

**Effects of dietary tuna dark muscle enzymatic hydrolysis and cooking drip supplementations on growth performance, antioxidant activity and gut microbiota modulation of Bama mini-piglets**

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**Table S1. The essential fatty acid composition of the swine diets.**

Fatty acid (%) (of total FA content)	Diets		
	Control	EH-TDM	EH-TCD
Myristic acids C14:0	0.54	0.58	0.63
Palmitic acid C16:0	14.09	14.37	14.58
Stearic acid C18:0	7.68	6.39	6.29
Oleic acid C18:1	27.88	26.77	26.99
Linoleic acid C18:2	40.64	42.86	42.39
$\alpha$ -Linolenic acid C18:3	5.52	5.92	6.29
Arachidonic acid C20:4	—	—	—
Eicosapentaenoic Acid C20:5	—	0.62	0.92
Docose Hexaenoie Acid C22:6	—	0.47	0.33

**Table S2. The chemical composition of the longissimus dorsi muscle in piglets fed experimental diets (mean±SEM).** The data marked with different letters represent significant differences between different groups ( $p<0.05$ ), whereas bars labelled with the same letter correspond to results that show no statistically significant differences.

Chemical composition (%)	Longissimus dorsi muscle		
	Control	EH-TDM	EH-TCD
Crude Protein	19.96 <sup>a</sup> ±0.23	21.65 <sup>b</sup> ±0.22	23.17 <sup>c</sup> ±0.34
Crude Fat	2.09 <sup>a</sup> ±0.06	1.74 <sup>b</sup> ±0.25	1.81 <sup>b</sup> ±0.09
Ash	1.23 <sup>a</sup> ±0.03	1.17 <sup>a</sup> ±0.02	1.21 <sup>a</sup> ±0.05
Moisture	71.90 <sup>a</sup> ±0.94	75.15 <sup>b</sup> ±1.00	76.32 <sup>b</sup> ±1.26

**Table S3. The essential amino acid composition of the longissimus dorsi muscle (mean±SEM).** The data marked with different letters represent significant differences between different groups ( $p<0.05$ ), whereas bars labelled with the same letter correspond to results that show no statistically significant differences.

Essential amino acids (mg/g)	Longissimus dorsi muscle		
	Control	EH-TDM	EH-TCD
Arginine	4.21 <sup>a</sup> ±0.07	4.46 <sup>a</sup> ±0.26	4.65 <sup>b</sup> ±0.52
Histidine	1.82 <sup>a</sup> ±0.01	2.69 <sup>b</sup> ±0.02	1.97 <sup>a</sup> ±0.42
Isoleucine	3.93 <sup>a</sup> ±0.07	3.98 <sup>a</sup> ±0.23	4.75 <sup>b</sup> ±0.53
Leucine	5.76 <sup>a</sup> ±0.10	5.32 <sup>a</sup> ±0.31	6.51 <sup>b</sup> ±0.73
Lysine	1.07 <sup>a</sup> ±0.02	0.95 <sup>a</sup> ±0.05	1.13 <sup>a</sup> ±0.13
Methionine	4.54 <sup>a</sup> ±0.08	4.59 <sup>a</sup> ±0.27	5.22 <sup>b</sup> ±0.58
Phenylalanine	1.59 <sup>a</sup> ±0.03	1.46 <sup>a</sup> ±0.09	1.47 <sup>a</sup> ±0.16
Threonine	4.73 <sup>a</sup> ±0.08	5.00 <sup>a</sup> ±0.29	4.05 <sup>b</sup> ±0.45
Tryptophan	0.42 <sup>a</sup> ±0.01	0.29 <sup>b</sup> ±0.02	0.37 <sup>a</sup> ±0.42
Valine	0.26 <sup>a</sup> ±0.01	0.29 <sup>a</sup> ±0.02	0.27 <sup>a</sup> ±0.03

**Table S4. The essential fatty acid composition of the longissimus dorsi muscle (mean).**

Fatty acid (%) (of total FA content)	Longissimus dorsi muscle		
	Control	EH-TDM	EH-TCD
Myristic acids C14:0	1.41	1.15	0.79
Palmitic acid C16:0	19.54	21.94	23.93
Stearic acid C18:0	14.78	13.71	12.11
Oleic acid C18:1	4.55	2.95	2.75
Linoleic acid C18:2	22.13	19.36	19.25
$\alpha$ -Linolenic acid C18:3	2.10	4.40	3.03
Arachidonic acid C20:4	—	0.51	0.45
Eicosapentaenoic Acid C20:5	0.22	1.08	0.85
Docose Hexaenoie Acid C22:6	0.15	0.45	0.39

