

1 Health and Disease

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3 **Gastrointestinal microbial population of turkey (*Meleagris gallopavo*) affected by**

4 **Haemorrhagic Enteritis virus**

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19 **ABSTRACT**

20 Haemorrhagic enteritis (HE) is an acute viral disease that affects avian species, particularly turkeys,  
21 compromising their commercial production and having a negative effect on animal welfare. Turkey  
22 adenovirus 3 (TAdV-3), is the main causal agent of the disease and in this study we considered  
23 three groups of turkeys to get two purposes: 1) A preliminary investigation on the microbiota  
24 content in the four parts of healthy turkey's intestine (group A), namely duodenum, jejunum, ileum  
25 and ceca were done; 2) an investigation on the relationship between natural infections with this  
26 virus and the intestinal microbiota in the jejunum, where HE mostly develops, comparing group A  
27 with group B (animals with molecular positivity for the virus and with clinical signs of HE) and  
28 group C (animals with molecular positivity for the virus but without clinical signs). Massive  
29 sequencing of the hypervariable V1-V2 regions of 16S rRNA gene and QIIME 1.9.1 software  
30 analysis was performed, and operation taxonomic units (OTUs) were classified into four abundant  
31 phyla: *Actinobacteria*, *Bacteroidetes*, *Firmicutes* and *Proteobacteria*. The microbial population of  
32 small intestine was distributed almost homogeneously in the healthy turkeys, and *Firmicutes* was  
33 the prevalent phylum (79.85% in duodenum, 89.57% in jejunum and 99.28% in ileum). As  
34 compared with small intestine, ceca microbial community was much more heterogeneous:  
35 *Firmicutes* (48.03%), *Bacteroidetes* (33.60%) and *Proteobacteria* (12.32%). In the natural  
36 infections of HEV, the main bacterial families were *Bacteroidaceae* (*Bacteroidetes*) and  
37 *Peptostreptococcaceae* (*Firmicutes*), uniquely detected in group B and C. Also *Clostridiaceae*  
38 (*Firmicutes*) was detected, uniquely in group B.

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40 Keywords: Gut microbiota, hemorrhagic enteritis, turkey, 16S

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## INTRODUCTION

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46 The gastrointestinal tract is colonized by beneficial bacteria that are essential for promoting normal  
47 intestinal development, physiology and digestion establishing meanwhile a mutualistic relationship  
48 with the host (Nicholson et al., 2012; Tremaroli and Bäckhed, 2012). Microbial communities have  
49 also adapted to colonize different locations in the intestine, allowing unique interactions with the  
50 immune system and collectively influencing its intestinal immune cell homeostasis (Cebra, 1999).  
51 Dysregulated localization of mutualistic bacteria and dysbiosis is associated with infectious and  
52 inflammatory diseases and can lead to inappropriate activation of the immune system (Ma et al.,  
53 2011; Oakley et al., 2014; Perumbakkam et al., 2014; Karst, 2016). In avian species, the  
54 gastrointestinal tract microbiota is composed by fungi, protozoa and bacteria, the last being the  
55 predominant microorganisms. The populations of bacteria keep changing during growth as related  
56 to age, diet, breed and geographic location (Pan and Yu, 2013a; Oakley et al., 2014). Avian  
57 microbiota is composed at phylum level by *Firmicutes*, *Bacteroidetes* and *Proteobacteria*:  
58 *Lactobacillus* (*Firmicutes*), *Bacilli* (*Firmicutes*) and *Enterococcus* (*Firmicutes*) are the most  
59 abundant genera (Wei et al., 2013; Mancabelli et al., 2016). In commercially important species such  
60 as chickens and turkeys, the microbiota has been recently reviewed (Pan and Yu, 2013b; Waite and  
61 Taylor, 2015) and a phylogenetic diversity census of poultry intestinal bacteria showed that  
62 chickens and turkeys share only 16% similarity between their respective microbiotas at the species-  
63 equivalent level (Wei et al., 2013). Information about the microbiota composition, using the 16S  
64 rRNA gene, of the regions of small intestine in turkey species such as duodenum and jejunum, we  
65 found that an investigation was carried out to identify the microbiota of heavy and light turkey  
66 flock, in order to study the relationship between bacterial community composition and the  
67 insurgency of Light Turkey Syndrome (Danzeisen et al., 2013). However the microbiota  
68 composition of the regions of small intestine is lacking, in healthy or in pathological conditions.  
69 Instead, a more recent study investigated the temporal relationship between ileal microbiota during  
70 development, and the impact of low-dose penicillin on bacterial community of ileum and cecum

71 (Danzeisen et al., 2015). At ceca level differences in the bacteria genera present in turkeys were  
72 determined (Scupham et al., 2008), and time-dependent differences in turkey intestinal tract were  
73 identified as well (Scupham, 2009) by means of culture-based or lower output molecular fingerprint  
74 methods, such as ARISA or T-RFLP. The methods used had limitations and biases that could be  
75 exceeded with the advent of next-generation sequencing (NGS). It has fuelled the metagenomics  
76 studies to identify the genomes of entire communities, including those of uncultivated organisms,  
77 using the 16S rRNA gene because it is a marker for investigating bacterial phylogeny (Tremblay et  
78 al., 2015).

79 Haemorrhagic enteritis is an acute viral disease affecting mainly turkeys of 4 weeks of age and  
80 older (*Meleagris gallopavo*) caused by turkey adenovirus 3 (TAdV-3), member of genus  
81 *Siadevovirus* (Sharma, 1991; Beach et al., 2009). The common clinical signs of the disease include  
82 depression, bloody droppings, and death; also is likely transmitted through the fecal-oral/cloacal  
83 route (Dhama et al., 2017). Oral infection of susceptible turkeys with pathogenic TAdV-3 strains  
84 results in well-characterized splenomegaly and intestinal bleeding in 4 to 6 days causing subclinical  
85 infections and mortality (Suresh and Sharma, 1996). Haemorrhagic adenovirus is one of the most  
86 important causes of economic loss to turkey industry and the mortality ranges between 10-15% but  
87 can reach 60% in some flocks (Dhama et al., 2017) . Infection with HE virus results in a transient  
88 immunosuppression, paving the ways for other diseases that can struck the animals that survived to  
89 the first wave of infection. This second wave of infections are lethal for the major part of animals,  
90 given that colisepticemia often follows clinical and subclinical infections with HE 12-14 days later  
91 (Moura-Alvarez et al., 2014). Gross pathology presents dilated intestine with blood content, and  
92 yellowish substance on the intestinal mucosa (Dhama et al., 2017). At microscopic level severe  
93 congestion in the intestinal mucosa, degeneration and shortening of the villi and bleeding at the tips  
94 of them are observed (Sharma, 1991). Given the background that viruses infecting the  
95 gastrointestinal tract are related with the host microbiota, and that emerging data suggest enteric  
96 viruses are regulated by microbial population through a series of processes termed “transkingdom

97 interactions” (Pfeiffer and Virgin, 2016), the aim of the present investigation was to characterize the  
98 relationship between HEV infection and the turkey intestinal microbiota by means of next  
99 generation sequencing of 16S rRNA genes. The first part of this study analysed the microbiota of  
100 the four intestinal tracts, including duodenum, jejunum, ileum, and cecum, collected from healthy  
101 turkeys. The second part aims to understand the changes at the jejunum microbiota in HEV-infected  
102 turkeys, by comparing HEV positive animals either with or without clinical signs versus healthy  
103 ones.

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## MATERIALS AND METHODS

107 ***Sample collection.*** The present study was carried out on commercial B.U.T. BIG6 hybrid turkeys.  
108 Ethical standards for commercial turkey production were therefore followed by the company during  
109 fattening and slaughtering of turkeys. All the samples were collected from prepuberal females of 80  
110 days-old.

111 The microbiota from intestinal tracts was determined from three groups of turkeys, including  
112 healthy turkeys (group A), HE affected turkeys (group B), and turkeys positive for HEV but without  
113 clinical signs (group C). Four clinically healthy turkeys were sorted out during routine slaughtering  
114 procedures (group A). Pathological analysis of the gastro enteric tract evidenced no sign of gross  
115 pathological lesions related to enteritis. Molecular diagnosis to rule out the presence of HEV was  
116 carried out in the four tracts of intestine and spleen by means of specific PCR (Hess et al., 1999)  
117 confirming that the animals were healthy and no virus was present in their organism. Intestinal  
118 content was collected from 2 cm tract of each district, including jejunum, duodenum, ileum and  
119 ceca, by scraping the intestinal mucosa with a sterile plastic scraper (Cell Scrapers, Sterile, Greiner  
120 Bio-One, VWR, Milano, Italy). Collected samples were snap frozen in liquid nitrogen.

121 A second set of samples (group B) was collected from a group of four turkeys with evident acute  
122 clinical signs of HE and animals were subjected to euthanasia due to their critical clinical

123 conditions, by cervical dislocation. Gross pathology confirmed the presence of enteritis lesions  
124 compatible with HE acute infection in jejunum, but no signs were found on the other districts of the  
125 intestine. The presence of HEV was confirmed with molecular diagnosis (PCR) which was positive  
126 in both jejunum and spleen. Samples for microbiota determination were collected as previously  
127 described for healthy animals.

128 A third set of four samples (group C) was collected during routine slaughtering procedures from  
129 animals that did not evidence any clinical sign of HE although being raised in the same barn of the  
130 infected turkeys. Gross pathology did not evidence any lesion throughout intestinal tracts.  
131 Molecular diagnosis of intestine sections was negative. On the contrary, presence of HEV was  
132 confirmed in spleen by PCR.

133 All the animals included in the experiment were never treated with antibiotic or probiotics.

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135 ***Bacterial DNA extraction and sequence analysis.*** The bacterial DNA was extracted using  
136 Powersoil® DNA extraction kit (Mobio), according to the manufacturer's instructions. DNA  
137 samples were eluted in 100 µl and stored at -20°C until further processing. The DNA concentration  
138 was quantified by NanoDrop ND-1000 UV–vis spectrophotometer (NanoDrop Technologies) and  
139  $A_{260}/A_{280}$  ratio was ~1.8. The bacterial hypervariable regions V1-V2 of 16S rRNA gene were  
140 amplified by PCR with primer pair F27 (5'-AGAGTTTGATCCTGGCTCAG-3') and R338 (5'-  
141 TGCTGCCTCCCGTAGGAGT-3'). Both primers included sequencing adaptors at the 5' end and  
142 forward primers were tagged with different barcodes. These hypervariable regions were chosen by  
143 the frequency with which they are used in research and because they contain a high discriminatory  
144 power for bacterial species (Chakravorty et al., 2007; Engelbrektsen et al., 2010; Fouhy et al.,  
145 2016). PCR mixture (50µL) contained 2 µl of DNA template (~5 ng), 5 µl of 10x AccuPrime™  
146 PCR Buffer II, 0.2 µM of each primer and 1 U of AccuPrime™ Taq DNA Polymerase High Fidelity  
147 (Life Technologies). The PCR thermal profile was 2 min at 94 °C, followed by 30 cycles of 1 min  
148 at 94 °C, 1 min at 55 °C, 1 min at 72 °C and a final extension of 7 min at 72 °C. For each amplicon,

149 both concentration and quality were determined using Agilent Bioanalyzer 2100. Samples were  
150 sequenced on an Ion Torrent Personal Genome Machine (PGM) with the Ion 318 Chip Kit v2 (Life  
151 Technologies) under manufacturer's conditions.

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153 ***Bioinformatics and Data Analysis.*** Raw reads (<https://www.ncbi.nlm.nih.gov>, BioProject  
154 PRJNA347549) were de-multiplexed, quality-filtered and analysed using QIIME 1.9.1 software  
155 (Caporaso et al., 2011). Reads included had: a length greater than 300 nt; a mean quality score  
156 above 25 in sliding window of 50 nucleotides; no mismatches on the primer; and default values for  
157 other quality parameters.

158 Quality-filtered reads were clustered into operational taxonomic units (OTUs) at 97% similarity,  
159 using UCLUST in an open reference approach for taxonomy analyses. Taxonomic assignment of  
160 representative OTUs was performed using the RDP Classifier (Wang et al., 2007) against  
161 Greengenes v13.8 database. Alignment of sequences was performed using PyNast (Caporaso et al.,  
162 2011) as default in QIIME pipeline. Via VSEARCH (Westcott and Schloss, 2015; Rognes et al.,  
163 2016), the chimeric sequences (24.1%) were removed, and then we applied two filtering steps in  
164 aligned and taxonomy-assigned OTU table: first, sequences corresponding to chloroplast class were  
165 filtered-out, and then sequences that represent less than 0.005% of total OTUs were also filtered-out  
166 from the OTU table. Downstream analyses were performed using QIIME 1.9.1 (Caporaso et al.,  
167 2011) at a depth of 78.500 sequences per sample for the healthy group and 93.300 sequences for the  
168 comparison of the jejunum tract for the three groups of turkeys to standardize for unequal  
169 sequencing depth of the samples. In alpha diversity (within a sample) we used two different metrics:  
170 observed species (that considers only the richness of OTUs) and Shannon index (that estimates the  
171 relative abundance of OTUs in addition to the richness). In beta diversity (between samples),  
172 Unweighted UniFrac distance matrix (Lozupone et al., 2011) was used to create PCoA plots.  
173 Adonis and ANOSIM were used to assess the statistical differences among the four intestinal tracts

174 of the healthy turkeys, and among the three jejunum groups corresponding to different health status  
175 of turkeys.

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## RESULTS

179 To assess composition of intestinal turkeys' microbiota in healthy birds and HEV infected one, we  
180 analysed 3 groups of animals (each group gather 4 animals): healthy (group A), HE affected (group  
181 B), and HEV positive but without clinical signs (group C).

