

Habitat and seasonality shape the structure of tench (*Tinca tinca* L.) gut
microbiome

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Table S1. Common and unique OTUs present in the four groups of tench.

Groups		Number of shared OTUs	Taxons
All groups	LakeAutumn2017 LakeSummer2018 PondAutumn2017 PondSummer2018	26	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Clostridium
			k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus
			k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; s__caviae
			k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae
			k__Bacteria; p__Proteobacteria; c__Betaproteobacteria
			k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales
			k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Rhodocyclales; f__Rhodocyclaceae
			k__Bacteria
			k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Alcaligenaceae; g__Achromobacter; s__
			k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Clostridium; s__gasigenes
			k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales
			k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Oxalobacteraceae; g__Polynucleobacter; s__
			k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Propionibacteriaceae; g__Propionibacterium; s__
			k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Acidovorax
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae
			k__Bacteria; p__Bacteroidetes
			k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Micrococcaceae; g__Micrococcus; s__
			k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__[Clostridium]; s__bifermentans
			k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Corynebacteriaceae; g__Corynebacterium; s__variable
			k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__u114; s__
			k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae
			k__Bacteria; p__Verrucomicrobia; c__[Spartobacteria]; o__[Chthoniobacteriales]; f__[Chthoniobacteraceae]; g__Candidatus Xiphinematobacter; s__
			k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Neisseriales; f__Neisseriaceae; g__Eikenella; s__
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Tolumonas; s__

From the same season	LakeAutumn2017 PondAutumn2017	14	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Dialister; s__
	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Geodermatophilaceae; g__s__		
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Leuconostocaceae; g__Leuconostoc; s__			
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales			
k__Bacteria; p__Acidobacteria; c__Acidobacteria-6; o__s__f__s__			
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Neisseriales; f__Neisseriaceae			
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__s__			
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae			
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__Xanthomonadaceae; g__Stenotrophomonas			
k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Arcobacter; s__cryaerophilus			
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__[Chromatiaceae]			
k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o__[Saprospirales]; f__Chitinophagaceae; g__Flavihumibacter; s__			
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__copri			
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus			
LakeSummer2018 PondSummer2018	2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Mannheimia; s__	
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Neisseriales; f__Neisseriaceae; g__Chitinilyticum; s__aquatile			
From the same environment	PondAutumn2017 PondSummer2018	16	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__frigidarium
			k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium
			k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Veillonella
			k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Cryomorphaceae
			k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__succinicans
			k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales
			k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Methylobacteriaceae; g__Methylobacterium; s__organophilum
			k__Bacteria; p__Cyanobacteria; c__Nostocophycideae; o__Nostocales; f__Nostocaceae; g__Cylindrospermopsis; s__
			k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Arcobacter
			k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__Cytophagales
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Acinetobacter; s__guillouiae
			k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__[Weeksellaceae]; g__Elizabethkingia; s__meningoseptica
			k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales
			k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae
			k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia; s__faecis
			k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Neisseriales; f__Neisseriaceae; g__Vogesella; s__

From the same environment	LakeAutumn2017 LakeSummer2018	29	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae
			k__Bacteria; p__Verrucomicrobia; c__[Spartobacteria]; o__[Chthoniobacterales]; f__[Chthoniobacteraceae]; g__Chthoniobacter; s__
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__Xanthomonadaceae
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales
			k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Lutimonas; s__
			k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Nocardioideaceae; g__Pimelobacter; s__
			k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Mycobacteriaceae; g__Mycobacterium; s__celatum
			k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Rhodocyclales; f__Rhodocyclaceae; g__Azovibrio; s__
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Chromatiaceae; g__Allochromatium; s__
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Crenotrichaceae; g__Crenothrix
			k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales; f__Desulfobacteraceae
			k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Intrasporangiaceae; g__Phycococcus; s__
			k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales; f__Desulfobulbaceae
			k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales; f__Desulfobulbaceae; g__Desulfobulbus; s__
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Crenotrichaceae; g__Crenothrix; s__
			k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Syntrophobacterales; f__Syntrophorhabdaceae; g__ ; s__
			k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__MSBL3; s__
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Crenotrichaceae; g__Crenothrix; s__polyspora
			k__Bacteria; p__Planctomycetes; c__Planctomycetia; o__Pirellulales; f__Pirellulaceae; g__planctomycete
			k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Dysgonomonas; s__
			k__Bacteria; p__Actinobacteria
			k__Bacteria; p__Proteobacteria
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Acidithiobacillales; f__ ; g__ ; s__
			k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales; f__Desulfobulbaceae; g__Desulforhopalus; s__
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Yersinia; s__
			k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__OM60; g__Congregibacter; s__
			k__Bacteria; p__Verrucomicrobia; c__[Methylacidiphilae]; o__Methylacidiphilales; f__LD19; g__ ; s__
			k__Bacteria; p__Planctomycetes; c__Planctomycetia; o__Pirellulales; f__Pirellulaceae; g__Pirellula; s__

