

**Release Notes 2022-03-01 :** I finally got a first list of enough organisms and antibiotics to motivate the argument for antibiotics for Beauty based on the 16s rRNA. There are over 330 organisms found in the two samples and only about 100 have been considered so far.

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**I am not a veterinarian or a doctor or health care professional**

**Note that any item given to a non-human must be checked for safety alone and in combination with other ingredients or medicines for that animal. Animals including dogs and cats have decreased tolerance for many common ingredients in things meant for human consumption.**

## CBeauty : linical Relevance of Vomit and Fecal Microbiome

Mike Marchywka\*

306 Charles Cox , Canton GA 30115

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\*Electronic address: [marchywka@hotmail.com](mailto:marchywka@hotmail.com); to cite or credit this work, see bibtex in Appendix F

## 1. INTRODUCTION

Beauty had been suffering from a variety of non-specific symptoms as detailed later. Recently 16s rRNA along with othre molecular techniques has become available to the general public. However, the large number of normal organisms present in many biological samples makes it difficult to establish clinical relevance of any particular "community structure" or small group of organisms except in specific cases. Organisms may become pathological simply due to location as bloodstream or organ infections with GI organisms may occur. These samples can not determine colonization in other locations. Virulence and various phenotypes canbe induced by specific environmental factors not revealed by the 16s rRNA sequences.

In the case of Beauty, considering her clinical picture, several organisms are highly suspicious due to their mere presence in the sample of propensity to become pathogens or to be associated with pathological states.

16s rRNA PCR analysis of the two samples from Beauty turned up a variety of suspicious organisms. In most cases, these organisms are described in the literature along with antibiotics that appear to work either in vitro, in humans, or in animals. The short list of relevant drugs includes,

Antibiotics
Cefovecin
clindamycin
amoxicillin plus clavulanate
doxycycline
ceftriaxone
metronidazole

TABLE I: Antibiotics thought to be useful against the most suspicious organisms found.

Currently she appears to be responding to silver and maybe copper as well as a low carbohydrate diet.

## 2. BACKGROUND

Two samples were collected from Beauty on 2022-01-22 and subsequently sent to Zymo Research for 16s rRNA PCR. The procedure generally followed [1] with more details in the company's full report. Results were reported on 2022-02-22 and can be found until approximated 2022-04-22 at these links,

[https://epiquest.s3.amazonaws.com/epiquest\\_zr5958/FZHH7JJPKPLH4T3FYTAKSYBQ2HBATFC/report/zr5958.16S\\_220218.zymo.zip](https://epiquest.s3.amazonaws.com/epiquest_zr5958/FZHH7JJPKPLH4T3FYTAKSYBQ2HBATFC/report/zr5958.16S_220218.zymo.zip)

[https://epiquest.s3.amazonaws.com/epiquest\\_zr5958/FZHH7JJPKPLH4T3FYTAKSYBQ2HBATFC/rawdata/zr5958.rawdata.220218.zip](https://epiquest.s3.amazonaws.com/epiquest_zr5958/FZHH7JJPKPLH4T3FYTAKSYBQ2HBATFC/rawdata/zr5958.rawdata.220218.zip)

The complete list of organisms found in the two samples is included in Appendix A along with their amounts.

Class	Genus	Species	Comments
Methanobacteria	Methanobrevibacter	oralis	(P) [2]
Actinobacteria	Actinomyces	bowdenii	(P) [3] [4]
Actinobacteria	Actinomyces	canis	(P) (C) [5]
Actinobacteria	Actinomyces	hordeovulneris	(P) [6]
Actinobacteria	Propionibacterium	acnes	(C) (P) [7]
Coriobacteriia	Atopobium	sp10394	(P) vaginosis [8]
Coriobacteriia	Paraeggerthella	hongkongensis	(P) renamed [9] [10]
Bacteroidia	Bacteroides	vulgatus	(C) (P) common in abscess [11]
Bacteroidia	Odoribacter	denticanis	(P) [12]
Bacteroidia	Parabacteroides	sp13269	(C) (P) (?) [13]
Bacteroidia	Porphyromonas	cangingivalis	(C) (P) [14] assoc [15]
Bacteroidia	Porphyromonas	canoris	(P) black subgingival [16]
Bacteroidia	Porphyromonas	crevioricanis	(P) Cefovecin effective [17]
Bacteroidia	Porphyromonas	gingivicanis	(P) [18]
Bacteroidia	Porphyromonas	gulae	(P) Cefovecin effective [17]
Bacteroidia	Porphyromonas	macacae	(P) clindamycin ok [19]
Bacteroidia	Tannerella	forsythia	(P) [20] sensitive including amoxicillin with clavulanate doxycycline clindamycin [21]
Bacteroidia	Prevotella	intermedia	(P) [22]
Bacilli	Staphylococcus	delphini intermedius pseudintermedius	(P) [23]
Bacilli	Abiotrophia	sp28087	possible (P) [24] likely clindamycin [25]
Bacilli	Streptococcus	canis	(P) [26]
Clostridia	Filifactor	alocis	(P) indicator of periodontal disease [27] antibiotics ceftriaxone (4 g/day) and metronidazole [28]
Deltaproteobacteria	Desulfomicrobium	orale	associated (P) [15]
Epsilonproteobacteria	Campylobacter	rectus showae	(P) CDT targets [29]
Spirochaetes	Treponema	denticola	(P) [20]

TABLE II: Currently annotated organisms based on a quick literature search. Organisms are identified by genus and species as well as class for context. Terse notes are indicated in the right most column. "(C)" indicates common or commensal not associated with disease under appropriate conditions. "(P)" indicates observed to be pathogenic at least under some conditions. Unusual features or antibiotic susceptibility are noted where they were thought helpful.