182 We investigated on 1) the composition of intestinal microbiota in 4 healthy turkeys (group A),  
183 collecting a total 16 samples, from the fourth intestinal tract: 4 duodenum, 4 jejunum, 4 ileum and 4  
184 ceca samples. Then 2) we compared the 4 jejunum samples of group A, with 8 jejunum samples of  
185 turkeys belonging to two different group, depending on the health status: 4 HE affected turkeys  
186 (group B) and 4 HEV positive turkeys but without clinical signs (group C).

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188 **Group A: Intestinal microbiota of healthy turkeys.** A total of 3400569 reads were obtained and  
189 divided in 654 OTUs. *Firmicutes* is the most abundant phylum, almost 80% in duodenum, then  
190 values rising almost to 90% in jejunum and to 98% in ileum. The abundance of *Firmicutes*  
191 diminishes in the ceca (46.44%). At the duodenum taxonomic level, the most abundant family from  
192 *Firmicutes* is *Lactobacillaceae* (72.45%). The remainder OTUs belonged to *Proteobacteria*  
193 (6.75%), *Actinobacteria* (3.65%), *Bacteroidetes* (3.22%) and *Cyanobacteria* (0.56%). In jejunum,  
194 with 87.82% of OTUs corresponding to *Firmicutes*, *Lactobacillaceae* provides the 86.47% of the  
195 sequences at family level. In ileum, *Firmicutes* represented the 97.94% of bacteria detected, and the  
196 main families are *Lactobacillaceae* (52.82%) and *Clostridiaceae* (42.93%). Comparing with  
197 duodenum and jejunum, in the ileum we observed a drop in the presence of *Lactobacillaceae* family  
198 and the appearance of OTUs from the *Clostridiaceae* family, which increases from 0.30% in the  
199 duodenum and 0.30% in the jejunum to 42.93% in the ileum (Table 1, Fig. 1 and, in explanation to



200 Fig.1, the supplementary Table S1). The present results mostly agree with those previously reported  
201 (Danzeisen et al., 2013, 2015), which identified *Lactobacillaceae* and *Clostridiaceae* as the most  
202 abundant families in the ileum and ceca respectively, in a commercial flock of turkeys (62% and  
203 36% respectively).

204 The ceca tract shows more diversity at the phylum level, with *Firmicutes* (46.44%), *Bacteroidetes*  
205 (31.32%) and *Proteobacteria* (11.51%) being the most abundant phyla, whereas at family level  
206 there are more bacterial communities as compared to the other tracts. The most abundant families  
207 are *Lachnospiraceae* (15.35%) and *Veillonellaceae* (16.66%) for *Firmicutes*; *Bacteroidaceae*  
208 (17.87%; *Bacteroidetes*), and *Alcaligenaceae* (11.43%; *Proteobacteria*) (Table 1, Fig. 1 and, in  
209 explanation to Fig.1, the supplementary Table S1). Although the present results are consistent to  
210 those previously reported in a meta-analytic investigation (Wei et al. 2013), they differ from others  
211 previously reported (Danzeisen et al., 2015), which demonstrated the presence of a higher  
212 concentration of *Clostridia* species in ceca (more than 70% of the bacterial population).

213 Differences in bacterial communities among the four intestinal parts of healthy turkeys (duodenum,  
214 jejunum, ileum and cecum) were analysed using the rarefaction curves, PCoA plots and phylogeny-  
215 based unweighted UniFrac distance matrix, obtained with QIIME pipeline. Rarefaction curves were  
216 generated with a depth of 78,500 for richness (observed species) and evenness (Shannon index) to  
217 describe the alpha diversity. Values of the Observed species and Shannon index in the different  
218 zone of the intestine in healthy turkeys are showed in Table 2. The species richness from the ceca  
219 tract is higher than the other tracts.

220 Beta diversity was calculated by unweighted UniFrac phylogenetic distance matrix. The PCoA plot  
221 in Fig. 2 shows a clustering of samples for ceca. For statistical testing, we applied ANOSIM and  
222 adonis test (analysis of similarity), to determine significant differences considering a probability (*p*-  
223 value) less than 0.05 to denote significance in microbial communities among these intestine tracts.  
224 Adonis test shows a *p*-value of 0.001 and the R<sup>2</sup> value (effect size) which shows a percentage of  
225 variation of 0.43. It means that clustering samples among different tracts of intestine, explained

226 43% of the distance among samples. The same was done for the ANOSIM test: obtaining a *p*-value  
227 of 0.002 and an R<sup>2</sup> value of 0.52, it indicates dissimilarity between the intestinal tracts; it is  
228 explicated by the changes of bacterial abundance in the alpha diversity analysis (Table 2).

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230 **Group A – Group B – Group C: Differences in jejunum tract during HEV infection.** A total of  
231 2199136 reads were obtained and divided in 654 OTUs. The second part of this study explored the  
232 relationship between natural HEV infection and the microbial community. Focus was on jejunum,  
233 on the background that this is the region of the gastro intestinal apparatus that is more affected by  
234 HEV infection. Microbial community was collected from healthy turkeys (group A), HE affected  
235 turkeys (group B), and turkeys positive for HEV but without clinical signs (group C). The most  
236 striking difference was the evident decrease of the *Lactobacillaceae* in HE affected animals  
237 (65.16%) as compared to the 86.47% of the healthy animals. *Clostridiaceae* had a higher percentage  
238 in HE affected animals (7.35%), compared with the other two groups of animals (<0.3%) (Table 3,  
239 Fig. 3 and, in explanation to Fig.3, the supplementary Table S2).

240 Interestingly, there are two families, *Bacteroidaceae* and *Peptostreptococcaceae*, which are  
241 detected in jejunum tract of groups B and C, but are absent in group A (Fig. 3).

242 The procedure was the same used for the analysis in the different tracts of the intestine in healthy  
243 animals. We obtained rarefaction curves with a depth of 93.300 and the observed species values  
244 were: 200.5 in group A; 202.5 in group B; 165 in group C (Table 4). The richness and the evenness  
245 of bacterial species is homogeneous in the three groups. When we analyse data with the unweighted  
246 UniFrac distance matrix (Fig. 4), we identified two clusters of samples: the group A, is separated  
247 from groups B and C but none statistically significant results were found with ANOSIM and adonis  
248 test.

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## DISCUSSION

252 **Group A: Intestinal microbiota of healthy turkeys.** The distribution of bacterial communities and  
253 the richness of bacterial families did not present any statistically significant difference among the  
254 healthy animals, probably due to the fact that the animals recruited in the present experiment were  
255 reared in the same flock, and homogeneous for feeding and sampling time. Age, sex, genetic  
256 background of the host and diet are regarded as the main factors influencing the composition of  
257 gastrointestinal microbiota in each intestinal tract in both mammalian (Langille and Zaneveld,  
258 2013) and avian species (Wilkinson et al., 2016). It can be ruled out any difference in ceca  
259 microbiota related to age, given that the analysis was carried out on animals with an age  
260 corresponding to that of previous experiments (Danzeisen et al. 2015). The differences between the  
261 present results and those previously reported may be related to genetic differences. The present  
262 investigation was carried out on a homogeneous population of hybrid B.U.T. BIG6 turkeys. The  
263 previous studies did not provide this information. Different genetic basis may have an impact on  
264 immune system, which is known to be related to the microbiota development in the gastro intestinal  
265 tract.

266 A recent study on Japanese quail (*Coturnix japonica*) demonstrated that sex differences can have a  
267 major impact on cecum microbiota (Wilkinson et al., 2016). We may also speculate that differences  
268 between the present investigation and the other previously reported might also be due to sex  
269 differences between the groups of animals included in the respective studies, at least for what  
270 concerns the study of Danzeisen et al. (2013), whereas the turkey microbiota of ceca and Ileum  
271 (Danzeisen et al. 2015) was determined on an homogeneous female population.

272 The microbial distribution agrees the result reported in a study on chicken, which demonstrated that  
273 the community of small intestine, namely duodenum, jejunum and ileum, is more homogeneous  
274 than the microbial community of ceca (Oakley et al. 2014). The small intestine harbours mostly  
275 *Lactobacillaceae* and *Clostridiaceae*, as confirmed by the present study, their role being to mediate  
276 starch breakdown and lactic acid fermentation. On the contrary, as compared to small intestine,  
277 microbial community is much more heterogeneous in ceca, which acts as a large reservoir for the

278 commensal bacteria that are involved in the fermentative digestion of the complex carbohydrates  
279 that cannot be dealt with by small intestinal enzymes (Waite and Taylor, 2014).

280

281 **Group A – Group B – Group C: Differences in jejunum tract during HEV infection.** The aim was  
282 to determine the relationship between the jejunum microbiota and natural HEV infection,  
283 considering turkeys with or without clinical sign and evident gross pathological lesions (group B  
284 and C respectively) and compare them with the healthy one (group A) to see if a difference in the  
285 distribution of bacterial communities occurs. From a genomic perspective, *Peptostreptococci* are  
286 more closely related to clostridia than *Streptococci* (Murray et al., 1991). *Peptostreptococcus*  
287 species are commensal organisms in chicken ileum (Mohd Shaufi et al., 2015), and their presence  
288 have been shown to be modified (albeit reduced) in faeces after Marek virus infection  
289 (Perumbakkam et al., 2014). In turkey, the caecal presence of *Peptostreptococci* was significantly  
290 increased in high fiber-fed turkeys (Bedbury and Duke, 1983). *Bacteroides* spp are anaerobic, non-  
291 spore forming, gram negative rods that are normally found in the lower digestive tract, especially  
292 ceca, of poultry. *Bacteroides* are rarely associated with diseases. *Bacteroides fragilis* has been  
293 isolated from salpingitis in laying hens (Bisgaard and dam, 1981), and *Bacteroides* has been  
294 associated with phallus inflammation of ganders (Behr et al., 1990).

295 Multiple hypotheses regarding the immunopathogenesis of HE and related viruses have been  
296 proposed. Based on the work of Rautenschlein and Sharma (2000) it was suggested the following,  
297 editorialized model. After oral exposure, HEV either undergoes an initial round of replication in B-  
298 lymphocytes located in the intestine and Bursa of Fabricius, or it travels directly to the spleen via  
299 the peripheral blood where it infects more B-cells and macrophages and replicates to high numbers.  
300 This results in an influx of CD4+ T-cells and macrophages into the white pulp, presumably in an  
301 attempt to clear virus and/or support the immune reaction, and accounts for the spleen hyperplasia  
302 observed during the acute phase of infection. We speculate that the animals of group C, on the  
303 background that they did not present any pathological nor histopathological lesion in duodenum,

304 were less susceptible to the lesions of the virus, which was still present at spleen level. We cannot  
305 rule out the possibility that the different composition of bacterial community lies at the background  
306 of this different susceptibility to the intestinal disease.

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308 The results presented in this investigation provides the background for future studies aimed at  
309 deciphering host-microbiota and microbe-microbe interactions to improve turkey health through the  
310 modulation of microbial intestinal population, providing the knowledge to enhance bird growth and  
311 improve turkey immune defences against enteric diseases.

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336 **Compliance with ethical standards**

337 **Conflict of interest.** All the authors declare that they have no conflict of interest.

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340 **Ethical approval.** Ethical standards for commercial turkey production were therefore followed by  
341 the company during fattening and slaughtering of the animal.

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## REFERENCES

- 343
- 344 Beach, N. M., R. B. Duncan, C. T. Larsen, X. J. Meng, N. Srianganathan, and W. F. Pierson. 2009.
- 345 Comparison of 12 turkey hemorrhagic enteritis virus isolates allows prediction of genetic
- 346 factors affecting virulence. *J. Gen. Virol.* 90:1978–1985.
- 347 Bedbury, H. P., and G. E. Duke. 1983. Cecal microflora of turkeys fed low or high fiber diets:
- 348 enumeration, identification, and determination of cellulolytic activity. *Poult Sci* 62:675–682
- 349 Behr KP, Hinz KH, Rottmann S. Phallus-inflammation of ganders: clinical observations and
- 350 comparative bacteriological examinations of healthy and altered organs. *Zentralbl*
- 351 *Veterinarmed B.* 1990 Dec;37(10):774-6.
- 352 Bisgaard M, Dam A (1981) Salpingitis in poultry. II. Prevalence, bacteriology, and possible
- 353 pathogenesis in egg-laying chickens. *Nord Vet Med.* 1981 Feb;33(2):81-9.
- 354 Caporaso, J. G., J. Kuczynski, J. Stombaugh, K. Bittinger, F. D. Bushman, E. K. Costello, N. Fierer,
- 355 A. G. Peña, K. Goodrich, J. I. Gordon, G. a Huttley, S. T. Kelley, D. Knights, E. Jeremy, R. E.
- 356 Ley, C. a Lozupone, D. Mcdonald, B. D. Muegge, J. Reeder, J. R. Sevinsky, P. J. Turnbaugh,
- 357 and W. a Walters. 2011. NIH Public Access. 7:335–336.
- 358 Cebra, J. J. 1999. Influences of microbiota on intestinal immune system. 69:1046–1051.
- 359 Chakravorty, S., D. Helb, M. Burday, and N. Connell. 2007. A detailed analysis of 16S ribosomal
- 360 RNA gene segments for the diagnosis of pathogenic bacteria. *J Microbiol Methods* 69:330–
- 361 339.
- 362 Danzeisen, J. L., A. J. Calvert, S. L. Noll, B. McComb, J. S. Sherwood, C. M. Logue, and T. J.
- 363 Johnson. 2013. Succession of the turkey gastrointestinal bacterial microbiome related to
- 364 weight gain. *PeerJ* 1:e237
- 365 Danzeisen, J. L., J. B. Clayton, H. Huang, D. Knights, B. McComb, S. S. Hayer, and T. J. Johnson.
- 366 2015. Temporal Relationships Exist Between Cecum, Ileum, and Litter Bacterial Microbiomes
- 367 in a Commercial Turkey Flock, and Subtherapeutic Penicillin Treatment Impacts Ileum
- 368 Bacterial Community Establishment. *Front. Vet. Sci.* 2:56

369 Dhama, K., V. Gowthaman, K. Karthik, R. Tiwari, S. Sachan, M. A. Kumar, M. Palanivelu, Y. S.  
370 Malik, R. K. Singh, and M. Munir. 2017. Haemorrhagic enteritis of turkeys – current  
371 knowledge. *Vet. Q.* 37:31–42

372 Engelbrektsen, A., V. Kunin, K. C. Wrighton, N. Zvenigorodsky, F. Chen, H. Ochman, and P.  
373 Hugenholtz. 2010. Experimental factors affecting PCR-based estimates of microbial species  
374 richness and evenness. *ISME J.* 4:642–647

375 Fouhy, F., A. G. Clooney, C. Stanton, M. J. Claesson, P. D. Cotter, J. Shendure, H. Ji, T. Glenn, E.  
376 Mardis, S. Shokralla, J. Spall, J. Gibson, M. Hajibabaei, G. Weinstock, D. Raoult, B.  
377 Henrissat, A. Walker, J. Martin, P. Scott, J. Parkhill, H. Flint, K. Scott, Z. Yu, M. Morrison,  
378 M. Nelson, H. Morrison, J. Benjamino, S. Grim, J. Graf, A. McOrist, M. Jackson, A. Bird, M.  
379 Claesson, S. Cusack, O. O’Sullivan, R. Greene-Diniz, H. Weerd, E. Flannery, E. Aronesty, R.  
380 Edgar, B. Haas, J. Clemente, C. Quince, R. Knight, G. Allard, F. Ryan, I. Jeffery, and M.  
381 Claesson. 2016. 16S rRNA gene sequencing of mock microbial populations- impact of DNA  
382 extraction method, primer choice and sequencing platform. *BMC Microbiol.*

383 Hess, M., R. Raue, and H. M. Hafez. 1999. PCR for specific detection of haemorrhagic enteritis  
384 virus of turkeys, an avian adenovirus. *J. Virol. Methods* 81:199–203.