Table S2. Statistical analysis of mean relative abundance (%) \pm SD of phyla and genera between groups. Statistical Analysis of Metagenomics Profiles (STAMP) software was used to test statistical significance between groups abundances, unclassified reads were retained only for calculating frequency. One-Way ANOVA ($P < 0.05$), with an effect size (ETA-Squared) with Benjamini-Hochberg FDR correction was applied followed by Tukey-Kramer post-hoc test.

Phylum	Autumn 2017				Summer 2018				p-values (corrected)	Effect size
	Pond		Lake		Pond		Lake			
	mean abu.(%)	\pm SD	mean abu. (%)	\pm SD	mean abun. (%)	\pm SD	mean abu. (%)	\pm SD		
<i>Verrucomicrobia</i>	0.32	0.59	1.92	2.26	0.28	0.62	2.91	1.60	0.02677	0.42
<i>Bacteroidetes</i>	8.70	5.22	3.94	2.34	8.81	8.35	0.73	1.09	0.13059	0.31
<i>Chloroflexi</i>	0.00	0.00	0.25	0.34	0.00	0.00	0.00	0.00	0.10285	0.31
<i>Planctomycetes</i>	0.00	0.00	1.57	2.52	0.10	0.19	0.30	0.23	0.33806	0.21
<i>Firmicutes</i>	16.57	10.10	21.72	20.47	7.86	12.92	5.65	7.43	0.37285	0.19
<i>Actinobacteria</i>	6.50	6.37	9.71	10.04	3.61	7.36	0.86	0.68	0.34879	0.18
<i>Proteobacteria</i>	66.41	19.12	57.61	29.13	74.74	24.16	83.49	11.14	0.41028	0.16
<i>Acidobacteria</i>	0.91	1.93	1.79	1.97	0.59	1.32	0.25	0.25	0.61478	0.11
<i>Synergistetes</i>	0.03	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.57378	0.11
<i>WS6</i>	0.04	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.52162	0.11
<i>Tenericutes</i>	0.00	0.00	0.00	0.00	0.07	0.18	0.00	0.00	0.58042	0.09
<i>Cyanobacteria</i>	0.09	0.19	0.09	0.18	0.42	1.00	0.39	0.20	0.65605	0.07
<i>Fusobacteria</i>	0.36	0.62	0.30	0.42	2.80	7.02	1.49	2.48	0.66832	0.06
Genus										
<i>Methylobacterium</i>	38.88	19.08	0	0	0.09	0.24	0	0	0.00003	0.76
<i>Candidatus Xiphinematobacter</i>	0.01	0.03	0.03	0.04	0.05	0.13	2.01	1.02	0.00007	0.72
<i>A17</i>	0	0	0.15	0.14	0	0	0	0	0.05071	0.49
<i>Desulfobulbus</i>	0	0	0.11	0.11	0	0	0.18	0.14	0.05514	0.46
<i>MSBL3</i>	0	0	0.05	0.08	0	0	0.18	0.15	0.05505	0.45
<i>Phycococcus</i>	0	0	0.13	0.13	0	0	0.01	0.02	0.06289	0.44
<i>Aeromonas</i>	10.05	14.86	17.38	17.71	47.93	38.14	62.61	18.94	0.07229	0.43
<i>Desulforhopalus</i>	0	0	1.87	1.9	0	0	0.38	0.24	0.08472	0.42
<i>Yersinia</i>	0	0	0.01	0.03	0	0	0.35	0.37	0.14502	0.38
<i>Crenothrix</i>	0	0	5.08	5.77	0	0	0.59	0.51	0.15432	0.37
<i>Flavobacterium</i>	1.84	2.18	0	0	5.28	5.16	0.03	0.08	0.15226	0.36
<i>Congregibacter</i>	0	0	0.1	0.13	0	0	0.31	0.32	0.15184	0.35
<i>Dysgonomonas</i>	0	0	0.73	0.9	0	0	0.01	0.02	0.1561	0.35
<i>C39</i>	0	0	0	0	0.55	0.65	0	0	0.17437	0.34
<i>Tolumonas</i>	0.06	0.14	0.14	0.27	0.54	0.53	0	0.01	0.17624	0.33
<i>Modestobacter</i>	0	0	0.27	0.35	0	0	0	0	0.20247	0.32
<i>Allochromatium</i>	0	0	0.51	0.68	0	0	0.03	0.05	0.21644	0.31
<i>Chthoniobacter</i>	0	0	0.31	0.41	0	0	0.02	0.04	0.21327	0.31
<i>Paulinella</i>	0	0	0	0	0	0	0.14	0.19	0.2234	0.3
<i>Acidovorax</i>	0.02	0.05	0.26	0.3	0.04	0.09	0	0.01	0.23668	0.29

