

Supplementary Material

Benefits of Gut Microbiota Reconstitution by Beta 1,3-1,6 Glucans in Subjects with Autism Spectrum Disorder and Other Neurodegenerative Diseases

Supplementary Table 1. Genus level: Mean and percentage abundance at baseline and post-intervention in Group 1 (Control)

S.No	Genus	Mean abundance		Percentage of abundance	
		Baseline	Post-Intervention	Baseline	Post-Intervention
1	<i>Bacteroides</i>	16395	16956	16.84	19.09
2	<i>Prevotella</i>	2019	7252	2.07	8.16
3	<i>Clostridium</i>	6277	5792	6.45	6.52
4	<i>Faecalibacterium</i>	4646	5398	4.77	6.08
5	<i>Bifidobacterium</i>	7375	4809	7.58	5.41
6	<i>Blautia</i>	6123	4175	6.29	4.70
7	<i>Roseburia</i>	3257	3564	3.35	4.01
8	<i>Eubacterium</i>	2268	3016	2.33	3.40
9	<i>Ruminococcus</i>	3484	2066	3.58	2.33
10	<i>Lachnospirillum</i>	1289	1682	1.32	1.89
11	<i>Hungatella</i>	66	1381	0.07	1.55
12	<i>Dialister</i>	983	1380	1.01	1.55
13	<i>Klebsiella</i>	1121	1357	1.15	1.53
14	<i>Alistipes</i>	2487	1352	2.55	1.52
15	<i>Enterococcus</i>	4721	1270	4.85	1.43
16	<i>Veillonella</i>	0	1244	0.00	1.40
17	<i>Akkermansia</i>	827	1126	0.85	1.27
18	<i>Streptococcus</i>	384	1093	0.39	1.23
19	<i>Megasphaera</i>	64	1084	0.07	1.22
20	<i>Anaerostipes</i>	393	1020	0.40	1.15
21	<i>Parabacteroides</i>	1686	971	1.73	1.09
22	<i>Lactobacillus</i>	1857	956	1.91	1.08
23	<i>Coprococcus</i>	897	915	0.92	1.03
24	<i>Dorea</i>	1352	862	1.39	0.97
25	<i>Butyricicoccus</i>	1339	835	1.38	0.94
26	<i>Flavonifractor</i>	669	825	0.69	0.93
27	<i>Escherichia</i>	1062	822	1.09	0.92
28	<i>Odoribacter</i>	1036	803	1.06	0.90
29	<i>Enterobacter</i>	355	757	0.36	0.85
30	<i>Subdoligranulum</i>	802	597	0.82	0.67
31	<i>Oscillibacter</i>	699	569	0.72	0.64
32	<i>Bilophila</i>	0	552	0.00	0.62
33	<i>Eggerthella</i>	829	548	0.85	0.62

34	<i>Collinsella</i>	1617	541	1.66	0.61
35	<i>Turicibacter</i>	0	415	0.00	0.47
36	<i>Mitsuokella</i>	0	409	0.00	0.46
37	<i>Catenibacterium</i>	540	403	0.55	0.45
38	<i>Fusicatenibacter</i>	434	392	0.45	0.44
39	<i>Romboutsia</i>	206	357	0.21	0.40
40	<i>Haemophilus</i>	88	346	0.09	0.39
41	<i>Gemmiger</i>	524	343	0.54	0.39
42	<i>Sutterella</i>	139	301	0.14	0.34
43	<i>Lachnospira</i>	0	294	0.00	0.33
44	<i>Mycoplasma</i>	292	251	0.30	0.28
45	<i>Holdemanella</i>	585	199	0.60	0.22
46	<i>Parasutterella</i>	0	197	0.00	0.22
47	<i>Weissella</i>	173	177	0.18	0.20
48	<i>Ruminiclostridium</i>	174	148	0.18	0.17
49	<i>Chlamydia</i>	133	147	0.14	0.16
50	<i>Dakarella</i>	97	147	0.10	0.16
51	<i>Lactococcus</i>	144	144	0.15	0.16
52	<i>Clostridioides</i>	107	126	0.11	0.14
53	<i>Terrisporobacter</i>	0	123	0.00	0.14
54	<i>Coprobacillus</i>	224	114	0.23	0.13
55	<i>Adlercreutzia</i>	405	101	0.42	0.11
56	<i>Butyrivibrio</i>	121	90	0.12	0.10
57	<i>Anaerotruncus</i>	135	81	0.14	0.09
58	<i>Bacillus</i>	262	69	0.27	0.08
59	<i>Agathobaculum</i>	54	67	0.05	0.08
60	<i>Shigella</i>	53	60	0.05	0.07
61	<i>Tyzzera</i>	13	59	0.01	0.07
62	<i>Oribacterium</i>	145	52	0.15	0.06
63	<i>Intestinimonas</i>	91	50	0.09	0.06
64	<i>Citrobacter</i>	0	49	0.00	0.06
65	<i>Fusobacterium</i>	0	46	0.00	0.05
66	<i>Acholeplasma</i>	0	41	0.00	0.05
67	<i>Pseudoflavonifractor</i>	68	40	0.07	0.05
68	<i>Raoultella</i>	0	32	0.00	0.04
69	<i>Muribaculum</i>	0	31	0.00	0.03
70	<i>Acidiphilium</i>	27	29	0.03	0.03
71	<i>Paenibacillus</i>	110	28	0.11	0.03
72	<i>Acidaminococcus</i>	0	25	0.00	0.03
73	<i>Salmonella</i>	0	22	0.00	0.03
74	<i>Anaeromassilibacillus</i>	179	22	0.18	0.02
75	<i>Pantoea</i>	0	21	0.00	0.02
76	<i>Intestinibacter</i>	0	21	0.00	0.02

77	<i>Eisenbergiella</i>	85	20	0.09	0.02
78	<i>Prevotellamassilia</i>	0	20	0.00	0.02
79	<i>Anaerotignum</i>	0	17	0.00	0.02
80	<i>Selenomonas</i>	0	16	0.00	0.02
81	<i>Actinomyces</i>	0	16	0.00	0.02
82	<i>Paraprevotella</i>	26	10	0.03	0.01
83	<i>Porphyromonas</i>	0	9	0.00	0.01
84	<i>Barnesiella</i>	129	0	0.13	0.00
85	<i>Anaerococcus</i>	141	0	0.14	0.00
86	<i>Stenotrophomonas</i>	13	0	0.01	0.00
87	<i>Finegoldia</i>	82	0	0.08	0.00
88	<i>Pediococcus</i>	10	0	0.01	0.00
89	<i>Solobacterium</i>	27	0	0.03	0.00
90	<i>Peptoniphilus</i>	929	0	0.95	0.00
91	<i>Urinacoccus</i>	144	0	0.15	0.00
92	<i>Enterorhabdus</i>	46	0	0.05	0.00
93	<i>Slackia</i>	69	0	0.07	0.00
94	<i>Achromobacter</i>	59	0	0.06	0.00
95	<i>Lysinibacillus</i>	1130	0	1.16	0.00
96	<i>Olsenella</i>	192	0	0.20	0.00
97	<i>Comamonas</i>	131	0	0.13	0.00
98	<i>Ruthenibacterium</i>	63	0	0.06	0.00
99	<i>Viridibacillus</i>	40	0	0.04	0.00
100	<i>Rummeliibacillus</i>	603	0	0.62	0.00
101	<i>Gordonibacter</i>	735	0	0.75	0.00
102	<i>Drancourtella</i>	19	0	0.02	0.00
103	<i>Monoglobus</i>	24	0	0.02	0.00
104	<i>Lagierella</i>	39	0	0.04	0.00
105	<i>Peptococcus</i>	27	0	0.03	0.00
106	<i>Senegalimassilia</i>	122	0	0.13	0.00
107	<i>Libanicoccus</i>	25	0	0.03	0.00
108	<i>Urmitella</i>	24	0	0.02	0.00
109	<i>Paraclostridium</i>	19	0	0.02	0.00
110	<i>Acinetobacter</i>	1273	0	1.31	0.00
111	<i>Anaerocolumna</i>	9	0	0.01	0.00
112	<i>Marvinbryantia</i>	22	0	0.02	0.00
113	<i>Robinsoniella</i>	50	0	0.05	0.00
114	<i>Neglecta</i>	33	0	0.03	0.00
115	<i>Butyricimonas</i>	180	0	0.19	0.00
116	unknown	6947	5101	7.14	5.74

Supplementary Table 2. Genus level: Mean and percentage abundance at baseline and post-intervention in Group 2 (Nichi Glucan)

S.No	Genus	Mean abundance		Percentage of abundance	
		Baseline	Post-Intervention	Baseline	Post-Intervention
1	<i>Bacteroides</i>	13463	14088	11.60	11.43
2	<i>Clostridium</i>	8728	12105	7.52	9.82
3	<i>Bifidobacterium</i>	6771	5625	5.84	4.57
4	<i>Faecalibacterium</i>	5291	9278	4.56	7.53
5	<i>Enterococcus</i>	4583	40	3.95	0.03
6	<i>Eubacterium</i>	4380	5007	3.78	4.06
7	<i>Ruminococcus</i>	4265	6143	3.68	4.99
8	<i>Blautia</i>	4196	3973	3.62	3.22
9	<i>Alistipes</i>	3187	2268	2.75	1.84
10	<i>Collinsella</i>	2542	1590	2.19	1.29
11	<i>Parabacteroides</i>	2419	1307	2.08	1.06
12	<i>Oscillibacter</i>	1956	2542	1.69	2.06
13	<i>Prevotella</i>	1887	5979	1.63	4.85
14	<i>Lactobacillus</i>	1860	1093	1.60	0.89
15	<i>Roseburia</i>	1756	7932	1.51	6.44
16	<i>Trichosporon</i>	1683	0	1.45	0.00
17	<i>Dorea</i>	1592	1585	1.37	1.29
18	<i>Lachnoclostridium</i>	1360	1056	1.17	0.86
19	<i>Olsenella</i>	1354	246	1.17	0.20
20	<i>Escherichia</i>	1346	505	1.16	0.41
21	<i>Klebsiella</i>	1067	80	0.92	0.06
22	<i>Gemmiger</i>	970	1161	0.84	0.94
23	<i>Streptococcus</i>	925	521	0.80	0.42
24	<i>Coprococcus</i>	910	1228	0.78	1.00
25	<i>Subdoligranulum</i>	904	1112	0.78	0.90
26	<i>Eggerthella</i>	871	190	0.75	0.15
27	<i>Dialister</i>	765	1062	0.66	0.86
28	<i>Hungatella</i>	732	175	0.63	0.14
29	<i>Lysinibacillus</i>	709	0	0.61	0.00
30	<i>Acinetobacter</i>	677	0	0.58	0.00
31	<i>Pediococcus</i>	662	0	0.57	0.00
32	<i>Holdemanella</i>	649	546	0.56	0.44
33	<i>Butyricoccus</i>	623	1257	0.54	1.02
34	<i>Catenibacterium</i>	620	470	0.53	0.38
35	<i>Cloacibacillus</i>	602	265	0.52	0.21
36	<i>Pichia</i>	588	0	0.51	0.00
37	<i>Odoribacter</i>	577	271	0.50	0.22
38	<i>Rummeliibacillus</i>	555	0	0.48	0.00

39	<i>Weissella</i>	555	24	0.48	0.02
40	<i>Flavonifractor</i>	545	729	0.47	0.59
41	<i>Senegalimassilia</i>	505	56	0.43	0.05
42	<i>Megasphaera</i>	464	1203	0.40	0.98
43	<i>Romboutsia</i>	463	130	0.40	0.11
44	<i>Desulfovibrio</i>	461	344	0.40	0.28
45	<i>Fusicatenibacter</i>	452	641	0.39	0.52
46	<i>Sutterella</i>	436	780	0.38	0.63
47	<i>Mycoplasma</i>	424	265	0.37	0.21
48	<i>Peptoniphilus</i>	413	0	0.36	0.00
49	<i>Ruminiclostridium</i>	411	387	0.35	0.31
50	<i>Anaerotruncus</i>	410	485	0.35	0.39
51	<i>Butyrivibrio</i>	404	315	0.35	0.26
52	<i>Methanobrevibacter</i>	395	368	0.34	0.30
53	<i>Megamonas</i>	392	501	0.34	0.41
54	<i>Bacillus</i>	326	150	0.28	0.12
55	<i>Butyricimonas</i>	319	39	0.28	0.03
56	<i>Anaerostipes</i>	318	485	0.27	0.39
57	<i>Phascolarctobacterium</i>	317	464	0.27	0.38
58	<i>Akkermansia</i>	305	498	0.26	0.40
59	<i>Gordonibacter</i>	304	0	0.26	0.00
60	<i>Coprobacillus</i>	295	438	0.25	0.36
61	<i>Coralimargarita</i>	294	339	0.25	0.28
62	<i>Methanosphaera</i>	282	0	0.24	0.00
63	<i>Enterobacter</i>	257	17	0.22	0.01
64	<i>Pyramidobacter</i>	231	15	0.20	0.01
65	<i>Acidaminococcus</i>	230	269	0.20	0.22
66	<i>Paenibacillus</i>	229	184	0.20	0.15
67	<i>Acidiphilium</i>	219	555	0.19	0.45
68	<i>Adlercreutzia</i>	210	334	0.18	0.27
69	<i>Actinomyces</i>	191	4	0.16	0.00
70	<i>Succinatimonas</i>	190	383	0.16	0.31
71	<i>Libanicoccus</i>	188	119	0.16	0.10
72	<i>Angelakisella</i>	184	79	0.16	0.06
73	<i>Pseudoflavonifractor</i>	183	173	0.16	0.14
74	<i>Chlamydia</i>	176	130	0.15	0.11
75	<i>Anaeromassilibacillus</i>	175	135	0.15	0.11
76	<i>Intestinimonas</i>	157	174	0.14	0.14
77	<i>Duodenibacillus</i>	150	181	0.13	0.15
78	<i>Oribacterium</i>	145	103	0.13	0.08
79	<i>Clostridioides</i>	129	64	0.11	0.05
80	<i>Barnesiella</i>	118	84	0.10	0.07
81	<i>Slackia</i>	109	0	0.09	0.00

82	<i>Eisenbergiella</i>	95	112	0.08	0.09
83	<i>Acidovorax</i>	93	0	0.08	0.00
84	<i>Lactococcus</i>	92	0	0.08	0.00
85	<i>Paraprevotella</i>	91	16	0.08	0.01
86	<i>Shigella</i>	90	90	0.08	0.07
87	<i>Oxalobacter</i>	87	0	0.08	0.00
88	<i>Selenomonas</i>	84	231	0.07	0.19
89	<i>Turcibacter</i>	74	36	0.06	0.03
90	<i>Haemophilus</i>	74	196	0.06	0.16
91	<i>Pygmaibacter</i>	69	0	0.06	0.00
92	<i>Urinacoccus</i>	64	0	0.06	0.00
93	<i>Bilophila</i>	63	613	0.05	0.50
94	<i>Allisonella</i>	62	54	0.05	0.04
95	<i>Ruthenibacterium</i>	51	69	0.04	0.06
96	<i>Raoultibacter</i>	50	0	0.04	0.00
97	<i>Comamonas</i>	44	0	0.04	0.00
98	<i>Neglecta</i>	42	37	0.04	0.03
99	<i>Atopobium</i>	40	11	0.03	0.01
100	<i>Christensenella</i>	38	41	0.03	0.03
101	<i>Massilimaliae</i>	37	32	0.03	0.03
102	<i>Finegoldia</i>	36	0	0.03	0.00
103	<i>Treponema</i>	36	48	0.03	0.04
104	<i>Robinsoniella</i>	36	0	0.03	0.00
105	<i>Enterorhabdus</i>	36	40	0.03	0.03
106	<i>Viridibacillus</i>	36	0	0.03	0.00
107	<i>Peptococcus</i>	35	0	0.03	0.00
108	<i>Fusobacterium</i>	34	30	0.03	0.02
109	<i>Terrisporobacter</i>	34	7	0.03	0.01
110	<i>Tyzzerella</i>	33	171	0.03	0.14
111	<i>Erysipelatoclostridium</i>	32	0	0.03	0.00
112	<i>Sporobacter</i>	32	36	0.03	0.03
113	<i>Mitsuokella</i>	31	432	0.03	0.35
114	<i>Cutaneotrichosporon</i>	31	0	0.03	0.00
115	<i>Marvinbryantia</i>	31	28	0.03	0.02
116	<i>Corallococcus</i>	30	143	0.03	0.12
117	<i>Anaerotignum</i>	28	18	0.02	0.01
118	<i>Prevotellamassilia</i>	24	158	0.02	0.13
119	<i>Anaerofilum</i>	24	35	0.02	0.03
120	<i>Synergistes</i>	22	0	0.02	0.00
121	<i>Alloprevotella</i>	22	22	0.02	0.02
122	<i>Isoptericola</i>	22	0	0.02	0.00
123	<i>Anaerococcus</i>	21	0	0.02	0.00
124	<i>Propionibacterium</i>	20	0	0.02	0.00