**Table S5. Alpha diversity of the sequencing analysis of 16S rDNA from microbiota in the fecal matter of pigs**

Item	Control	EH-TDM	EH-TCD
Sequence number	21846	41171	42129
OUT number	1249	4003	3391
Coverage	0.9652	0.9394	0.9513
ACE index	5202.49	16155.90	13234.26
Chao1 index	3323.96	10238.00	8337.53
Shannon index	3.8824	5.4010	5.2489
Simpson index	0.0785	0.0273	0.0269

**Table S6. The RDP classification of the sequences from the three groups at the phylum level.**

Phylum (%)	Control	EH-TDM	EH-TCD
Firmicutes	89.65	53.54	52.11
unclassified	5.18	13.32	19.08
Proteobacteria	3.00	16.98	17.06
Bacteroidetes	1.24	12.32	7.85
Planctomycetes	0.27	1.08	1.31
Chloroflexi	0.22	0.89	0.79
Gemmatimonadetes	0.18	0.48	0.53
Cyanobacteria	0.08	0.06	0.15
Verrucomicrobia	0.06	0.41	0.26
others	0.12	0.92	0.86

**Table S7. The RDP classification of the sequences from the three groups at the family level.**

Family (%)	Control	EH-TDM	EH-TCD
Ruminococcaceae	71.06	36.87	31.93
unclassified	4.55	10.56	17.14
Lactobacillaceae	3.9	5.57	4.65
Streptococcaceae	2.55	0.55	0.64
Enterobacteriaceae	0.75	4.35	6.1
Porphyromonadaceae	0.33	3.84	2.19
Lachnospiraceae	4.94	3.5	4.44
Peptostreptococcaceae	6.78	2.81	7.42
Rikenellaceae	0.27	2.38	1.83
Prevotellaceae	0.04	2.26	0.58
others	4.83	27.31	23.08



1 **Table S8. The eighteen most abundant genera within the three groups.**

Genus	Phylum	Class	Order	Family	Control (%)	EH-TDM (%)	EH-TCD (%)
<i>unclassified_Ruminococcaceae</i>	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	2.9	28.09	18.86
<i>unclassified</i>	—	—	—	—	4.55	10.56	17.14
<i>Subdoligranulum</i>	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	67.8	5.28	11.14
<i>unclassified_Peptostreptococcaceae</i>	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	6.78	2.81	7.4
<i>Lactobacillus</i>	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	3.9	5.56	4.64
<i>Citrobacter</i>	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	0.27	1.14	2.85
<i>unclassified_Porphyrmonadaceae</i>	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	0.31	2.93	2.06
<i>unclassified_Lachnospiraceae</i>	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	4.06	2.09	1.88
<i>Alistipes</i>	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	0.25	2.37	1.81
<i>Blautia</i>	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	0.53	0.85	1.38
<i>Enterobacter</i>	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	0.1	0.61	1.33
<i>Pseudomonas</i>	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.29	1.31	1.22
<i>Rhodobacter</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	0	0.25	1.15
<i>Serratia</i>	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	0.29	1.65	1.12
<i>Ruminococcus</i>	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	0.02	2.29	1.06
<i>Streptococcus</i>	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	2.47	0.19	0.35
<i>unclassified_Christensenellaceae</i>	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	0.04	1.27	0.33
<i>Prevotella</i>	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	0.02	1.41	0.17
others	—	—	—	—	5.42	29.34	24.11

2

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4 **Table S9. The taxonomic assignments of 100 OTUs that changed upon EH-TDM and EH-TCD treatment as identified by the**  
5 **RDA.**

OTU name	Phylum	Class	Order	Family	Genus
OTU4667	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcus</i>
OTU1207	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU4228	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU0027	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU4396	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU3881	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU4290	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU3754	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU4390	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU0018	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU0891	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Faecalibacterium</i>
OTU5312	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Subdoligranulum</i>
OTU3882	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcus</i>
OTU5534	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcus</i>
OTU2872	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	<i>unclassified_Erysipelotrichaceae</i>
OTU3920	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU0023	Firmicutes	Bacilli	Bacillales	Bacillaceae	<i>Bacillus</i>
OTU1501	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU1081	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU4178	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	<i>Enterorhabdus</i>
OTU0332	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU5944	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	<i>unclassified_Peptostreptococcaceae</i>