### 3. CONCLUSIONS

### 4. SUPPLEMENTAL INFORMATION

#### 4.1. Computer Code

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## Appendix A: Full List of Organisms found in 16s rRNA Sequencing

0	k	p	c	o	f	
1		g	s	sample 0	sample 1	
2	None	Other	Other	Other	Other	
3		<b>Other</b>	<b>Other</b>	2.44	0.0181	
4	Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	
5		<b>Methanobrevibacter</b>	<b>oralis</b>	0.0254		(P) [2]
6	Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	Methanosarcinaceae	
7		<b>Methanimicrococcus</b>	<b>blatticola</b>	0.0701		[30]
8	Archaea	Euryarchaeota	Thermoplasmata	Thermoplasmatales	NA	
9		<b>*Methanomethylophilus</b>	<b>sp1266</b>	0.0242		
10		<b>NA</b>	<b>sp1275</b>	0.0326		
11	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	
12		<b>Actinomyces</b>	<b>bowdenii</b>	0.0326		(P) [3] [4]
13		<b>Actinomyces</b>	<b>canis</b>	1.23		(P) (C) [5]
14		<b>Actinomyces</b>	<b>cardiffensis</b>	0.122		
15		<b>Actinomyces</b>	<b>coleocanis</b>	0.752		
16		<b>Actinomyces</b>	<b>hordeovulneris</b>	0.487		(P) [6]
17		<b>Actinomyces</b>	<b>oris</b>	0.081		
18		<b>Actinomyces</b>	<b>slackii</b>	0.0943		
19		<b>Actinomyces</b>	<b>sp4755</b>	0.0363		
20		<b>Actinomyces</b>	<b>sp4762</b>	0.173		
21	Bacteria	Actinobacteria	Actinobacteria	Corynebacteriales	Corynebacteriaceae	
22		<b>Corynebacterium</b>	<b>canis</b>	0.254		
23		<b>Corynebacterium</b>	<b>freiburgense</b>	0.48		
24		<b>Corynebacterium</b>	<b>matruchotii</b>	0.337		
25		<b>Corynebacterium</b>	<b>sp5220</b>	0.302		
26	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	
27		<b>Leucobacter</b>	<b>sp6730</b>	0.0798		
28	Bacteria	Actinobacteria	Actinobacteria	Propionibacteriales	Propionibacteriaceae	
29		<b>NA</b>	<b>sp7814</b>	0.0375		
30		<b>NA</b>	<b>sp7833</b>	0.0411		
31		<b>NA</b>	<b>sp7836</b>	0.029		
32		<b>Propionibacterium</b>	<b>acnes</b>	0.0387		(C) (P) [7]
33		<b>Propionibacterium</b>	<b>propionicum</b>	0.0338		[31]
34		<b>Propioniciclava</b>	<b>sp7799</b>	0.0483		likely decaying matter
35		<b>Propioniciclava</b>	<b>sp7803</b>	0.0314		
36	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	
37		<b>Atopobium</b>	<b>sp10394</b>	0.0169		(P) vaginosis [8]
38		<b>Collinsella</b>	<b>intestinalis</b>		3.98	
			<b>stercoris</b>			
39		<b>Paraeggerthella</b>	<b>hongkongensis</b>	0.058		(P) renamed [9]
40		<b>Slackia</b>	<b>piriformis</b>		0.166	[10]
41	Bacteria	Actinobacteria	Nitriliruptoria	Euzebyales	Euzebyaceae	
42		<b>Euzebya</b>	<b>sp10631</b>	0.244		(?) marine organisms [32]
43	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	
44		<b>Bacteroides</b>	<b>clarus</b>	0.0471		(C) [33]

TABLE III: Summary of all of the organisms identified in Beauty's two samples from 2021-01-22. Two line types exist. The first line indicates the higher level classifications of the following lines which only contain genus and species along with percentage of total abundance in the two samples. The first sample was spit up clear fluid while the second one was a fecal sample. During this time here symptoms were fairly controlled.