125	<i>Leuconostoc</i>	20	0	0.02	0.00
126	<i>Brachyspira</i>	19	95	0.02	0.08
127	<i>Lachnospira</i>	18	386	0.02	0.31
128	<i>Lagierella</i>	17	0	0.02	0.00
129	<i>Mogibacterium</i>	16	0	0.01	0.00
130	<i>Agathobaculum</i>	15	61	0.01	0.05
131	<i>Pseudobutyrvibrio</i>	15	35	0.01	0.03
132	<i>Hydrogenoanaerobacterium</i>	14	14	0.01	0.01
133	<i>Holdemania</i>	14	0	0.01	0.00
134	<i>Desulfotomaculum</i>	14	0	0.01	0.00
135	<i>Veillonella</i>	14	324	0.01	0.26
136	<i>Succinivibrio</i>	14	32	0.01	0.03
137	<i>Anaerocolumna</i>	14	14	0.01	0.01
138	<i>Mobilibacterium</i>	12	0	0.01	0.00
139	<i>Arabia</i>	12	0	0.01	0.00
140	<i>Enorma</i>	11	0	0.01	0.00
141	<i>Candida</i> <Debaryomycetaceae>	11	0	0.01	0.00
142	<i>Intestinibacter</i>	11	13	0.01	0.01
143	<i>Kurthia</i>	10	0	0.01	0.00
144	<i>Paeniclostridium</i>	9	0	0.01	0.00
145	<i>Paraclostridium</i>	8	0	0.01	0.00
146	<i>Listeria</i>	8	0	0.01	0.00
147	<i>Kwoniella</i>	8	0	0.01	0.00
148	<i>Cryptococcus</i>	7	0	0.01	0.00
149	<i>Fournierella</i>	0	23	0.00	0.02
150	<i>Sellimonas</i>	0	23	0.00	0.02
151	<i>Blastocystis</i>	0	34	0.00	0.03
152	<i>Acholeplasma</i>	0	126	0.00	0.10
153	<i>Azospirillum</i>	0	162	0.00	0.13
154	<i>Porphyromonas</i>	0	7	0.00	0.01
155	<i>Emergencia</i>	0	14	0.00	0.01
156	<i>Acetobacter</i>	0	13	0.00	0.01
157	<i>Dakarella</i>	0	64	0.00	0.05
158	<i>Parasutterella</i>	0	133	0.00	0.11
159	<i>Elusimicrobium</i>	0	128	0.00	0.10
160	<i>Drancourtella</i>	0	32	0.00	0.03
161	<i>Anaerovorax</i>	0	15	0.00	0.01
162	<i>Caldicoprobacter</i>	0	15	0.00	0.01
163	unknown	12707	16408	10.95	13.32

Supplementary Table 3. Species level: Mean abundance at baseline and post-intervention in Group 1 (Control)

S.No	Species	Mean abundance	
		Baseline	Post-Intervention
1	<i>Prevotella copri</i>	530	2058
2	uncultured <i>Clostridium</i> sp.	2459	1860
3	<i>Bifidobacterium longum</i>	2150	1433
4	<i>Hungatella hathewayi</i>	65	1287
5	<i>Bacteroides fragilis</i>	2052	1189
6	<i>Bacteroides thetaiotaomicron</i>	1432	1172
7	<i>Blautia producta</i>	25	985
8	<i>Bifidobacterium bifidum</i>	941	946
9	<i>Roseburia intestinalis</i>	144	930
10	<i>Bacteroides vulgatus</i>	364	866
11	<i>Bacteroides ovatus</i>	1186	846
12	<i>Clostridium neonatale</i>	0	770
13	<i>Escherichia coli</i>	998	767
14	<i>Akkermansia muciniphila</i>	464	760
15	uncultured <i>Butyricicoccus</i> sp.	948	751
16	<i>Prevotella copri</i> CAG:164	362	700
17	<i>Flavonifractor plautii</i>	445	640
18	[<i>Eubacterium</i>] <i>rectale</i>	380	594
19	<i>Anaerostipes</i> sp. BG01	0	584
20	<i>Dialister</i> sp. CAG:357	0	540
21	<i>Lactobacillus ruminis</i>	628	536
22	<i>Bacteroides uniformis</i>	265	519
23	<i>Roseburia faecis</i>	625	507
24	<i>Prevotella</i> sp. CAG:386	61	481
25	<i>Eubacterium</i> sp. CAG:252	0	472
26	[<i>Clostridium</i>] <i>bolteae</i>	0	471
27	[<i>Eubacterium</i>] <i>eligens</i>	0	470
28	<i>Bifidobacterium adolescentis</i>	574	466
29	<i>Klebsiella pneumoniae</i>	397	461
30	<i>Prevotella</i> sp. CAG:1092	0	457
31	<i>Dialister succinatiphilus</i>	412	454
32	<i>Clostridium</i> sp. AT4	12	450
33	<i>Prevotella</i> sp. CAG:604	154	445
34	Firmicutes bacterium CAG:124	806	439
35	uncultured <i>Blautia</i> sp.	1136	435
36	<i>Bacteroides xylanisolvens</i>	402	414
37	<i>Bilophila wadsworthia</i>	0	412
38	<i>Blautia obeum</i>	1024	410
39	<i>Prevotella</i> sp. 885	48	406

40	<i>Fusicatenibacter saccharivorans</i>	432	391
41	<i>[Clostridium] clostridioforme</i>	76	379
42	<i>Megasphaera elsdenii</i>	0	376
43	<i>Bacteroides nordii</i>	56	369
44	<i>Faecalibacterium</i> sp. CAG:82	296	362
45	<i>[Ruminococcus] gnavus</i>	367	361
46	<i>Ruminococcus</i> sp. CAG:177	427	359
47	<i>Dorea longicatena</i>	402	358
48	<i>Mitsuokella multacida</i>	0	356
49	<i>Blautia wexlerae</i>	738	355
50	<i>Eubacterium</i> sp. CAG:251	0	351
51	<i>[Ruminococcus] torques</i>	790	342
52	<i>Prevotella multisaccharivorax</i>	72	334
53	<i>Odoribacter splanchnicus</i>	417	330
54	Firmicutes bacterium CAG:176	653	329
55	<i>Dialister</i> sp. CAG:486	143	328
56	<i>Gemmiger formicilis</i>	481	320
57	Firmicutes bacterium CAG:41	334	311
58	<i>Streptococcus thermophilus</i>	0	305
59	<i>Romboutsia timonensis</i>	171	299
60	<i>Subdoligranulum</i> sp. 60_17	438	296
61	<i>Bacteroides oleiciplenus</i>	0	286
62	<i>Subdoligranulum variabile</i>	275	281
63	<i>Bacteroides plebeius</i>	0	280
64	uncultured <i>Faecalibacterium</i> sp.	168	280
65	<i>Roseburia hominis</i>	94	273
66	<i>Anaerostipes hadrus</i>	350	266
67	<i>Alistipes putredinis</i>	568	266
68	butyrate-producing bacterium SS3/4	0	259
69	Firmicutes bacterium CAG:103	872	255
70	<i>Eggerthella lenta</i>	392	254
71	<i>Catenibacterium</i> sp. CAG:290	324	240
72	<i>Mycoplasma</i> sp. CAG:956	229	238
73	<i>Veillonella dispar</i>	0	238
74	<i>Oscillibacter</i> sp. ER4	283	238
75	<i>Clostridium</i> sp. CAG:81	0	236
76	<i>Collinsella aerofaciens</i>	715	236
77	<i>Bacteroides timonensis</i>	0	235
78	<i>Turicibacter sanguinis</i>	0	233
79	<i>Bifidobacterium</i> sp. N5G01	550	230
80	<i>Bacteroides caccae</i>	548	224
81	Clostridiales bacterium KLE1615	0	216
82	uncultured <i>Ruminococcus</i> sp.	760	213

83	<i>Bacteroides cellulosilyticus</i>	0	213
84	<i>Clostridium</i> sp. CAG:7	55	213
85	<i>Parabacteroides merdae</i>	40	211
86	<i>Clostridium</i> sp. CAG:389	291	208
87	<i>Blautia</i> sp. CAG:37	162	208
88	<i>Coprococcus eutactus</i>	158	200
89	<i>Veillonella atypica</i>	0	200
90	<i>Ruminococcus callidus</i>	32	200
91	<i>Holdemanella biformis</i>	585	199
92	Lachnospiraceae bacterium TF01-11	0	199
93	uncultured <i>Lachnospira</i> sp.	0	190
94	<i>Bacteroides stercoris</i>	0	187
95	<i>Bifidobacterium catenulatum</i>	142	183
96	[<i>Eubacterium</i>] <i>hallii</i>	346	174
97	<i>Prevotella</i> sp. CAG:520	0	173
98	<i>Roseburia</i> sp. CAG:18	283	173
99	<i>Alistipes</i> sp. HGB5	27	172
100	<i>Haemophilus parainfluenzae</i>	52	172
101	<i>Streptococcus salivarius</i>	71	169
102	<i>Coprococcus catus</i>	49	167
103	Firmicutes bacterium CAG:65	89	164
104	<i>Bacteroides plebeius</i> CAG:211	0	163
105	<i>Ruminococcus bromii</i>	158	163
106	<i>Megasphaera massiliensis</i>	12	161
107	<i>Enterobacter hormaechei</i>	47	158
108	<i>Roseburia intestinalis</i> CAG:13	0	153
109	<i>Catenibacterium mitsuokai</i>	198	149
110	<i>Dakarella massiliensis</i>	97	147
111	<i>Chlamydia trachomatis</i>	132	146
112	<i>Enterobacter cloacae</i>	70	145
113	<i>Bifidobacterium pseudocatenulatum</i>	251	145
114	Clostridiales bacterium VE202-06	0	144
115	Firmicutes bacterium CAG:65_45_313	0	142
116	[<i>Clostridium</i>] <i>symbiosum</i>	0	140
117	<i>Veillonella parvula</i>	0	139
118	Clostridiales bacterium 1_7_47FAA	0	136
119	Burkholderiales bacterium 1_1_47	0	135
120	<i>Roseburia</i> sp. CAG:18_43_25	158	134
121	<i>Bacteroides</i> sp. HPS0048	64	132
122	<i>Weissella confusa</i>	124	132
123	<i>Clostridium</i> sp. CAG:122	0	131
124	Firmicutes bacterium CAG:424	146	131
125	<i>Prevotella stercorea</i>	0	127

126	<i>Ruminococcus</i> sp. CAG:254	445	127
127	<i>Bacteroides</i> sp. 2_2_4	64	127
128	<i>Enterococcus asini</i>	0	126
129	<i>Blautia</i> sp. KLE 1732	185	126
130	<i>Clostridioides difficile</i>	107	125
131	Firmicutes bacterium CAG:129_59_24	164	124
132	[<i>Eubacterium</i>] <i>siraeum</i>	50	124
133	Clostridiales bacterium 42_27	184	120
134	<i>Bifidobacterium kashiwanohense</i>	125	117
135	<i>Roseburia inulinivorans</i>	482	117
136	<i>Prevotella</i> sp. CAG:732	28	114
137	Firmicutes bacterium CAG:170	235	113
138	<i>Clostridium</i> sp. CAG:12237_41	0	113
139	<i>Clostridium bolteae</i> CAG:59	0	113
140	<i>Clostridium</i> sp. ATCC BAA-442	67	113
141	<i>Lactobacillus ruminis</i> CAG:367	87	113
142	Firmicutes bacterium CAG:102	0	111
143	<i>Ruminococcus</i> sp. 5_1_39BFAA	166	105
144	Firmicutes bacterium CAG:114	480	103
145	<i>Alistipes senegalensis</i>	628	102
146	<i>Alistipes finegoldii</i>	41	101
147	<i>Adlercreutzia equolifaciens</i>	405	101
148	<i>Sutterella</i> sp. CAG:351	132	100
149	<i>Parabacteroides distasonis</i>	67	100
150	<i>Parasutterella excrementihominis</i>	0	98
151	uncultured <i>Eubacterium</i> sp.	294	98
152	<i>Enterococcus avium</i>	292	97
153	<i>Bacteroides dorei</i>	235	97
154	<i>Bacteroides stercorisoris</i>	0	97
155	<i>Collinsella</i> sp. CAG:166	156	96
156	uncultured bacterium	89	95
157	<i>Lactococcus garvieae</i>	0	95
158	<i>Prevotella</i> sp. CAG:474	21	95
159	<i>Terrisporobacter glycolicus</i>	0	94
160	<i>Oscillibacter</i> sp. 57_20	66	94
161	<i>Veillonella</i> sp. DORA_A_3_16_22	0	94
162	<i>Ruminococcus</i> sp. CAG:90	118	92
163	<i>Prevotella</i> sp. CAG:592	0	92
164	<i>Lachnospira pectinoschiza</i>	0	92
165	<i>Bacteroides intestinalis</i>	0	89
166	<i>Bacteroides caccae</i> CAG:21	231	88
167	<i>Bacteroides</i> sp. 3_1_23	12	87
168	Clostridiales bacterium 41_21_two_genomes	21	87

169	<i>Faecalibacterium</i> sp. CAG:82-related_59_9	74	85
170	<i>Klebsiella michiganensis</i>	0	85
171	<i>Bifidobacterium</i> sp. N4G05	217	83
172	Proteobacteria bacterium CAG:139	0	81
173	Clostridiales bacterium 41_12_two_minus	83	81
174	<i>Eubacterium</i> sp. CAG:248	0	80
175	<i>Dorea formicigenerans</i>	292	80
176	<i>Megasphaera</i> sp. DISK 18	0	79
177	<i>Coprobacillus</i> sp. CAG:235	197	79
178	<i>Prevotella stercorea</i> CAG:629	0	79
179	Clostridiales bacterium 52_15	218	79
180	Clostridiales bacterium 59_14	133	77
181	<i>Blautia</i> sp. CAG:237	163	77
182	uncultured <i>Bacteroides</i> sp.	0	76
183	<i>Alistipes finegoldii</i> CAG:68	0	75
184	<i>Dorea</i> sp. CAG:105	39	74
185	<i>Ruminococcus obeum</i> CAG:39	163	73
186	<i>Bacteroides cellulosilyticus</i> CAG:158	0	70
187	<i>Ruminococcus</i> sp. CAG:17	170	69
188	<i>Eubacterium</i> sp. CAG:38	0	69
189	<i>Clostridium</i> sp. CAG:91	0	69
190	<i>Klebsiella oxytoca</i>	0	68
191	<i>Bacteroides</i> sp. 43_46	134	68
192	<i>Prevotella</i> sp. P3-122	0	68
193	<i>Roseburia</i> sp. CAG:471	101	68
194	<i>Agathobaculum desmolans</i>	54	67
195	<i>Sutterella parvirubra</i>	0	66
196	<i>Eubacterium rectale</i> CAG:36	35	66
197	<i>Collinsella</i> sp. 4_8_47FAA	144	65
198	<i>Blautia</i> sp. Marseille-P3201T	68	65
199	<i>Bacteroides</i> sp. 4_1_36	75	63
200	<i>Odoribacter</i> sp. 43_10	61	62
201	<i>Parasutterella excrementihominis</i> CAG:233	0	60
202	<i>Bilophila</i> sp. 4_1_30	0	60
203	<i>Eubacterium eligens</i> CAG:72	0	60
204	<i>Parabacteroides merdae</i> CAG:48	0	59
205	<i>Blautia</i> sp. CAG:37_48_57	87	59
206	<i>Bifidobacterium breve</i>	485	58
207	<i>Ruminococcus</i> sp. CAG:108	45	58
208	Firmicutes bacterium CAG:83	430	57
209	<i>Bacteroides</i> sp. 41_26	0	57
210	<i>Anaerostipes caccae</i>	0	56
211	uncultured <i>Flavonifractor</i> sp.	65	56

