

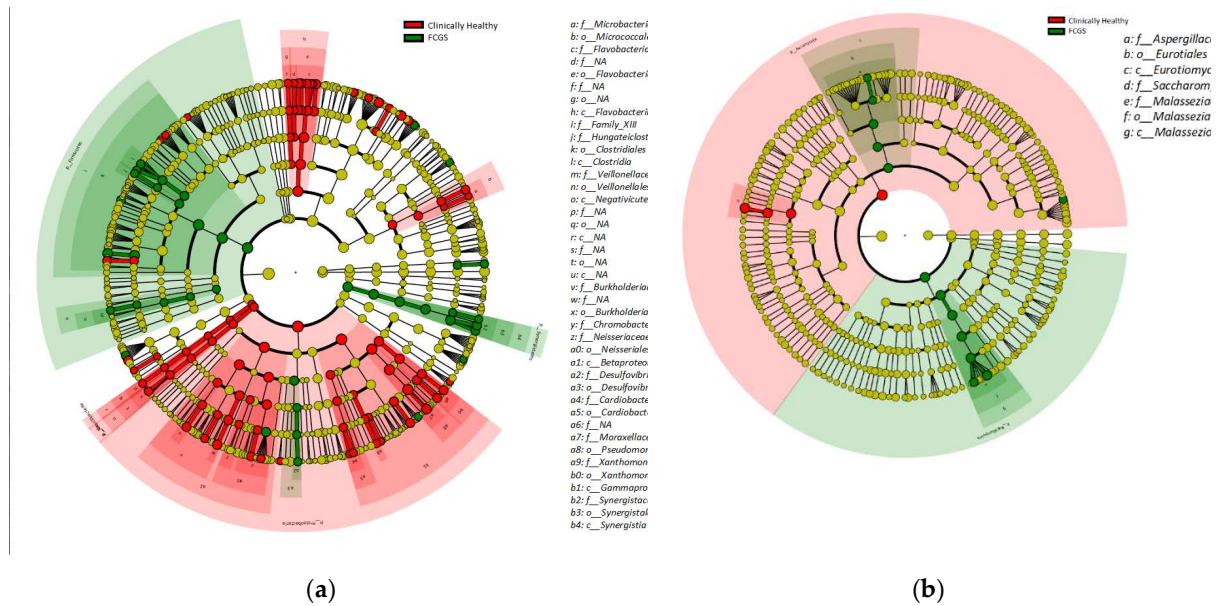
Supplementary Table

Species	Oxygen dependence	FCGS		CH		LEfSe P-value
		ReA (%)	Frequency	ReA (%)	Frequency	
Fungi						
<i>Saccharomyces cerevisiae</i>	AE/MAE/AN	11.54	8	36.41	10	0.0307
<i>Malassezia restricta</i>	AE/MAE/AN	16.93	10	4.12	4	0.0001
<i>Cladosporium penidielloides/salinae</i>	AE/MAE/AN	8.48	4	0.00	0	0.0413
<i>Malassezia arunalokei</i>	AE/MAE/AN	6.78	7	1.31	2	0.0007
<i>Aspergillaceae sp.</i>	AE/MAE/AN	6.07	1	0.00	0	0.0275
Bacteria						
Bacteroidales sp. (order)	O-AN	5.97	9	2.57	14	0.0341
<i>Xanthomonadaceae sp.</i> (family)	AE	3.22	5	1.75	13	0.0079
<i>Moraxella sp.</i>	AE	3.18	9	8.46	12	0.0117
<i>Arenimonas sp.</i>	AE/F-AN	2.37	4	1.80	11	0.0177
<i>Burkholderiaceae sp.</i> (family)	AE/F-AN	2.01	8	1.59	13	0.0465
<i>Alloprevotella sp.</i>	O-AN	1.72	10	1.74	12	0.0007
<i>Pseudoclavibacter sp.</i>	AE	1.53	4	1.04	10	0.0392
<i>Porphyromonas sp.</i>	O-AN	1.29	13	2.76	14	0.0234
<i>Fusibacter sp.</i>	F-AN	1.11	10	0.98	14	0.0047
<i>Lampropedia sp.</i>	AE/F-AN	1.06	5	0.53	11	0.0470
<i>Porphyromonas canoris</i>	O-AN	0.89	8	2.36	13	0.0095
<i>Pasteurellaceae sp.</i> (family)	F-AN	0.72	8	1.77	13	0.0041
<i>Fusobacterium sp.</i>	(O)-AN	0.69	11	1.19	14	0.0047
Burkholderiales sp. (order)	AE/F-AN	0.55	10	2.14	14	0.0015
<i>Bergeyella zoohelcum</i>	AE	0.36	4	2.80	12	0.0002
<i>Bacteroides sp.</i>	O-AN	0.28	11	1.54	13	0.0128
<i>Flavobacterium sp.</i>	AE	0.20	1	1.01	10	0.0008
<i>Flavobacteriaceae sp.</i> (family)	AE	0.16	2	2.39	12	0.0001
<i>Peptostreptococcus canis</i>	O-AN.	6.87	10	2.27	4	0.0080
<i>Fretibacterium sp.</i>	O/F-AN	3.73	13	1.10	14	0.0069
<i>Propionibacteriaceae sp.</i> (family)	AE/F-AN	3.71	10	0.66	14	0.0346
<i>Spirochaetaceae sp.</i> (family)	O/F-AN	2.27	12	1.29	13	0.0416
<i>FamilyXIII sp.</i> (family)	O-AN	1.79	9	0.58	4	0.0074
<i>Fusobacterium nucleatum</i>	O-AN	1.30	8	0.60	3	0.0420
<i>Lachnospiraceae sp.</i> (family)	O-AN	1.11	11	0.36	13	0.0476
<i>Methanobrevibacter oralis</i>	O-AN	1.07	6	1.87	1	0.0462

Abbreviations; AE: Aerobic; MAE: microaerobic; AN.: Anaerobic; F: Facultative; O: Obligate; ReA: Relative Abundance

**Table S1.** Average relative abundances of bacteria and fungi significantly different between FCGS and CH feline samples. Frequency lists how many samples in each group had that given species present. Those with a grey background were significantly enriched in FCGS samples. For brevity of the table, only those species that had at least 1% relative abundances in one the two groups are shown.

## Supplementary Figure



**Figure S1.** LefSe cladogram highlighting species that are significantly different between groups for (a) bacteria and (b) fungi. Each ring represents a taxonomic level, with the phylum being in the center and species on the outermost ring. Nodes colored in moss green are not significantly different between groups. The large number of identified taxa limits the readability of the graph. Therefore, those species that represented on average at least 1% of the microbiota per group are listed in Table S1. Taxa significantly enriched in FCGS samples are shown in green, taxa significantly enriched in CH samples are shown in red.