45	k	p	c	o	f	
46		g	s	sample 0	sample 1	
47		<b>Bacteroides</b>	<b>coprocola</b>		5.67	
48		<b>Bacteroides</b>	<b>denticanum</b>	0.759		bite related [34]
49			<b>pyogenes</b>			
50		<b>Bacteroides</b>	<b>sp12145</b>	1.24		
51		<b>Bacteroides</b>	<b>sp12206</b>	0.517		
52		<b>Bacteroides</b>	<b>sp12209</b>		4.06	
53		<b>Bacteroides</b>	<b>stercoris</b>		3.57	
54	Bacteria	<b>Bacteroides</b>	<b>vulgatus</b>		9.22	(C) (P) common in abscess [11]
55		<b>Bacteroidetes</b>	<b>Bacteroidia</b>	<b>Bacteroidales</b>	NA	
56		<b>NA</b>	<b>sp12425</b>	0.359		
57		<b>NA</b>	<b>sp12429</b>	0.0145		
58	Bacteria	<b>NA</b>	<b>sp13034</b>	0.108		
59		<b>Bacteroidetes</b>	<b>Bacteroidia</b>	<b>Bacteroidales</b>	<b>Porphyromonadaceae</b>	
60		<b>Microbacter</b>	<b>sp13164</b>	0.0278		
61		<b>Odoribacter</b>	<b>denticanis</b>	0.39		(P) [12]
62		<b>Paludibacter</b>	<b>sp13190</b>	0.0701		plant residue (?) [35]
63		<b>Parabacteroides</b>	<b>sp13269</b>	0.0713		(C) (P) (?) [13]
64		<b>Petrimonas</b>	<b>sp13305</b>	0.0205		
65		<b>Porphyromonas</b>	<b>cangingivalis</b>	6.57		(C) (P) [14] assoc [15]
66		<b>Porphyromonas</b>	<b>canoris</b>	3.61		(P) black subgingival [16]
67		<b>Porphyromonas</b>	<b>crevioricanis</b>	0.609		(P) Cefovecin effective [17]
68		<b>Porphyromonas</b>	<b>gingivicanis</b>	2.95		(P) [18]
69		<b>Porphyromonas</b>	<b>gulae</b>	5.23		(P) Cefovecin effective [17]
70		<b>Porphyromonas</b>	<b>macacae</b>	0.527		(P) clindamycin ok [19]
71		<b>Porphyromonas</b>	<b>sp13363</b>	0.84		
72		<b>Porphyromonas</b>	<b>sp13364</b>	0.178		
73		<b>Porphyromonas</b>	<b>sp13368</b>			
74		<b>Porphyromonas</b>	<b>sp13365</b>	1.32		
75		<b>Porphyromonas</b>	<b>sp13366</b>	0.0616		
76		<b>Porphyromonas</b>	<b>sp13367</b>	1.02		
77		<b>Porphyromonas</b>	<b>sp13368</b>	1.8		
78		<b>Proteiniphilum</b>	<b>sp13394</b>	0.0508		
79		<b>Tannerella</b>	<b>sp13418</b>			
80		<b>Tannerella</b>	<b>forsythia</b>	0.227		(P) [20] sensitive including amoxicillin with clavulanate doxycycline clindamycin [21]
81	Bacteria	<b>Bacteroidetes</b>	<b>Bacteroidia</b>	<b>Bacteroidales</b>	<b>Prevotellaceae</b>	
82		<b>Alloprevotella</b>	<b>sp13484</b>	2.4		
83		<b>Alloprevotella</b>	<b>sp13488</b>	0.648		
84		<b>Alloprevotella</b>	<b>sp13489</b>	0.0568		
85		<b>Alloprevotella</b>	<b>sp13490</b>	1.64		
86		<b>Alloprevotella</b>	<b>sp13512</b>	0.173		
87		<b>NA</b>	<b>sp13517</b>			
88		<b>NA</b>	<b>sp12884</b>	0.355		
89		<b>NA</b>	<b>sp13774</b>	0.0387		
90		<b>NA</b>	<b>sp14118</b>		0.191	
91		<b>NA</b>	<b>sp14284</b>	0.168		
92		<b>Prevotella</b>	<b>intermedia</b>	0.54		(P) [22]
93		<b>Prevotella</b>	<b>sp14101</b>	1.34		

TABLE IV: Summary of all of the organisms identified in Beauty’s two samples from 2021-01-22. Two line types exist. The first line indicates the higher level classifications of the following lines which only contain genus and species along with percentage of total abundance in the two samples. The first sample was spit up clear fluid while the second one was a fecal sample. During this time here symptoms were fairly controlled.



90	k	p	c	o	f	
91		g	s	sample 0	sample 1	
92	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	
93		<b>NA</b>	<b>sp14589</b>	0.023		
94		<b>NA</b>	<b>sp14717</b>	0.135		
95	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	
96		<b>Bergeyella</b>	<b>sp16466</b>	0.0846		
97		<b>Bergeyella</b>	<b>zoohelcum</b>	0.874		(C) human pathogen [36]
98		<b>Capnocytophaga</b>	<b>canimorsus</b>	0.116		(C) human pathogen [37]
99		<b>Capnocytophaga</b>	<b>cynodegmi</b>	0.39		(C) human pathogen [38]
100		<b>Capnocytophaga</b>	<b>sp16516</b>	0.349		
101		<b>Capnocytophaga</b>	<b>sp16518</b>	0.0387		
102		<b>Flavobacterium</b>	<b>sp16983</b>	0.0894		
103	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	NA	
104		<b>NA</b>	<b>bacterium</b>	0.0145		
105	Bacteria	Chlorobi	Chlorobia	Chlorobiales	NA	
106		<b>NA</b>	<b>sp20053</b>	0.586		
107	Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	
108		<b>NA</b>	<b>sp20572</b>	0.114		
109	Bacteria	Cyanobacteria	Chloroplast	NA	NA	
110		<b>Castanea</b>	<b>mollissima</b>	0.0157		suspect floor contamination
111	Bacteria	Cyanobacteria	NA	NA	NA	
112		<b>NA</b>	<b>sp23682</b>	0.108		
113	Bacteria	Firmicutes	Bacilli	Bacillales	Family XI	
114		<b>Gemella</b>	<b>palaticanis</b>	0.512		(C) dog specific [39]
115	Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	
116		<b>Staphylococcus</b>	<b>delphini intermedius pseudintermedius</b>	0.853		
117	Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	
118		<b>Abiotrophia</b>	<b>sp28087</b>	0.357		possible (P) [24] likely clindamycin [25]
119		<b>NA</b>	<b>sp28129</b>	0.462		
120	Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	
121		<b>Granulicatella</b>	<b>adiacens</b>	0.656		(C)
122	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	
123		<b>Enterococcus</b>	<b>NA</b>	0.0313		
124		<b>Enterococcus</b>	<b>lemanii</b>	0.0181		(C) manure [40]
125	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	
126		<b>Streptococcus</b>	<b>NA</b>	0.146		
127		<b>Streptococcus</b>	<b>cameli</b>	0.0435		
128		<b>Streptococcus</b>	<b>canis</b>	0.164		(P) [26]
129		<b>Streptococcus</b>	<b>equinus infantarius lutetiensis</b>	0.0363	0.181	
130		<b>Streptococcus</b>	<b>fryi</b>	1.27		
131		<b>Streptococcus</b>	<b>minor</b>	0.112		
132		<b>Streptococcus</b>	<b>mitis oralis sanguinis</b>	0.133		
133		<b>Streptococcus</b>	<b>sp30072</b>	0.0254		
134	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	