385 Karst, S. M. 2016. The influence of commensal bacteria on infection with enteric viruses. *Nat Rev*  
386 *Micro advance on:*197–204.

387 Langille, M. G. I., and J. Zaneveld. 2013. Predictive functional profiling of microbial communities  
388 using 16S rRNA marker gene sequences. *Nat. Biotechnol.* 31:1–20

389 Lozupone, C., M. E. Lladser, D. Knights, J. Stombaugh, and R. Knight. 2011. UniFrac: An  
390 effective distance metric for microbial community comparison. *ISME J.* 5:169–172

391 Ma, C., X. Wu, M. Nawaz, J. Li, P. Yu, J. E. Moore, and J. Xu. 2011. Molecular characterization of  
392 fecal microbiota in patients with viral diarrhea. *Curr. Microbiol.* 63:259–266.

393 Mancabelli, L., C. Ferrario, C. Milani, M. Mangifesta, F. Turrone, S. Duranti, G. A. Lugli, A.  
394 Viappiani, M. C. Ossiprandi, D. van Sinderen, and M. Ventura. 2016. Insights into the



395 biodiversity of the gut microbiota of broiler chickens. *Environ. Microbiol.* 0:1462–2912

396 Mohd Shaufi, M. A., C. C. Sieo, C. W. Chong, H. M. Gan, and Y. W. Ho. 2015. Deciphering  
397 chicken gut microbial dynamics based on high-throughput 16S rRNA metagenomics analyses.  
398 *Gut Pathog.* 7:4

399 Moura-Alvarez, J., L. F. N. Nuñez, C. S. Astolfi-Ferreira, T. Knöbl, J. L. Chacón, A. M. Moreno,  
400 R. C. Jones, and A. J. P. Ferreira. 2014. Detection of enteric pathogens in Turkey flocks  
401 affected with severe enteritis, in Brazil. *Trop. Anim. Health Prod.* 46:1051–1058.

402 Murray, B. E., Singh, K. V., Markowitz, S. M., Lopardo, H. A., Patterson, J. E., Zervos, M. J.,  
403 Rubeglio, E., Eliopoulos, G. M., Rice, L. B., Goldstein, F. W., Jenkins, S. G., Caputo, G. M.,  
404 Nasnas, R., Moore, L. S., Wong, E. S., Weinstock G. (1991). Evidence for clonal spread of a  
405 single strain of  $\beta$ -lactamase-producing *Enterococcus* (*Streptococcus*) *faecalis* to six hospitals in  
406 five states. *Journal of Infectious Diseases*, 163(4), 780-785.

407 Nicholson, J. K., E. Holmes, J. Kinross, R. Burcelin, G. Gibson, W. Jia, and S. Pettersson. 2012.  
408 *Metabolic Interactions. Science* (80-. ). 108:1262–1268.

409 Oakley, B. B., H. S. Lillehoj, M. H. Kogut, W. K. Kim, J. J. Maurer, A. Pedroso, M. D. Lee, S. R.  
410 Collett, T. J. Johnson, and N. A. Cox. 2014. The chicken gastrointestinal microbiome. *FEMS*  
411 *Microbiol. Lett.* 360:100–112.

412 Pan, D., and Z. Yu. 2013a. Intestinal microbiome of poultry and its interaction with host and diet.  
413 *Gut Microbes* 5.

414 Pan, D., and Z. Yu. 2013b. Intestinal microbiome of poultry and its interaction with host and diet.  
415 *Gut Microbes* 5:108–119.

416 Perumbakkam, S., H. D. Hunt, and H. H. Cheng. 2014. Marek’s disease virus influences the core  
417 gut microbiome of the chicken during the early and late phases of viral replication. *FEMS*  
418 *Microbiol. Ecol.* 90:300–312.

419 Pfeiffer, J. K., and H. W. Virgin. 2016. Transkingdom control of viral infection and immunity in the  
420 mammalian intestine. *Science* (80-. ). 351:aad5872-aad5872 .

421 Rautenschlein S, Sharma JM (2000) Immunopathogenesis of haemorrhagic enteritis virus (HEV) in  
422 turkeys. *Dev Comp Immunol* 24:237–246.

423 Rognes, T., T. Flouri, B. Nichols, C. Quince, and F. Mahé. 2016. VSEARCH: a versatile open  
424 source tool for metagenomics. *PeerJ Prepr.* 4:e2409v1.

425 Scupham, A. J. 2009. *Campylobacter* colonization of the turkey intestine in the context of microbial  
426 community development. *Appl. Environ. Microbiol.* 75:3564–3571.

427 Scupham, A. J., T. G. Patton, E. Bent, and D. O. Bayles. 2008. Comparison of the cecal microbiota  
428 of domestic and wild turkeys. *Microb. Ecol.* 56:322–331.

429 Sharma, J. M. 1991. Hemorrhagic enteritis of turkeys. *Vet. Immunol. Immunopathol.* 30:67–71.

430 Suresh, M., and J. M. Sharma. 1996. Pathogenesis of type II avian adenovirus infection in turkeys:  
431 in vivo immune cell tropism and tissue distribution of the virus. *J. Virol.* 70:30–6.

432 Tremaroli, V., and F. Bäckhed. 2012. Functional interactions between the gut microbiota and host  
433 metabolism. *Nature* 489:242–249.

434 Tremblay, J., K. Singh, A. Fern, E. S. Kirton, S. He, T. Woyke, J. Lee, F. Chen, J. L. Dangl, and S.  
435 G. Tringe. 2015. Primer and platform effects on 16S rRNA tag sequencing. *Front. Microbiol.*  
436 6:1–15.

437 Waite, D. W., and M. W. Taylor. 2014. Characterizing the avian gut microbiota: Membership,  
438 driving influences, and potential function. *Front. Microbiol.* 5:1–12.

439 Waite, D. W., and M. W. Taylor. 2015. Exploring the avian gut microbiota : current trends and  
440 future directions. 6:1–12.

441 Wang, Q., G. M. Garrity, J. M. Tiedje, and J. R. Cole. 2007. Naive Bayesian classifier for rapid  
442 assignment of rRNA sequences into the new bacterial taxonomy. *Appl. Environ. Microbiol.*  
443 73:5261–5267.

444 Wei, S., M. Morrison, and Z. Yu. 2013. Bacterial census of poultry intestinal microbiome. *Poult.*  
445 *Sci.* 92:671–683

446 Westcott, S. L., and P. D. Schloss. 2015. De novo clustering methods outperform reference-based

447 methods for assigning 16S rRNA gene sequences to operational taxonomic units. PeerJ  
448 3:e1487

449 Wilkinson, N., R. J. Hughes, W. J. Aspden, J. Chapman, R. J. Moore, and D. Stanley. 2016. The  
450 gastrointestinal tract microbiota of the Japanese quail, *Coturnix japonica*. Appl. Microbiol.  
451 Biotechnol.:1–9.

452

Fig. 1: Main bacterial families and corresponding phyla, in the four tracts of the intestine in the healthy turkeys (group A): duodenum, jejunum, ileum and cecum. At family level, “Other” means that level that have a percentage too low for assigning the taxonomy. Percentage details are showed in table 1 and supplementary table S1.

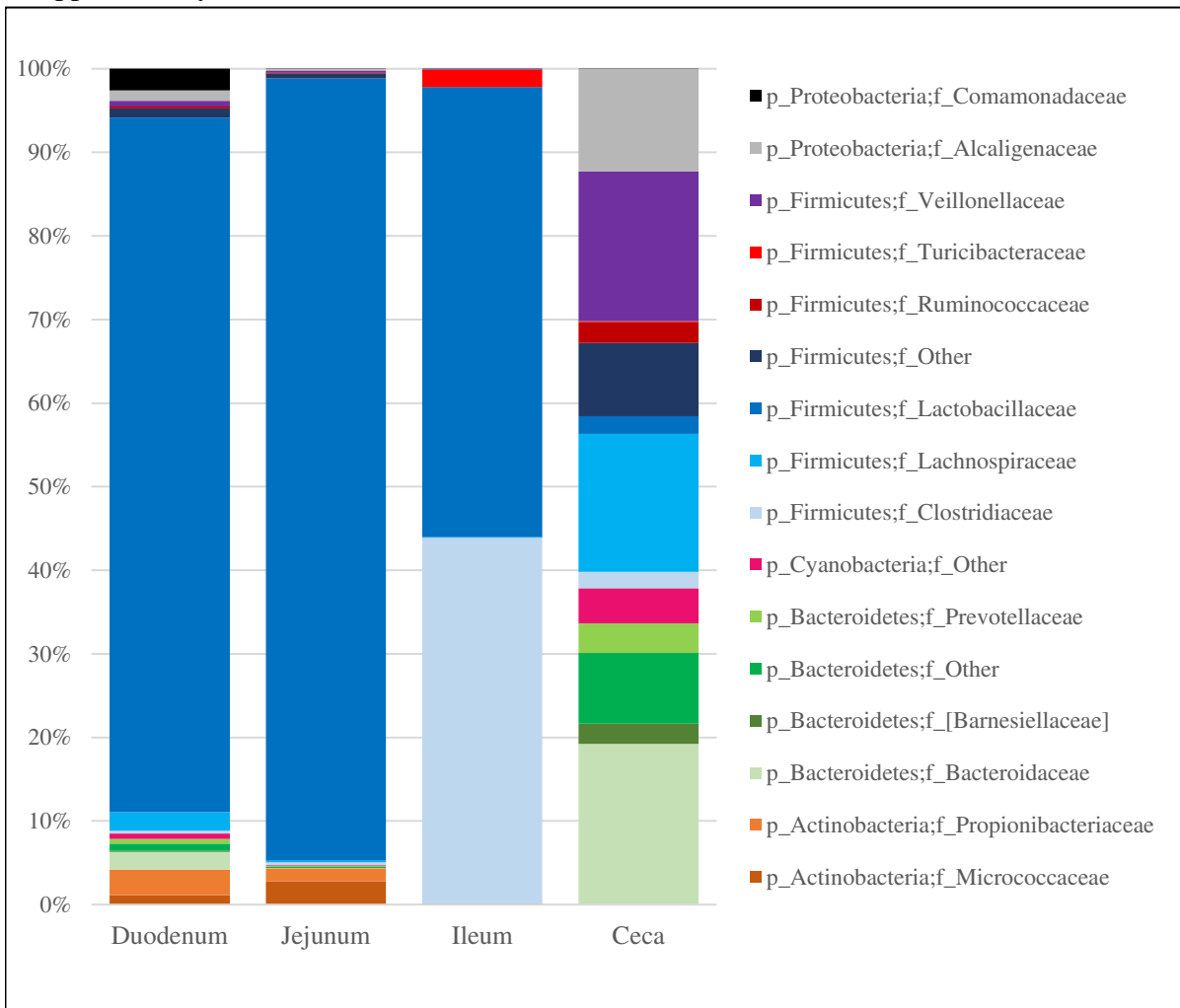


Fig. 2: Unweighted UniFrac analysis among the four intestine tracts in 4 healthy turkeys (group A). Sample from ceca are clustered separately from the other tracts of the intestine.