<i>Lactobacillus</i>	0.52	0.59	0.21	0.42	0	0	0	0	0.26428	0.28
<i>Propionibacterium</i>	0.93	0.54	0.81	1.15	0.34	0.32	0.03	0.03	0.25333	0.28
<i>Shewanella</i>	0	0	0.84	0.82	0	0.01	0.8	1.1	0.30064	0.26
<i>Luteolibacter</i>	0	0	1.52	1.93	0.24	0.62	0.29	0.2	0.30448	0.26
<i>Chitinibacter</i>	0	0	0.04	0.08	0.1	0.19	0.27	0.27	0.30303	0.26
<i>Deefgea</i>	0	0	1.6	1.89	0.05	0.08	0.87	1.26	0.30532	0.26
<i>Arenimonas</i>	0	0	0	0	0	0	0.04	0.06	0.34298	0.24
<i>Streptococcus</i>	1.14	1.17	0	0	0.98	1.33	0.04	0.06	0.35122	0.24
<i>planctomycete</i>	0	0	0.62	0.98	0	0	0.05	0.07	0.36173	0.24
<i>[Clostridium]</i>	0.06	0.14	1.8	3.27	0.1	0.25	4.29	5.6	0.38117	0.23
<i>Anaerococcus</i>	0.09	0.15	0	0	0	0	0	0	0.42719	0.22
<i>Prevotella</i>	0.6	0.97	0.01	0.02	0	0	0	0	0.42028	0.22
<i>Flaviumibacter</i>	0.85	1.37	0.08	0.15	0	0	0	0	0.4381	0.22
<i>Mannheimia</i>	0	0	0	0	6.06	9.73	0.05	0.12	0.43764	0.22
<i>Corynebacterium</i>	3.68	5.68	1.17	1.75	0.07	0.1	0.01	0.02	0.44198	0.21
<i>Bacillus</i>	0.3	0.51	0	0	0	0	0	0	0.43602	0.21
<i>Anaeromyxobacter</i>	0	0	0.57	1.02	0	0	0	0	0.4405	0.21
<i>Clostridium</i>	0.46	0.97	4.47	6.86	0.67	1.22	0.29	0.19	0.4365	0.21
<i>Rothia</i>	0.21	0.36	0	0	0	0	0	0	0.46391	0.2
<i>Clostridium I</i>	0	0	0.19	0.35	0	0	0	0	0.4782	0.2
<i>Pseudomonas</i>	7.78	13.38	0.76	0.8	0.4	0.46	0.14	0.13	0.52458	0.19
<i>Haemophilus</i>	0.57	1.05	0	0	0	0	0	0	0.53372	0.18
<i>Lutimonas</i>	0	0	1.09	1.92	0	0	0.41	0.56	0.55596	0.18
<i>Xanthomonas</i>	0	0	0	0	0	0	0.02	0.04	0.57052	0.18
<i>Veillonella</i>	0.21	0.33	0	0	0.08	0.14	0	0	0.56388	0.18
<i>Achromobacter</i>	1.35	2.37	0	0	0.22	0.49	0.01	0.01	0.5649	0.17
<i>Pelosinus</i>	0	0	0.14	0.29	0	0	0	0	0.57484	0.17
<i>Geobacter</i>	0	0	0.08	0.16	0	0	0	0	0.54645	0.17
<i>Salinibacterium</i>	0	0	0.19	0.38	0	0	0	0	0.53979	0.17
<i>Neorickettsia</i>	0	0	0.3	0.6	0	0	0	0	0.53329	0.17
<i>Cellulomonas</i>	0	0	0.05	0.11	0	0	0	0	0.52074	0.17
<i>Solirubrobacter</i>	0	0	0.04	0.08	0	0	0	0	0.50877	0.17
<i>Carnobacterium</i>	0	0	0.1	0.2	0	0	0	0	0.50299	0.17
<i>Legionella</i>	0	0	0.09	0.18	0	0	0	0	0.49181	0.17
<i>Aeromicrobium</i>	0	0	0.13	0.27	0	0	0	0	0.47594	0.17
<i>Actinoplanes</i>	0	0	0.16	0.32	0	0	0	0	0.45632	0.17
<i>Pirellula</i>	0	0	0.53	1.05	0	0	0	0.01	0.4554	0.17
<i>Kocuria</i>	0	0	1.16	2.32	0.07	0.19	0	0	0.47582	0.16
<i>Bacteroides</i>	1.34	1.74	0.46	0.9	0.45	1.17	0	0	0.48416	0.16
<i>Cloacibacterium</i>	0	0	1.27	2.54	0.12	0.31	0	0	0.4857	0.16
<i>Acinetobacter</i>	0.38	0.67	0	0	0.88	1.37	0.08	0.21	0.49159	0.16
<i>Mycobacterium</i>	0	0	0.19	0.38	0	0	0.06	0.04	0.49067	0.16
<i>Azovibrio</i>	0	0	0.12	0.24	0	0	0.02	0.03	0.49162	0.16
<i>Rheinheimera</i>	0	0	0	0	0.27	0.53	0	0	0.48602	0.15
<i>Eikenella</i>	0.44	1.09	11.77	23.5	10.04	12.94	0.42	0.5	0.48678	0.15
<i>Pimelobacter</i>	0	0	0.28	0.57	0	0	0.04	0.11	0.48867	0.15

