

## SUPPLEMENTARY MATERIAL

**TABLE S1. 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.

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	21bd78cd9b6f375f755f9dfc18fe86f2	1	0	0	1	0	8	0.9541976	0.005	d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Marinifilac eae	g_Odoribacter	NA
2	4e4abbe815c85701ae77ecf9fd3bc702	1	1	0	1	1	28	0.9862709	0.01	d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Prevotellac eae	g_Prevotella	NA
3	4c724a66250d4b7df2c1ec1327f497e4	1	1	0	1	0	17	0.8731771	0.02	d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Barnesiella ceae	g_Barnesiella	NA
4	c8164226ba504a5b3b562dcf668c0bb	1	1	0	1	0	17	0.9060716	0.02	d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales	f_Peptostrep tocaceae	g_Romboutsia	NA
5	4ce51f16d8ff9477e967d4a18a679209	1	1	0	1	0	17	0.9535488	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales	f_Anaerovora ceae	g_Family_XIII_AD301_1_group	s_uncultured_bacterium
6	51c76082684b9ede8eb0be0631dc09de	1	1	1	1	0	26	0.9360773	0.03	d_Bacteria	p_Firmicutes	c_Negativicutes	o_Veillonellales-Selenomonadales	f_Veillonella ceae	g_Dialister	NA
7	a5c4caa215030992b4ef28757309392d	1	1	0	1	0	17	0.9602705	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christense nellaceae	g_Christensenellaceae	NA
8	2aa65c3d547af543184eef9178a65728	1	1	0	1	0	17	0.8994939	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Monoglobales	f_Monogloba ceae	g_Monoglobus	s_uncultured_o rganism
9	7d24ffc8eb8226313fd5a493092d6853	1	1	0	1	0	17	0.9825264	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Clostridiac eae	g_Clostridium_sensu_stricto_1	s_Clostridium_chauvoei
10	1a5c25f5fe7c368dc1976e13e3003e22	1	1	0	1	0	17	0.8776201	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Oscillospir aceae	g_UCG-003	NA
11	a7d57b1f7d6047cdd27889df35ad63b5	1	1	0	1	0	17	0.9603384	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Oscillospir aceae	g_UCG-002	NA
12	3d66830b6306d630db430b63b5f7a467	1	1	0	1	0	17	0.9407876	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococ ceae	g_uncultured	s_gut_metagenome
13	599f9468ff7781407bfff160b574e0ddf	1	1	0	1	0	17	0.9575573	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococ ceae	g_Ruminococcus	NA
14	2fc3c1d34aff06dd96e71f8e9858e8f	1	0	0	1	0	8	0.9442675	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_UCG-010	g_UCG-010	NA
15	5b659c92c3442dcbc5926bfac940ceb	1	0	0	1	0	8	0.8801247	0.01	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococ ceae	g_[Eubacterium]_sira eum_group	s_[Eubacterium]_sira eum
16	17d294491c706b3f4bf05e2ecb1b4aa7	1	1	0	1	0	17	0.9431663	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Oscillospir aceae	g_UCG-005	s_uncultured_o rganism
17	4a89cac13e971f8e928f1e979fb707ae	1	1	0	1	0	17	0.9330268	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococ ceae	g_Subdoligranulum	NA
18	c1a5986dd95b9ee50e3a7723be159d4d	1	1	0	1	0	17	0.9867395	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococ ceae	g_Faecalibacterium	NA
19	f676fb863d1139641d306d0a2f07a14b	1	1	1	1	0	26	0.939508	0.01	d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Butyricicoc ceae	g_Butyricicoccus	NA
20	86acaa700437671e9f8c38b903e9b0c1	1	1	0	1	0	17	0.9166255	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospir aceae	g_[Eubacterium]_vent riosum_group	s_uncultured_r umen
21	c536cb40d0686dfe706ceab3b90146a2	1	0	0	1	0	8	0.8787139	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospir aceae	g_Moryella	s_human_gut
22	33f91e62a000ed593c352f0c7f976f8a	1	1	0	1	0	17	0.9368454	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospir aceae	g_Lachnospiraceae_ND3007_group	s_metagenome
23	e679760656821248d941dccc0b1ca39e	1	1	0	1	0	17	0.9581176	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospir aceae	g_[Eubacterium]_elig ens_group	NA
24	f0143441c5a8a01ba31592825d9e47ef	1	1	0	1	0	17	0.9483575	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospir aceae	g_Agathobacter	NA
25	5f3d16b803aaa2896227ae65b06ff9d5	1	1	1	1	0	26	0.8990931	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospir aceae	g_Roseburia	NA
26	34ecf8ad93a52ec913a59abaca0d39ca	1	1	0	1	0	17	0.8783473	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospir aceae	g_uncultured	s_uncultured_E ubacterium
27	b91f30e253a2f78f0722bbdc236b9f8a	1	1	0	1	0	17	0.887274	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospir aceae	g_Lachnospiraceae_FCS020_group	s_uncultured_o rganism
28	d0f21126697b2318d28dd79e2ffe491b	1	1	0	1	0	17	0.9600533	0.005	d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospir aceae	g_Lachnospiraceae_NK4A136_group	NA