TABLE V: Summary of all of the organisms identified in Beauty’s two samples from 2021-01-22. Two line types exist. The first line indicates the higher level classifications of the following lines which only contain genus and species along with percentage of total abundance in the two samples. The first sample was spit up clear fluid while the second one was a fecal sample. During this time here symptoms were fairly controlled.



135	k	p	c	o	f	
136		g	s	sample 0	sample 1	
137		NA	sp30201	0.0399		
138		NA	sp30214	0.0496		
139		NA	sp30247	0.0858		
140		NA	sp30248	0.0302		
141		NA	sp30313	0.436		
142		NA	sp30336	0.312		
143	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	
144		<b>Clostridium</b>	<b>colicanis</b>		0.296	
145		<b>Clostridium</b>	<b>perfringens</b>	0.0387	13	
146	Bacteria	Firmicutes	Clostridia	Clostridiales	Defluviitaleaceae	
147		NA	sp31140	0.686		
148	Bacteria	Firmicutes	Clostridia	Clostridiales	Family XI	
149		<b>Ezakiella</b>	<b>sp31233</b>	0.236		
150		<b>Helcococcus</b>	<b>sp31258</b>	1.01		
151		NA	sp31397	0.193		
152		NA	sp31414	0.0302		
153		<b>Parvimonas</b>	<b>micra</b>	0.0761		
154		<b>Parvimonas</b>	<b>sp31278</b>	0.0278		
155		<b>Parvimonas</b>	<b>sp31283</b>	0.966		
156		<b>Peptoniphilus</b>	<b>sp31312</b>	0.227		
157	Bacteria	Firmicutes	Clostridia	Clostridiales	Family XII	
158		<b>Fusibacter</b>	<b>sp31441</b>	0.412		
159		<b>Fusibacter</b>	<b>sp31447</b>	0.0447		
160		<b>Fusibacter</b>	<b>sp31454</b>	0.167		
161		<b>Fusibacter</b>	<b>sp31458</b>	0.0302		
162		<b>Fusibacter</b>	<b>sp31462</b>	0.205		
163		<b>Fusibacter</b>	<b>sp31467</b>	0.035		
164	Bacteria	Firmicutes	Clostridia	Clostridiales	Family XIII	
165		<b>Anaerovorax</b>	<b>sp31493</b>	0.0157		
166		<b>Anaerovorax</b>	<b>sp31513</b>	0.0314		
167		<b>Eubacterium</b>	<b>sp31674</b>	0.0266		
168		NA	sp31535	0.0834		
169		NA	sp31550	0.0822		
170		NA	sp31556	0.0471		
171		NA	sp31583	0.0278		
172		NA	sp31623	0.0266		
173		NA	sp31624	0.1		
174		NA	sp31635	0.0882		
175		NA	sp31677	0.126		
176		NA	sp31686	0.0496		
177		NA	sp31699	0.0532		
178		NA	sp31701	0.15		
179	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	

TABLE VI: Summary of all of the organisms identified in Beauty's two samples from 2021-01-22. Two line types exist. The first line indicates the higher level classifications of the following lines which only contain genus and species along with percentage of total abundance in the two samples. The first sample was spit up clear fluid while the second one was a fecal sample. During this time here symptoms were fairly controlled.