OTU1286	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU1584	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Streptococcus</i>
OTU0257	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Variovorax</i>
OTU0673	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU3914	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	<i>unclassified_Christensenellaceae</i>
OTU0016	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU3704	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	<i>Olsenella</i>
OTU0033	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU4053	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	<i>unclassified_Christensenellaceae</i>
OTU1345	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Serratia</i>
OTU0765	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Enterobacter</i>
OTU0541	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Faecalibacterium</i>
OTU2446	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	<i>Bacteroides</i>
OTU4852	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcus</i>
OTU2695	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	<i>Prevotella</i>
OTU4037	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	<i>unclassified_Christensenellaceae</i>
OTU0911	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU0024	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Stenotrophomonas</i>
OTU0505	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU1127	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Pantoea</i>
OTU3078	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	<i>Alistipes</i>
OTU0759	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Blautia</i>
OTU1307	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Citrobacter</i>
OTU2422	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	<i>unclassified_Porphyromonadaceae</i>
OTU0133	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Escherichia-Shigella</i>
OTU3665	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	<i>Bifidobacterium</i>

OTU0125	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU4811	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcus</i>
OTU4957	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcus</i>
OTU0436	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU5189	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcus</i>
OTU5292	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	<i>Collinsella</i>
OTU0029	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Pseudomonas</i>
OTU2548	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	<i>Barnesiella</i>
OTU0536	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU4488	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU0907	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU0028	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Streptococcus</i>
OTU0291	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Blautia</i>
OTU3034	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	<i>Solobacterium</i>
OTU2458	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	<i>Prevotella</i>
OTU4039	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Subdoligranulum</i>
OTU0032	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU6015	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	<i>unclassified_Peptostreptococcaceae</i>
OTU0143	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	<i>Enterococcus</i>
OTU4352	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	<i>Collinsella</i>
OTU4648	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Subdoligranulum</i>
OTU1444	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU1401	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU5334	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU0031	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU5171	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Rhodobacter</i>

OTU4387	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	<i>Slackia</i>
OTU1541	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU5766	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Subdoligranulum</i>
OTU4986	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>unclassified_Lachnospiraceae</i>
OTU5444	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Subdoligranulum</i>
OTU0186	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	<i>Burkholderia</i>
OTU5266	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>unclassified_Lachnospiraceae</i>
OTU5452	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Subdoligranulum</i>
OTU2219	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	<i>Solobacterium</i>
OTU1834	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU0015	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Citrobacter</i>
OTU5268	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Subdoligranulum</i>
OTU5054	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Subdoligranulum</i>
OTU1482	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>
OTU3731	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	<i>Aeriscardovia</i>
OTU5877	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Anaerotruncus</i>
OTU2978	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	<i>Solobacterium</i>
OTU1614	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Streptococcus</i>
OTU1507	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Streptococcus</i>
OTU4051	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU1615	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Streptococcus</i>
OTU5622	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU1635	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Blautia</i>
OTU3774	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	<i>Aeriscardovia</i>
OTU4064	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>
OTU4301	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>unclassified_Ruminococcaceae</i>

**Table S10. The relative abundance of the 100 OTUs that changed upon EH-TDM and EH-TCD treatment as identified by the RDA.**