<i>Nostocoida</i>	0	0	0.08	0.15	0	0	0.03	0.04	0.50824	0.15
<i>Pantoea</i>	0	0	1.27	2.55	0.35	0.57	0	0	0.50577	0.15
<i>Micrococcus</i>	0.22	0.35	0.74	1.48	0.04	0.1	0.01	0.01	0.5243	0.14
<i>Staphylococcus</i>	5.34	3.01	10.3	18.55	3.42	6.7	0.16	0.26	0.56351	0.13
<i>u114</i>	0.01	0.02	0.3	0.42	0.19	0.48	1.32	2.51	0.57408	0.13
<i>Elizabethkingia</i>	0.34	0.84	0.09	0.18	1.58	3.11	0	0	0.58422	0.13
<i>Actinobacillus</i>	0.13	0.32	0.63	1.27	0.1	0.25	0	0	0.58626	0.13
<i>Arcobacter</i>	0.11	0.18	0.12	0.24	0.03	0.07	0	0	0.62783	0.12
<i>Paracoccus</i>	0	0	0.02	0.04	0.03	0.08	0.08	0.12	0.63202	0.12
<i>Stenotrophomonas</i>	0.1	0.24	0.18	0.35	0	0	0	0	0.65154	0.12
<i>Wandonia</i>	0	0	0	0	0.24	0.56	0	0	0.64972	0.12
<i>Vogesella</i>	0.03	0.07	0	0	0.1	0.2	0	0	0.6557	0.11
<i>Friedmanniella</i>	0	0	0.08	0.17	0.04	0.1	0	0	0.6656	0.11
<i>Neisseria</i>	0.13	0.33	0	0	0	0	0	0	0.65271	0.11
<i>Blastomonas</i>	0.03	0.08	0	0	0	0	0	0	0.64791	0.11
<i>Allobaculum</i>	0.09	0.23	0	0	0	0	0	0	0.63852	0.11
<i>Akkermansia</i>	0.25	0.6	0	0	0	0	0	0	0.6294	0.11
<i>Pseudoxanthomonas</i>	0.52	1.27	0	0	0	0	0	0	0.62494	0.11
<i>Sedimentibacter</i>	0.13	0.31	0	0	0	0	0	0	0.62053	0.11
<i>Ruminococcus</i>	0.47	1.15	0	0	0	0	0	0	0.61619	0.11
<i>Methylopila</i>	0.05	0.12	0	0	0	0	0	0	0.61192	0.11
<i>Pedobacter</i>	0.12	0.29	0	0	0	0	0	0	0.6077	0.11
<i>Oscillospira</i>	0.06	0.16	0	0	0	0	0	0	0.59943	0.11
<i>Porphyromonas</i>	0.05	0.11	0	0	0	0	0	0	0.59538	0.11
<i>rc4-4</i>	0.06	0.14	0	0	0	0	0	0	0.59138	0.11
<i>HA73</i>	0.03	0.06	0	0	0	0	0	0	0.58744	0.11
<i>Parabacteroides</i>	0.53	1.29	0	0	0	0	0	0	0.58355	0.11
<i>Blautia</i>	0.05	0.13	0	0	0	0	0	0	0.57218	0.11
<i>Selenomonas</i>	0.11	0.26	0	0	0	0	0	0	0.56849	0.11
<i>Bilophila</i>	0.14	0.35	0	0	0	0	0	0	0.56485	0.11
<i>02d06</i>	0.06	0.15	0	0	0	0	0	0	0.55419	0.11
<i>Syntrophus</i>	0.1	0.25	0	0	0	0	0	0	0.55072	0.11
<i>Peptoniphilus</i>	0.04	0.1	0	0	0	0	0	0	0.5473	0.11
<i>Actinomyces</i>	0.06	0.14	0	0	0	0	0	0	0.53404	0.11
<i>[Prevotella]</i>	0.13	0.32	0	0	0	0	0	0	0.53082	0.11
<i>Clostridium 2</i>	0.35	0.86	0	0	0	0	0	0	0.52764	0.11
<i>Polynucleobacter</i>	0.63	0.98	0.01	0.03	0.85	1.79	0	0	0.52573	0.11
<i>Dialister</i>	0.38	0.94	0.02	0.02	0	0	0	0	0.53187	0.11
<i>Leuconostoc</i>	0.23	0.55	0.01	0.02	0	0	0	0	0.53114	0.11
<i>Cylindrospermopsis</i>	0.09	0.19	0	0	0.02	0.05	0	0	0.54514	0.11
<i>Enhydrobacter</i>	0.09	0.23	0.11	0.23	0	0	0	0.01	0.56204	0.1
<i>Lactococcus</i>	0.37	0.89	0.74	1.48	0.15	0.24	0	0	0.56079	0.1
<i>Roseburia</i>	0.04	0.09	0	0	0.01	0.02	0	0	0.57372	0.1
<i>Dyadobacter</i>	0	0	0	0	0.04	0.12	0	0	0.59095	0.09
<i>Alistipes</i>	0	0	0	0	0.07	0.19	0	0	0.58771	0.09
<i>Roseococcus</i>	0	0	0	0	0.32	0.84	0	0	0.5845	0.09