212	<i>Enterococcus</i> sp. HMSC05C03	31	56
213	<i>Butyricoccus</i> sp. BB10	347	56
214	<i>Alistipes putredinis</i> CAG:67	57	55
215	<i>Bacteroides</i> sp. D20	18	54
216	<i>Lachnoclostridium</i> sp. An196	34	54
217	<i>Dorea longicatena</i> CAG:42	29	53
218	<i>Klebsiella variicola</i>	0	53
219	<i>Akkermansia muciniphila</i> CAG:154	21	48
220	<i>Streptococcus pneumoniae</i>	36	48
221	Firmicutes bacterium CAG:129	73	48
222	<i>Eubacterium</i> sp. 45_250	0	48
223	<i>Bacteroides</i> sp. D22	51	47
224	<i>Eubacterium</i> sp. CAG:76	0	47
225	Clostridiales bacterium VE202-28	0	47
226	<i>Oscillibacter</i> sp. CAG:241	69	46
227	<i>Blautia massiliensis</i>	69	46
228	<i>Blautia</i> sp. SF-50	77	46
229	<i>Parabacteroides</i> sp. D13	39	45
230	<i>Enterococcus faecium</i>	844	45
231	<i>Mitsuokella jalaludinii</i>	0	45
232	<i>Sutterella wadsworthensis</i>	0	44
233	Clostridiales bacterium 36_14	48	44
234	<i>Coprococcus</i> sp. CAG:131	66	44
235	<i>Lachnoclostridium</i> sp. An14	0	43
236	Lachnospiraceae bacterium 7_1_58FAA	18	43
237	<i>Blautia</i> sp. Marseille-P2398	86	43
238	<i>Eubacterium hallii</i> CAG:12	85	42
239	<i>Bacteroides</i> sp. 1_1_30	49	42
240	Clostridiales bacterium VE202-03	25	41
241	<i>Acholeplasma</i> sp. CAG:878	0	40
242	<i>Blautia</i> sp. CAG:52	175	40
243	<i>Veillonella</i> sp. HPA0037	0	40
244	<i>Alistipes indistinctus</i>	91	39
245	<i>Ruminococcus</i> sp. SR1/5	57	39
246	<i>Roseburia</i> sp. CAG:50	0	38
247	Erwinia phage vB_EamM_Y3	0	38
248	<i>Bacteroides</i> sp. D2	0	38
249	<i>Eubacterium ramulus</i>	34	37
250	<i>Veillonella</i> sp. oral taxon 158	0	37
251	Clostridia bacterium UC5.1-2H11	22	36
252	<i>Turcibacter</i> sp. H121	0	36
253	<i>Fusobacterium</i> sp. CAG:815	0	36
254	<i>Alistipes</i> sp. 58_9_plus	0	35

255	<i>Prevotella</i> sp. CAG:873	0	34
256	<i>Clostridium</i> sp. CAG:448	0	34
257	<i>Clostridium</i> sp. CAG:492	0	34
258	Firmicutes bacterium CAG:822	0	34
259	<i>Veillonella</i> sp. ACP1	0	34
260	<i>Bacteroides</i> sp. 14(A)	0	33
261	Clostridiales bacterium NK3B98	0	33
262	<i>Ruminococcus</i> sp. CAG:108-related_41_35	25	33
263	<i>Bacteroides intestinalis</i> CAG:315	0	32
264	<i>Lactobacillus rogosae</i>	0	32
265	<i>Alistipes timonensis</i>	77	32
266	<i>Anaerotruncus</i> sp. CAG:390	26	31
267	<i>Prevotella</i> sp. P4-65	0	31
268	<i>Blautia</i> sp. An81	27	31
269	<i>Bacteroides fragilis</i> CAG:558	57	31
270	<i>Tyzzerella nexilis</i>	0	30
271	<i>Romboutsia ilealis</i>	0	30
272	[<i>Clostridium</i>] <i>citroniae</i>	0	29
273	<i>Prevotella</i> sp. P5-108	0	29
274	<i>Prevotella</i> sp. P4-76	0	29
275	<i>Acidiphilium</i> sp. CAG:727	27	29
276	<i>Muribaculum intestinale</i>	0	29
277	<i>Eubacterium</i> sp. 41_20	27	29
278	<i>Shigella sonnei</i>	0	28
279	<i>Terrisporobacter othiniensis</i>	0	28
280	<i>Bifidobacterium adolescentis</i> CAG:119	0	28
281	<i>Veillonella</i> sp. ICM51a	0	28
282	<i>Prevotella</i> sp. AGR2160	0	27
283	<i>Bacteroides</i> sp. 3_1_13	11	27
284	<i>Prevotella</i> sp. CAG:279	320	27
285	<i>Intestinimonas butyriciproducens</i>	72	27
286	<i>Prevotella bryantii</i>	0	27
287	<i>Streptococcus parasanguinis</i>	12	27
288	<i>Clostridium</i> sp. CAG:43	0	27
289	<i>Klebsiella aerogenes</i>	503	27
290	<i>Ruminococcus</i> sp. CAG:330	37	26
291	<i>Clostridium</i> sp. SS2/1	43	26
292	uncultured <i>Oscillibacter</i> sp.	53	26
293	<i>Prevotella</i> sp. P5-64	0	26
294	Firmicutes bacterium CAG:341	281	25
295	<i>Oscillibacter</i> sp. CAG:241_62_21	32	25
296	<i>Megasphaera</i> sp. MJR8396C	0	25
297	<i>Coprococcus</i> sp. CAG:131-related_45_246	0	25

298	<i>Ruminococcus</i> sp. CAG:9	61	25
299	<i>Prevotella</i> sp. P5-60	0	25
300	<i>Bacteroides</i> sp. CAG:927	0	24
301	<i>Megasphaera</i> sp. BL7	0	24
302	Bacteroidales bacterium 52_46	0	24
303	<i>Odoribacter splanchnicus</i> CAG:14	50	24
304	<i>Bacteroides</i> sp. 43_108	0	24
305	<i>Citrobacter koseri</i>	0	24
306	<i>Clostridium</i> sp. CAG:221	0	23
307	<i>Veillonella tobetsuensis</i>	0	23
308	<i>Collinsella</i> sp. TF06-26	144	23
309	<i>Prevotella</i> sp. P2-180	0	23
310	<i>Bacteroides intestinalis</i> CAG:564	0	23
311	<i>Lachnoclostridium edouardi</i>	0	23
312	<i>Eggerthella</i> sp. 1_3_56FAA	25	22
313	<i>Klebsiella</i> sp. MS 92-3	24	22
314	<i>Ruminococcus faecis</i>	39	22
315	<i>Bacteroides</i> sp. 3_1_19	0	22
316	<i>Bacteroides stercoris</i> CAG:120	0	22
317	<i>Bacteroides</i> sp. 1_1_14	170	21
318	<i>Parabacteroides johnsonii</i>	0	21
319	<i>Weissella cibaria</i>	0	21
320	<i>Prevotella</i> sp. P4-67	0	21
321	<i>Intestinibacter bartlettii</i>	0	21
322	Lachnospiraceae bacterium 6_1_63FAA	21	21
323	<i>Eubacterium siraeum</i> CAG:80	0	21
324	<i>Salmonella enterica</i>	0	21
325	<i>Prevotella</i> sp. P4-51	0	21
326	<i>Clostridium botulinum</i>	0	20
327	<i>Clostridium nexile</i> CAG:348	0	20
328	<i>Prevotellamassilia timonensis</i>	0	20
329	<i>Prevotella</i> sp. P5-125	0	20
330	Clostridiales bacterium VE202-09	0	20
331	<i>Shigella flexneri</i>	0	20
332	<i>Eubacterium</i> sp. CAG76_36_125	0	20
333	<i>Prevotella</i> sp. P5-119	0	20
334	<i>Prevotella ruminicola</i>	0	19
335	<i>Prevotella lascolaii</i>	0	19
336	<i>Prevotella buccae</i>	0	19
337	<i>Clostridium butyricum</i>	0	19
338	<i>Blautia</i> sp. An46	20	19
339	<i>Eggerthella</i> sp. HGA1	19	19
340	<i>Coprococcus comes</i>	85	18

341	<i>Prevotella</i> sp. CAG:1185	0	18
342	Lachnospiraceae bacterium 5_1_63FAA	35	18
343	<i>Bifidobacterium ruminantium</i>	263	18
344	<i>Bacteroides finegoldii</i>	0	18
345	<i>Bacteroides</i> sp. 4_3_47FAA	0	17
346	<i>Bacteroides</i> sp. 3_1_40A	0	17
347	<i>Bacteroides</i> sp. CAG:530	0	17
348	Lachnospiraceae bacterium CAG:364	15	16
349	<i>Prevotella</i> sp. CAG:1124	0	16
350	<i>Bacteroides vulgatus</i> CAG:6	0	16
351	<i>Prevotella baroniae</i>	0	16
352	<i>Anaerotignum lactatifermentans</i>	0	16
353	<i>Blautia hansenii</i>	14	15
354	<i>Prevotella</i> sp. CAG:487	0	15
355	<i>Prevotella timonensis</i>	0	15
356	<i>Ruminococcus gnavus</i> CAG:126	17	15
357	<i>Megasphaera</i> sp. NM10	0	15
358	<i>Prevotella buccalis</i>	0	14
359	<i>Prevotella</i> sp. P5-92	0	14
360	<i>Streptococcus infantarius</i>	0	14
361	<i>Bacteroides</i> sp. AR20	0	14
362	<i>Enterobacter</i> sp. BIDMC 29	0	14
363	Lachnospiraceae bacterium 2_1_58FAA	13	14
364	<i>Bacteroides uniformis</i> CAG:3	18	14
365	<i>Prevotella</i> sp. CAG:5226	0	14
366	<i>Bacteroides sartorii</i>	0	14
367	<i>Blautia schinkii</i>	0	14
368	[<i>Clostridium</i>] <i>lavalense</i>	0	13
369	<i>Prevotella intermedia</i>	0	13
370	<i>Bacteroides mediterraneensis</i>	0	13
371	<i>Veillonella</i> sp. 6_1_27	0	13
372	<i>Lactococcus lactis</i>	140	13
373	<i>Bacteroides faecis</i>	0	12
374	Lachnospiraceae bacterium JC7	37	12
375	<i>Prevotella histicola</i>	0	11
376	<i>Sutterella</i> sp. KLE1602	0	11
377	<i>Prevotella oralis</i>	0	11
378	<i>Bifidobacterium bifidum</i> CAG:234	0	10
379	<i>Prevotella</i> sp. P4-119	0	10
380	<i>Prevotella paludivivens</i>	0	10
381	<i>Prevotella</i> sp. tc2-28	0	10
382	<i>Prevotella</i> sp. P5-126	0	10
383	<i>Prevotella</i> sp. 109	0	10

384	<i>Prevotella brevis</i>	0	10
385	<i>Prevotella oris</i>	0	9
386	<i>Prevotella</i> sp. DNF00663	0	9
387	<i>Prevotella oryzae</i>	0	9
388	<i>Prevotella</i> sp. CAG:255	0	9
389	<i>Prevotella</i> sp. S7-1-8	0	9
390	<i>Prevotella dentalis</i>	0	9
391	<i>Prevotella</i> sp. KH2C16	0	9
392	<i>Prevotella</i> sp. CAG:1058	0	9
393	<i>Prevotella maculosa</i>	0	9
394	<i>Prevotella bergensis</i>	0	9
395	Ruminococcaceae bacterium D16	14	8
396	<i>Dorea formicigenerans</i> CAG:28	31	0
397	<i>Rummeliibacillus stabekisii</i>	41	0
398	<i>Bifidobacterium pseudolongum</i>	30	0
399	<i>Clostridium</i> sp. CAG:138	415	0
400	<i>Blautia</i> sp. CAG:257	39	0
401	<i>Enterococcus</i> sp. HMSC072H05	14	0
402	<i>Bacteroides dorei</i> CAG:222	22	0
403	<i>Bacteroides</i> sp. CAG:189	67	0
404	<i>[Desulfotomaculum] guttoideum</i>	17	0
405	<i>Tissierellia</i> bacterium S5-A11	21	0
406	<i>Ruminococcus</i> sp. CAG:382	21	0
407	<i>Peptococcus niger</i>	27	0
408	<i>Oribacterium</i> sp. C9	24	0
409	<i>Olsenella provencensis</i>	22	0
410	<i>Collinsella</i> sp. CAG:289	85	0
411	<i>Ruthenibacterium lactatiformans</i>	63	0
412	<i>Acinetobacter</i> sp. NIPH 899	71	0
413	<i>Oribacterium</i> sp. WCC10	33	0
414	<i>Clostridium</i> sp. CAG:609	259	0
415	<i>Clostridium</i> sp. CAG:571	33	0
416	<i>Butyricimonas virosa</i>	146	0
417	<i>Slackia piriformis</i>	52	0
418	Firmicutes bacterium CAG:110	278	0
419	<i>Achromobacter xylosoxidans</i>	12	0
420	<i>Lactobacillus mucosae</i>	321	0
421	<i>Clostridium</i> sp. CAG:433	54	0
422	<i>Clostridium</i> sp. CAG:226	155	0
423	<i>Solobacterium moorei</i>	27	0
424	bacterium LF-3	22	0
425	<i>Anaerococcus prevotii</i>	17	0
426	<i>Olsenella</i> sp. An188	24	0

427	<i>Clostridium minihomine</i>	16	0
428	<i>Acinetobacter</i> sp. NIPH 2171	133	0
429	<i>Anaeromassilibacillus senegalensis</i>	19	0
430	<i>Dialister invisus</i>	60	0
431	Firmicutes bacterium CAG:646	12	0
432	bacterium MS4	32	0
433	<i>Gordonibacter pamelaee</i>	82	0
434	<i>Parabacteroides</i> sp. HGS0025	18	0
435	<i>Anaeromassilibacillus</i> sp. Marseille-P3371	12	0
436	<i>Peptoniphilus senegalensis</i>	37	0
437	<i>Clostridium</i> sp. 7_2_43FAA	17	0
438	<i>Peptoniphilus duerdenii</i>	16	0
439	<i>Comamonas testosteroni</i>	90	0
440	<i>Anaeromassilibacillus</i> sp. An200	9	0
441	<i>Lysinibacillus</i> sp. ZYM-1	44	0
442	<i>Mycoplasma</i> sp. CAG:472	53	0
443	<i>Clostridium</i> sp. L2-50	37	0
444	<i>Collinsella</i> sp. MS5	44	0
445	Firmicutes bacterium CAG:555	26	0
446	<i>Bacillus kochii</i>	12	0
447	<i>Faecalibacterium</i> sp. CAG:74_58_120	295	0
448	<i>Clostridium</i> sp. CAG:793	270	0
449	<i>Neglecta timonensis</i>	26	0
450	[<i>Clostridium</i>] <i>celerecrescens</i>	750	0
451	<i>Clostridium</i> sp. ASBs410	20	0
452	<i>Enterococcus casseliflavus</i>	251	0
453	<i>Eggerthella timonensis</i>	23	0
454	<i>Faecalibacterium</i> sp. CAG:74	439	0
455	Clostridiales bacterium Marseille-P2846	187	0
456	<i>Anaerococcus vaginalis</i>	30	0
457	<i>Anaeromassilibacillus</i> sp. An250	39	0
458	<i>Acinetobacter</i> sp. CIP 101934	13	0
459	Firmicutes bacterium CAG:24	145	0
460	Firmicutes bacterium HGW-Firmicutes-16	22	0
461	<i>Barnesiella intestinihominis</i>	121	0
462	<i>Enterococcus gallinarum</i>	214	0
463	<i>Lysinibacillus</i> sp. FJAT-14222	245	0
464	<i>Alistipes shahii</i>	40	0
465	<i>Peptoniphilus timonensis</i>	41	0
466	<i>Akkermansia</i> sp. CAG:344	85	0
467	<i>Lagierella massiliensis</i>	39	0
468	<i>Acinetobacter</i> sp. LCT-H3	26	0
469	<i>Drancourtella massiliensis</i>	12	0

