063	0.019	0.039	0.046	0.086	0.92
Lachnospiraceae	16.394	7.402	20.378	9.795	24.522	4.405	<0.01**
Lactobacillaceae	0.004	0.008	0.004	0.008	0	0	<0.05*
Leptotrichiaceae	0.009	0.017	0.007	0.016	0.008	0.021	0.62
Leuconostocaceae	0.446	0.821	0.4	0.75	0.311	0.493	0.91
Micrococcaceae	0.003	0.006	0.005	0.011	0.008	0.02	0.97
Pasteurellaceae	1.268	2.244	1.353	2.045	1.011	1.144	0.56
Peptococcaceae	0.085	0.183	0.162	0.368	0.109	0.196	0.41
Peptostreptococcaceae.Clostridiales.	0.102	0.062	0.125	0.093	0.197	0.287	0.57
Planctomycetaceae	0	0	0.005	0.011	0.049	0.086	<0.01**
Porphyromonadaceae	2.918	1.811	2.404	1.392	1.434	0.796	<0.05*
Prevotellaceae	5.789	6.128	5.201	5.587	3.617	3.262	0.54
Rhodospirillaceae	0.126	0.188	0.129	0.187	0.098	0.128	0.87
Rikenellaceae	3.973	2.618	3.519	3.149	2.631	2.48	0.11
Ruminococcaceae	16.463	8.557	16.463	7.98	23.258	7.836	<0.05*
Staphylococcaceae	0	0	0	0	0.01	0.035	0.27
Streptococcaceae	0.666	1.231	0.577	0.946	1.202	1.881	0.23



Synergistaceae	0.023	0.038	0.013	0.035	0.02	0.045	0.35
Veillonellaceae	1.333	0.944	1.099	0.586	1.009	0.773	0.27
Victivallaceae	0.004	0.011	0	0	0	0	0.19
X4C0d_2	0.025	0.052	0.047	0.111	0.039	0.081	0.52
Xanthomonadaceae	0	0	0.002	0.008	0.164	0.586	0.11

\*Uncorrected p-values as determined by the Kruskal-Wallis test. Significance values: <0.05=\*, <0.01=\*\*, <0.001=\*\*\*.

Table S5b: Family-level abundances between luminal and mucosal samples in UC

	Lumen (UC)		Mucosa (UC)		Mucus gel (UC)		*P-value
	Mean	SD	Mean	SD	Mean	SD	
Actinomycetaceae.Actinomycetales.	0.083	0.092	0.095	0.108	0.199	0.221	0.15
Akkermansiaceae	0.042	0.155	0.013	0.049	0	0	<0.05*
Alcaligenaceae	4.061	3.115	3.015	2.327	1.826	1.796	<0.05*
Anaeroplasmataceae	0.295	0.648	0.407	0.852	0.245	0.461	0.93
Bacteroidaceae	13.521	6.994	11.544	6.298	5.891	3.512	<0.01**
Bifidobacteriaceae	0.901	0.824	1.396	0.854	2.223	1.395	<0.001***
Clostridiaceae	1.196	2.446	1.429	2.459	1.249	1.785	0.47
Comamonadaceae	0	0	0	0	0.008	0.028	0.13
Coriobacteriaceae	0.3	0.536	0.175	0.188	0.564	0.35	<0.01**
Desulfovibrionaceae	0.637	1.002	0.74	1.098	0.377	0.59	0.46
Enterobacteriaceae	2.533	5.132	1.477	1.652	1.019	1.782	<0.05*
Enterococcaceae	0.016	0.044	0.013	0.046	0.006	0.016	0.7
Erysipelotrichaceae	6.252	8.036	7.031	7.89	11.343	11.487	0.14
Family_XI_Incertae_Sedis_.Bacillales.	0.015	0.033	0.011	0.026	0.004	0.016	0.2
Family_XI_Incertae_Sedis_.Clostridiales.	1.859	3.944	1.583	3.449	1.468	3.116	0.89
Family_XIII_Incertae_Sedis	0.07	0.128	0.132	0.234	0.206	0.177	<0.05*
FJ440089	0.049	0.079	0.026	0.041	0.015	0.024	0.35
Fusobacteriaceae	0.307	1.128	0.242	0.835	0	0	0.09
Lachnospiraceae	18.01	9.58	21.55	8.669	23.308	7.886	0.06
Lactobacillaceae	0.011	0.02	0.015	0.045	0.091	0.194	0.09
Leuconostocaceae	0.003	0.01	0.002	0.005	0.004	0.017	0.67
Micrococcaceae	0.02	0.031	0.039	0.067	0.026	0.043	0.84
Pasteurellaceae	0.751	1.848	1.131	3.601	0.245	0.475	0.7
Peptococcaceae	0.004	0.008	0.01	0.022	0.012	0.024	0.58
Peptostreptococcaceae.Clostridiales.	0.68	0.719	1.205	1.333	2.66	2.073	<0.001***
Planctomycetaceae	0	0	0	0	0.003	0.01	0.29
Porphyromonadaceae	2.266	0.943	2.305	1.355	1.066	0.794	<0.01**
Prevotellaceae	2.721	2.474	2.851	2.49	1.33	1.19	0.19
RF3	0.025	0.083	0.018	0.049	0.009	0.029	0.33

