

Indicator Number	ASV	s.Healthy Control	s.inflammation_no_surgery	s.inflammation_with_surgery	s.no_inflammation_no_surgery	s.no_inflammation_with_surgery	index	stat	p.value	Domain	Phylum	Class	Order	Family	Genus	Species
1	21bd78cd9b6f375f7559dcf18fe86f2	1	0	0	1	0	8	0.954197569	0.005	d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Marinifilaceae	g_Odoribacter	NA
2	4e4abbe815c85701ae77ec9fd3bc702	1	1	0	1	1	28	0.986270882	0.01	d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Prevotellaceae	g_Prevotella	NA
3	4c724a66250d4b7df2c1ec1327f497e4	1	1	0	1	0	17	0.873177144	0.02	d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Barnesiellaceae	g_Barnesiella	NA
4	c8164226bba504a5b3b562dcf668c0bb	1	1	0	1	0	17	0.906071635	0.02	d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales	f_Peptostreptococcaceae	g_Romboutsia	NA
5	4ce5f1f6d8ff9477e967d4a18a679209	1	1	0	1	0	17	0.953548839	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales	f_Anaerovoracaceae	g_Family_XIII_AD3011_group	s_uncultured_bacterium
6	51c76082684b9ede8eb0be0631dc09de	1	1	1	1	0	26	0.936077277	0.03	d_Bacteria	p_Firmicutes	c_Negativicutes	o_Veillonellales-Selenomonadales	f_Veillonellaceae	g_Dialister	NA
7	a5c4caa215030992b4e28757309392d	1	1	0	1	0	17	0.960270475	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christensenellaceae	g_Christensenellaceae_R-7_group	NA
8	2aa65c3d547af543184ee9f178a65728	1	1	0	1	0	17	0.899493854	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Monoglobales	f_Monoglobaceae	g_Monoglobus	s_uncultured_organism
9	7d24ffc8eb8226313fd5a493092d6853	1	1	0	1	0	17	0.982526433	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Clostridiaceae	g_Clostridium_sensu_stricto_1	s_Clostridium_chauvoei
10	1a5c25f5fe7c368dc1976e13e3003e22	1	1	0	1	0	17	0.877620121	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Oscillospiraceae	g_UCG-003	NA
11	a7d57b17f06047cdd27889df35ad63b5	1	1	0	1	0	17	0.960338402	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Oscillospiraceae	g_UCG-002	NA
12	3d66830b6306d630db430b63b5f7a467	1	1	0	1	0	17	0.940787599	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococcaceae	g_uncultured	s_gut_metagenome
13	599f9468ff781407bf160b574e0ddf	1	1	0	1	0	17	0.957557311	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococcaceae	g_Ruminococcus	NA
14	2f9c31d34af06dd96e71f8e9858e8f	1	0	0	1	0	8	0.944267484	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_UCG-010	g_UCG-010	NA
15	5b659c92c3442dcbc5926bfcac940ceb	1	0	0	1	0	8	0.880124691	0.01	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococcaceae	g_[Eubacterium]_siraeum_group	s_[Eubacterium]_siraeum
16	17d294491c706b3f4bf05e2ecb1b4aa7	1	1	0	1	0	17	0.943166322	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Oscillospiraceae	g_UCG-005	s_uncultured_organism
17	4a89cac13e971f8e928f1e979fb707ae	1	1	0	1	0	17	0.933026843	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococcaceae	g_Subdoligranulum	NA
18	c1a5986dd95b9ee50e347723be159d4d	1	1	0	1	0	17	0.986739509	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococcaceae	g_Faecalibacterium	NA
19	f676fb863d1139641d306d0a2f07a14b	1	1	1	1	0	26	0.939508004	0.01	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Butyricocccaceae	g_Butyricoccus	NA
20	86acaa700437671e9f8c38b903e9b0c1	1	1	0	1	0	17	0.916625521	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_[Eubacterium]_ventriosum_group	s_uncultured_rumen
21	c536cb40d0686dfe760ceab3b90146a2	1	0	0	1	0	8	0.878713893	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Moryella	s_human_gut
22	33f91e62a000ed593c352f0c7f976f8a	1	1	0	1	0	17	0.936845365	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Lachnospiraceae_ND3007_group	s_metagenome
23	e679760656821248d941dcecb0b1ca39e	1	1	0	1	0	17	0.958117633	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_[Eubacterium]_eligen_s_group	NA
24	f0143441c5a8a01ba31592825d9e47ef	1	1	0	1	0	17	0.948357501	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Agathobacter	NA
25	5f3d16b803aaa2896227ae65b06ff9d5	1	1	1	1	0	26	0.899093122	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Roseburia	NA
26	34ecf8ad93a52ec913a59abaca0d39ca	1	1	0	1	0	17	0.87834728	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_uncultured	s_uncultured_Eubacterium
27	b91f30e253a2f78f0722bbdc236b9f8a	1	1	0	1	0	17	0.887274034	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Lachnospiraceae_FC5020_group	s_uncultured_organism
28	d0f21126697b2318d28dd79e2fe491b	1	1	0	1	0	17	0.960053345	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Lachnospiraceae_NK4A136_group	NA

**Supplemental Table 1.** Indicator Species Analysis Table for Crohn’s Disease Patients with Inflammation or Surgery. Indicator species analysis was performed on Crohn's Disease patients using their inflammation and surgical status. Table was filtered for the association statistic value (column ‘stat’) and p-value to be above 0.87 and less than 0.05 respectively. If an ASV was associated with a group, it was assigned a value of 1; if not associated, the value was 0.