470	<i>Subdoligranulum</i> sp. 4_3_54A2FAA	88	0
471	<i>Peptoniphilus harei</i>	30	0
472	<i>Ruminococcus</i> sp. CAG:9-related_41_34	11	0
473	<i>Ruminococcus lactaris</i>	22	0
474	Firmicutes bacterium CAG:24053_14	48	0
475	<i>Enterorhabdus caecimuris</i>	28	0
476	<i>Alistipes</i> sp. Marseille-P2431	21	0
477	<i>Bacteroides thetaiotaomicron</i> CAG:40	42	0
478	<i>Ruminococcus flavefaciens</i>	30	0
479	<i>Blautia</i> sp. Marseille-P3087	46	0
480	<i>Oribacterium</i> sp. P6A1	25	0
481	<i>Clostridium</i> sp. C105KSO15	124	0
482	<i>Achromobacter</i> sp. Root170	21	0
483	<i>Clostridium</i> sp. CAG:264	101	0
484	<i>Lysinibacillus sphaericus</i>	108	0
485	<i>Clostridium</i> sp. CAG:1024	39	0
486	<i>Urinacoccus</i> sp. Marseille-P3926	136	0
487	<i>Enterococcus</i> sp. FDAARGOS_375	30	0
488	Clostridiales bacterium	81	0
489	<i>Lysinibacillus boronitolerans</i>	27	0
490	<i>Collinsella bouchesdurhonensis</i>	32	0
491	<i>Rummeliibacillus pycnus</i>	562	0
492	Erysipelotrichaceae bacterium NK3D112	33	0
493	<i>Collinsella</i> sp. 60_9	26	0
494	<i>Alistipes obesi</i>	352	0
495	<i>Dialister invisus</i> CAG:218	290	0
496	<i>Eubacterium</i> sp. CAG:161	21	0
497	<i>Bacteroides</i> sp. 3_1_33FAA	22	0
498	Firmicutes bacterium CAG:110_56_8	45	0
499	uncultured <i>Coprococcus</i> sp.	83	0
500	<i>Paraclostridium bifermentans</i>	17	0
501	<i>Monoglobus pectinilyticus</i>	24	0
502	<i>Oribacterium</i> sp. NK2B42	20	0
503	<i>Lactobacillus brevis</i>	32	0
504	<i>Senegalimassilia anaerobia</i>	122	0
505	<i>Acinetobacter baumannii</i>	228	0
506	<i>Clostridium</i> sp. CAG:567	236	0
507	<i>Coprococcus</i> sp. ART55/1	22	0
508	<i>Peptoniphilus</i> sp. HMSC075B08	105	0
509	<i>Enterococcus pallens</i>	17	0
510	<i>Fingoldia magna</i>	82	0
511	<i>Lysinibacillus</i> sp. FJAT-14745	97	0
512	<i>Coprobacillus</i> sp. 8_1_38FAA	10	0

513	<i>Peptoniphilus</i> sp. oral taxon 375	118	0
514	uncultured <i>crAssphage</i>	31	0
515	<i>Gordonibacter massiliensis</i>	20	0
516	<i>Olsenella</i> sp. An290	19	0
517	<i>Peptoniphilus grossensis</i>	71	0
518	<i>Bacteroides</i> sp. 9_1_42FAA	31	0
519	Firmicutes bacterium CAG:176_63_11	30	0
520	<i>Enterococcus faecalis</i>	238	0
521	<i>Lactobacillus plantarum</i>	259	0
522	<i>Lysinibacillus fusiformis</i>	42	0
523	<i>Eubacterium</i> sp. 38_16	21	0
524	<i>Peptoniphilus</i> sp. HMSC062D09	42	0
525	<i>Alistipes</i> sp. CAG:53	39	0
526	Bacteroidales bacterium 43_8	22	0
527	<i>Peptoniphilus phoceensis</i>	55	0
528	<i>Peptoniphilus</i> sp. BV3AC2	12	0
529	<i>Clostridium</i> sp. CAG:302	267	0
530	<i>Gordonibacter urolithinifaciens</i>	567	0
531	<i>Acinetobacter</i> sp. YZS-X1-1	115	0
532	<i>Lysinibacillus xylanilyticus</i>	242	0
533	<i>Acinetobacter schindleri</i>	91	0
534	<i>Bacteroides</i> sp. CAG:20	60	0
535	<i>Clostridium</i> sp. CAG:269	67	0
536	<i>Alistipes</i> sp. cv1	20	0
537	<i>Roseburia inulinivorans</i> CAG:15	111	0
538	<i>Urmitella timonensis</i>	24	0
539	<i>Olsenella</i> sp. An293	20	0
540	<i>Eisenbergiella tayi</i>	73	0
541	<i>Enterococcus saccharolyticus</i>	16	0
542	<i>Parabacteroides goldsteinii</i>	602	0
543	<i>Marvinbryantia formatexigens</i>	22	0
544	<i>Lysinibacillus macroides</i>	49	0
545	<i>Bacteroides salyersiae</i>	248	0
546	<i>Eubacterium</i> sp. CAG:146	52	0
547	<i>Peptoniphilus coxii</i>	318	0
548	<i>Libanicoccus massiliensis</i>	25	0
549	<i>Roseburia</i> sp. CAG:182	36	0
550	<i>Clostridium</i> sp. CAG:413	26	0
551	<i>Dorea</i> sp. AGR2135	24	0
552	<i>Acinetobacter lwoffii</i>	12	0

Supplementary Table 4. Species level: Mean abundance at baseline and post-intervention in Group 2 (Nichi Glucan)

S.No	Species	Mean abundance	
		Baseline	Post-Intervention
1	<i>Faecalibacterium prausnitzii</i>	3613	6596
2	<i>Bifidobacterium longum</i>	2012	1446
3	Firmicutes bacterium CAG:124	1684	1308
4	<i>Trichosporon asahii</i>	1683	0
5	<i>Bifidobacterium adolescentis</i>	1376	931
6	<i>Escherichia coli</i>	1264	471
7	uncultured Clostridium sp.	1062	2726
8	<i>Collinsella aerofaciens</i>	1048	729
9	uncultured Blautia sp.	981	879
10	Ruminococcus sp. CAG:177	977	565
11	Firmicutes bacterium CAG:103	972	925
12	<i>Bacteroides fragilis</i>	960	1186
13	<i>Blautia obeum</i>	877	777
14	<i>Gemmiger formicilis</i>	865	1022
15	Firmicutes bacterium CAG:170	847	989
16	<i>Dorea longicatena</i>	819	785
17	Firmicutes bacterium CAG:110	787	604
18	<i>Clostridium sp. CAG:226</i>	779	321
19	<i>Clostridium sp. CAG:138</i>	743	528
20	uncultured Ruminococcus sp.	726	913
21	<i>Bacteroides uniformis</i>	707	512
22	<i>Alistipes sp. CAG:435</i>	690	721
23	<i>Hungatella hathewayi</i>	681	171
24	<i>Holdemanella bififormis</i>	649	546
25	Oscillibacter sp. CAG:241	634	419
26	Firmicutes bacterium CAG:176	617	945
27	Firmicutes bacterium CAG:83	612	400
28	<i>Subdoligranulum sp. 60_17</i>	588	734
29	<i>Pichia kudriavzevii</i>	582	0
30	<i>Bacteroides thetaiotaomicron</i>	581	562
31	<i>Prevotella copri</i>	568	1458
32	Eubacterium sp. CAG:202	536	0
33	<i>Enterococcus faecium</i>	528	0
34	<i>Klebsiella pneumoniae</i>	524	44
35	<i>Rummeliibacillus pycnus</i>	516	0
36	<i>Senegalimassilia anaerobia</i>	505	56
37	<i>[Eubacterium] rectale</i>	499	1165
38	Firmicutes bacterium CAG:114	489	386
39	<i>Bifidobacterium bifidum</i>	476	418

40	<i>Bacteroides ovatus</i>	472	448
41	<i>Bacteroides vulgatus</i>	467	375
42	<i>Blautia wexlerae</i>	464	486
43	<i>Lactobacillus ruminis</i>	464	634
44	<i>[Ruminococcus] torques</i>	452	347
45	<i>Fusicatenibacter saccharivorans</i>	450	624
46	<i>[Eubacterium] hallii</i>	442	218
47	<i>Olsenella umbonata</i>	441	37
48	<i>Desulfovibrio piger</i>	434	303
49	<i>Dialister</i> sp. CAG:486	433	447
50	uncultured <i>Eubacterium</i> sp.	429	294
51	<i>Enterococcus avium</i>	425	0
52	<i>Faecalibacterium</i> sp. CAG:74	415	485
53	<i>Bacteroides caccae</i>	398	152
54	<i>Oscillibacter</i> sp. CAG:241_62_21	392	469
55	<i>Romboutsia timonensis</i>	388	112
56	<i>Eubacterium</i> sp. CAG:180	379	338
57	<i>Parabacteroides merdae</i>	377	101
58	<i>Pediococcus pentosaceus</i>	371	0
59	<i>Enterococcus faecalis</i>	362	0
60	Clostridiales bacterium Marseille-P2846	358	355
61	<i>Clostridium</i> sp. CAG:221	355	326
62	<i>Butyricoccus</i> sp. BB10	334	177
63	<i>[Clostridium] celerecrescens</i>	333	0
64	Lentisphaerae bacterium GWF2_44_16	332	307
65	<i>[Clostridium] bolteae</i>	331	43
66	Clostridiales bacterium 42_27	329	463
67	<i>Prevotella</i> sp. CAG:279	326	754
68	<i>Bifidobacterium</i> sp. N5G01	325	383
69	Firmicutes bacterium CAG:129	324	380
70	<i>Cloacibacillus porcorum</i>	322	248
71	<i>Clostridium</i> sp. CAG:1024	319	488
72	<i>Prevotella copri</i> CAG:164	318	771
73	<i>Catenibacterium mitsuokai</i>	312	274
74	<i>Eggerthella lenta</i>	309	60
75	<i>Mycoplasma</i> sp. CAG:956	306	117
76	<i>Oscillibacter</i> sp. ER4	302	587
77	<i>Roseburia faecis</i>	301	662
78	<i>Coralimargarita</i> sp. CAG:312	292	338
79	Clostridiales bacterium 52_15	290	332
80	<i>Catenibacterium</i> sp. CAG:290	287	180
81	<i>Pediococcus acidilactici</i>	282	0
82	<i>Bacteroides dorei</i>	281	357

83	Clostridiales bacterium 59_14	280	386
84	Firmicutes bacterium CAG:176_63_11	280	400
85	<i>Alistipes putredinis</i>	278	201
86	<i>Odoribacter splanchnicus</i>	277	129
87	bacterium OL-1	275	15
88	<i>Parabacteroides</i> sp. SN4	274	249
89	<i>[Eubacterium] eligens</i>	273	552
90	<i>Alistipes indistinctus</i>	272	13
91	<i>Alistipes obesi</i>	272	0
92	<i>Clostridium</i> sp. CAG:510	270	449
93	<i>Dialister</i> sp. CAG:357	270	360
94	<i>Faecalibacterium</i> sp. CAG:74_58_120	264	368
95	<i>Lactobacillus brevis</i>	262	0
96	<i>Bifidobacterium ruminantium</i>	261	257
97	<i>Anaerostipes hadrus</i>	260	422
98	<i>Enterococcus casseliflavus</i>	259	0
99	<i>Cloacibacillus</i> sp. An23	257	0
100	<i>Bacteroides plebeius</i>	250	250
101	<i>Weissella confusa</i>	249	12
102	<i>Lactobacillus plantarum</i>	249	0
103	<i>Bacteroides</i> sp. CAG:545	246	379
104	<i>Clostridium</i> sp. CAG:452	245	120
105	uncultured <i>Faecalibacterium</i> sp.	243	437
106	<i>Collinsella</i> sp. 4_8_47FAA	239	166
107	Firmicutes bacterium CAG:555	237	281
108	<i>Ruminococcus</i> sp. CAG:724	236	367
109	<i>Roseburia inulinivorans</i>	233	1197
110	Lentisphaerae bacterium GWF2_45_14	232	228
111	<i>Bacteroides xylanisolvens</i>	232	285
112	uncultured <i>Butyricoccus</i> sp.	230	995
113	<i>Butyricimonas virosa</i>	230	0
114	<i>Bacteroides intestinalis</i>	230	135
115	<i>Collinsella</i> sp. CAG:166	228	187
116	<i>Ruminococcus</i> sp. CAG:488	225	211
117	<i>Coprococcus catus</i>	225	412
118	<i>Klebsiella aerogenes</i>	224	0
119	<i>Phascolarctobacterium</i> sp. CAG:207	220	21
120	<i>Acidiphilium</i> sp. CAG:727	219	555
121	<i>Parabacteroides gordonii</i>	217	0
122	<i>[Eubacterium] siraeum</i>	212	189
123	<i>Adlercreutzia equolifaciens</i>	210	334
124	<i>Butyrivibrio</i> sp. CAG:318	208	0
125	<i>Blautia</i> sp. CAG:37	207	203

126	<i>Clostridium</i> sp. CAG:448	203	192
127	<i>Bacteroides salyersiae</i>	203	193
128	<i>Coprobaecillus</i> sp. CAG:235	197	145
129	Clostridiales bacterium	194	147
130	<i>Bifidobacterium pseudocatenulatum</i>	194	174
131	<i>Collinsella</i> sp. TF06-26	189	155
132	<i>Alistipes</i> sp. CAG:53	189	180
133	<i>Clostridium</i> sp. CAG:571	189	14
134	<i>Sutterella</i> sp. CAG:397	188	193
135	<i>Libanicoccus massiliensis</i>	188	119
136	<i>Succinatimonas</i> sp. CAG:777	187	376
137	<i>Subdoligranulum variabile</i>	187	244
138	<i>Anaerotruncus</i> sp. CAG:390	185	275
139	<i>Bifidobacterium angulatum</i>	185	332
140	<i>Angelakisella massiliensis</i>	184	79
141	<i>Alistipes senegalensis</i>	183	57
142	<i>Megamonas funiformis</i>	182	175
143	<i>Ruminococcus obeum</i> CAG:39	180	137
144	<i>Acidaminococcus fermentans</i>	180	199
145	<i>Lactobacillus mucosae</i>	178	0
146	Firmicutes bacterium CAG:129_59_24	174	400
147	<i>Chlamydia trachomatis</i>	174	127
148	Lentisphaerae bacterium GWF2_52_8	172	173
149	<i>Ruminococcus bromii</i>	172	301
150	<i>Eubacterium</i> sp. CAG:581	171	148
151	<i>Clostridium</i> sp. CAG:433	170	8
152	<i>Weissella cibaria</i>	170	0
153	<i>Methanobrevibacter smithii</i>	161	159
154	<i>Enterococcus gallinarum</i>	161	0
155	Firmicutes bacterium CAG:240	159	135
156	<i>Clostridium</i> sp. CAG:302	159	20
157	<i>Bacteroides plebeius</i> CAG:211	158	160
158	Firmicutes bacterium CAG:24053_14	158	158
159	<i>Eubacterium limosum</i>	157	0
160	<i>Clostridium</i> sp. CAG:349	157	143
161	<i>Clostridium</i> sp. CAG:43	156	162
162	<i>Parabacteroides</i> sp. HGS0025	155	0
163	<i>Akkermansia muciniphila</i>	153	218
164	<i>Clostridium</i> sp. CAG:245	152	15
165	<i>Enterococcus hirae</i>	151	0
166	<i>Duodenibacillus massiliensis</i>	150	181
167	Firmicutes bacterium CAG:272	149	254
168	<i>Coprococcus eutactus</i>	148	100

169	Verrucomicrobia bacterium CAG:312_58_20	148	273
170	<i>Faecalibacterium</i> sp. CAG:82	147	398
171	<i>Lysinibacillus xylanilyticus</i>	147	0
172	Firmicutes bacterium CAG:460	144	166
173	<i>Peptoniphilus coxii</i>	141	0
174	uncultured bacterium	141	176
175	<i>Lysinibacillus</i> sp. FJAT-14222	141	0
176	<i>Bifidobacterium breve</i>	139	132
177	<i>Clostridium</i> sp. CAG:245_30_32	138	9
178	<i>Clostridium</i> sp. CAG:451	136	30
179	<i>Sutterella wadsworthensis</i>	136	279
180	<i>Parabacteroides goldsteinii</i>	135	13
181	<i>Streptococcus mutans</i>	133	0
182	<i>Roseburia hominis</i>	132	630
183	<i>Streptococcus salivarius</i>	131	110
184	<i>Alistipes</i> sp. CAG:514	131	147
185	Firmicutes bacterium CAG:137	131	72
186	<i>Roseburia</i> sp. CAG:18	130	229
187	<i>Ruminococcus</i> sp. 5_1_39BFAA	129	152
188	<i>Clostridioides difficile</i>	127	64
189	<i>Flavonifractor plautii</i>	125	221
190	<i>Gordonibacter urolithinifaciens</i>	125	0
191	Firmicutes bacterium CAG:110_56_8	123	87
192	<i>Pyramidobacter</i> sp. C12-8	122	0
193	<i>Ruminococcus</i> sp. CAG:17	122	151
194	<i>Bifidobacterium</i> sp. N4G05	119	125
195	<i>Streptococcus thermophilus</i>	118	0
196	<i>Clostridium</i> sp. CAG:568	117	204
197	<i>Blautia</i> sp. KLE 1732	115	51
198	<i>Parabacteroides merdae</i> CAG:48	114	30
199	<i>Dorea formicigenerans</i>	114	119
200	<i>Barnesiella intestinihominis</i>	112	77
201	<i>[Clostridium] clostridioforme</i>	111	124
202	<i>Intestinimonas butyriciproducens</i>	110	124
203	<i>Olsenella scatoligenes</i>	107	13
204	<i>Clostridium</i> sp. CAG:413	107	472
205	uncultured <i>Flavonifractor</i> sp.	105	138
206	<i>Clostridium</i> sp. CAG:343	104	0
207	<i>Alistipes shahii</i>	104	102
208	<i>Pyramidobacter piscolens</i>	103	0
209	Firmicutes bacterium CAG:238	103	75
210	<i>Collinsella</i> sp. CAG:289	102	0
211	<i>Bacteroides caccae</i> CAG:21	102	107

