Table S3. Relative abundances of gut microbes on phylum and genus level in the cohort.

	Phylum	**Mean (%)**	**Median (%)**	**Min (%)**	**Max (%)**
1	*Bacteroidetes*	52	46.2	0.4	97.5
2	*Firmicutes*	40.6	44.2	1.8	95.7
3	*Proteobacteria*	4	3.4	0	24
4	*Actinobacteria*	2.7	1.3	0	51.6
5	NA	0.3	0	0	10
6	*Verrucomicrobia*	0.2	0	0	4.3
7	*Tenericutes*	0.1	0	0	9.1
8	*Euryarchaeota*	0	0	0	2.4
9	*Lentisphaerae*	0	0	0	0.6
	Genus	**Mean (%)**	**Median (%)**	**Min (%)**	**Max (%)**
1	*Bacteroides*	18.4	17.3	0	59.1
2	*Prevotella*	18.4	0.2	0	96.6
3	*Faecalibacterium*	7.3	6.5	0	27.8
4	*Barnesiella*	5.6	0.7	0	92.1
5	*Roseburia*	5.3	4	0	30.6
6	*Paraprevotella*	4.1	0	0	61.6
7	*Clostridium* XlVa	3.5	2.8	0.1	27.9
8	*Lachnospiracea incertae sedis*	3.1	2.4	0	24.6
9	*Phascolarctobacterium*	2.8	0	0	45
10	*Alistipes*	2.5	1.9	0	34
11	*Bifidobacterium*	2.2	0.8	0	51.6
12	*Ruminococcus*	2.2	1.2	0	17.8
13	*Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_*NA	1.8	1.4	0	14.6
14	*Sutterella*	1.7	0.9	0	14.4
15	*Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_*NA	1.5	1	0	15
16	*Parabacteroides*	1.4	1	0	17.8
17	*Blautia*	1.2	0.9	0	12.2
18	*Fusicatenibacter*	1.1	0.8	0	7.2
19	*Oscillibacter*	1.1	0.8	0	19.6
20	*Odoribacter*	1	0.7	0	5.6
21	*Coprococcus*	1	0.5	0	6.8
22	*Bacteria_Firmicutes_Clostridia_Clostridiales_*NA_NA	0.9	0.5	0	9.2
23	*Clostridium IV*	0.9	0.4	0	12.5
24	*Gemmiger*	0.9	0.4	0	13.8
25	*Parasutterella*	0.8	0.1	0	11.2
26	*Ruminococcus2*	0.6	0.3	0	5.3
27	*Bacteria_Firmicutes_*NA_NA_NA_NA	0.6	0.1	0	5.8
28	*Dialister*	0.6	0.3	0	5.2
29	*Eubacterium*	0.5	0.4	0	5.3

30	*Collinsella*	0.4	0.2	0	5.9
31	*Veillonella*	0.4	0.1	0	12.9
32	*Escherichia/Shigella*	0.4	0	0	23.7
33	*Butyricimonas*	0.3	0	0	2.6
34	*Coprobacter*	0.3	0	0	3.9
35	*Dorea*	0.3	0.2	0	3.6
36	*Flavonifractor*	0.3	0.2	0	6.5
37	*Sporobacter*	0.3	0.1	0	4.7
38	*Bacteria*_NA_NA_NA_NA_NA	0.3	0	0	10
39	*Streptococcus*	0.2	0.1	0	2.8
40	*Clostridium sensu stricto*	0.2	0	0	5.8
41	*Anaerostipes*	0.2	0.1	0	2.5
42	*Clostridium* XlVb	0.2	0.1	0	2.5
43	*Clostridium* III	0.2	0	0	5.8
44	*Acidaminococcus*	0.2	0	0	16.8
45	*Succiniclasticum*	0.2	0	0	19
46	*Bacteria_Proteobacteria_Alphaproteobacteria*_NA_NA_NA	0.2	0	0	7.2
47	*Bacteria_Proteobacteria_Alphaproteobacteria_Rhodospirillales_Rhodospirillaceae*_NA	0.2	0	0	7.3
48	*Bilophila*	0.2	0.1	0	1.7
49	*Akkermansia*	0.2	0	0	4.3
50	*Adlercreutzia*	0.1	0	0	1.6
51	*Butyrivibrio*	0.1	0	0	5.6
52	*Romboutsia*	0.1	0	0	3.1
53	*Intestinimonas*	0.1	0.1	0	1.3
54	*Subdoligranulum*	0.1	0	0	4.1
55	*Megasphaera*	0.1	0	0	20.8
56	*Aestuariispira*	0.1	0	0	6.7
57	*Bacteria_Proteobacteria_Betaproteobacteria_Burkholderiales*_NA_NA	0.1	0	0	4.9
58	*Haemophilus*	0.1	0	0	4.9
59	*Bacteria_Proteobacteria*_NA_NA_NA_NA	0.1	0	0	4.9
60	*Bacteria_Tenericutes_Mollicutes*_NA_NA_NA	0.1	0	0	9.1
61	*Methanobrevibacter*	0	0	0	2.4
62	*Eggerthella*	0	0	0	1.2
63	*Bacteria_Actinobacteria_Actinobacteria_Coriobacteriales_Coriobacteriaceae*_NA	0	0	0	0.5
64	*Senegalimassilia*	0	0	0	1.3
65	*Slackia*	0	0	0	0.6
66	*Lactococcus*	0	0	0	0.8
67	*Anaerosporobacter*	0	0	0	0.5
68	*Filifactor*	0	0	0	0.9
69	*Intestinibacter*	0	0	0	0.8

70	*Terrisporobacter*	0	0	0	0.3
71	*Papillibacter*	0	0	0	1.8
72	*Clostridium XVIII*	0	0	0	0.4
73	*Turicibacter*	0	0	0	0.7
74	*Megamonas*	0	0	0	6.5
75	*Victivallis*	0	0	0	0.6
76	*Desulfovibrio*	0	0	0	1.7
77	*Salmonella*	0	0	0	3.2