180	k	p	c	o	f	
181		g	s	sample 0	sample 1	
182		<b>Acetitomaculum</b>	<b>sp31920</b>	0.613		
183		<b>Blautia</b>	<b>hansenii</b>		1.4	
184		<b>Blautia</b>	<b>producta</b>		2.32	
185		<b>Blautia</b>	<b>sp32002</b>		0.028	
			<b>sp32027</b>			
186		<b>Blautia</b>	<b>sp32032</b>		0.0214	
187		<b>Blautia</b>	<b>sp32042</b>		0.485	
188		<b>Catonella</b>	<b>sp32118</b>	0.174		
189		<b>Catonella</b>	<b>sp32118</b>	0.0399		
			<b>sp32120</b>			
190		<b>Catonella</b>	<b>sp32119</b>	0.0737		
191		<b>Catonella</b>	<b>sp32120</b>	1.07		
192		<b>Catonella</b>	<b>sp32121</b>	0.0145		
193		<b>Johnsonella</b>	<b>sp32284</b>	0.0931		
194		<b>Johnsonella</b>	<b>sp32285</b>	0.0508		
195		<b>Johnsonella</b>	<b>sp32287</b>	0.0556		
196		<b>Lachnoclostridium</b>	<b>sp32341</b>		0.438	
			<b>sp32430</b>			
197		<b>Lachnoclostridium</b>	<b>sp32345</b>		4.75	
198		<b>Lachnoclostridium</b>	<b>sp32364</b>		0.0938	
199		<b>Lachnoclostridium</b>	<b>sp32369</b>		0.0214	
200		<b>Lachnoclostridium</b>	<b>sp32386</b>		0.179	
201		<b>Lachnoclostridium</b>	<b>sp32408</b>	0.111		
202		<b>Lachnoclostridium</b>	<b>sp32424</b>		0.244	
203		<b>Lachnoclostridium</b>	<b>sp32443</b>		0.257	
204		NA	<b>sp32167</b>		0.0329	
205		NA	<b>sp32615</b>		0.0576	
			<b>sp32802</b>			
206		NA	<b>sp33271</b>		0.0741	
207		NA	<b>sp33387</b>		0.137	
208		NA	<b>sp33411</b>	0.0193		
209		NA	<b>sp33422</b>		0.474	
210		NA	<b>sp33656</b>		0.133	
211		NA	<b>sp33707</b>		0.862	
212		NA	<b>sp33756</b>		0.051	
213		<b>Roseburia</b>	<b>sp33161</b>		0.0346	
			<b>sp33189</b>			
214		<b>Roseburia</b>	<b>sp33201</b>	0.156		
215		<b>Tyzzereella</b>	<b>sp33301</b>		0.0477	may be diet related [41]
216	Bacteria	Firmicutes	Clostridia	Clostridiales	NA	
217		NA	NA		8.48	
218		NA	<b>sp31126</b>	0.0556		
219	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	
220		<b>Peptococcus</b>	<b>sp34115</b>	0.163		
221		<b>Peptococcus</b>	<b>sp34120</b>	0.52		
222	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	
223		<b>Filifactor</b>	<b>alocis</b>	0.533		(P) indicator of periodontal disease [27] antibiotics ceftriaxone (4 g/day) and metronidazole [28]
224		<b>Filifactor</b>	<b>sp34271</b>	0.665		

TABLE VII: Summary of all of the organisms identified in Beauty's two samples from 2021-01-22. Two line types exist. The first line indicates the higher level classifications of the following lines which only contain genus and species along with percentage of total abundance in the two samples. The first sample was spit up clear fluid while the second one was a fecal sample. During this time here symptoms were fairly controlled.

225	k	p	c	o	f
226		g	s	sample 0	sample 1
227		<b>Filifactor</b>	<b>villosus</b>	0.632	
228		<b>Intestinibacter</b>	<b>sp34281</b>		0.665
229		<b>NA</b>	<b>sp34397</b>	0.299	
230		<b>NA</b>	<b>sp34399</b>	0.0846	
231		<b>NA</b>	<b>sp34402</b>	0.191	
232		<b>Paeniclostridium</b>	<b>sordellii</b>		1.48
233		<b>Peptoclostridium</b>	<b>sp34343</b>	0.0568	
234		<b>Peptoclostridium</b>	<b>sp34345</b>	0.213	
235		<b>Peptostreptococcus</b>	<b>canis</b>	0.927	
236		<b>Peptostreptococcus</b>	<b>sp34368</b>	0.423	
237		<b>Proteocatella</b>	<b>sp34372</b>	0.0411	
238		<b>Proteocatella</b>	<b>sp34373</b>	0.464	
239	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae
240		<b>Anaerotruncus</b>	<b>sp34464</b>		2.24
241		<b>Faecalibacterium</b>	<b>prausnitzii</b>		0.148
242		<b>Fastidiosipila</b>	<b>sp34580</b>	0.0628	
243		<b>NA</b>	<b>sp34794</b>		0.028
244		<b>NA</b>	<b>sp35348</b>	0.248	
245		<b>NA</b>	<b>sp35348</b>	0.0242	
			<b>sp35356</b>		
246		<b>NA</b>	<b>sp35734</b>	0.0218	
247		<b>NA</b>	<b>sp35829</b>		0.0872
248		<b>NA</b>	<b>sp35859</b>	0.0725	
249		<b>Oscillospira</b>	<b>sp34659</b>		0.0313
250		<b>Ruminiclostridium</b>	<b>sp34905</b>		0.132
			<b>sp34912</b>		
251		<b>Ruminiclostridium</b>	<b>sp34943</b>	0.0665	
252	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae
253		<b>Allobaculum</b>	<b>stercoricanis</b>		0.309
254		<b>Erysipelothrix</b>	<b>sp36653</b>	0.308	
255		<b>Faecalitalea</b>	<b>sp36732</b>		0.0889
256		<b>NA</b>	<b>sp36724</b>	0.0314	
257		<b>NA</b>	<b>sp36726</b>	0.213	
258		<b>NA</b>	<b>sp36764</b>	0.546	
259		<b>NA</b>	<b>sp36778</b>	0.0882	
260		<b>NA</b>	<b>sp36784</b>	0.0894	
261	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae
262		<b>Megamonas</b>	<b>funiformis</b>		2.95
263		<b>Succinoclasticum</b>	<b>sp36849</b>	0.158	
			<b>sp36859</b>		
264		<b>Succinoclasticum</b>	<b>sp36859</b>	0.0906	
265	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae
266		<b>NA</b>	<b>sp37039</b>	0.0677	
267		<b>Selenomonas</b>	<b>sp37072</b>	0.0677	
268		<b>Veillonella</b>	<b>parvula</b>	0.0157	
269		<b>Veillonella</b>	<b>sp37198</b>	0.212	