212	<i>Acinetobacter baumannii</i>	101	0
213	Lentisphaerae bacterium GWF2_50_93	100	109
214	<i>Bacteroides</i> sp. 2_2_4	97	83
215	<i>Eubacterium</i> sp. CAG:841	93	105
216	<i>Ruminococcus</i> sp. CAG:382	93	170
217	Firmicutes bacterium CAG:270	92	45
218	<i>Olsenella</i> sp. kh2p3	90	13
219	<i>Phascolarctobacterium succinatutens</i>	90	420
220	<i>Lactobacillus fermentum</i>	90	0
221	<i>Mycoplasma</i> sp. CAG:877	89	41
222	<i>Bacteroides intestinalis</i> CAG:564	87	60
223	<i>Oxalobacter formigenes</i>	87	0
224	<i>Eisenbergiella tayi</i>	86	99
225	<i>Parabacteroides distasonis</i>	86	157
226	Lentisphaerae bacterium GWF2_49_21	84	96
227	<i>Dorea longicatena</i> CAG:42	84	83
228	<i>Ruminococcus</i> sp. CAG:563	83	191
229	<i>Olsenella</i> sp. KH3B4	83	16
230	<i>Lactobacillus ruminis</i> CAG:367	82	106
231	<i>Blautia</i> sp. CAG:37_48_57	82	140
232	<i>Alistipes</i> sp. 56_sp_Nov_56_25	82	62
233	<i>Enterococcus thailandicus</i>	80	0
234	<i>Alistipes</i> sp. HGB5	80	0
235	<i>Blautia</i> sp. CAG:237	78	207
236	<i>Bacteroides stercoris</i>	77	19
237	Firmicutes bacterium HGW-Firmicutes-9	75	94
238	<i>Clostridium</i> sp. CAG:1193	75	125
239	<i>Roseburia</i> sp. CAG:18_43_25	75	173
240	Firmicutes bacterium HGW-Firmicutes-16	74	73
241	<i>Oscillibacter</i> sp. 57_20	74	403
242	<i>Olsenella provencensis</i>	74	7
243	<i>Olsenella</i> sp. An188	74	0
244	<i>Anaerotruncus colihominis</i>	73	71
245	<i>Clostridium</i> sp. CAG:524	73	71
246	<i>Bacteroides coprocola</i> CAG:162	72	79
247	Firmicutes bacterium CAG:41	72	310
248	<i>Coprococcus comes</i>	71	125
249	<i>Ruminococcus</i> sp. CAG:90	71	9
250	<i>Clostridium</i> sp. CAG:492	70	0
251	<i>Pygmaibacter massiliensis</i>	69	0
252	<i>Lysinibacillus sphaericus</i>	69	0
253	<i>Roseburia intestinalis</i>	69	1218
254	<i>Ruminococcus flavefaciens</i>	69	267

255	uncultured <i>Coprococcus</i> sp.	68	22
256	<i>Lactococcus lactis</i>	68	0
257	uncultured <i>Oscillibacter</i> sp.	66	87
258	<i>Gordonibacter pamelaiae</i>	65	0
259	<i>Bacteroides eggerthii</i>	64	0
260	<i>Bifidobacterium kashiwanohense</i>	64	82
261	Clostridiales bacterium 41_12_two_minus	63	195
262	<i>Collinsella</i> sp. 60_9	63	17
263	<i>Allisonella histaminiformans</i>	62	54
264	<i>Megasphaera elsdenii</i>	61	262
265	<i>Lysinibacillus</i> sp. FJAT-14745	61	0
266	<i>Ruminococcus</i> sp. CAG:9	60	59
267	<i>Urinacoccus</i> sp. Marseille-P3926	60	0
268	<i>Bacteroides coprocola</i>	60	99
269	<i>Olsenella</i> sp. An285	59	0
270	<i>Acinetobacter</i> sp. NIPH 2171	59	0
271	<i>Clostridium</i> sp. CAG:7	59	396
272	<i>Bifidobacterium catenulatum</i>	58	75
273	<i>Olsenella</i> sp. An290	58	0
274	<i>Eubacterium hallii</i> CAG:12	57	41
275	<i>Streptococcus pneumoniae</i>	57	8
276	<i>Collinsella</i> sp. MS5	56	0
277	<i>Eggerthella</i> sp. CAG:209	56	0
278	<i>Bacteroides</i> sp. CAG:20	56	37
279	<i>Clostridium</i> sp. C105KSO15	55	0
280	<i>Bacteroides</i> sp. CAG:189	55	36
281	<i>Clostridium</i> sp. CAG:594	55	0
282	<i>Bacteroides</i> sp. AR29	55	0
283	<i>Subdoligranulum</i> sp. 4_3_54A2FAA	54	65
284	<i>Ruminococcus bicirculans</i>	54	172
285	<i>Oscillibacter</i> sp. 1-3	53	70
286	<i>Blautia</i> sp. Marseille-P3087	53	39
287	<i>Turicibacter sanguinis</i>	52	26
288	<i>Peptoniphilus</i> sp. oral taxon 375	52	0
289	<i>Olsenella</i> sp. An293	52	0
290	<i>Bacteroides intestinalis</i> CAG:315	51	32
291	<i>Acinetobacter</i> sp. YZS-X1-1	51	0
292	<i>Ruthenibacterium lactatiformans</i>	51	69
293	<i>Coprococcus eutactus</i> CAG:665	51	0
294	Firmicutes bacterium CAG:321	51	69
295	<i>Bacteroides</i> sp. D20	50	32
296	<i>Clostridium</i> sp. CAG:264	50	38
297	<i>Blautia producta</i>	49	0

298	Firmicutes bacterium CAG:176_59_8	49	90
299	<i>Bacteroides</i> sp. 1_1_14	48	18
300	Erysipelotrichaceae bacterium 6_1_45	48	0
301	<i>Peptoniphilus</i> sp. HMSC075B08	47	0
302	<i>Selenomonas bovis</i>	47	168
303	<i>Bacteroides</i> sp. 4_1_36	45	27
304	<i>Slackia piriformis</i>	44	0
305	<i>Enterobacter cloacae</i>	44	0
306	<i>[Clostridium] citroniae</i>	43	0
307	Ruminococcus sp. CAG:254	43	486
308	<i>Alistipes finegoldii</i>	43	143
309	<i>Haemophilus parainfluenzae</i>	43	87
310	<i>Alistipes onderdonkii</i>	42	14
311	<i>Actinomyces</i> sp. HPA0247	42	0
312	<i>Roseburia</i> sp. CAG:182	42	317
313	<i>Parabacteroides</i> sp. merdae-related_45_40	41	10
314	butyrate-producing bacterium SS3/4	41	248
315	<i>Collinsella vaginalis</i>	41	8
316	<i>Faecalibacterium</i> sp. CAG:82-related_59_9	41	99
317	<i>Acinetobacter schindleri</i>	40	0
318	<i>Bacteroides oleiciplenus</i>	40	55
319	<i>Megamonas rupellensis</i>	40	35
320	<i>Blautia</i> sp. Marseille-P2398	40	44
321	<i>Clostridium</i> sp. CAG:81	40	238
322	<i>Comamonas kerstersii</i>	40	0
323	<i>Eggerthella</i> sp. 1_3_56FAA	39	0
324	<i>Enterobacter hormaechei</i>	39	0
325	<i>Rummelibacillus stabekisii</i>	39	0
326	<i>Acinetobacter bereziniae</i>	39	0
327	<i>Lactobacillus pentosus</i>	39	0
328	<i>Eubacterium eligens</i> CAG:72	39	102
329	<i>Oscillibacter valericigenes</i>	38	58
330	<i>Bacteroides nordii</i>	38	0
331	<i>Clostridium</i> sp. CAG:127	37	628
332	<i>Eggerthella</i> sp. HGA1	37	0
333	<i>[Ruminococcus] gnavus</i>	37	96
334	Ruminococcus sp. CAG:108	37	100
335	<i>Olsenella mediterranea</i>	37	0
336	<i>Oscillibacter</i> sp. PC13	37	56
337	<i>Subdoligranulum</i> sp. CAG:314	37	36
338	<i>Oscillibacter ruminantium</i>	37	68
339	<i>Roseburia inulinivorans</i> CAG:15	37	161
340	<i>Finegoldia magna</i>	36	0

341	<i>Bacteroides</i> sp. 3_1_23	36	42
342	<i>Peptococcus niger</i>	35	0
343	<i>Bacteroides</i> sp. HPS0048	35	0
344	<i>Oribacterium</i> sp. WCC10	35	15
345	Firmicutes bacterium CAG:552_39_19	34	68
346	<i>Paraprevotella clara</i> CAG:116	34	0
347	Clostridiales bacterium 41_21_two_genomes	34	338
348	<i>Prevotella</i> sp. CAG:604	34	247
349	<i>Intestinimonas massiliensis</i>	34	34
350	<i>Clostridium</i> sp. L2-50	34	123
351	<i>Clostridium</i> sp. CAG:1000	34	0
352	Firmicutes bacterium CAG:24	33	9
353	<i>Enterococcus</i> sp. FDAARGOS_375	33	0
354	<i>Prevotella</i> sp. CAG:891	33	34
355	<i>Parabacteroides</i> sp. D13	33	60
356	<i>Enterococcus</i> sp. HMSC05C03	33	0
357	<i>Eubacterium siraeum</i> CAG:80	33	39
358	<i>Megasphaera</i> sp. BL7	33	74
359	<i>Bacteroides</i> sp. D22	33	41
360	<i>Lysinibacillus macroides</i>	32	0
361	<i>Klebsiella</i> sp. MS 92-3	32	0
362	<i>Sporobacter termitidis</i>	32	36
363	<i>Acinetobacter</i> sp. NIPH 899	32	0
364	<i>Pseudoflavonifractor capillosus</i>	31	31
365	<i>Lysinibacillus fusiformis</i>	31	0
366	<i>Peptoniphilus grossensis</i>	31	0
367	Firmicutes bacterium CAG:102	31	206
368	<i>Ruminococcus albus</i>	31	33
369	<i>Cutaneotrichosporon oleaginosum</i>	31	0
370	Firmicutes bacterium HGW-Firmicutes-21	31	0
371	<i>Marvinbryantia formatexigens</i>	31	28
372	<i>Collinsella bouchedurhonensis</i>	31	0
373	<i>Acidovorax</i> sp. 12322-1	31	0
374	Firmicutes bacterium CAG:321_26_22	31	51
375	<i>Corallocooccus</i> sp. CAG:1435	30	143
376	<i>Bacteroides</i> sp. 3_1_40A	30	17
377	Ruminococcaceae bacterium D5	30	31
378	Bacteroidales bacterium 43_8	30	0
379	<i>Anaerotruncus rubiinfantis</i>	30	14
380	<i>Ruminococcus champanellensis</i>	30	57
381	<i>Clostridium</i> sp. CAG:349_48_7	30	25
382	<i>Eubacterium rectale</i> CAG:36	29	95
383	<i>Clostridium</i> sp. CAG:91	29	107

384	<i>Butyricimonas</i> sp. An62	29	0
385	Clostridiales bacterium GWF2_36_10	29	0
386	<i>Alistipes fingoldii</i> CAG:68	29	0
387	<i>Flavonifractor</i> sp. An10	28	30
388	<i>Lactobacillus salivarius</i>	28	0
389	<i>Butyricimonas synergistica</i>	28	0
390	Firmicutes bacterium CAG:65	28	160
391	<i>Prevotella</i> sp. CAG:5226	28	188
392	<i>Romboutsia ilealis</i>	27	8
393	<i>Eubacterium</i> sp. CAG:146	27	27
394	<i>Clostridium</i> sp. CAG:609	27	19
395	<i>Blautia schinkii</i>	27	0
396	<i>Methanosphaera stadtmanae</i>	27	0
397	<i>Alistipes timonensis</i>	26	0
398	<i>Lysinibacillus</i> sp. ZYM-1	26	0
399	Lachnospiraceae bacterium JC7	26	17
400	<i>Bacteroides</i> sp. CAG:709	26	140
401	<i>Terrisporobacter glycolicus</i>	26	0
402	<i>Bacteroides</i> sp. 3_1_19	25	22
403	bacterium LF-3	25	20
404	<i>Bacteroides stercorisoris</i>	24	31
405	<i>Peptoniphilus phoceensis</i>	24	0
406	<i>Oribacterium</i> sp. P6A1	24	0
407	<i>Prevotellamassilia timonensis</i>	24	158
408	<i>Ruminococcus faecis</i>	24	10
409	<i>Anaerofilum</i> sp. An201	24	35
410	<i>Dorea</i> sp. 42_8	24	17
411	<i>Eubacterium</i> sp. CAG:251	24	290
412	<i>Clostridium</i> sp. CAG:389	23	45
413	<i>Blautia</i> sp. SF-50	23	9
414	<i>Eubacterium</i> sp. CAG:76	23	76
415	Clostridiales bacterium NK3B98	23	33
416	Firmicutes bacterium ASF500	23	46
417	<i>Bacteroides bouchesdurhonensis</i>	23	0
418	<i>Eubacterium</i> sp. 38_16	22	22
419	<i>Clostridium</i> sp. HGF2	22	0
420	<i>Bacteroides</i> sp. 9_1_42FAA	22	16
421	<i>Mitsuokella jalaludinii</i>	22	280
422	<i>Paraprevotella clara</i>	22	0
423	<i>Blautia massiliensis</i>	22	7
424	Coriobacteriaceae bacterium 68-1-3	22	0
425	<i>Bacteroides</i> sp. 43_108	22	22
426	<i>Olsenella</i> sp. An270	22	0

427	<i>Isoptericola variabilis</i>	22	0
428	<i>Clostridium</i> sp. KNHs209	21	13
429	<i>Streptococcus parasanguinis</i>	21	61
430	<i>Gordonibacter massiliensis</i>	21	0
431	<i>Bilophila wadsworthia</i>	21	436
432	uncultured <i>Bacteroides</i> sp.	21	46
433	Firmicutes bacterium CAG:552	21	31
434	<i>Clostridium</i> sp. SS2/1	21	60
435	<i>Parabacteroides johnsonii</i>	21	8
436	<i>Flavonifractor</i> sp. An100	20	50
437	<i>Propionibacterium acidifaciens</i>	20	0
438	<i>Clostridium</i> sp. CAG:914	20	29
439	<i>Clostridium</i> sp. 26_22	20	0
440	<i>Bacteroides cellulosilyticus</i>	20	82
441	Ruminococcaceae bacterium D16	20	163
442	<i>Butyricoccus pullicaecorum</i>	20	30
443	<i>Actinomyces</i> sp. ICM47	20	0
444	<i>Olsenella</i> sp. Marseille-P2300	20	0
445	<i>Collinsella tanakaei</i>	20	15
446	<i>Gemmiger</i> sp. An120	19	39
447	<i>Pseudoflavonifractor</i> sp. An184	19	35
448	<i>Peptoniphilus</i> sp. HMSC062D09	19	0
449	<i>Bacteroides</i> sp. 3_1_13	19	36
450	<i>Flavonifractor</i> sp. An306	19	32
451	Firmicutes bacterium CAG:145	19	15
452	<i>Peptoniphilus timonensis</i>	18	0
453	<i>Eubacterium ventriosum</i>	18	70
454	Clostridiales bacterium 43-6	18	0
455	<i>Cloacibacillus evryensis</i>	18	0
456	<i>Akkermansia muciniphila</i> CAG:154	18	13
457	<i>Oribacterium</i> sp. C9	18	0
458	<i>Olsenella uli</i>	18	11
459	<i>Prevotella</i> sp. CAG:1092	17	299
460	<i>Slackia heliotrinireducens</i>	17	0
461	<i>Lagierella massiliensis</i>	17	0
462	Firmicutes bacterium CAG:194	17	14
463	Lachnospiraceae bacterium 28-4	17	0
464	<i>Oribacterium</i> sp. NK2B42	17	0
465	<i>Bacteroides eggerthii</i> CAG:109	17	0
466	<i>Eggerthella timonensis</i>	17	0
467	<i>Clostridium</i> sp. CAG:762	17	79
468	<i>Brachyspira</i> sp. CAG:484	17	91
469	methanogenic archaeon mixed culture ISO4-G1	17	38