OUT name	Species	Control (%)	EH-TDM (%)	EH-TCD (%)
OTU4667	<i>uncultured_bacterium</i>	0	11.58414	4.878243
OTU1207	<i>uncultured_bacterium</i>	5.453865	8.163577	6.739154
OTU4228	<i>uncultured_Ruminococcaceae_bacterium</i>	0	5.195697	2.124096
OTU0027				
OTUs	<i>uncultured_bacterium</i>	1.043959	3.270517	0.398766
OTU4396	<i>uncultured_bacterium</i>	0.004681	2.690674	0.451935
OTU3881	<i>uncultured_bacterium</i>	0.341744	2.644897	0.194066
OTU4290	<i>uncultured_bacterium</i>	0.06554	2.573688	1.914079
OTU3754	<i>uncultured_bacterium</i>	0.028089	2.090486	0.786899
OTU4390	<i>uncultured_bacterium</i>	0.009363	2.067597	0.132922
OTU0018	<i>uncultured_Lactobacillus_sp.</i>	7.551145	1.640345	13.39324
OTU0891	<i>uncultured_bacterium</i>	0	1.330078	0.17014
OTU5312	<i>uncultured_bacterium</i>	16.03857	1.078304	1.948639
OTU3882	<i>uncultured_bacterium</i>	0	1.045243	1.026159
OTU5534	<i>uncultured_bacterium</i>	1.619774	0.854505	1.733305
OTU2872	<i>uncultured_bacterium</i>	0.592851	0.830612	0.708996
OTU3920	<i>uncultured_bacterium</i>	0	0.821444	0.061144
OTU0023	<i>uncultured_Bacillus_sp.</i>	0.107673	0.793469	0.805508
OTU1501	<i>uncultured_bacterium</i>	5.238519	0.775667	1.751914
OTU1081	<i>Lactobacillus_reuteri_ATCC_53608</i>	0.26216	0.770581	0.108996
OTU4178	<i>uncultured_bacterium</i>	0	0.768666	0.350915
OTU0332	<i>uncultured_bacterium</i>	0	0.747692	0.026584
OTU5944	<i>uncultured_bacterium</i>	1.807032	0.671397	1.531263
OTU1286	<i>Lactobacillus_delbrueckii_subsp._bulgaricus</i>	0.004681	0.503548	0.06912
OTU1584	<i>uncultured_bacterium</i>	19.57305	0.488289	2.735538
OTU0257	<i>bacterium_enrichment_culture_clone_heteroB90_4W</i>	0.051496	0.462857	0.340281
OTU0673	<i>Lactobacillus_reuteri_ATCC_53608</i>	0.145124	0.455227	0.643343
OTU3914	<i>uncultured_bacterium</i>	0	0.439968	0.002658
OTU0016	<i>uncultured_bacterium</i>	0.182576	0.432339	1.145789
OTU3704	<i>uncultured_bacterium</i>	0.173213	0.419623	0.263186
OTU0033	<i>uncultured_bacterium</i>	1.844483	0.406907	0.935772
OTU4053	<i>uncultured_bacterium</i>	0	0.371303	0
OTU1345	<i>uncultured_bacterium</i>	0.06554	0.350958	0.212675
OTU0765	<i>uncultured_bacterium</i>	0.056177	0.350958	0.571565
OTU0541	<i>uncultured_bacterium</i>	0	0.350958	0.260527
OTU2446	<i>uncultured_bacterium</i>	0.093629	0.345871	0.215334
OTU4852	<i>uncultured_bacterium</i>	0	0.333155	0.111655
OTU2695	<i>uncultured_bacterium</i>	0.004681	0.330612	0.007975
OTU4037	<i>uncultured_bacterium</i>	0	0.325526	0