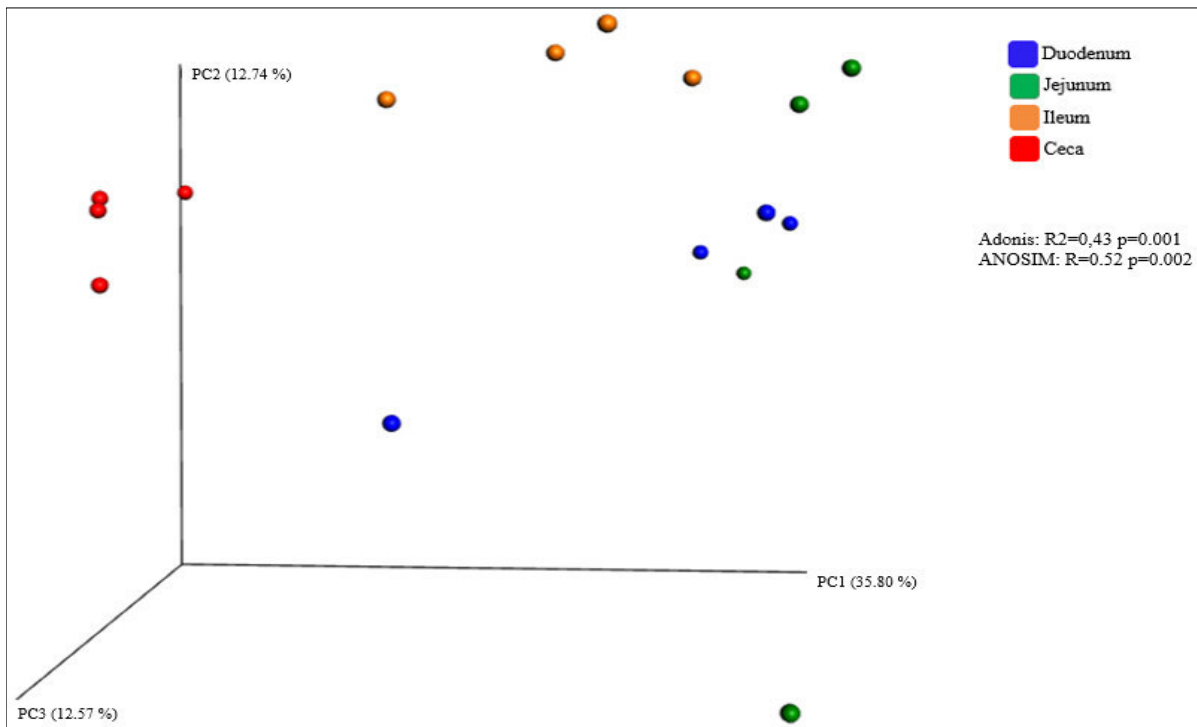


Fig. 3: Main bacterial families and corresponding phyla among the three groups of turkeys. Healthy turkeys (group A), HEV-affected turkeys (group B) and turkeys positive for HEV but without clinical signs (group C). Percentage details are showed in Table 3 and supplementary table S2.

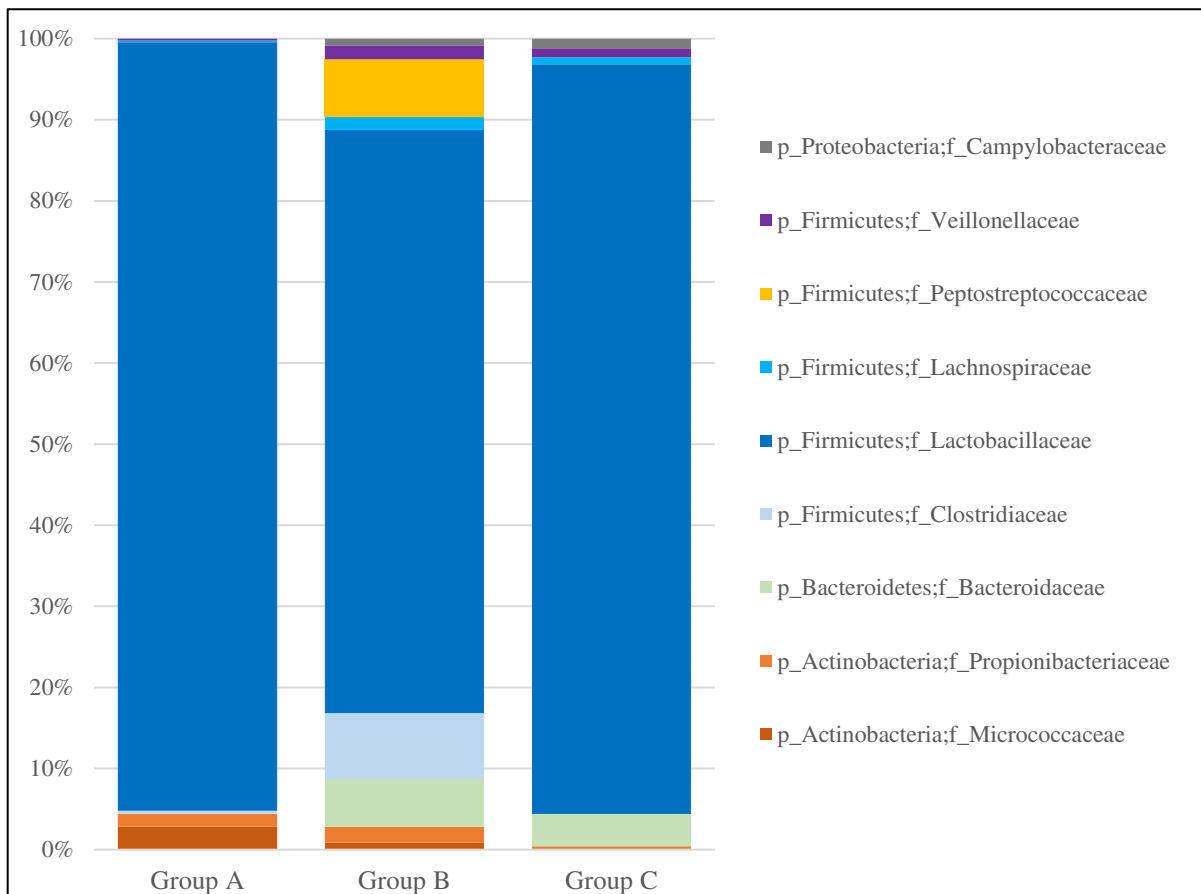


Fig. 4: Unweighted UniFrac analysis among the three health status of animals; 4 healthy turkeys (group A), 4 HEV-affected turkey (group B) and 4 turkeys positive for HEV but without clinical signs (group C).

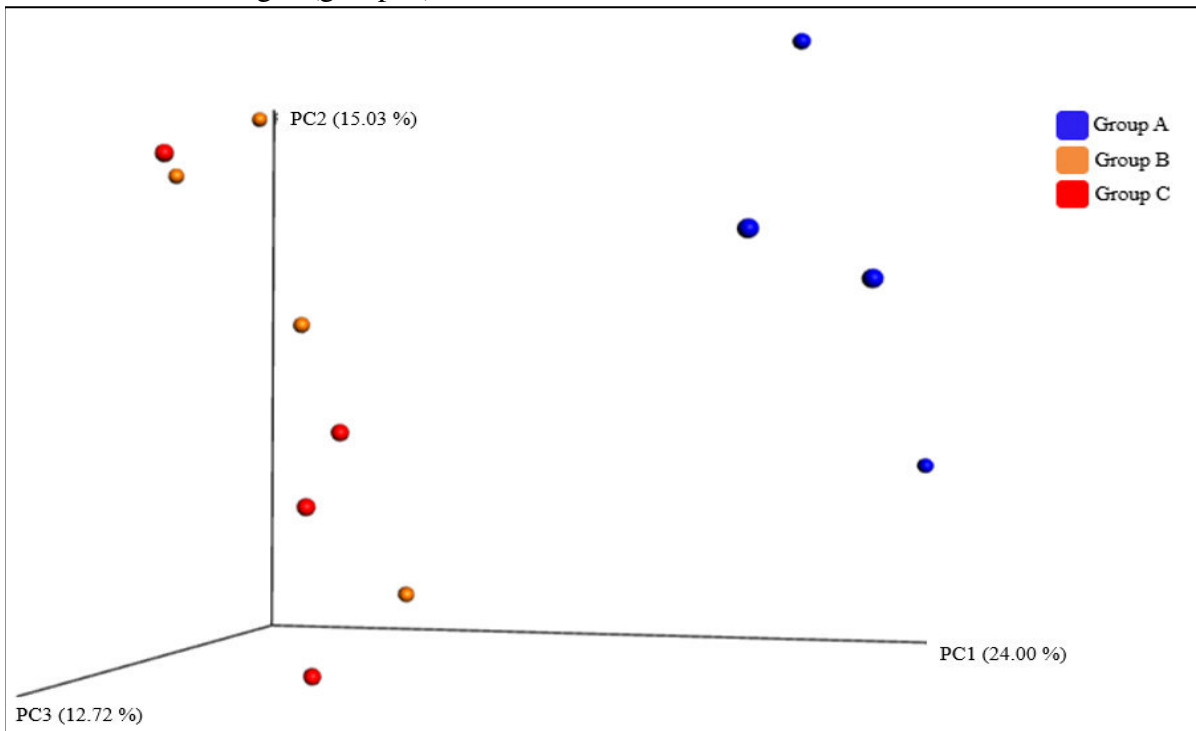


TABLE 1: Main bacterial phyla and families obtained for intestine tracts in healthy turkeys. Bacterial phyla (*italic*) and families (*italic*) that showed a percentage higher than 0.99% at least in one tract of the intestine were represented. Bacterial families that showed a

	Duodenum	Jejunum	Ileum	Cecum
<b>ACTINOBACTERIA</b>	<b>3.65%</b>	<b>4.01%</b>	<b>0.00%</b>	<b>0.02%</b>
<i>Micrococcaceae</i>	1.01%	2.56%	0.00%	0.01%
<i>Propionibacteriaceae</i>	2.64%	1.45%	0.00%	0.01%
<b>BACTEROIDETES</b>	<b>3.22%</b>	<b>0.28%</b>	<b>0.10%</b>	<b>31.32%</b>
<i>Bacteroidaceae</i>	1.87%	0.05%	0.06%	17.87%
<i>[Barnesiellaceae]</i>	0.08%	0.00%	0.01%	2.26%
<i>Prevotellaceae</i>	0.49%	0.11%	0.01%	3.31%
<i>Others &lt; 0.99%</i>	0.77%	0.11%	0.02%	7.89%
<b>CYANOBACTERIA</b>	<b>0.56%</b>	<b>0.08%</b>	<b>0.02%</b>	<b>3.89%</b>
<i>Others &lt; 0.99%</i>	0.56%	0.08%	0.02%	3.89%
<b>FIRMICUTES</b>	<b>76.39%</b>	<b>87.82%</b>	<b>97.94%</b>	<b>46.44%</b>
<i>Clostridiaceae</i>	0.30%	0.30%	42.93%	1.85%
<i>Lactobacillaceae</i>	72.45%	86.47%	52.82%	1.98%
<i>Lachnospiraceae</i>	1.91%	0.20%	0.07%	15.35%
<i>Ruminococcaceae</i>	0.20%	0.11%	0.01%	2.31%
<i>Turicibacteraceae</i>	0.00%	0.01%	2.01%	0.12%
<i>Veillonellaceae</i>	0.60%	0.20%	0.07%	16.66%
<i>Others &lt; 0.99%</i>	0.93%	0.53%	0.04%	8.16%
<b>PROTEOBACTERIA</b>	<b>6.75%</b>	<b>0.30%</b>	<b>0.08%</b>	<b>11.51%</b>
<i>Alcaligenaceae</i>	1.07%	0.17%	0.04%	11.43%
<i>Campylobacteraceae</i>	1.79%	0.04%	0.04%	0.07%
<i>Comamonadaceae</i>	2.27%	0.03%	0.00%	0.01%
<i>Neisseriaceae</i>	1.62%	0.06%	0.00%	0.01%
<b>SYNERGISTETES</b>	<b>0.01%</b>	<b>0.00%</b>	<b>0.01%</b>	<b>1.38%</b>
<i>Others &lt; 0.99%</i>	0.01%	0.00%	0.01%	1.38%

percentage lower than 0.99% were gathered in the “*Others < 0.99%*” group.



TABLE 2: Values of Observed species and Shannon index in different tract of the intestine in healthy turkeys.

<b>SHANNON</b>	<b>MEAN</b>	<b>STD</b>
Duodenum	4.83	0.61
Jejunum	4.29	0.54
Ileum	4	0.55
Cecum	5.71	0.57

<b>OBSERVED SPECIES</b>	<b>MEAN</b>	<b>STD</b>
Duodenum	233	28.24
Jejunum	199.25	31.11
Ileum	255.75	33.01
Cecum	390.5	25

TABLE 3: Comparison of bacterial composition in the jejunum tract in 12 turkeys from three different groups. Group (A): 4 healthy animals. Group (B): 4 HEV affected turkeys positive for PCR at intestinal level and with clinical signs and evident gross pathological lesions. Group (C): 4 positive turkeys for HEV PCR at spleen level, but without clinical signs or gross pathological lesions. Bacterial phyla (bold) and families (italic) that showed a percentage higher than 0.99% at least in one tract of the intestine were represented.

Bacterial families that showed a percentage lower than 0.99% were gathered in the “Others

	Group A	Group B	Group C
<b>ACTINOBACTERIA</b>	<b>4.01%</b>	<b>2.57%</b>	<b>0.39%</b>
<i>Micrococcaceae</i>	2.56%	0.76%	0.05%
<i>Propionibacteriaceae</i>	1.45%	1.81%	0.34%
<b>BACTEROIDETES</b>	<b>0.05%</b>	<b>5.33%</b>	<b>3.61%</b>
<i>Bacteroidaceae</i>	0.05%	5.33%	3.61%
<b>FIRMICUTES</b>	<b>87.17%</b>	<b>81.96%</b>	<b>89.95%</b>
<i>Clostridiaceae</i>	0.30%	7.35%	0.09%
<i>Lactobacillaceae</i>	86.47%	65.16%	83.85%
<i>Lachnospiraceae</i>	0.20%	1.42%	0.80%
<i>Peptostreptococcaceae</i>	0.00%	6.48%	4.21%
<i>Veillonellaceae</i>	0.20%	1.55%	1.00%
<b>PROTEOBACTERIA</b>	<b>0.04%</b>	<b>0.75%</b>	<b>1.06%</b>
<i>Campylobacteraceae</i>	0.04%	0.75%	1.06%

<  
0.99%  
”  
group.