470	<i>Eggerthella</i> sp. 51_9	17	0
471	<i>Ruminococcus</i> sp. CAG:379	17	27
472	<i>Bacteroides timonensis</i>	17	98
473	<i>Oscillibacter</i> sp. CAG:155	17	36
474	<i>Peptoniphilus senegalensis</i>	17	0
475	<i>Lachnospira pectinoschiza</i>	16	117
476	Firmicutes bacterium CAG:95	16	197
477	<i>Megamonas</i> sp. Calf98-2	16	10
478	<i>Massilimallia massiliensis</i>	16	14
479	<i>Anaeromassilibacillus</i> sp. An200	16	17
480	<i>Odoribacter</i> sp. 43_10	16	0
481	<i>Bacteroides mediterraneensis</i>	16	11
482	<i>Bacteroides dorei</i> CAG:222	16	7
483	<i>Bacteroides</i> sp. 4_3_47FAA	16	13
484	Firmicutes bacterium CAG:534	16	314
485	Ruminococcaceae bacterium FB2012	16	0
486	<i>Clostridium disporicum</i>	16	0
487	<i>Neglecta timonensis</i>	16	13
488	<i>Bacteroides uniformis</i> CAG:3	15	9
489	<i>Clostridium bolteae</i> CAG:59	15	0
490	<i>Agathobaculum desmolans</i>	15	61
491	<i>Bacteroides sartorii</i>	15	5
492	<i>Bacteroides</i> sp. D2	15	63
493	<i>Lachnoclostridium</i> sp. An196	15	151
494	<i>Acidaminococcus massiliensis</i>	15	0
495	<i>Raoultibacter massiliensis</i>	15	0
496	<i>Clostridium</i> sp. SN20	15	0
497	<i>Eggerthella</i> sp. YY7918	15	0
498	<i>Bacteroides</i> sp. 43_46	15	0
499	Lachnospiraceae bacterium 7_1_58FAA	15	25
500	Eggerthellaceae bacterium AT8	15	0
501	<i>Alistipes</i> sp. AL-1	15	10
502	<i>Ruminococcus</i> sp. SR1/5	15	0
503	<i>Bacteroides fragilis</i> CAG:558	15	0
504	<i>[Clostridium] thermosuccinogenes</i>	14	0
505	<i>Hydrogenoanaerobacterium saccharovorans</i>	14	14
506	<i>Alistipes</i> sp. 58_9_plus	14	0
507	<i>Eubacterium</i> sp. CAG:86	14	92
508	<i>Faecalibacterium</i> sp. CAG:1138	14	29
509	<i>Actinomyces oris</i>	14	0
510	<i>Dorea</i> sp. CAG:105	14	0
511	Eubacteriaceae bacterium CHKCI005	14	17
512	<i>Succinivibrio dextrinosolvans</i>	14	32

513	<i>Lactococcus garvieae</i>	14	0
514	<i>Bacteroides</i> sp. 1_1_30	14	33
515	[<i>Clostridium</i>] <i>asparagiforme</i>	14	9
516	<i>Ruminococcus</i> sp. CAG:9-related_41_34	14	13
517	<i>Enterococcus</i> sp. HMSC072H05	14	0
518	Firmicutes bacterium CAG:475	14	39
519	<i>Clostridium</i> sp. CAG:440	14	0
520	<i>Coprobacillus</i> sp. 8_1_38FAA	14	35
521	<i>Alloprevotella rava</i>	14	14
522	<i>Collinsella ihuae</i>	13	0
523	<i>Coprobacillus</i> sp. CAG:235_29_27	13	0
524	<i>Megasphaera</i> sp. NM10	13	39
525	<i>Enterorhabdus caecimuris</i>	13	21
526	<i>Peptoniphilus hareii</i>	13	0
527	<i>Prevotella</i> sp. CAG:755	13	13
528	<i>Ruminococcus</i> sp. CAG:579	13	0
529	<i>Paraprevotella xylaniphila</i>	13	0
530	<i>Enterococcus</i> sp. 5B7_DIV0075	12	0
531	<i>Tyzzerella nexilis</i>	12	81
532	<i>Ruminococcus</i> sp. CAG:57	12	36
533	<i>Parabacteroides</i> sp. Marseille-P3763	12	0
534	<i>Raoultibacter timonensis</i>	12	0
535	<i>Bacteroides thetaiotaomicron</i> CAG:40	12	0
536	Clostridiales bacterium SK-Y3	12	0
537	<i>Eubacterium</i> sp. 41_20	12	62
538	<i>Mobilibacterium timonense</i>	12	0
539	<i>Arabia massiliensis</i>	12	0
540	<i>Bacteroides vulgatus</i> CAG:6	12	7
541	<i>Lysinibacillus boronitolerans</i>	12	0
542	<i>Ruminococcus</i> sp. CAG:108-related_41_35	11	50
543	<i>Acinetobacter</i> sp. LCT-H3	11	0
544	<i>Odoribacter splanchnicus</i> CAG:14	11	0
545	<i>Synergistes jonesii</i>	11	0
546	<i>Olsenella profusa</i>	11	6
547	<i>Synergistes</i> sp. 3_1_syn1	11	0
548	<i>Bilophila</i> sp. 4_1_30	11	78
549	<i>Clostridium</i> sp. CAG:798	11	61
550	<i>Bacteroides</i> sp. 2_1_33B	11	0
551	<i>Prevotella</i> sp. 885	11	146
552	<i>Intestinibacter bartlettii</i>	11	13
553	<i>Enterorhabdus mucosicola</i>	10	11
554	<i>Bacteroides cellulosilyticus</i> CAG:158	10	30
555	<i>Enterococcus</i> sp. 3H8_DIV0648	10	0

556	<i>Clostridium</i> sp. CAG:269	10	115
557	<i>Candida parapsilosis</i>	10	0
558	<i>Clostridium nexile</i> CAG:348	10	74
559	<i>Weissella</i> sp. DD23	10	0
560	<i>Actinomyces dentalis</i>	9	0
561	uncultured <i>crAssphage</i>	9	9
562	<i>Tissierellia bacterium</i> S5-A11	9	0
563	<i>Clostridium</i> sp. ASBs410	9	0
564	<i>Roseburia</i> sp. CAG:471	9	119
565	<i>Paeniclostridium sordellii</i>	9	0
566	<i>Collinsella stercoris</i>	9	0
567	<i>Bacteroides coprophilus</i>	9	8
568	<i>Bacteroides</i> sp. 3_1_33FAA	9	17
569	<i>Enterococcus gilvus</i>	9	0
570	<i>Acidaminococcus</i> sp. CAG:542	8	0
571	<i>Alistipes</i> sp. CAG:29	8	30
572	<i>Prevotella</i> sp. CAG:617	8	8
573	<i>Leuconostoc lactis</i>	8	0
574	<i>Collinsella</i> sp. An2	8	0
575	<i>Actinomyces</i> sp. oral taxon 175	8	0
576	<i>Clostridiales bacterium</i> VE202-21	8	0
577	<i>Listeria monocytogenes</i>	8	0
578	<i>Clostridium</i> sp. 7_2_43FAA	8	0
579	<i>Paraclostridium bifermentans</i>	8	0
580	<i>Enterococcus pallens</i>	8	0
581	<i>[Desulfotomaculum] guttoideum</i>	7	0
582	<i>Anaerococcus prevotii</i>	7	0
583	<i>Actinomyces viscosus</i>	7	0
584	<i>Bacteroides finegoldii</i>	7	33
585	<i>Clostridium celatum</i>	7	0
586	<i>Bacteroides stercoris</i> CAG:120	7	0
587	<i>Enterococcus saccharolyticus</i>	7	0
588	<i>Enterococcus malodoratus</i>	7	0
589	<i>Clostridium</i> sp. CAG:470	7	10
590	<i>Actinomyces odontolyticus</i>	7	0
591	<i>Peptoniphilus duerdenii</i>	7	0
592	<i>Actinomyces</i> sp. ICM58	7	0
593	<i>Ruminococcus</i> sp. 37_24	7	0
594	<i>Alistipes putredinis</i> CAG:67	7	9
595	<i>Fusobacterium mortiferum</i>	7	0
596	<i>Collinsella phocaeensis</i>	7	0
597	<i>Dialister succinatiphilus</i>	7	196
598	<i>Enterococcus</i> sp. kppr-6	6	0

599	<i>Eubacterium callanderi</i>	6	0
600	<i>Sutterella wadsworthensis</i> CAG:135	6	18
601	Clostridiales bacterium 36_14	6	52
602	<i>Prevotella lascolaii</i>	6	11
603	<i>Collinsella intestinalis</i>	6	0
604	Lachnospiraceae bacterium 5_1_63FAA	6	33
605	<i>Actinomyces</i> sp. ICM39	6	0
606	<i>Acinetobacter</i> sp. CIP 101934	6	0
607	<i>Acinetobacter lwoffii</i>	5	0
608	<i>Peptoniphilus</i> sp. BV3AC2	5	0
609	<i>Bifidobacterium bifidum</i> CAG:234	5	0
610	<i>Bifidobacterium pseudocatenulatum</i> CAG:263	5	0
611	<i>Lactobacillus rhamnosus</i>	5	0
612	<i>Prevotella</i> sp. CAG:732	5	65
613	<i>Megamonas funiformis</i> CAG:377	5	0
614	<i>Megamonas hypermegale</i>	4	124
615	<i>Eubacterium</i> sp. CAG76_36_125	4	30
616	<i>Bifidobacterium adolescentis</i> CAG:119	4	18
617	<i>Roseburia</i> sp. CAG:197	0	47
618	<i>Bacteroides</i> sp. CAG:98	0	41
619	<i>Parasutterella excrementihominis</i> CAG:233	0	48
620	<i>Clostridium</i> sp. CAG:122	0	98
621	Firmicutes bacterium CAG:313	0	124
622	Clostridiales bacterium KLE1615	0	301
623	<i>Elusimicrobium</i> sp. An273	0	124
624	<i>Bifidobacterium dentium</i>	0	5
625	Clostridia bacterium UC5.1-1D1	0	8
626	<i>Tyzzereella</i> sp. Marseille-P3062	0	35
627	<i>Acidaminococcus intestini</i>	0	7
628	<i>Prevotella</i> sp. CAG:386	0	64
629	uncultured <i>Lachnospira</i> sp.	0	248
630	<i>Clostridium</i> sp. M62/1	0	10
631	<i>Sellimonas intestinalis</i>	0	23
632	<i>Clostridium</i> sp. CAG:780	0	114
633	<i>Clostridium</i> sp. AT4	0	26
634	<i>Roseburia</i> sp. CAG:380	0	16
635	<i>Ruminococcus</i> sp. CAG:330	0	23
636	<i>Clostridium</i> sp. CAG:575	0	4
637	<i>Clostridium</i> sp. CAG:62	0	74
638	Lachnospiraceae bacterium 8_1_57FAA	0	11
639	<i>Eubacterium</i> sp. CAG:603	0	22
640	Ruminococcaceae bacterium cv2	0	15
641	<i>Akkermansia</i> sp. CAG:344	0	58

642	<i>Clostridium</i> sp. 44_14	0	54
643	<i>Clostridium</i> sp. CAG:628	0	107
644	<i>Ruminococcus</i> sp. CAG:624	0	32
645	<i>Roseburia</i> sp. CAG:303	0	451
646	<i>Lactobacillus rogosae</i>	0	33
647	<i>Roseburia</i> sp. CAG:309	0	25
648	<i>Acholeplasma</i> sp. CAG:878	0	115
649	<i>Shigella sonnei</i>	0	35
650	<i>Megasphaera elsdenii</i> CAG:570	0	7
651	<i>Fusobacterium</i> sp. CAG:439	0	8
652	<i>Bifidobacterium pseudolongum</i>	0	9
653	<i>Bacteroides</i> sp. CAG:770	0	38
654	<i>Bacteroides</i> sp. 14(A)	0	11
655	<i>Anaerovorax odorimutans</i>	0	15
656	<i>Bifidobacterium merycicum</i>	0	7
657	<i>Ruminococcus callidus</i>	0	268
658	<i>Eubacterium</i> sp. CAG:252	0	27
659	<i>Clostridium</i> sp. CAG:253	0	42
660	<i>Clostridium</i> sp. ATCC BAA-442	0	20
661	<i>Coprobacillus</i> sp. 28_7	0	21
662	<i>Clostridium</i> sp. SCN 57-10	0	40
663	<i>Ruminococcus</i> sp. CAG:403	0	7
664	<i>Clostridium</i> sp. 42_12	0	14
665	Firmicutes bacterium CAG:65_45_313	0	108
666	Lachnospiraceae bacterium CAG:25	0	8
667	<i>Sutterella parvirubra</i>	0	15
668	<i>Eubacterium</i> sp. 45_250	0	17
669	Firmicutes bacterium CAG:272_52_7	0	26
670	<i>Clostridium</i> sp. 29_15	0	18
671	<i>Veillonella dispar</i>	0	94
672	<i>Bacteroides</i> sp. CAG:530	0	145
673	<i>Flavonifractor</i> sp. An82	0	15
674	Firmicutes bacterium CAG:449	0	81
675	<i>Eubacterium ramulus</i>	0	27
676	<i>Clostridium</i> sp. CAG:75	0	26
677	<i>Shigella flexneri</i>	0	10
678	<i>Coprococcus comes</i> CAG:19	0	9
679	Firmicutes bacterium CAG:341	0	52
680	Candidatus Gastranaerophilales bacterium HUM_1	0	102
681	<i>Clostridium</i> sp. CAG:813	0	49
682	Proteobacteria bacterium CAG:495	0	31
683	<i>Coprobacillus</i> sp. CAG:698	0	130
684	<i>Prevotella stercorea</i>	0	117