TABLE VIII: Summary of all of the organisms identified in Beauty’s two samples from 2021-01-22. Two line types exist. The first line indicates the higher level classifications of the following lines which only contain genus and species along with percentage of total abundance in the two samples. The first sample was spit up clear fluid while the second one was a fecal sample. During this time here symptoms were fairly controlled.

270	k	p	c	o	f	
271		g	s	sample 0	sample 1	
272	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	
273		<b>Fusobacterium</b>	<b>canifelinum</b>	0.624		
274		<b>Fusobacterium</b>	<b>nucleatum</b>			
			<b>equinum</b>	2.31		
			<b>gonidiaformans</b>			
275		<b>Fusobacterium</b>	<b>mortiferum</b>		17.4	
276		<b>Fusobacterium</b>	<b>nucleatum</b>	0.434		
277		<b>Fusobacterium</b>	<b>sp37444</b>	1.26		
278		<b>Fusobacterium</b>	<b>sp37445</b>	2.71		
279		<b>Fusobacterium</b>	<b>sp37458</b>		9.99	
280		<b>Fusobacterium</b>	<b>sp37464</b>		1.91	
281	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae	
282		<b>Leptotrichia</b>	<b>sp37508</b>	0.0689		
283		<b>Leptotrichia</b>	<b>sp37508</b>	0.0773		
			<b>sp37510</b>			
284		<b>Leptotrichia</b>	<b>sp37518</b>	0.166		
285		<b>NA</b>	<b>sp37541</b>	1.38		
286		<b>Streptobacillus</b>	<b>moniliformis</b>	0.321		
287	Bacteria	Gracilibacteria	NA	NA	NA	
288		<b>Gracilibacteria</b>	<b>bacterium</b>	0.0375		
289		<b>NA</b>	<b>sp38143</b>	0.0471		
290		<b>NA</b>	<b>sp38170</b>	0.0846		
291		<b>NA</b>	<b>sp38230</b>	0.0363		
292	Bacteria	NA	NA	NA	NA	
293		<b>NA</b>	<b>sp19816</b>	1.5		
294		<b>NA</b>	<b>sp19817</b>	0.0749		
295		<b>NA</b>	<b>sp19824</b>	0.289		
296	Bacteria	Parcubacteria	NA	NA	NA	
297		<b>NA</b>	<b>sp40081</b>	0.0302		
298	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	
299		<b>NA</b>	<b>sp46470</b>	0.155		
300	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	
301		<b>Sutterella</b>	<b>stercoricanis</b>		1.44	
302	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	
303		<b>Lautropia</b>	<b>mirabilis</b>	0.375		
304	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	
305		<b>Brachymonas</b>	<b>denitrificans</b>	0.0314		
306		<b>Brachymonas</b>	<b>sp48850</b>	0.16		
307		<b>Brachymonas</b>	<b>sp48857</b>	0.149		
308		<b>Comamonas</b>	<b>sp48916</b>	0.0604		
309		<b>Lampropedia</b>	<b>hyalina</b>	0.253		
310		<b>Lampropedia</b>	<b>sp49018</b>	0.226		
311	Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	
312		<b>Conchiformibius</b>	<b>sp49784</b>	0.156		
313		<b>Conchiformibius</b>	<b>steedae</b>	0.369		
314		<b>Neisseria</b>	<b>animaloris</b>	0.0592		

TABLE IX: Summary of all of the organisms identified in Beauty's two samples from 2021-01-22. Two line types exist. The first line indicates the higher level classifications of the following lines which only contain genus and species along with percentage of total abundance in the two samples. The first sample was spit up clear fluid while the second one was a fecal sample. During this time here symptoms were fairly controlled.