TABLE 4: Values of Observed species and Shannon index among three group of turkeys in three different healthy status. We compare the jejunum tract of the three group. Group A: healthy turkeys, Group B: HEV affected turkeys, Group C: turkeys positive for HEV but without clinical signs.

SHANNON		
	MEAN	STD
Group A	4.29	0.53
Group B	4.07	0.58
Group C	3.25	1.16

OBSERVED SPECIES		
	MEAN	STD
Group A	200.5	33.55
Group B	202.5	43.04
Group C	165	24.5

Table S1. Complete table of bacteria species found up to Phylum level (L2), Class level (L3), Order level (L4), Family level (5) and Genus level (L6), in the four tracts of the intestine. The value 0.00% indicates a percentage lower than 0.0005%. “Other”: Class, Order, Family or Genus level that have a percentage too low for assigning the taxonomy. “N.C.”: bacteria that can’t be classified until corresponding Class, Order, Family or Genus level.

Duodenum	Jejunum	Ileum	Cecum	L2
				Phylum
0.00%	0.00%	0.00%	0.09%	Other
0.00%	0.06%	0.08%	0.00%	Acidobacteria
6.43%	6.21%	0.02%	0.10%	Actinobacteria
0.04%	0.00%	0.00%	0.00%	Armatimonadetes
3.88%	0.66%	0.19%	33.60%	Bacteroidetes
0.00%	0.00%	0.05%	0.00%	Chloroflexi
0.56%	0.18%	0.02%	3.89%	Cyanobacteria
0.00%	0.00%	0.00%	0.30%	Deferribacteres
79.85%	89.57%	99.28%	48.03%	Firmicutes
0.04%	0.12%	0.00%	0.00%	Fusobacteria
0.00%	0.00%	0.04%	0.00%	GN02
9.18%	3.20%	0.23%	12.32%	Proteobacteria
0.01%	0.00%	0.01%	1.51%	Synergistetes
0.00%	0.00%	0.08%	0.00%	TM7
0.01%	0.00%	0.00%	0.15%	Tenericutes

Duodenum	Jejunum	Ileum	Cecum	L3	
				Phylum	Class
0.00%	0.00%	0.00%	0.09%	Other	Other
0.00%	0.00%	0.03%	0.00%	Acidobacteria	Acidobacteria-6
0.00%	0.06%	0.00%	0.00%	Acidobacteria	Solibacteres
0.00%	0.00%	0.06%	0.00%	Acidobacteria	Sva0725
0.09%	0.00%	0.00%	0.00%	Actinobacteria	Acidimicrobiia
6.25%	6.12%	0.02%	0.04%	Actinobacteria	Actinobacteria
0.07%	0.05%	0.00%	0.06%	Actinobacteria	Coriobacteriia
0.03%	0.03%	0.00%	0.00%	Actinobacteria	Rubrobacteria
0.04%	0.00%	0.00%	0.00%	Armatimonadetes	Chthonomonadetes
3.42%	0.29%	0.11%	33.60%	Bacteroidetes	Bacteroidia
0.00%	0.00%	0.03%	0.00%	Bacteroidetes	Cytophagia
0.46%	0.04%	0.01%	0.00%	Bacteroidetes	Flavobacteriia
0.00%	0.33%	0.03%	0.00%	Bacteroidetes	Sphingobacteriia
0.00%	0.00%	0.05%	0.00%	Chloroflexi	Anaerolineae
0.56%	0.08%	0.02%	3.89%	Cyanobacteria	4C0d-2
0.00%	0.10%	0.00%	0.00%	Cyanobacteria	Oscillatoriothycideae
0.00%	0.00%	0.00%	0.30%	Deferribacteres	Deferribacteres
0.12%	0.00%	0.00%	0.71%	Firmicutes	Other
75.11%	87.89%	56.03%	2.26%	Firmicutes	Bacilli
4.49%	1.68%	43.25%	44.52%	Firmicutes	Clostridia
0.12%	0.00%	0.00%	0.53%	Firmicutes	Erysipelotrichi
0.04%	0.12%	0.00%	0.00%	Fusobacteria	Fusobacteriia
0.00%	0.00%	0.04%	0.00%	GN02	GKS2-174
0.68%	2.13%	0.00%	0.15%	Proteobacteria	Alphaproteobacteria
6.06%	0.40%	0.07%	11.45%	Proteobacteria	Betaproteobacteria
0.02%	0.00%	0.00%	0.22%	Proteobacteria	Deltaproteobacteria
1.80%	0.04%	0.04%	0.22%	Proteobacteria	Epsilonproteobacteria
0.62%	0.64%	0.12%	0.28%	Proteobacteria	Gammaproteobacteria
0.01%	0.00%	0.01%	1.51%	Synergistetes	Synergistia
0.00%	0.00%	0.08%	0.00%	TM7	TM7-1
0.01%	0.00%	0.00%	0.15%	Tenericutes	Mollicutes

Duodenum	Jejunum	Ileum	Cecum	L4		
				Phylum	Class	Order
0.00%	0.00%	0.00%	0.09%	Other	Other	Other
0.00%	0.00%	0.03%	0.00%	Acidobacteria	Acidobacteria-6	iii1-15
0.00%	0.06%	0.00%	0.00%	Acidobacteria	Solibacteres	Solibacterales
0.00%	0.00%	0.06%	0.00%	Acidobacteria	Sva0725	Sva0725
0.09%	0.00%	0.00%	0.00%	Actinobacteria	Acidimicrobiia	Acidimicrobiales
6.25%	6.12%	0.02%	0.04%	Actinobacteria	Actinobacteria	Actinomycetales
0.07%	0.05%	0.00%	0.06%	Actinobacteria	Coriobacteriia	Coriobacteriales
0.03%	0.03%	0.00%	0.00%	Actinobacteria	Rubrobacteria	Rubrobacterales
0.04%	0.00%	0.00%	0.00%	Armatimonadetes	Chthonomonadetes	Chthonomonadales
3.42%	0.29%	0.11%	33.60%	Bacteroidetes	Bacteroidia	Bacteroidales
0.00%	0.00%	0.03%	0.00%	Bacteroidetes	Cytophagia	Cytophagales
0.46%	0.04%	0.01%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales
0.00%	0.33%	0.03%	0.00%	Bacteroidetes	Sphingobacteriia	Sphingobacteriales
0.00%	0.00%	0.05%	0.00%	Chloroflexi	Anaerolineae	SBR1031

0.56%	0.08%	0.02%	3.89%	Cyanobacteria	4C0d-2	YS2
0.00%	0.10%	0.00%	0.00%	Cyanobacteria	Oscillatoriophycideae	Chroococcales
0.00%	0.00%	0.00%	0.30%	Deferribacteres	Deferribacteres	Deferribacterales
0.12%	0.00%	0.00%	0.71%	Firmicutes	Other	Other
1.04%	0.67%	0.01%	0.09%	Firmicutes	Bacilli	Bacillales
0.08%	0.07%	0.00%	0.00%	Firmicutes	Bacilli	Gemellales
74.00%	87.14%	54.00%	2.06%	Firmicutes	Bacilli	Lactobacillales
0.00%	0.01%	2.01%	0.12%	Firmicutes	Bacilli	Turicibacterales
4.49%	1.68%	43.25%	44.48%	Firmicutes	Clostridia	Clostridiales
0.00%	0.00%	0.00%	0.04%	Firmicutes	Clostridia	SHA-98
0.12%	0.00%	0.00%	0.53%	Firmicutes	Erysipelotrichi	Erysipelotrichales
0.04%	0.12%	0.00%	0.00%	Fusobacteria	Fusobacteriia	Fusobacteriales
0.00%	0.00%	0.04%	0.00%	GN02	GKS2-174	N.C.
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Caulobacterales
0.00%	0.00%	0.00%	0.14%	Proteobacteria	Alphaproteobacteria	RF32
0.20%	0.55%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales
0.03%	0.69%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodobacterales
0.00%	0.33%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodospirillales
0.46%	0.55%	0.00%	0.01%	Proteobacteria	Alphaproteobacteria	Sphingomonadales
0.00%	0.00%	0.03%	0.00%	Proteobacteria	Betaproteobacteria	Other
4.22%	0.27%	0.04%	11.44%	Proteobacteria	Betaproteobacteria	Burkholderiales
0.00%	0.07%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Methylophilales
1.62%	0.06%	0.00%	0.01%	Proteobacteria	Betaproteobacteria	Neisseriales
0.22%	0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Rhodocyclales
0.02%	0.00%	0.00%	0.22%	Proteobacteria	Deltaproteobacteria	Desulfovibrionales
1.80%	0.04%	0.04%	0.22%	Proteobacteria	Epsilonproteobacteria	Campylobacterales
0.13%	0.03%	0.00%	0.22%	Proteobacteria	Gammaproteobacteria	Other
0.00%	0.00%	0.00%	0.05%	Proteobacteria	Gammaproteobacteria	Aeromonadales
0.00%	0.00%	0.12%	0.00%	Proteobacteria	Gammaproteobacteria	Enterobacteriales
0.47%	0.46%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Pseudomonadales
0.02%	0.15%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Xanthomonadales
0.01%	0.00%	0.01%	1.51%	Synergistetes	Synergistia	Synergistales
0.00%	0.00%	0.08%	0.00%	TM7	TM7-1	N.C.
0.00%	0.00%	0.00%	0.05%	Tenericutes	Mollicutes	Anaeroplasmatales
0.01%	0.00%	0.00%	0.10%	Tenericutes	Mollicutes	RF39

Duodenum	Jejunum	Ileum	Cecum	L5			
				Phylum	Class	Order	Family
0.00%	0.00%	0.00%	0.09%	Other	Other	Other	Other
0.00%	0.00%	0.03%	0.00%	Acidobacteria	Acidobacteria-6	iii1-15	mb2424
0.00%	0.06%	0.00%	0.00%	Acidobacteria	Solibacteres	Solibacterales	N.C.
0.00%	0.00%	0.06%	0.00%	Acidobacteria	Sva0725	Sva0725	N.C.
0.05%	0.00%	0.00%	0.00%	Actinobacteria	Acidimicrobiia	Acidimicrobiales	N.C.
0.04%	0.00%	0.00%	0.00%	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111
0.02%	0.09%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Other
0.16%	0.01%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae
0.22%	0.87%	0.01%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae
0.00%	0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae
0.29%	0.25%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Gordoniaceae
0.07%	0.21%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae
0.00%	0.09%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae
0.97%	0.37%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae
1.01%	2.56%	0.00%	0.01%	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae
0.58%	0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae
0.00%	0.07%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae
0.30%	0.09%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae
2.64%	1.45%	0.00%	0.01%	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae
0.00%	0.08%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Sporichthyaceae
0.07%	0.05%	0.00%	0.06%	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae
0.03%	0.03%	0.00%	0.00%	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae
0.04%	0.00%	0.00%	0.00%	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae
0.19%	0.04%	0.01%	1.97%	Bacteroidetes	Bacteroidia	Bacteroidales	Other
0.58%	0.07%	0.02%	5.92%	Bacteroidetes	Bacteroidia	Bacteroidales	N.C.
1.87%	0.05%	0.06%	17.87%	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae
0.01%	0.00%	0.00%	0.61%	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae
0.49%	0.11%	0.01%	3.31%	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae
0.09%	0.00%	0.00%	0.98%	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae
0.06%	0.00%	0.00%	0.61%	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7
0.08%	0.00%	0.01%	2.26%	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]
0.04%	0.00%	0.00%	0.09%	Bacteroidetes	Bacteroidia	Bacteroidales	[Paraprevotellaceae]
0.00%	0.00%	0.03%	0.00%	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
0.05%	0.00%	0.00%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	Other
0.41%	0.00%	0.00%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae
0.00%	0.04%	0.01%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]