<i>Flectobacillus</i>	0	0	0	0	0.14	0.37	0	0	0.58132	0.09
<i>Candidatus Hamiltonella</i>	0	0	0	0	0.22	0.59	0	0	0.57199	0.09
<i>Sulfurospirillum</i>	0	0	0	0	0.07	0.2	0	0	0.56895	0.09
<i>Aquabacterium</i>	0	0	0	0	0	0	0.01	0.02	0.56296	0.09
<i>Serratia</i>	0	0	0	0	0	0	0.07	0.19	0.5571	0.09
<i>Peredibacter</i>	0	0	0	0	0.03	0.08	0	0	0.55135	0.09
<i>Cetobacterium</i>	0.35	0.62	0	0	2.61	6.53	0.17	0.13	0.55328	0.09
<i>Morganella</i>	0.01	0.02	0	0	0	0	0.16	0.42	0.55447	0.09
<i>Sediminibacterium</i>	0.51	1.24	0.01	0.01	0.19	0.39	0	0	0.55805	0.09
<i>Chitinilyticum</i>	0	0	0	0	0.02	0.04	0.02	0.04	0.56265	0.09
<i>Enterococcus</i>	0	0	0.02	0.05	0.06	0.17	0	0	0.57218	0.08
<i>Desulfovibrio</i>	0	0	0	0	0.33	0.87	0.16	0.18	0.59531	0.08
<i>Methylocaldum</i>	0	0	0.33	0.58	0.64	1.6	0.36	0.32	0.67444	0.06