Rhodospirillaceae	0.256	0.351	0.228	0.28	0.13	0.164	0.55
Rikenellaceae	8.439	10.03	5.693	5.938	3.439	3.053	0.1
Ruminococcaceae	31.999	10.044	32.718	8.362	39.02	6.241	<0.01**
Staphylococcaceae	0.006	0.019	0.02	0.035	0.027	0.05	0.13
Streptococcaceae	0.73	0.837	1.085	1.257	0.914	1.041	0.4
Synergistaceae	0.042	0.156	0.067	0.271	0	0	0.18
Veillonellaceae	1.824	1.232	1.616	0.984	0.989	0.84	<0.01**
Victivallaceae	0.077	0.227	0.123	0.261	0.065	0.157	0.85
Xanthomonadaceae	0	0	0	0	0.018	0.057	0.13

\*Uncorrected p-values as determined by the Kruskal-Wallis test. Significance values: <0.05=\*, <0.01=\*\*, <0.001=\*\*\*.

Table S6: Diversity indices between cohorts, compared by sampling locations

	Lumen		Mucosa		Mucus Gel		Sampling technique (Kruskal-Wallis) P-value
	Median	IQR	Median	IQR	Median	IQR	
<b>Health</b>							
<b>Simpson Index</b>	0.91	0.07	0.92	0.07	0.91	0.07	0.82
<b>Shannon Diversity Index</b>	4.77	1.31	4.97	1.17	4.79	0.88	0.89
<b>chao1</b>	745.14	1690.34	581.07	911.99	565.84	412.48	0.09
<b>Phylogenetic Diversity</b>	26.65	31.1	25.22	22	27.16	15.41	0.35
<b>Observed species</b>	425	817	360	487.25	329	202	0.13
<b>Ulcerative colitis</b>							
<b>Simpson Index</b>	0.93	0.04	0.93	0.04	0.94	0.03	0.32
<b>Shannon Diversity Index</b>	5.16	0.49	5.16	0.49	5.31	0.44	0.43
<b>chao1</b>	1534.14	901.38	1534.14	901.38	810.72	530.55	<0.01**
<b>Phylogenetic Diversity</b>	45.12	19.65	45.12	19.65	30.4	11.77	0.01
<b>Observed species</b>	702.5	350.5	702.5	350.5	481.5	222	<0.01**
<b>Between cohorts (Wilcoxon rank sum)</b>	P-value		P-value		P-value		
<b>Simpson Index</b>	0.42		0.15		0.3		
<b>Shannon Diversity Index</b>	0.3		0.11		0.1		
<b>chao1</b>	0.31		0.3		<0.001***		
<b>Phylogenetic Diversity</b>	0.31		0.31		0.02		
<b>Observed species</b>	0.36		0.6		<0.01**		

Significance values: <0.05=\*, <0.01=\*\*, <0.001=\*\*\*.

**Table S7: Correlation of bacterial diversity with local inflammation**

	Spearman rho	P-value
<b>Lumen</b>		
Shannon	-0.185	0.464
Simpson	-0.023	0.926
chao1	-0.37	0.131
PD	-0.288	0.247
Observed species	-0.284	0.254
<b>Mucosa</b>		
Shannon	0.13	0.607
Simpson	0.155	0.54
chao1	-0.383	0.117
PD	-0.365	0.137
Observed species	-0.338	0.17
<b>Mucus gel</b>		
Shannon	0.314	0.236
Simpson	0.437	0.091
chao1	-0.135	0.618
PD	-0.074	0.784
Observed species	-0.108	0.691