0.00%	0.00%	0.03%	0.00%	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	N.C.
0.00%	0.33%	0.00%	0.00%	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae
0.00%	0.00%	0.05%	0.00%	Chloroflexi	Anaerolineae	SBR1031	A4b
0.56%	0.08%	0.02%	3.89%	Cyanobacteria	4C0d-2	YS2	N.C.
0.00%	0.10%	0.00%	0.00%	Cyanobacteria	Oscillatoriophycideae	Chroococcales	Xenococcaceae
0.00%	0.00%	0.00%	0.30%	Deferribacteres	Deferribacteres	Deferribacterales	Deferribacteraceae
0.12%	0.00%	0.00%	0.71%	Firmicutes	Other	Other	Other
0.14%	0.11%	0.00%	0.08%	Firmicutes	Bacilli	Bacillales	Bacillaceae
0.33%	0.35%	0.00%	0.00%	Firmicutes	Bacilli	Bacillales	Listeriaceae
0.57%	0.21%	0.01%	0.00%	Firmicutes	Bacilli	Bacillales	Staphylococcaceae
0.08%	0.02%	0.00%	0.00%	Firmicutes	Bacilli	Gemellales	N.C.
0.00%	0.05%	0.00%	0.00%	Firmicutes	Bacilli	Gemellales	Gemellaceae
0.31%	0.36%	0.19%	0.01%	Firmicutes	Bacilli	Lactobacillales	Other
0.08%	0.00%	0.00%	0.00%	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae
72.45%	86.47%	52.82%	1.98%	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae
0.45%	0.03%	0.01%	0.00%	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae
0.71%	0.28%	0.99%	0.06%	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae
0.00%	0.01%	2.01%	0.12%	Firmicutes	Bacilli	Turicibacterales	Turicibacteraceae
0.65%	0.52%	0.02%	4.88%	Firmicutes	Clostridia	Clostridiales	Other
0.28%	0.00%	0.01%	3.28%	Firmicutes	Clostridia	Clostridiales	N.C.
0.30%	0.30%	42.93%	1.85%	Firmicutes	Clostridia	Clostridiales	Clostridiaceae
1.91%	0.20%	0.07%	15.35%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae
0.02%	0.00%	0.00%	0.14%	Firmicutes	Clostridia	Clostridiales	Peptococcaceae
0.33%	0.00%	0.13%	0.01%	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae
0.20%	0.11%	0.01%	2.31%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae
0.60%	0.20%	0.07%	16.66%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae
0.19%	0.34%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]
0.00%	0.00%	0.00%	0.04%	Firmicutes	Clostridia	SHA-98	N.C.
0.12%	0.00%	0.00%	0.53%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae
0.04%	0.00%	0.00%	0.00%	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae
0.00%	0.12%	0.00%	0.00%	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae
0.00%	0.00%	0.04%	0.00%	GN02	GKS2-174	N.C.	N.C.
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae
0.00%	0.00%	0.00%	0.14%	Proteobacteria	Alphaproteobacteria	RF32	N.C.
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae
0.00%	0.04%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae
0.20%	0.13%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae
0.00%	0.38%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae
0.03%	0.69%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae
0.00%	0.31%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae
0.00%	0.03%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae
0.46%	0.55%	0.00%	0.01%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae
0.00%	0.00%	0.03%	0.00%	Proteobacteria	Betaproteobacteria	Other	Other
1.07%	0.17%	0.04%	11.43%	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae
0.21%	0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae
2.27%	0.03%	0.00%	0.01%	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae
0.67%	0.06%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae
0.00%	0.07%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae
1.62%	0.06%	0.00%	0.01%	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae
0.22%	0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae
0.02%	0.00%	0.00%	0.22%	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae
1.79%	0.04%	0.04%	0.07%	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae
0.01%	0.00%	0.00%	0.16%	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae
0.13%	0.03%	0.00%	0.22%	Proteobacteria	Gammaproteobacteria	Other	Other
0.00%	0.00%	0.00%	0.05%	Proteobacteria	Gammaproteobacteria	Aeromonadales	Succinivibrionaceae
0.00%	0.00%	0.12%	0.00%	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae
0.01%	0.09%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae
0.46%	0.38%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae
0.02%	0.01%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae
0.00%	0.14%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae
0.01%	0.00%	0.01%	1.38%	Synergistetes	Synergistia	Synergistales	N.C.
0.00%	0.00%	0.00%	0.12%	Synergistetes	Synergistia	Synergistales	Synergistaceae
0.00%	0.00%	0.08%	0.00%	TM7	TM7-1	N.C.	N.C.
0.00%	0.00%	0.00%	0.05%	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae
0.01%	0.00%	0.00%	0.10%	Tenericutes	Mollicutes	RF39	N.C.

Duodenum	Jejunum	Ileum	Cecum	L6				
				Phylum	Class	Order	Family	Genus
0.00%	0.00%	0.09%	0.00%	Other	Other	Other	Other	Other
0.00%	0.03%	0.00%	0.00%	Acidobacteria	Acidobacteria-6	iii1-15	mb2424	N.C.
0.06%	0.00%	0.00%	0.00%	Acidobacteria	Solibacteres	Solibacterales	N.C.	N.C.
0.00%	0.06%	0.00%	0.00%	Acidobacteria	Sva0725	Sva0725	N.C.	N.C.
0.00%	0.00%	0.00%	0.05%	Actinobacteria	Acidimicrobiia	Acidimicrobiales	N.C.	N.C.

0.00%	0.00%	0.00%	0.04%	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111	N.C.
0.09%	0.00%	0.00%	0.02%	Actinobacteria	Actinobacteria	Actinomycetales	Other	Other
0.01%	0.00%	0.00%	0.11%	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces
0.00%	0.00%	0.00%	0.04%	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Arcanobacterium
0.87%	0.01%	0.00%	0.22%	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium
0.00%	0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	N.C.
0.25%	0.00%	0.00%	0.29%	Actinobacteria	Actinobacteria	Actinomycetales	Gordoniaceae	Gordonia
0.21%	0.00%	0.00%	0.07%	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Janibacter
0.09%	0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	N.C.
0.04%	0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Clavibacter
0.32%	0.00%	0.00%	0.89%	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium
0.00%	0.00%	0.00%	0.07%	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Salinibacterium
0.00%	0.00%	0.00%	0.05%	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	N.C.
0.29%	0.00%	0.00%	0.12%	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria
2.24%	0.00%	0.01%	0.85%	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Micrococcus
0.03%	0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia
0.00%	0.00%	0.00%	0.58%	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Actinoplanes
0.07%	0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus
0.09%	0.00%	0.00%	0.30%	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	N.C.
1.45%	0.00%	0.01%	2.64%	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacterium
0.08%	0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Sporichthyaceae	Sporichthya
0.05%	0.00%	0.06%	0.07%	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	N.C.
0.03%	0.00%	0.00%	0.03%	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae	Rubrobacter
0.00%	0.00%	0.00%	0.04%	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	N.C.
0.04%	0.01%	1.97%	0.19%	Bacteroidetes	Bacteroidia	Bacteroidales	Other	Other
0.07%	0.02%	5.92%	0.58%	Bacteroidetes	Bacteroidia	Bacteroidales	N.C.	N.C.
0.05%	0.06%	17.87%	1.87%	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
0.00%	0.00%	0.61%	0.01%	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
0.00%	0.00%	0.00%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Porphyromonas
0.11%	0.01%	3.31%	0.49%	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
0.00%	0.00%	0.06%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Other
0.00%	0.00%	0.40%	0.09%	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	N.C.
0.00%	0.00%	0.26%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
0.00%	0.00%	0.26%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Rikenella
0.00%	0.00%	0.61%	0.06%	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	N.C.
0.00%	0.00%	0.13%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	Other
0.00%	0.00%	0.04%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	N.C.
0.00%	0.01%	2.09%	0.08%	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	Barnesiella
0.00%	0.00%	0.09%	0.01%	Bacteroidetes	Bacteroidia	Bacteroidales	[Paraprevotellaceae]	Other
0.00%	0.00%	0.00%	0.03%	Bacteroidetes	Bacteroidia	Bacteroidales	[Paraprevotellaceae]	[Prevotella]
0.00%	0.03%	0.00%	0.00%	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	N.C.
0.00%	0.00%	0.00%	0.00%	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter
0.00%	0.00%	0.00%	0.05%	Bacteroidetes	Flavobacteriia	Flavobacteriales	Other	Other
0.00%	0.00%	0.00%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
0.00%	0.00%	0.00%	0.41%	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Myroides
0.04%	0.00%	0.00%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium
0.00%	0.01%	0.00%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Cloacibacterium
0.00%	0.03%	0.00%	0.00%	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	N.C.	N.C.
0.33%	0.00%	0.00%	0.00%	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
0.00%	0.05%	0.00%	0.00%	Chloroflexi	Anaerolineae	SBR1031	A4b	N.C.
0.08%	0.02%	3.89%	0.56%	Cyanobacteria	4C0d-2	YS2	N.C.	N.C.
0.10%	0.00%	0.00%	0.00%	Cyanobacteria	Oscillatoriohycideae	Chroococcales	Xenococcaceae	Chroococcidiopsis
0.00%	0.00%	0.30%	0.00%	Deferribacteres	Deferribacteres	Deferribacterales	Deferribacteraceae	Mucispirillum
0.00%	0.00%	0.71%	0.12%	Firmicutes	Other	Other	Other	Other
0.07%	0.00%	0.08%	0.00%	Firmicutes	Bacilli	Bacillales	Bacillaceae	Other
0.04%	0.00%	0.00%	0.00%	Firmicutes	Bacilli	Bacillales	Bacillaceae	Anoxybacillus
0.00%	0.00%	0.00%	0.10%	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
0.00%	0.00%	0.00%	0.04%	Firmicutes	Bacilli	Bacillales	Bacillaceae	Marinibacillus
0.35%	0.00%	0.00%	0.33%	Firmicutes	Bacilli	Bacillales	Listeriaceae	Brochothrix
0.00%	0.00%	0.00%	0.00%	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Jeotgalicoccus
0.20%	0.01%	0.00%	0.56%	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus
0.02%	0.00%	0.00%	0.08%	Firmicutes	Bacilli	Gemellales	N.C.	N.C.
0.05%	0.00%	0.00%	0.00%	Firmicutes	Bacilli	Gemellales	Gemellaceae	N.C.
0.36%	0.19%	0.01%	0.31%	Firmicutes	Bacilli	Lactobacillales	Other	Other
0.00%	0.00%	0.00%	0.08%	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Granulicatella
86.47%	52.82%	1.98%	72.45%	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
0.01%	0.00%	0.00%	0.44%	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Leuconostoc
0.02%	0.01%	0.00%	0.01%	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Weissella
0.00%	0.00%	0.00%	0.00%	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	N.C.
0.28%	0.99%	0.06%	0.71%	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
0.01%	2.01%	0.12%	0.00%	Firmicutes	Bacilli	Turicibacterales	Turicibacteraceae	Turicibacter
0.52%	0.02%	4.88%	0.65%	Firmicutes	Clostridia	Clostridiales	Other	Other
0.00%	0.01%	3.28%	0.28%	Firmicutes	Clostridia	Clostridiales	N.C.	N.C.
0.00%	0.02%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	02d06

0.05%	0.44%	0.01%	0.09%	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	<i>Clostridium</i>
0.24%	42.46%	1.83%	0.21%	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	<i>SMB53</i>
0.03%	0.01%	2.13%	0.16%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Other</i>
0.17%	0.05%	11.53%	1.54%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>N.C.</i>
0.00%	0.00%	0.16%	0.06%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Blautia</i>
0.00%	0.00%	0.43%	0.06%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Coprococcus</i>
0.00%	0.00%	0.07%	0.00%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Dorea</i>
0.00%	0.00%	0.00%	0.08%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Roseburia</i>
0.00%	0.00%	1.04%	0.01%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>[Ruminococcus]</i>
0.00%	0.00%	0.14%	0.02%	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	<i>Peptococcus</i>
0.00%	0.13%	0.00%	0.18%	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	<i>N.C.</i>
0.00%	0.00%	0.00%	0.15%	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	<i>Filifactor</i>
0.00%	0.00%	0.21%	0.00%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Other</i>
0.01%	0.01%	0.67%	0.15%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>N.C.</i>
0.00%	0.00%	0.12%	0.00%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Butyricoccus</i>
0.00%	0.00%	0.37%	0.00%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Faecalibacterium</i>
0.00%	0.00%	0.75%	0.04%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Oscillospira</i>
0.10%	0.00%	0.19%	0.00%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcus</i>
0.00%	0.00%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	<i>Anaerovibrio</i>
0.15%	0.06%	13.88%	0.46%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	<i>Megamonas</i>
0.00%	0.00%	0.71%	0.07%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	<i>Megasphaera</i>
0.04%	0.01%	2.08%	0.07%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	<i>Phascolarctobacterium</i>
0.00%	0.00%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	<i>Veillonella</i>
0.00%	0.00%	0.00%	0.15%	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]	<i>Anaerococcus</i>
0.06%	0.00%	0.00%	0.01%	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]	<i>Fingoldia</i>
0.00%	0.00%	0.00%	0.03%	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]	<i>Gallicola</i>
0.28%	0.00%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]	<i>Peptoniphilus</i>
0.00%	0.00%	0.04%	0.00%	Firmicutes	Clostridia	SHA-98	<i>N.C.</i>	<i>N.C.</i>
0.00%	0.00%	0.04%	0.00%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>Other</i>
0.00%	0.00%	0.11%	0.00%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>N.C.</i>
0.00%	0.00%	0.09%	0.10%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>Clostridium</i>
0.00%	0.00%	0.05%	0.00%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>RFN20</i>
0.00%	0.00%	0.03%	0.01%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>[Eubacterium]</i>
0.00%	0.00%	0.21%	0.01%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>cc_115</i>
0.00%	0.00%	0.00%	0.00%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>p-75-a5</i>
0.00%	0.00%	0.00%	0.04%	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	<i>Fusobacterium</i>
0.12%	0.00%	0.00%	0.00%	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae	<i>Leptotrichia</i>
0.00%	0.04%	0.00%	0.00%	GN02	GKS2-174	<i>N.C.</i>	<i>N.C.</i>	<i>N.C.</i>
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	<i>Mycoplana</i>
0.00%	0.00%	0.14%	0.00%	Proteobacteria	Alphaproteobacteria	RF32	<i>N.C.</i>	<i>N.C.</i>
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Chelatococcus</i>
0.04%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	<i>Afipia</i>
0.13%	0.00%	0.00%	0.20%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	<i>Methylobacterium</i>
0.23%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Agrobacterium</i>
0.15%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Rhizobium</i>
0.40%	0.00%	0.00%	0.01%	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Other</i>
0.29%	0.00%	0.00%	0.02%	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Paracoccus</i>
0.31%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	<i>Roseomonas</i>
0.03%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	<i>N.C.</i>
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	<i>N.C.</i>
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Other</i>
0.41%	0.00%	0.00%	0.04%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Novosphingobium</i>
0.01%	0.00%	0.00%	0.31%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingobium</i>
0.10%	0.00%	0.00%	0.11%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingomonas</i>
0.03%	0.00%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingopyxis</i>
0.00%	0.03%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Other	Other	<i>Other</i>
0.17%	0.04%	11.43%	1.07%	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	<i>Sutterella</i>
0.00%	0.00%	0.00%	0.21%	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	<i>Lautropia</i>
0.00%	0.00%	0.00%	0.27%	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Other</i>
0.00%	0.00%	0.01%	2.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>N.C.</i>
0.03%	0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Delftia</i>
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Schlegelella</i>
0.06%	0.00%	0.00%	0.24%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Other</i>
0.00%	0.00%	0.00%	0.23%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>N.C.</i>
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Cupriavidus</i>
0.00%	0.00%	0.00%	0.07%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Massilia</i>
0.00%	0.00%	0.00%	0.13%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Ralstonia</i>
0.07%	0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	<i>Methylobacillus</i>
0.00%	0.00%	0.00%	1.40%	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	<i>N.C.</i>
0.06%	0.00%	0.00%	0.21%	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	<i>Neisseria</i>
0.00%	0.00%	0.00%	0.22%	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	<i>Methyloversatilis</i>
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	<i>Petrobacter</i>
0.00%	0.00%	0.05%	0.00%	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	<i>N.C.</i>
0.00%	0.00%	0.16%	0.02%	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	<i>Desulfovibrio</i>