315	k	p	c	o	f	
316		g	s	sample 0	sample 1	
317		<b>Neisseria</b>	<b>animaloris</b>	0.0363		
			<b>zoodegmatis</b>			
318		<b>Neisseria</b>	<b>canis</b>	0.0786		
319		<b>Neisseria</b>	<b>shayeganii</b>	0.302		
320		<b>Neisseria</b>	<b>sp49941</b>	0.404		
321		<b>Neisseria</b>	<b>weaveri</b>	0.411		
322		<b>Neisseria</b>	<b>zoodegmatis</b>	0.0532		
323	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	
324		<b>Propionivibrio</b>	<b>sp50395</b>	0.0278		
325	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	
326		<b>Desulfobulbus</b>	<b>sp51846</b>	0.0205		
327	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfohalobiaceae	
328		<b>NA</b>	<b>sp52441</b>	0.365		
329	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfomicrobiaceae	
330		<b>Desulfomicrobium</b>	<b>orale</b>	0.0363		associated (P) [15]
331	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	
332		<b>Desulfovibrio</b>	<b>sp52597</b>	0.157		
333	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	NA	
334		<b>NA</b>	<b>bacterium</b>	0.0375		
335	Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	
336		<b>Arcobacter</b>	<b>thereius</b>	0.305		
337		<b>Campylobacter</b>	<b>mucosalis</b>	0.0254		
338		<b>Campylobacter</b>	<b>rectus</b>	0.88		
			<b>showae</b>			
339	Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	
340		<b>NA</b>	<b>sp55662</b>	0.029		
341		<b>Wolinella</b>	<b>succinogenes</b>	0.0459		
342	Bacteria	Proteobacteria	Gammaproteobacteria	Cardiobacteriales	Cardiobacteriaceae	
343		<b>Cardiobacterium</b>	<b>sp57123</b>	0.023		
344		<b>Cardiobacterium</b>	<b>sp57124</b>	0.848		
345		<b>NA</b>	<b>sp57146</b>	0.0773		
346	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	
347		<b>Escherichia Shigella</b>	<b>coli</b>		0.0197	
348	Bacteria	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	
349		<b>Aggregatibacter</b>	<b>Haemophilus</b>	0.0532		
			<b>sp62087</b>			
			<b>sp62189</b>			
350		<b>Bibersteinia</b>	<b>sp62095</b>	0.618		
351		<b>Bibersteinia</b>	<b>sp62096</b>	0.12		
352		<b>Haemophilus</b>	<b>sp62184</b>	0.14		
353		<b>Haemophilus</b>	<b>sp62189</b>	1.15		
354		<b>NA</b>	<b>sp62273</b>	1.21		
355		<b>Pasteurella</b>	<b>aerogenes</b>	0.0761		
356		<b>Pasteurella</b>	<b>dagmatis</b>	1.3		
357	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	
358		<b>Moraxella</b>	<b>caprae</b>	0.245		
			<b>equi</b>			
359		<b>Moraxella</b>	<b>catarrhalis</b>	0.143		
			<b>nonliquefaciens</b>			

TABLE X: Summary of all of the organisms identified in Beauty's two samples from 2021-01-22. Two line types exist. The first line indicates the higher level classifications of the following lines which only contain genus and species along with percentage of total abundance in the two samples. The first sample was spit up clear fluid while the second one was a fecal sample. During this time here symptoms were fairly controlled.

360	k	p	c	o	f
361		g	s	sample 0	sample 1
362		<b>Moraxella</b>	<b>caviae</b>	0.375	
363		<b>Moraxella</b>	<b>cuniculi</b>	1.25	
364		<b>Moraxella</b>	<b>sp62638</b>	3.06	
365		<b>Psychrobacter</b>	<b>sp62723</b>	0.0338	
366	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae
367		<b>Pseudomonas</b>	<b>aeruginosa</b>	0.0193	
368	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae
369		<b>Arenimonas</b>	<b>sp64995</b>	0.081	
370		<b>Luteimonas</b>	<b>sp65067</b>	0.0931	
371		<b>NA</b>	<b>sp65479</b>	0.218	
372	Bacteria	Saccharibacteria	NA	NA	NA
373		<b>*Saccharimonas</b>	<b>sp65943</b>	0.271	
374		<b>*Saccharimonas</b>	<b>sp65946</b>	0.175	
375		<b>*Saccharimonas</b>	<b>sp65948</b>	0.0508	
376		<b>*Saccharimonas</b>	<b>sp65955</b>	0.247	
377		<b>*Saccharimonas</b>	<b>sp65968</b>	0.0157	
378		<b>NA</b>	<b>*Saccharibacteria</b>	0.0641	
379		<b>NA</b>	<b>*Saccharibacteria</b>	0.0302	
380		<b>NA</b>	<b>sp65941</b>	0.415	
381		<b>NA</b>	<b>sp66045</b>	0.0181	
382		<b>NA</b>	<b>sp66119</b>	0.0483	
383	Bacteria	Spirochaetae	Spirochaetes	Spirochaetales	NA
384		<b>Firmicutes</b>	<b>bacterium</b>	0.0967	
385	Bacteria	Spirochaetae	Spirochaetes	Spirochaetales	Spirochaetaceae
386		<b>NA</b>	<b>sp66621</b>	0.0592	
387		<b>NA</b>	<b>sp66653</b>	0.0399	
388		<b>NA</b>	<b>sp66672</b>	0.0157	
389		<b>NA</b>	<b>sp66678</b>	0.0133	
390		<b>NA</b>	<b>sp66695</b>	0.0133	
391		<b>NA</b>	<b>sp66723</b>	0.0302	
392		<b>NA</b>	<b>sp67037</b>	0.0302	
393		<b>Spirochaeta</b>	<b>sp66555</b>	0.197	
394		<b>Treponema</b>	<b>denticola</b>	0.708	(P) [20]
395		<b>Treponema</b>	<b>medium</b>	0.129	
396		<b>Treponema</b>	<b>vincentii</b>		
397		<b>Treponema</b>	<b>parvum</b>	0.0145	
398		<b>Treponema</b>	<b>pectinovorum</b>	0.0133	
399		<b>Treponema</b>	<b>pedis</b>	0.0266	
400		<b>Treponema</b>	<b>sp66795</b>	0.117	
401		<b>Treponema</b>	<b>sp66797</b>	0.0628	
402	Bacteria	<b>Treponema</b>	<b>sp66801</b>	0.29	
403		Synergistetes	Synergistia	Synergistales	Synergistaceae
404		<b>Fretibacterium</b>	<b>fastidiosum</b>	0.0181	
		<b>Fretibacterium</b>	<b>feline</b>	0.0713	