OTU0911	<i>Lactobacillus_reuteri_ATCC_53608</i>	0.042133	0.315353	0.015951
OTU0024	<i>uncultured_bacterium</i>	0.042133	0.31281	0.135581
OTU0505	<i>uncultured_bacterium</i>	0.028089	0.297551	0.462569
OTU1127	<i>uncultured_bacterium</i>	0.060859	0.292465	0.151531
OTU3078	<i>uncultured_bacterium</i>	0.046814	0.289921	0.15419
OTU0759	<i>uncultured_bacterium</i>	0.018726	0.287378	0.704487
OTU1307	<i>uncultured_Citrobacter_sp.</i>	0.102991	0.277206	0.539664
OTU2422	<i>uncultured_bacterium</i>	0.060859	0.274662	0.172799
OTU0133	<i>uncultured_bacterium</i>	0.051496	0.267033	0.039877
OTU3665	<i>Bifidobacterium_thermophilum_RBL67</i>	0.107673	0.261947	0.840068
OTU0125	<i>Lactobacillus_sp._RA2113</i>	0.004681	0.259403	0.106338
OTU4811	<i>uncultured_bacterium</i>	0	0.259403	0.079753
OTU4957	<i>uncultured_bacterium</i>	0	0.239058	0.053169
OTU0436	<i>Lactobacillus_sp._ACD7</i>	0.028089	0.233972	0.489154
OTU5189	<i>uncultured_bacterium</i>	0	0.233972	0.015951
OTU5292	<i>uncultured_bacterium</i>	0	0.233972	0
OTU0029	<i>Pseudomonas_plecoglossicida</i>	0.023407	0.231428	0.364207
OTU2548	<i>uncultured_bacterium</i>	0	0.226342	0.281795
OTU0536	<i>uncultured_bacterium</i>	0.018726	0.213626	0.412059
OTU4488	<i>uncultured_bacterium</i>	0.004681	0.213626	0.042535
OTU0907	<i>uncultured_bacterium</i>	0.037451	0.203454	0.010634
OTU0028	<i>uncultured_bacterium</i>	3.927719	0.185651	0.893237
OTU0291	<i>uncultured_bacterium</i>	0.009363	0.162763	0.414717
OTU3034	<i>uncultured_bacterium</i>	0	0.15259	1.685453
OTU2458	<i>uncultured_bacterium</i>	0.018726	0.144961	0.401425
OTU4039	<i>uncultured_bacterium</i>	1.980244	0.124615	0.132922
OTU0032	<i>Lactobacillus_reuteri_ATCC_53608</i>	0.416647	0.114443	0.808167
OTU6015	<i>uncultured_bacterium</i>	0.149806	0.09664	0.220651
OTU0143	<i>Enterococcus_casseliflavus</i>	0.042133	0.094097	0.329647
OTU4352	<i>uncultured_bacterium</i>	0.03277	0.094097	0.313696
OTU4648	<i>uncultured_bacterium</i>	1.151631	0.089011	0.093046
OTU1444	<i>uncultured_bacterium</i>	0.257479	0.078838	0.159507
OTU1401	<i>Lactobacillus_reuteri_ATCC_53608</i>	0.215346	0.071209	0.122288
OTU5334	<i>uncultured_bacterium</i>	0.585179	0.066122	0.042535
OTU0031	<i>uncultured_bacterium</i>	0.477506	0.053407	0.707146
OTU5171	<i>uncultured_bacterium</i>	0.004681	0.053407	0.231285
OTU4387	<i>uncultured_bacterium</i>	1.320163	0.043234	0.287112
OTU1541	<i>Lactobacillus_reuteri_ATCC_53608</i>	0.308974	0.043234	0.087729
OTU5766	<i>uncultured_bacterium</i>	0.62263	0.040691	0.066461
OTU4986	<i>uncultured_bacterium</i>	0.575816	0.033061	0.026584
OTU5444	<i>uncultured_bacterium</i>	0.346426	0.025432	0.047852
OTU0186	<i>uncultured_bacterium</i>	0.223407	0.023906	0.013026
OTU5266	<i>uncultured_bacterium</i>	0.889471	0.022889	0.093046
OTU5452	<i>uncultured_bacterium</i>	0.243434	0.022889	0.210017

OTU2219	<i>uncultured_bacterium</i>	0	0.022889	0.207359
OTU1834	<i>uncultured_bacterium</i>	0.215346	0.020345	0.066461
OTU0015	<i>uncultured_Citrobacter_sp.</i>	0.004681	0.020345	0.199383
OTU5268	<i>uncultured_bacterium</i>	0.68817	0.017802	0.026584
OTU5054	<i>uncultured_bacterium</i>	0.22939	0.017802	0.039877
OTU1482	<i>uncultured_Lactobacillus_sp.</i>	0.318337	0.015259	0.11963
OTU3731	<i>Bifidobacteriaceae_genomosp._C1</i>	0.26216	0.015259	0.319013
OTU5877	<i>uncultured_bacterium</i>	0	0.012716	0.178116
OTU2978	<i>uncultured_bacterium</i>	0	0.010173	0.180774
OTU1614	<i>uncultured_bacterium</i>	0.257479	0.005086	0.013292
OTU1507	<i>uncultured_bacterium</i>	0.220027	0.005086	0.010634
OTU4051	<i>uncultured_bacterium</i>	0	0.005086	1.374415
OTU1615	<i>uncultured_bacterium</i>	0.257479	0.002543	0
OTU5622	<i>uncultured_bacterium</i>	0	0.002543	0.337622
OTU1635	<i>uncultured_bacterium</i>	0.992463	0	0
OTU3774	<i>Aeriscardovia_aeriphila</i>	0.716259	0	0.786899
OTU4064	<i>uncultured_bacterium</i>	0	0	0.481178
OTU4301	<i>uncultured_bacterium</i>	0	0	0.345598

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