0.04%	0.04%	0.07%	1.79%	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	<i>Campylobacter</i>
0.00%	0.00%	0.16%	0.01%	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	<i>Helicobacter</i>
0.03%	0.00%	0.22%	0.13%	Proteobacteria	Gammaproteobacteria	Other	Other	<i>Other</i>
0.00%	0.00%	0.05%	0.00%	Proteobacteria	Gammaproteobacteria	Aeromonadales	Succinivibrionaceae	<i>Succinatimonas</i>
0.00%	0.04%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Other</i>
0.00%	0.01%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>N.C.</i>
0.00%	0.07%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Trabulsiella</i>
0.00%	0.00%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>
0.09%	0.00%	0.00%	0.01%	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Enhydrobacter</i>
0.38%	0.00%	0.00%	0.46%	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Pseudomonas</i>
0.01%	0.00%	0.00%	0.02%	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	<i>N.C.</i>
0.14%	0.00%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Stenotrophomonas</i>
0.00%	0.01%	1.38%	0.01%	Synergistetes	Synergistia	Synergistales	<i>N.C.</i>	<i>N.C.</i>
0.00%	0.00%	0.12%	0.00%	Synergistetes	Synergistia	Synergistales	Synergistaceae	<i>N.C.</i>
0.00%	0.08%	0.00%	0.00%	TM7	TM7-1	<i>N.C.</i>	<i>N.C.</i>	<i>N.C.</i>
0.00%	0.00%	0.05%	0.00%	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	<i>Anaeroplasma</i>
0.00%	0.00%	0.10%	0.01%	Tenericutes	Mollicutes	RF39	<i>N.C.</i>	<i>N.C.</i>

Table S2. Complete table of bacteria species found up to Phylum level (L2), Class level (L3), Order level (L4), Family level (5) and Genus level (L6). Group A: healthy turkeys, Group B: turkeys with clinical signs of HEV, Group C: positive turkeys to HEV but without clinical signs. The value 0.00% indicates a percentage lower than 0.0005%. “Other”: Class, Order, Family or Genus level that have a percentage too low for assigning the taxonomy. “N.C.”: bacteria that can’t be classified until corresponding Class, Order, Family or Genus level.

Group A	Group B	Group C	L2
			Phylum
0.00%	0.00%	0.00%	Other
0.06%	0.01%	0.00%	Acidobacteria
6.21%	3.15%	1.53%	Actinobacteria
0.00%	0.00%	0.00%	Armatimonadetes
0.66%	6.47%	4.99%	Bacteroidetes
0.00%	0.00%	0.00%	Chloroflexi
0.18%	0.56%	0.00%	Cyanobacteria
0.00%	0.00%	0.09%	Deferribacteres
89.57%	84.98%	91.07%	Firmicutes
0.12%	0.00%	0.00%	Fusobacteria
0.00%	0.00%	0.00%	GN02
3.20%	4.75%	2.29%	Proteobacteria
0.00%	0.04%	0.00%	Synergistetes
0.00%	0.02%	0.00%	TM7
0.00%	0.03%	0.04%	Tenericutes

Group A	Group B	Group C	L3	
			Phylum	Class
0.00%	0.00%	0.00%	Other	Other
0.00%	0.00%	0.00%	Acidobacteria	Acidobacteria-6
0.06%	0.00%	0.00%	Acidobacteria	Solibacteres
0.00%	0.01%	0.00%	Acidobacteria	Sva0725
0.00%	0.00%	0.00%	Actinobacteria	Acidimicrobiia
6.12%	3.14%	1.42%	Actinobacteria	Actinobacteria
0.05%	0.00%	0.09%	Actinobacteria	Coriobacteriia
0.03%	0.01%	0.03%	Actinobacteria	Rubrobacteria
0.00%	0.00%	0.00%	Armatimonadetes	Chthonomonadetes
0.29%	5.98%	4.16%	Bacteroidetes	Bacteroidia
0.00%	0.07%	0.00%	Bacteroidetes	Cytophagia
0.04%	0.42%	0.83%	Bacteroidetes	Flavobacteriia
0.33%	0.00%	0.00%	Bacteroidetes	Sphingobacteriia
0.00%	0.00%	0.00%	Chloroflexi	Anaerolineae
0.08%	0.56%	0.00%	Cyanobacteria	4C0d-2
0.10%	0.00%	0.00%	Cyanobacteria	Oscillatoriothycideae
0.00%	0.00%	0.09%	Deferribacteres	Deferribacteres
0.00%	0.04%	0.00%	Firmicutes	Other
87.89%	66.88%	84.22%	Firmicutes	Bacilli
1.68%	17.78%	6.74%	Firmicutes	Clostridia
0.00%	0.28%	0.10%	Firmicutes	Erysipelotrichi
0.12%	0.00%	0.00%	Fusobacteria	Fusobacteriia
0.00%	0.00%	0.00%	GN02	GKS2-174
2.13%	0.61%	0.49%	Proteobacteria	Alphaproteobacteria
0.40%	2.05%	0.13%	Proteobacteria	Betaproteobacteria
0.00%	0.00%	0.03%	Proteobacteria	Deltaproteobacteria
0.04%	0.75%	1.06%	Proteobacteria	Epsilonproteobacteria
0.64%	1.33%	0.59%	Proteobacteria	Gammaproteobacteria
0.00%	0.04%	0.00%	Synergistetes	Synergistia
0.00%	0.02%	0.00%	TM7	TM7-1
0.00%	0.03%	0.04%	Tenericutes	Mollicutes

Group A	Group B	Group C	L4		
			Phylum	Class	Order
0.00%	0.00%	0.00%	Other	Other	Other
0.00%	0.00%	0.00%	Acidobacteria	Acidobacteria-6	iii1-15
0.06%	0.00%	0.00%	Acidobacteria	Solibacteres	Solibacterales
0.00%	0.01%	0.00%	Acidobacteria	Sva0725	Sva0725
0.00%	0.00%	0.00%	Actinobacteria	Acidimicrobiia	Acidimicrobiales
6.12%	3.14%	1.42%	Actinobacteria	Actinobacteria	Actinomycetales
0.05%	0.00%	0.09%	Actinobacteria	Coriobacteriia	Coriobacteriales
0.03%	0.01%	0.03%	Actinobacteria	Rubrobacteria	Rubrobacterales
0.00%	0.00%	0.00%	Armatimonadetes	Chthonomonadetes	Chthonomonadales
0.29%	5.98%	4.16%	Bacteroidetes	Bacteroidia	Bacteroidales
0.00%	0.07%	0.00%	Bacteroidetes	Cytophagia	Cytophagales
0.04%	0.42%	0.83%	Bacteroidetes	Flavobacteriia	Flavobacteriales
0.33%	0.00%	0.00%	Bacteroidetes	Sphingobacteriia	Sphingobacteriales
0.00%	0.00%	0.00%	Chloroflexi	Anaerolineae	SBR1031

0.08%	0.56%	0.00%	Cyanobacteria	4C0d-2	YS2
0.10%	0.00%	0.00%	Cyanobacteria	Oscillatoriothycideae	Chroococcales
0.00%	0.00%	0.09%	Deferribacteres	Deferribacteres	Deferribacterales
0.00%	0.04%	0.00%	Firmicutes	Other	Other
0.67%	0.67%	0.32%	Firmicutes	Bacilli	Bacillales
0.07%	0.13%	0.01%	Firmicutes	Bacilli	Gemellales
87.14%	66.08%	83.89%	Firmicutes	Bacilli	Lactobacillales
0.01%	0.00%	0.00%	Firmicutes	Bacilli	Turcibacterales
1.68%	17.78%	6.74%	Firmicutes	Clostridia	Clostridiales
0.00%	0.00%	0.00%	Firmicutes	Clostridia	SHA-98
0.00%	0.28%	0.10%	Firmicutes	Erysipelotrichi	Erysipelotrichales
0.12%	0.00%	0.00%	Fusobacteria	Fusobacteriia	Fusobacteriales
0.00%	0.00%	0.00%	GN02	GKS2-174	N.C.
0.00%	0.00%	0.03%	Proteobacteria	Alphaproteobacteria	Caulobacterales
0.00%	0.05%	0.00%	Proteobacteria	Alphaproteobacteria	RF32
0.55%	0.05%	0.25%	Proteobacteria	Alphaproteobacteria	Rhizobiales
0.69%	0.43%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodobacterales
0.33%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodospirillales
0.55%	0.08%	0.20%	Proteobacteria	Alphaproteobacteria	Sphingomonadales
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Other
0.27%	0.97%	0.12%	Proteobacteria	Betaproteobacteria	Burkholderiales
0.07%	0.02%	0.00%	Proteobacteria	Betaproteobacteria	Methylophilales
0.06%	0.86%	0.00%	Proteobacteria	Betaproteobacteria	Neisseriales
0.00%	0.21%	0.00%	Proteobacteria	Betaproteobacteria	Rhodocyclales
0.00%	0.00%	0.03%	Proteobacteria	Deltaproteobacteria	Desulfovibrionales
0.04%	0.75%	1.06%	Proteobacteria	Epsilonproteobacteria	Campylobacterales
0.03%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Other
0.00%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Aeromonadales
0.00%	0.94%	0.02%	Proteobacteria	Gammaproteobacteria	Enterobacteriales
0.46%	0.26%	0.54%	Proteobacteria	Gammaproteobacteria	Pseudomonadales
0.15%	0.14%	0.02%	Proteobacteria	Gammaproteobacteria	Xanthomonadales
0.00%	0.04%	0.00%	Synergistetes	Synergistia	Synergistales
0.00%	0.02%	0.00%	TM7	TM7-1	N.C.
0.00%	0.00%	0.00%	Tenericutes	Mollicutes	Anaeroplasmatales
0.00%	0.03%	0.04%	Tenericutes	Mollicutes	RF39

Group A	Group B	Group C	L5			
			Phylum	Class	Order	Family
0.00%	0.00%	0.00%	Other	Other	Other	Other
0.00%	0.00%	0.00%	Acidobacteria	Acidobacteria-6	iii1-15	mb2424
0.06%	0.00%	0.00%	Acidobacteria	Solibacteres	Solibacterales	N.C.
0.00%	0.01%	0.00%	Acidobacteria	Sva0725	Sva0725	N.C.
0.00%	0.00%	0.00%	Actinobacteria	Acidimicrobiia	Acidimicrobiales	N.C.
0.00%	0.00%	0.00%	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111
0.09%	0.01%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Other
0.01%	0.24%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae
0.87%	0.22%	0.61%	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae
0.00%	0.01%	0.11%	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae
0.25%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Gordoniaceae
0.21%	0.04%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae
0.09%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae
0.37%	0.00%	0.04%	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae
2.56%	0.76%	0.05%	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae
0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae
0.07%	0.05%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae
0.09%	0.00%	0.26%	Actinobacteria	Actinobacteria	Actinomycetales	Nocardoidaceae
1.45%	1.81%	0.34%	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae
0.08%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Sporichthyaceae
0.05%	0.00%	0.09%	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae
0.03%	0.01%	0.03%	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae
0.00%	0.00%	0.00%	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae
0.04%	0.00%	0.29%	Bacteroidetes	Bacteroidia	Bacteroidales	Other
0.07%	0.01%	0.02%	Bacteroidetes	Bacteroidia	Bacteroidales	N.C.
0.05%	5.33%	3.61%	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae
0.00%	0.21%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae
0.11%	0.00%	0.17%	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae
0.00%	0.35%	0.07%	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae
0.00%	0.00%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7
0.00%	0.07%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]
0.00%	0.01%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	[Paraprevotellaceae]
0.00%	0.07%	0.00%	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
0.00%	0.00%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	Other
0.00%	0.19%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae
0.04%	0.23%	0.83%	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]