TABLE XI: Summary of all of the organisms identified in Beauty's two samples from 2021-01-22. Two line types exist. The first line indicates the higher level classifications of the following lines which only contain genus and species along with percentage of total abundance in the two samples. The first sample was spit up clear fluid while the second one was a fecal sample. During this time here symptoms were fairly controlled.

405	k	p	c	o	f
406		g	s	sample 0	sample 1
407		<b>Fretibacterium</b>	<b>sp67103</b>	0.0665	
408		<b>Fretibacterium</b>	<b>sp67106</b>	0.0967	
409	Bacteria	Tenericutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae
410		<b>Acholeplasma</b>	<b>morum</b>	0.32	
411		<b>Acholeplasma</b>	<b>sp67593</b>	0.283	
412		<b>Acholeplasma</b>	<b>sp67613</b>	0.0906	
413	Bacteria	Tenericutes	Mollicutes	Mycoplasmatales	Mycoplasmataceae
414		<b>Mycoplasma</b>	<b>canis</b>	0.0483	
415		<b>Mycoplasma</b>	<b>edwardii</b>	0.0254	
416		<b>Mycoplasma</b>	<b>lipophilum</b>	0.0278	
417		<b>Mycoplasma</b>	<b>neophronis</b>	0.0157	
418		<b>Ureaplasma</b>	<b>parvum</b>	0.0967	
			<b>urealyticum</b>		
419	Bacteria	Tenericutes	Mollicutes	NA	NA
420		<b>Acholeplasmatales</b>	<b>bacterium</b>	0.0737	
421		<b>Firmicutes</b>	<b>oral</b>	0.0157	
422		<b>NA</b>	<b>sp68302</b>	0.0798	

TABLE XII: Summary of all of the organisms identified in Beauty's two samples from 2021-01-22. Two line types exist. The first line indicates the higher level classifications of the following lines which only contain genus and species along with percentage of total abundance in the two samples. The first sample was spit up clear fluid while the second one was a fecal sample. During this time here symptoms were fairly controlled.

### Appendix B: Statement of Conflicts

No specific funding was used in this effort and there are no relationships with others that could create a conflict of interest. I would like to develop these ideas further and have obvious bias towards making them appear successful. Barbara Cade, the dog owner, has worked in the pet food industry but this does not likely create a conflict. We have no interest in the makers of any of the products named in this work.

### Appendix C: About the Authors and Facility

This work was performed at a dog rescue run by Barbara Cade and housed in rural Georgia. The author of this report, Mike Marchywka, has a background in electrical engineering and has done extensive research using free online literature sources. I hope to find additional people interested in critically examining the results and verify that they can be reproduced effectively to treat other dogs.

### Appendix D: Symbols, Abbreviations and Colloquialisms

TERM definition and meaning

### Appendix E: General caveats and disclaimer

This document was created in the hope it will be interesting to someone including me by providing information about some topic that may include personal experience or a literature review or description of a speculative theory or idea. There is no assurance that the content of this work will be useful for any particular purpose.

All statements in this document were true to the best of my knowledge at the time they were made and every attempt is made to assure they are not misleading or confusing. However, information provided by others and observations that can be manipulated by unknown causes ( "gaslighting" ) may be misleading. Any use of this information should be preceded by validation including replication where feasible. Errors may enter into the final work at every step from conception and research to final editing.

Documents labelled "NOTES" or "not public" contain substantial informal or speculative content that may be terse and poorly edited or even sarcastic or profane. Documents labelled as "public" have generally been edited to be more coherent but probably have not been reviewed or proof read.



Generally non-public documents are labelled as such to avoid confusion and embarrassment and should be read with that understanding.

## Appendix F: Citing this as a tech report or white paper

Note: This is mostly manually entered and not assured to be error free.  
This is tech report MJM-2022-003.

Version	Date	Comments
0.01	2022-01-10	Create from empty.tex template
-	March 1, 2022	version 0.10 MJM-2022-003
0.1	2022-03-01	First revision for consideration
1.0	20xx-xx-xx	First revision for distribution

Released versions,  
build script needs to include empty releases.tex

Version	Date	URL
0.1	2022-03-01	email circulation RFC

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author ="Mike J Marchywka " ,
type ="techreport" ,
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day ="1" ,
month ="3" ,
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contact ="marchywka@hotmail.com" ,
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pages =" 17" ,
filename ="beauty"
}
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Supporting files. Note that some dates,sizes, and md5's will change as this is rebuilt.

This really needs to include the data analysis code but right now it is auto generated picking up things from prior build in many cases

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