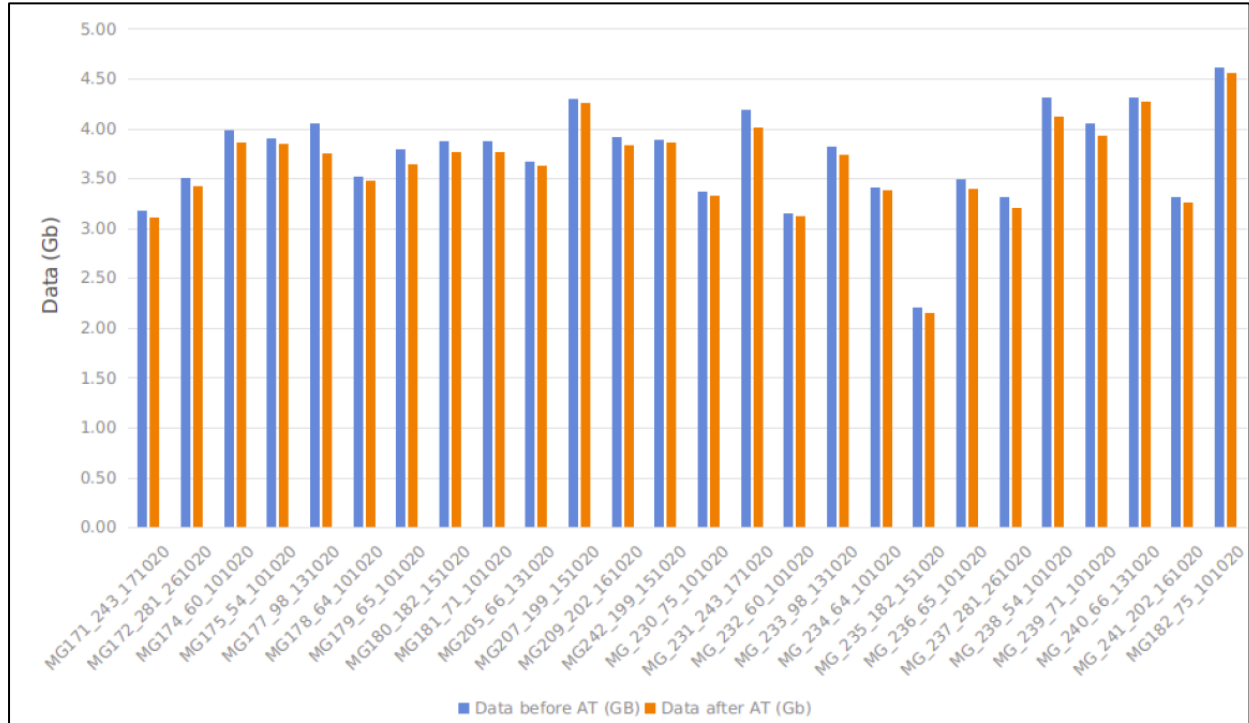
685	<i>Gemmiger</i> sp. An50	0	16
686	<i>Clostridium</i> sp. 26_21	0	12
687	<i>Clostridium</i> sp. CAG:217	0	20
688	<i>Butyrivibrio crossotus</i>	0	11
689	<i>Coprococcus</i> sp. CAG:782	0	11
690	<i>Prevotella</i> sp. P3-122	0	18
691	<i>Blautia</i> sp. CAG:52	0	31
692	uncultured organism	0	7
693	<i>Roseburia</i> sp. 499	0	46
694	<i>Clostridium</i> sp. CAG:277	0	170
695	<i>Mitsuokella multacida</i>	0	126
696	<i>Azospirillum</i> sp. 51_20	0	8
697	<i>Ruminococcus</i> sp. DSM 100440	0	37
698	<i>Clostridium</i> sp. CAG:62_40_43	0	30
699	<i>Butyrivibrio crossotus</i> CAG:259	0	10
700	<i>Azospirillum</i> sp. CAG:239	0	82
701	<i>Prevotella</i> sp. CAG:520	0	540
702	Lachnospiraceae bacterium TF01-11	0	111
703	Burkholderiales bacterium 1_1_47	0	118
704	<i>Bacteroides massiliensis</i>	0	134
705	<i>Eubacterium</i> sp. CAG:248	0	294
706	Clostridiales bacterium VE202-14	0	17
707	<i>Eubacterium</i> sp. 36_13	0	36
708	<i>Veillonella atypica</i>	0	41
709	<i>Sutterella</i> sp. 54_7	0	5
710	<i>Dakarella massiliensis</i>	0	64
711	<i>Clostridium ventriculi</i>	0	119
712	<i>Sutterella</i> sp. CAG:351	0	44
713	<i>Bacteroides acidifaciens</i>	0	9
714	Lachnospiraceae bacterium KHCPX20	0	7
715	<i>Roseburia</i> sp. CAG:10041_57	0	38
716	<i>Veillonella</i> sp. DORA_A_3_16_22	0	33
717	<i>Selenomonas ruminantium</i>	0	6
718	<i>Emergencia timonensis</i>	0	14
719	<i>Roseburia</i> sp. CAG:45	0	62
720	<i>Azospirillum</i> sp. 47_25	0	8
721	<i>Fournierella massiliensis</i>	0	23
722	Tenericutes bacterium HGW-Tenericutes-4	0	16
723	<i>Blastocystis</i> sp. subtype 1	0	33
724	<i>Prevotella bryantii</i>	0	8
725	<i>Roseburia</i> sp. 831b	0	46
726	<i>Bacteroides</i> sp. CAG:754	0	25
727	<i>Roseburia</i> sp. 40_7	0	11

728	<i>Roseburia</i> sp. CAG:100	0	70
729	<i>Bacteroides congongensis</i>	0	14
730	<i>Clostridium</i> sp. CAG:12237_41	0	36
731	Lachnospiraceae bacterium 10-1	0	20
732	<i>Eubacterium</i> sp. CAG:38	0	452
733	<i>Azospirillum</i> sp. CAG:260	0	16
734	<i>Bacteroides ovatus</i> CAG:22	0	36
735	Firmicutes bacterium CAG_194_44_15	0	7
736	<i>Veillonella parvula</i>	0	14
737	<i>Clostridium</i> sp. CAG:265	0	41
738	<i>Coprococcus</i> sp. ART55/1	0	9
739	<i>Parasutterella excrementihominis</i>	0	63
740	<i>Roseburia intestinalis</i> CAG:13	0	190
741	<i>Roseburia</i> sp. CAG:50	0	13
742	uncultured <i>Roseburia</i> sp.	0	36
743	<i>Akkermansia glycaniphila</i>	0	18
744	<i>Mycoplasma</i> sp. CAG:611	0	61
745	<i>Eggerthella</i> sp. CAG:298	0	43
746	<i>Clostridium</i> sp. CAG:632	0	226
747	<i>Prevotella ruminicola</i>	0	7
748	<i>Drancourtella massiliensis</i>	0	18
749	<i>Lachnoclostridium</i> sp. An14	0	19
750	<i>Eubacterium</i> sp. CAG:115	0	14
751	<i>Bacteroides</i> sp. CAG:1076	0	4
752	<i>Coprococcus</i> sp. CAG:131	0	26
753	<i>Veillonella</i> sp. oral taxon 158	0	12
754	<i>Phascolarctobacterium</i> sp. CAG:266	0	14
755	<i>Lachnoclostridium edouardi</i>	0	11
756	<i>Prevotella stercorea</i> CAG:629	0	24
757	<i>Alloprevotella tannerae</i>	0	7
758	<i>Olsenella</i> sp. oral taxon 807	0	8

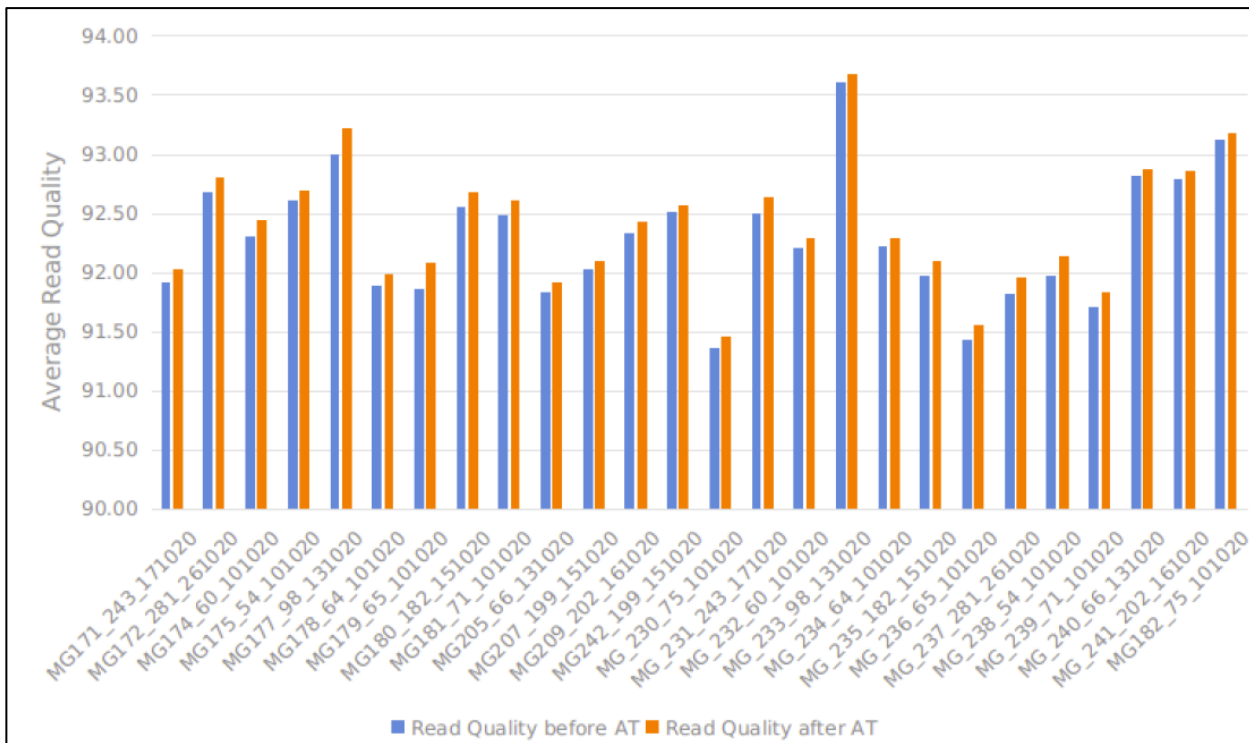
Supplementary Table 4. Post Intervention Control versus Post Intervention Treatment Seed Average Values

IDs	Baseline Control Average	Post Intervention Control Average	Difference	Increase/Decrease	Baseline Treatment Average	Post Intervention Treatment Average	Difference	Increase/Decrease
Carbohydrates	6182	5990	-193	Decrease	6549	4636	-1914	Decrease
Cofactors, Vitamins, Prosthetic Groups, Pigments	5849	5968	119	Increase	6164	4931	-1233	Decrease
Amino Acids and Derivatives	4772	4619	-153	Decrease	4817	3889	-927	Decrease
Protein Metabolism	2735	2540	-195	Decrease	2811	2387	-424	Decrease
RNA Metabolism	1715	1719	5	Increase	1841	1488	-354	Decrease
Cell Wall and Capsule	1263	1211	-52	Decrease	1318	992	-326	Decrease
Fatty Acids, Lipids, and Isoprenoids	1215	1199	-17	Decrease	1279	999	-280	Decrease
Nucleosides and Nucleotides	1054	1045	-9	Decrease	1103	832	-271	Decrease
DNA Metabolism	1029	990	-39	Decrease	1094	938	-156	Decrease
Respiration	994	976	-19	Decrease	1002	780	-222	Decrease
Stress Response	974	933	-41	Decrease	1032	746	-287	Decrease
Metabolite damage and its repair or mitigation	857	856	-1	Decrease	913	740	-173	Decrease
Virulence	743	720	-24	Decrease	775	611	-164	Decrease
Membrane Transport	626	585	-41	Decrease	644	467	-177	Decrease
Phosphorus Metabolism	505	484	-20	Decrease	500	396	-104	Decrease
Regulation and Cell signaling	446	428	-19	Decrease	467	326	-141	Decrease
Cell Division and Cell Cycle	416	401	-15	Decrease	452	385	-67	Decrease
Iron acquisition and metabolism	366	369	4	Increase	370	303	-68	Decrease
Potassium metabolism	343	340	-3	Decrease	341	279	-61	Decrease
Sulfur Metabolism	330	310	-20	Decrease	343	276	-67	Decrease
Virulence, Disease and Defense	258	245	-13	Decrease	268	193	-75	Decrease
Phages, Prophages, Transposable elements, Plasmids	231	214	-18	Decrease	241	184	-56	Decrease
Metabolism of Aromatic Compounds	201	202	0		207	113	-94	Decrease
Motility and Chemotaxis	185	199	14	Increase	174	148	-26	Decrease
Thiamin	167	174	7	Increase	172	158	-14	Decrease
Nitrogen Metabolism	166	161	-5	Decrease	171	133	-38	Decrease
Predictions based on plant-prokaryote comparative analysis	163	144	-19	Decrease	179	132	-47	Decrease
Mitochondrial electron transport system in plants	122	114	-8	Decrease	128	124	-3	Decrease
Dormancy and Sporulation	71	96	26	Decrease	83	71	-11	Decrease

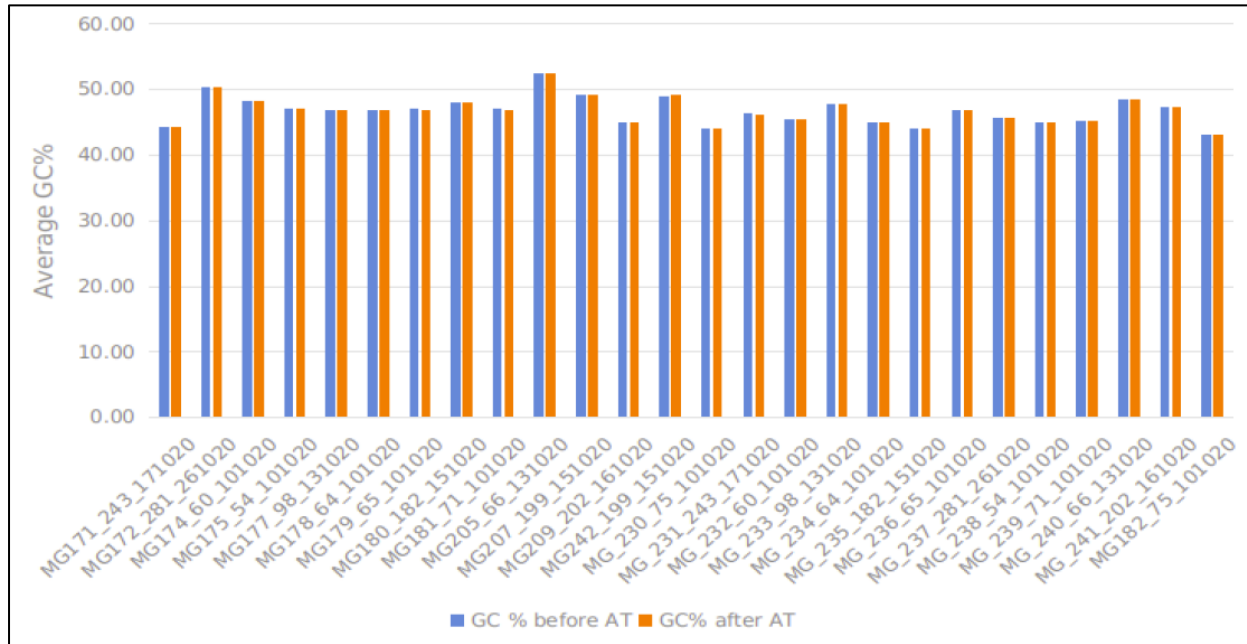
Nucleotide sugars	70	62	-8	Decrease	73	55	-19	Decrease
Secondary Metabolism	63	57	-6	Decrease	62	47	-15	Decrease
Plant Glucosinolates	50	46	-5	Decrease	44	40	-4	Decrease
Transcriptional regulation	43	39	-5	Decrease	46	36	-10	Decrease
Phages, Prophages, Transposable elements	42	38	-4	Decrease	43	27	-15	Decrease
Plant cell walls and outer surfaces	19	17	-1	Decrease	19	6	-12	Decrease
Central metabolism	12	15	2	Increase	13	12	0	
Autotrophy	11	10	-1	Decrease	11	10	-2	Decrease
Arabinose Sensor and transport module	9	9	-1	Decrease	8	4	-3	Decrease
Polyamines	4	4	0		4	6	1	Decrease
General Stress Response and Stationary Phase Response	2	2	0		3	1	-2	Decrease
Plastidial (cyanobacterial) electron transport system	0	1	1	Increase	0	1	0	



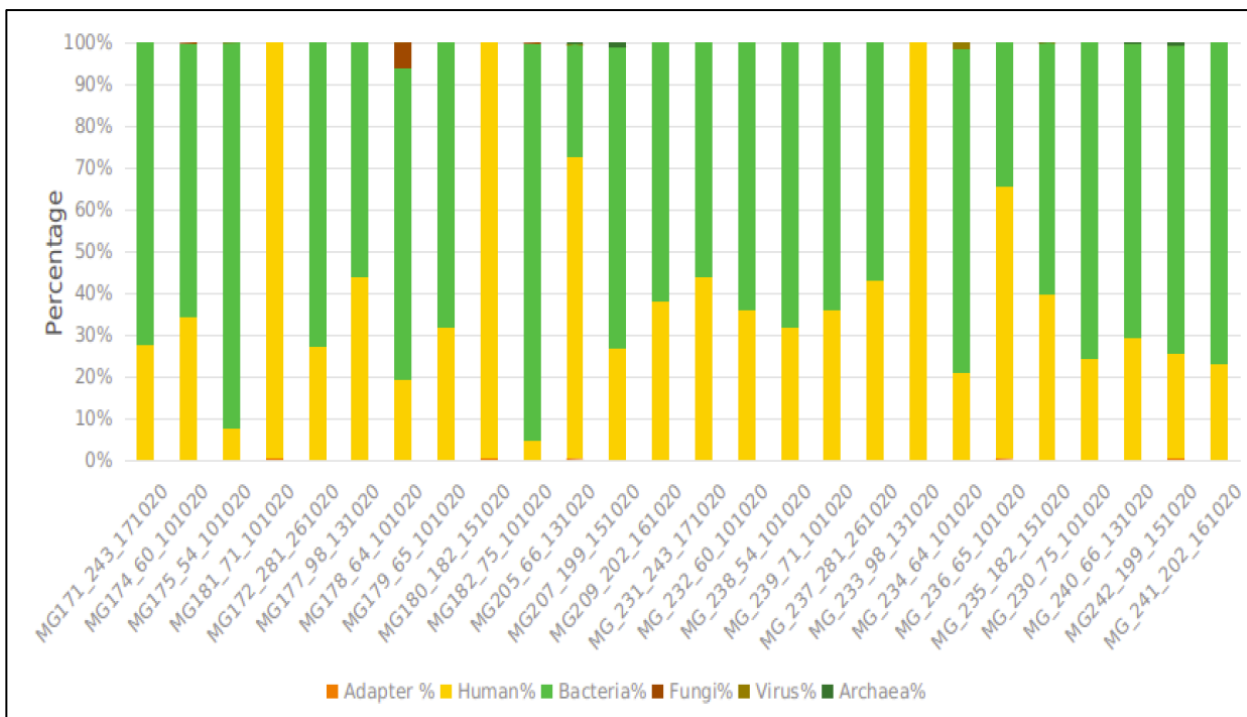
Supplementary Figure 1. Data before and after adapter trimming