0.00%	0.00%	0.00%	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	N.C.
0.33%	0.00%	0.00%	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae
0.00%	0.00%	0.00%	Chloroflexi	Anaerolineae	SBR1031	A4b
0.08%	0.56%	0.00%	Cyanobacteria	4C0d-2	YS2	N.C.
0.10%	0.00%	0.00%	Cyanobacteria	Oscillatoriophycideae	Chroococcales	Xenococcaceae
0.00%	0.00%	0.09%	Deferribacteres	Deferribacteres	Deferribacterales	Deferribacteraceae
0.00%	0.04%	0.00%	Firmicutes	Other	Other	Other
0.11%	0.00%	0.00%	Firmicutes	Bacilli	Bacillales	Bacillaceae
0.35%	0.04%	0.01%	Firmicutes	Bacilli	Bacillales	Listeriaceae
0.21%	0.63%	0.32%	Firmicutes	Bacilli	Bacillales	Staphylococcaceae
0.02%	0.02%	0.00%	Firmicutes	Bacilli	Gemellales	N.C.
0.05%	0.11%	0.00%	Firmicutes	Bacilli	Gemellales	Gemellaceae
0.36%	0.00%	0.00%	Firmicutes	Bacilli	Lactobacillales	Other
0.00%	0.14%	0.00%	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae
86.47%	65.16%	83.85%	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae
0.03%	0.00%	0.00%	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae
0.28%	0.78%	0.04%	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae
0.01%	0.00%	0.00%	Firmicutes	Bacilli	Turicibacterales	Turicibacteraceae
0.52%	0.14%	0.30%	Firmicutes	Clostridia	Clostridiales	Other
0.00%	0.32%	0.13%	Firmicutes	Clostridia	Clostridiales	N.C.
0.30%	7.35%	0.09%	Firmicutes	Clostridia	Clostridiales	Clostridiaceae
0.20%	1.42%	0.80%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae
0.00%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	Peptococcaceae
0.00%	6.48%	4.21%	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae
0.11%	0.35%	0.18%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae
0.20%	1.55%	1.00%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae
0.34%	0.17%	0.04%	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]
0.00%	0.00%	0.00%	Firmicutes	Clostridia	SHA-98	N.C.
0.00%	0.28%	0.10%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae
0.00%	0.00%	0.00%	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae
0.12%	0.00%	0.00%	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae
0.00%	0.00%	0.00%	GN02	GKS2-174	N.C.	N.C.
0.00%	0.00%	0.03%	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae
0.00%	0.05%	0.00%	Proteobacteria	Alphaproteobacteria	RF32	N.C.
0.00%	0.00%	0.05%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae
0.04%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae
0.13%	0.05%	0.02%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae
0.38%	0.00%	0.18%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae
0.69%	0.43%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae
0.31%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae
0.03%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae
0.00%	0.00%	0.07%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae
0.55%	0.08%	0.13%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Other	Other
0.17%	0.42%	0.06%	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae
0.03%	0.30%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae
0.06%	0.24%	0.06%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae
0.07%	0.02%	0.00%	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae
0.06%	0.86%	0.00%	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae
0.00%	0.21%	0.00%	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae
0.00%	0.00%	0.03%	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae
0.04%	0.75%	1.06%	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae
0.00%	0.00%	0.00%	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae
0.03%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Other	Other
0.00%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Aeromonadales	Succinivibrionaceae
0.00%	0.94%	0.02%	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae
0.09%	0.21%	0.32%	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae
0.38%	0.05%	0.22%	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae
0.01%	0.14%	0.02%	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae
0.14%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae
0.00%	0.04%	0.00%	Synergistetes	Synergistia	Synergistales	N.C.
0.00%	0.00%	0.00%	Synergistetes	Synergistia	Synergistales	Synergistaceae
0.00%	0.02%	0.00%	TM7	TM7-1	N.C.	N.C.
0.00%	0.00%	0.00%	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae
0.00%	0.03%	0.04%	Tenericutes	Mollicutes	RF39	N.C.

Group A	Group B	Group C	L6				
			Phylum	Class	Order	Family	Genus
0.00%	0.00%	0.00%	Other	Other	Other	Other	Other
0.00%	0.00%	0.00%	Acidobacteria	Acidobacteria-6	iii1-15	mb2424	N.C.
0.06%	0.00%	0.00%	Acidobacteria	Solibacteres	Solibacterales	N.C.	N.C.
0.00%	0.01%	0.00%	Acidobacteria	Sva0725	Sva0725	N.C.	N.C.
0.00%	0.00%	0.00%	Actinobacteria	Acidimicrobiia	Acidimicrobiales	N.C.	N.C.

0.00%	0.00%	0.00%	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111	N.C.
0.09%	0.01%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Other	Other
0.01%	0.24%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces
0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Arcanobacterium
0.87%	0.22%	0.61%	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium
0.00%	0.01%	0.11%	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	N.C.
0.25%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Gordoniaceae	Gordonia
0.21%	0.04%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Janibacter
0.09%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	N.C.
0.04%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Clavibacter
0.32%	0.00%	0.04%	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium
0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Salinibacterium
0.00%	0.05%	0.01%	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	N.C.
0.29%	0.18%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria
2.24%	0.50%	0.02%	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Micrococcus
0.03%	0.02%	0.02%	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia
0.00%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Actinoplanes
0.07%	0.05%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus
0.09%	0.00%	0.26%	Actinobacteria	Actinobacteria	Actinomycetales	Nocardoidaceae	N.C.
1.45%	1.81%	0.34%	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacterium
0.08%	0.00%	0.00%	Actinobacteria	Actinobacteria	Actinomycetales	Sporichthyaceae	Sporichthya
0.05%	0.00%	0.09%	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	N.C.
0.03%	0.01%	0.03%	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae	Rubrobacter
0.00%	0.00%	0.00%	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	N.C.
0.04%	0.00%	0.29%	Bacteroidetes	Bacteroidia	Bacteroidales	Other	Other
0.07%	0.01%	0.02%	Bacteroidetes	Bacteroidia	Bacteroidales	N.C.	N.C.
0.05%	5.33%	3.61%	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
0.00%	0.00%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
0.00%	0.21%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Porphyromonas
0.11%	0.00%	0.17%	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
0.00%	0.00%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Other
0.00%	0.35%	0.07%	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	N.C.
0.00%	0.00%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
0.00%	0.00%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Rikenella
0.00%	0.00%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	N.C.
0.00%	0.00%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	Other
0.00%	0.07%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	N.C.
0.00%	0.00%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	Barnesiella
0.00%	0.00%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	[Paraprevotellaceae]	Other
0.00%	0.01%	0.00%	Bacteroidetes	Bacteroidia	Bacteroidales	[Paraprevotellaceae]	[Prevotella]
0.00%	0.00%	0.00%	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	N.C.
0.00%	0.07%	0.00%	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter
0.00%	0.00%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	Other	Other
0.00%	0.19%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
0.00%	0.00%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Myroides
0.04%	0.18%	0.00%	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium
0.00%	0.05%	0.83%	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Cloacibacterium
0.00%	0.00%	0.00%	Bacteroidetes	Sphingobacteriia	Sphingobacteriales		N.C.
0.33%	0.00%	0.00%	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
0.00%	0.00%	0.00%	Chloroflexi	Anaerolineae	SBR1031	A4b	N.C.
0.08%	0.56%	0.00%	Cyanobacteria	4C0d-2	YS2	N.C.	N.C.
0.10%	0.00%	0.00%	Cyanobacteria	Oscillatoriohycideae	Chroococcales	Xenococcaceae	Chroococcidiopsis
0.00%	0.00%	0.09%	Deferribacteres	Deferribacteres	Deferribacterales	Deferribacteraceae	Mucispirillum
0.00%	0.04%	0.00%	Firmicutes	Other	Other	Other	Other
0.07%	0.00%	0.00%	Firmicutes	Bacilli	Bacillales	Bacillaceae	Other
0.04%	0.00%	0.00%	Firmicutes	Bacilli	Bacillales	Bacillaceae	Anoxybacillus
0.00%	0.00%	0.00%	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
0.00%	0.00%	0.00%	Firmicutes	Bacilli	Bacillales	Bacillaceae	Marinibacillus
0.35%	0.04%	0.01%	Firmicutes	Bacilli	Bacillales	Listeriaceae	Brochothrix
0.00%	0.20%	0.14%	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Jeotgalicoccus
0.20%	0.43%	0.18%	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus
0.02%	0.02%	0.00%	Firmicutes	Bacilli	Gemellales	N.C.	N.C.
0.05%	0.11%	0.00%	Firmicutes	Bacilli	Gemellales	Gemellaceae	N.C.
0.36%	0.00%	0.00%	Firmicutes	Bacilli	Lactobacillales	Other	Other
0.00%	0.14%	0.00%	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Granulicatella
86.47%	65.16%	83.85%	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
0.01%	0.00%	0.00%	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Leuconostoc
0.02%	0.00%	0.00%	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Weissella
0.00%	0.20%	0.00%	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	N.C.
0.28%	0.58%	0.04%	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
0.01%	0.00%	0.00%	Firmicutes	Bacilli	Turicibacterales	Turicibacteraceae	Turicibacter
0.52%	0.14%	0.30%	Firmicutes	Clostridia	Clostridiales	Other	Other
0.00%	0.32%	0.13%	Firmicutes	Clostridia	Clostridiales	N.C.	N.C.
0.00%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	02d06

0.05%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	<i>Clostridium</i>
0.24%	7.35%	0.09%	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	<i>SMB53</i>
0.03%	0.25%	0.44%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Other</i>
0.17%	0.87%	0.29%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>N.C.</i>
0.00%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Blautia</i>
0.00%	0.20%	0.00%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Coproccoccus</i>
0.00%	0.01%	0.01%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Dorea</i>
0.00%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Roseburia</i>
0.00%	0.08%	0.07%	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>[Ruminococcus]</i>
0.00%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	<i>Peptococcus</i>
0.00%	6.48%	4.21%	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	<i>N.C.</i>
0.00%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	<i>Filifactor</i>
0.00%	0.01%	0.00%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Other</i>
0.01%	0.08%	0.08%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>N.C.</i>
0.00%	0.05%	0.03%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Butyricoccus</i>
0.00%	0.20%	0.07%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Faecalibacterium</i>
0.00%	0.01%	0.00%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Oscillospira</i>
0.10%	0.01%	0.00%	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcus</i>
0.00%	0.05%	0.00%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	<i>Anaerovibrio</i>
0.15%	1.26%	0.96%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	<i>Megamonas</i>
0.00%	0.00%	0.02%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	<i>Megasphaera</i>
0.04%	0.08%	0.02%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	<i>Phascolarctobacterium</i>
0.00%	0.16%	0.00%	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	<i>Veillonella</i>
0.00%	0.17%	0.00%	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]	<i>Anaerococcus</i>
0.06%	0.00%	0.04%	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]	<i>Finegoldia</i>
0.00%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]	<i>Gallicola</i>
0.28%	0.00%	0.00%	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]	<i>Peptoniphilus</i>
0.00%	0.00%	0.00%	Firmicutes	Clostridia	SHA-98	N.C.	<i>N.C.</i>
0.00%	0.00%	0.00%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>Other</i>
0.00%	0.00%	0.00%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	
0.00%	0.00%	0.10%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>Clostridium</i>
0.00%	0.00%	0.00%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>RFN20</i>
0.00%	0.00%	0.00%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>[Eubacterium]</i>
0.00%	0.00%	0.00%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>cc_115</i>
0.00%	0.28%	0.00%	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	<i>p-75-a5</i>
0.00%	0.00%	0.00%	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	<i>Fusobacterium</i>
0.12%	0.00%	0.00%	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae	<i>Leptotrichia</i>
0.00%	0.00%	0.00%	GN02	GKS2-174	N.C.	N.C.	<i>N.C.</i>
0.00%	0.00%	0.03%	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	<i>Mycoplana</i>
0.00%	0.05%	0.00%	Proteobacteria	Alphaproteobacteria	RF32	N.C.	<i>N.C.</i>
0.00%	0.00%	0.05%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Chelatococcus</i>
0.04%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	<i>Afipia</i>
0.13%	0.05%	0.02%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	<i>Methylobacterium</i>
0.23%	0.00%	0.18%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Agrobacterium</i>
0.15%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Rhizobium</i>
0.40%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Other</i>
0.29%	0.43%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Paracoccus</i>
0.31%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	<i>Roseomonas</i>
0.03%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	<i>N.C.</i>
0.00%	0.00%	0.07%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	<i>N.C.</i>
0.00%	0.00%	0.12%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Other</i>
0.41%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Novosphingobium</i>
0.01%	0.07%	0.01%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingobium</i>
0.10%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingomonas</i>
0.03%	0.00%	0.00%	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingopyxis</i>
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Other	Other	<i>Other</i>
0.17%	0.42%	0.06%	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	<i>Sutterella</i>
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	<i>Lautropia</i>
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Other</i>
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>N.C.</i>
0.03%	0.24%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Delftia</i>
0.00%	0.06%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Schlegelella</i>
0.06%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Other</i>
0.00%	0.24%	0.01%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>N.C.</i>
0.00%	0.00%	0.05%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Cupriavidus</i>
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Massilia</i>
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Ralstonia</i>
0.07%	0.02%	0.00%	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	<i>Methylobacillus</i>
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	<i>N.C.</i>
0.06%	0.86%	0.00%	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	<i>Neisseria</i>
0.00%	0.00%	0.00%	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	<i>Methyloversatilis</i>
0.00%	0.21%	0.00%	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	<i>Petrobacter</i>
0.00%	0.00%	0.00%	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	<i>N.C.</i>
0.00%	0.00%	0.03%	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	<i>Desulfovibrio</i>

0.04%	0.75%	1.06%	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	<i>Campylobacter</i>
0.00%	0.00%	0.00%	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	<i>Helicobacter</i>
0.03%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Other	Other	<i>Other</i>
0.00%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Aeromonadales	Succinivibrionaceae	<i>Succinatimonas</i>
0.00%	0.04%	0.00%	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Other</i>
0.00%	0.19%	0.00%	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>N.C.</i>
0.00%	0.72%	0.02%	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Trabulsiella</i>
0.00%	0.04%	0.30%	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>
0.09%	0.17%	0.02%	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Enhydrobacter</i>
0.38%	0.05%	0.22%	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Pseudomonas</i>
0.01%	0.14%	0.02%	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	<i>N.C.</i>
0.14%	0.00%	0.00%	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Stenotrophomonas</i>
0.00%	0.04%	0.00%	Synergistetes	Synergistia	Synergistales	<i>N.C.</i>	<i>N.C.</i>
0.00%	0.00%	0.00%	Synergistetes	Synergistia	Synergistales	Synergistaceae	<i>N.C.</i>
0.00%	0.02%	0.00%	TM7	TM7-1	<i>N.C.</i>	<i>N.C.</i>	<i>N.C.</i>
0.00%	0.00%	0.00%	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	<i>Anaeroplasma</i>
0.00%	0.03%	0.04%	Tenericutes	Mollicutes	RF39	<i>N.C.</i>	<i>N.C.</i>