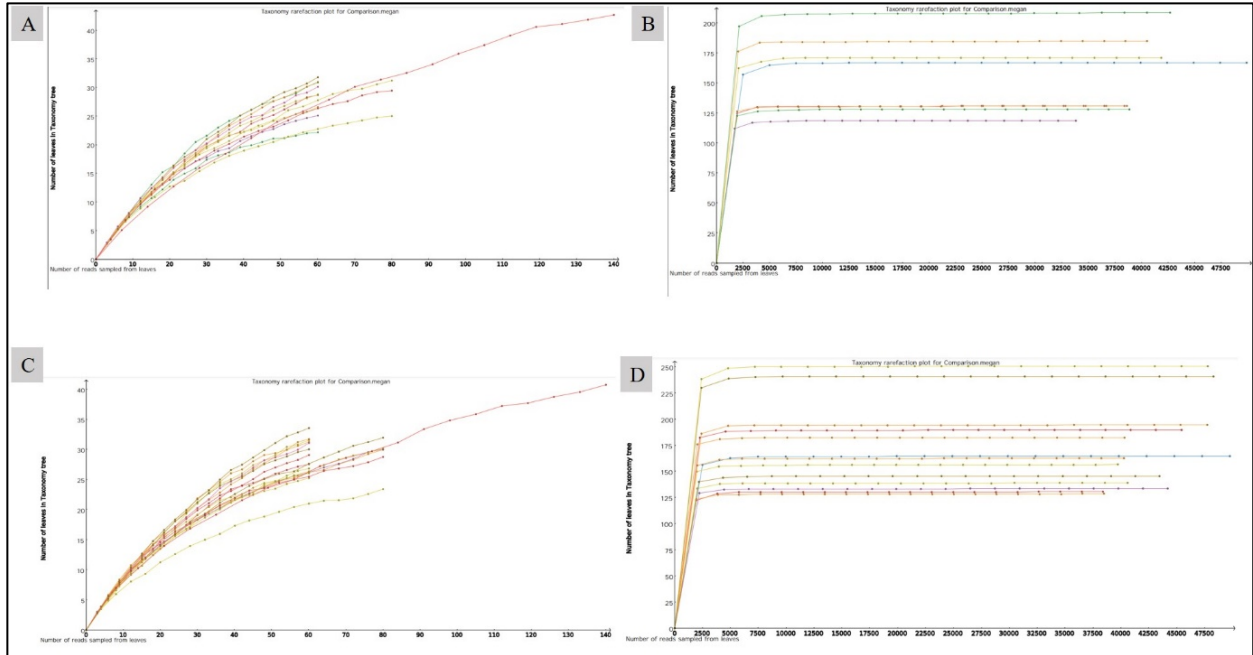
Supplementary Figure 2. Average Read quality before and after adapter trimming



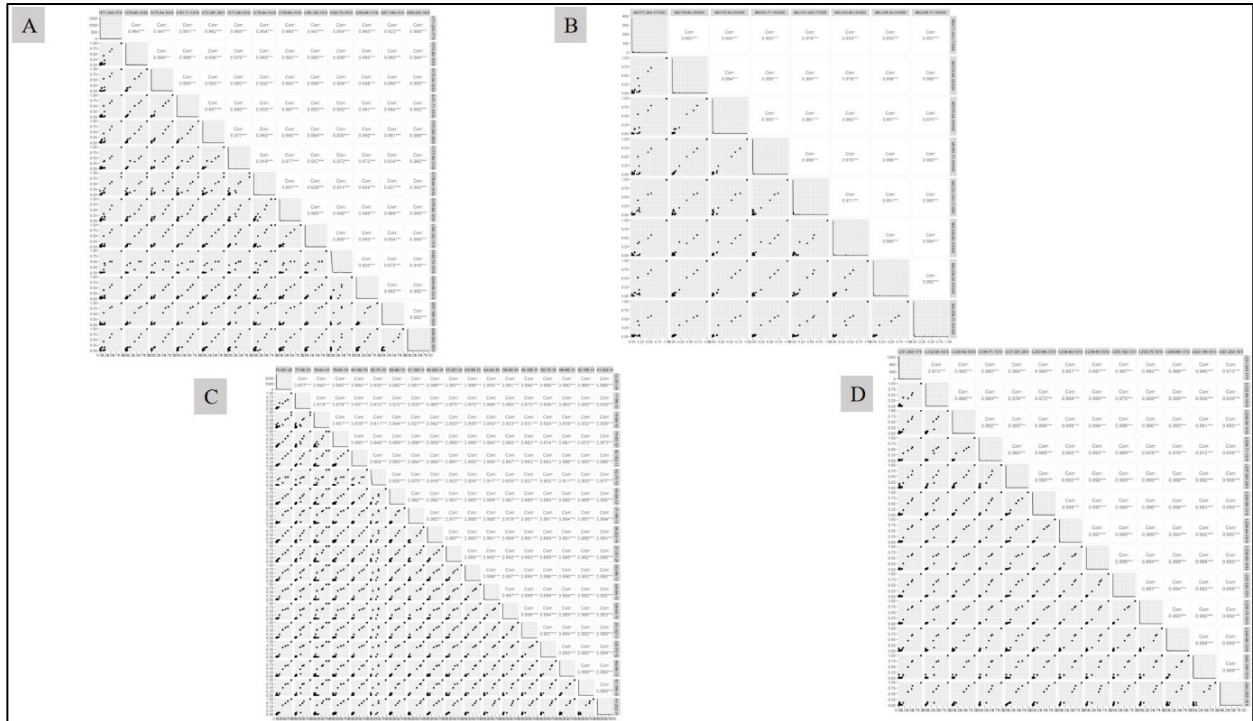
Supplementary Figure 3. Average GC% before and after adapter trimming



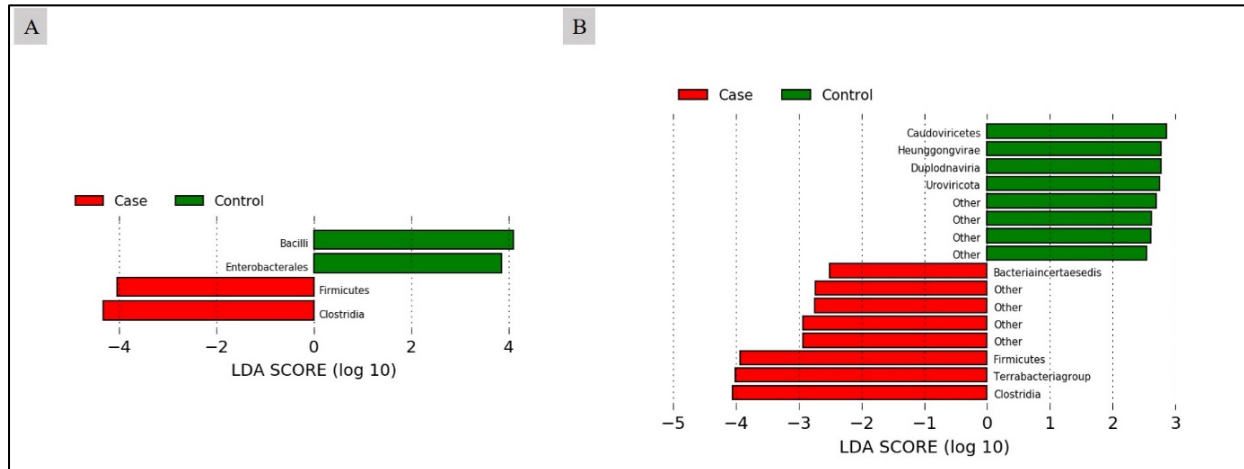
Supplementary Figure 4. Percentage of alignment to Bacteria, Fungi, Virus, Archae Bacteria, and Human genomes



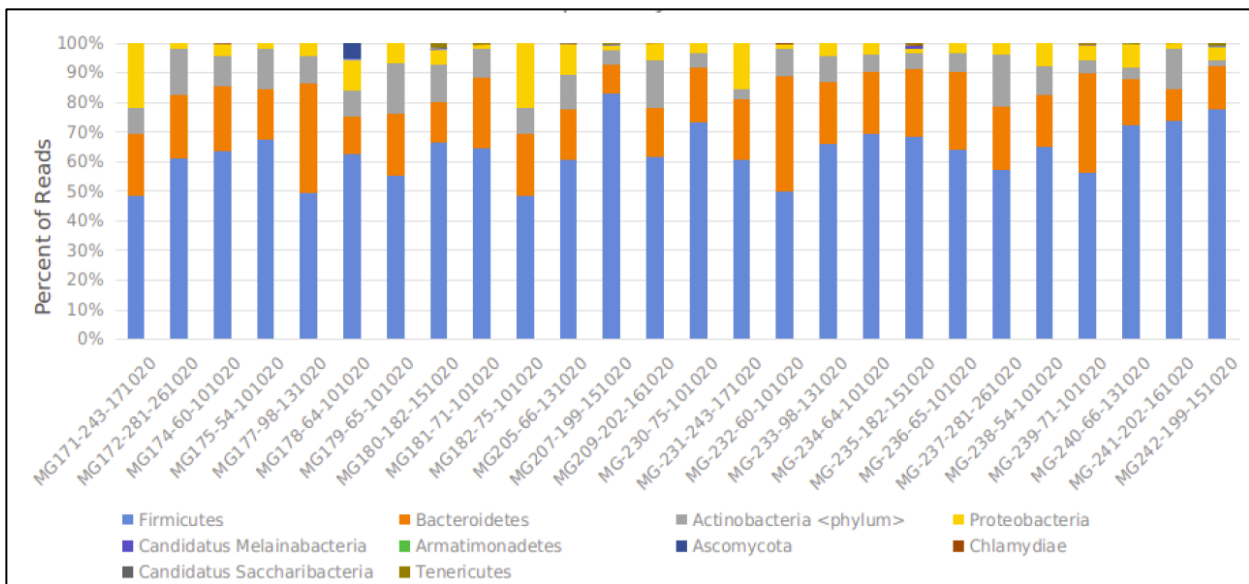
Supplementary Figure 5. Shannon Alpha Diversity Plots. A) Baseline control versus baseline treatment; B) Baseline control versus post-intervention control; C) Baseline treatment versus post-intervention treatment; D) Post-intervention control versus post-intervention treatment.



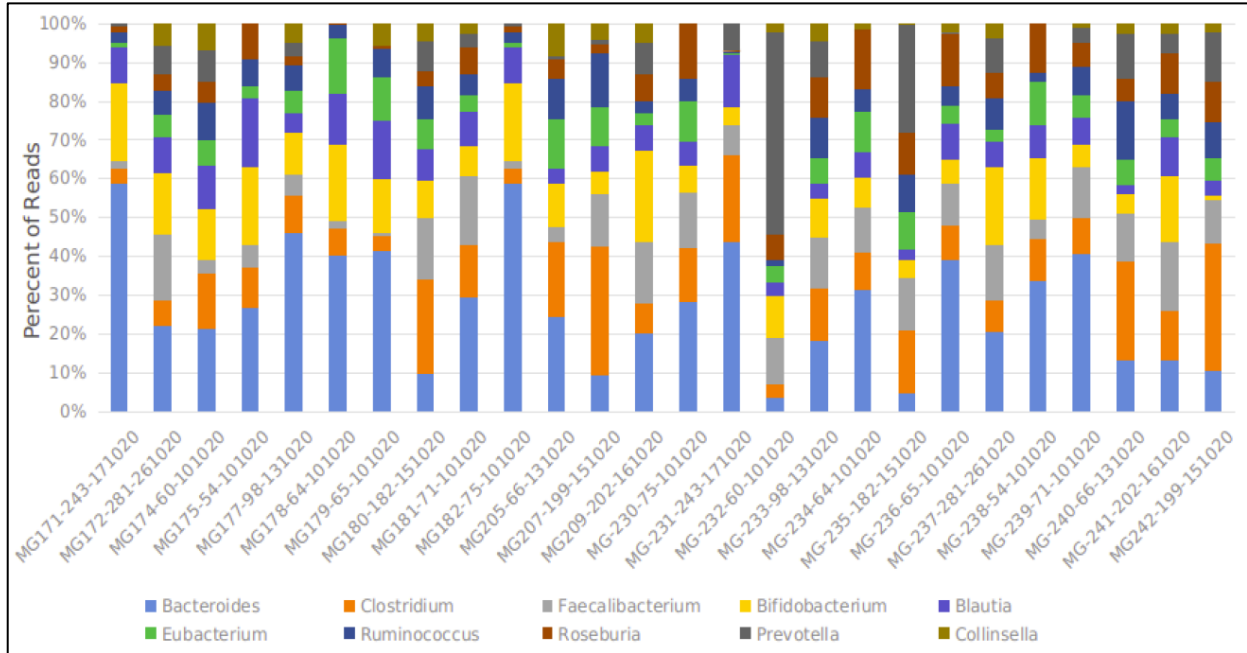
Supplementary Figure 6. L6 (Genus level) Correlation Plots. A) Baseline control versus baseline treatment; B) Baseline control versus post-intervention control; C) Baseline treatment versus post-intervention treatment; D) Post-intervention control versus post-intervention treatment.



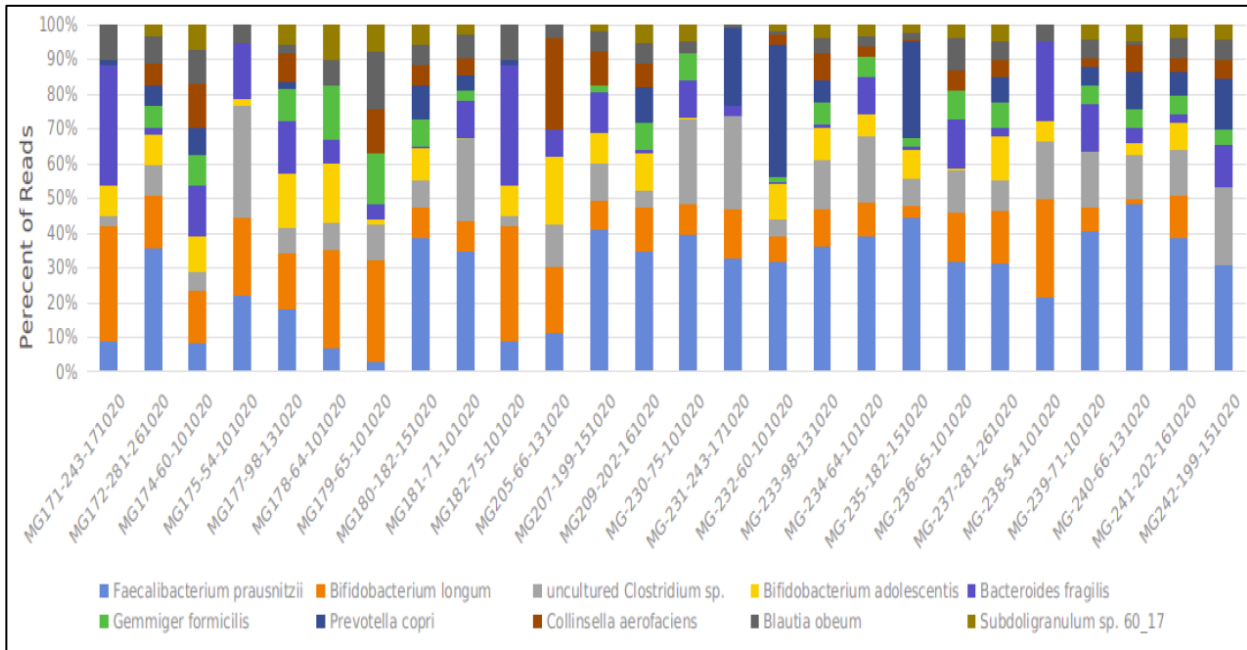
Supplementary Figure 7. Linear discriminant analysis (LDA) effect size (LEfSe): A) Baseline treatment versus post-intervention treatment and B) Post-intervention control versus post-intervention treatment



Supplementary Figure 8. Distribution of Phyla: Phylum Proteobacteria was the most abundant followed by phylum Firmicutes.



Supplementary Figure 9. Distribution of Genera



Supplementary Figure 10. Distribution of Species