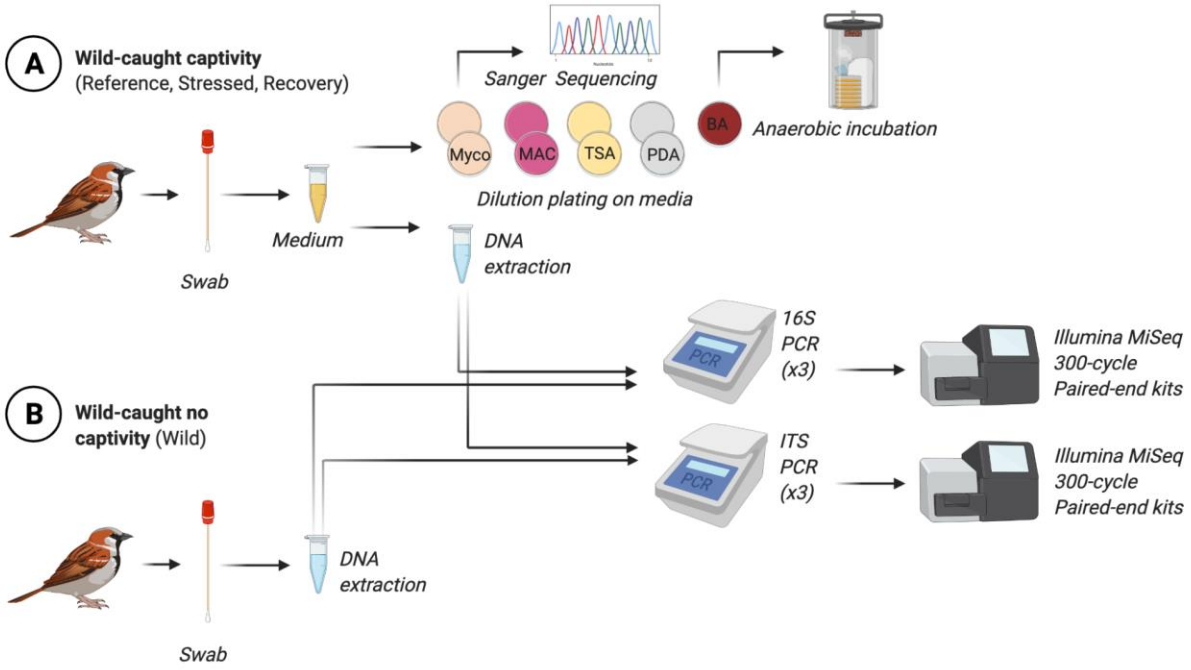

Fig. S1. Schematic of the microbial measurement scheme used in this study. (A) Measurement scheme for wild-caught, captive animals (Reference = unstressed wild-caught captive house sparrows, Stressed = wild-caught captive house sparrows experiencing a chronic mild stress protocol, Recovery = wild-caught captive house sparrows that had previously experienced a chronic mild stress protocol). (B) Measurement scheme for wild-caught animals that experienced no captivity. Image created with BioRender.com.

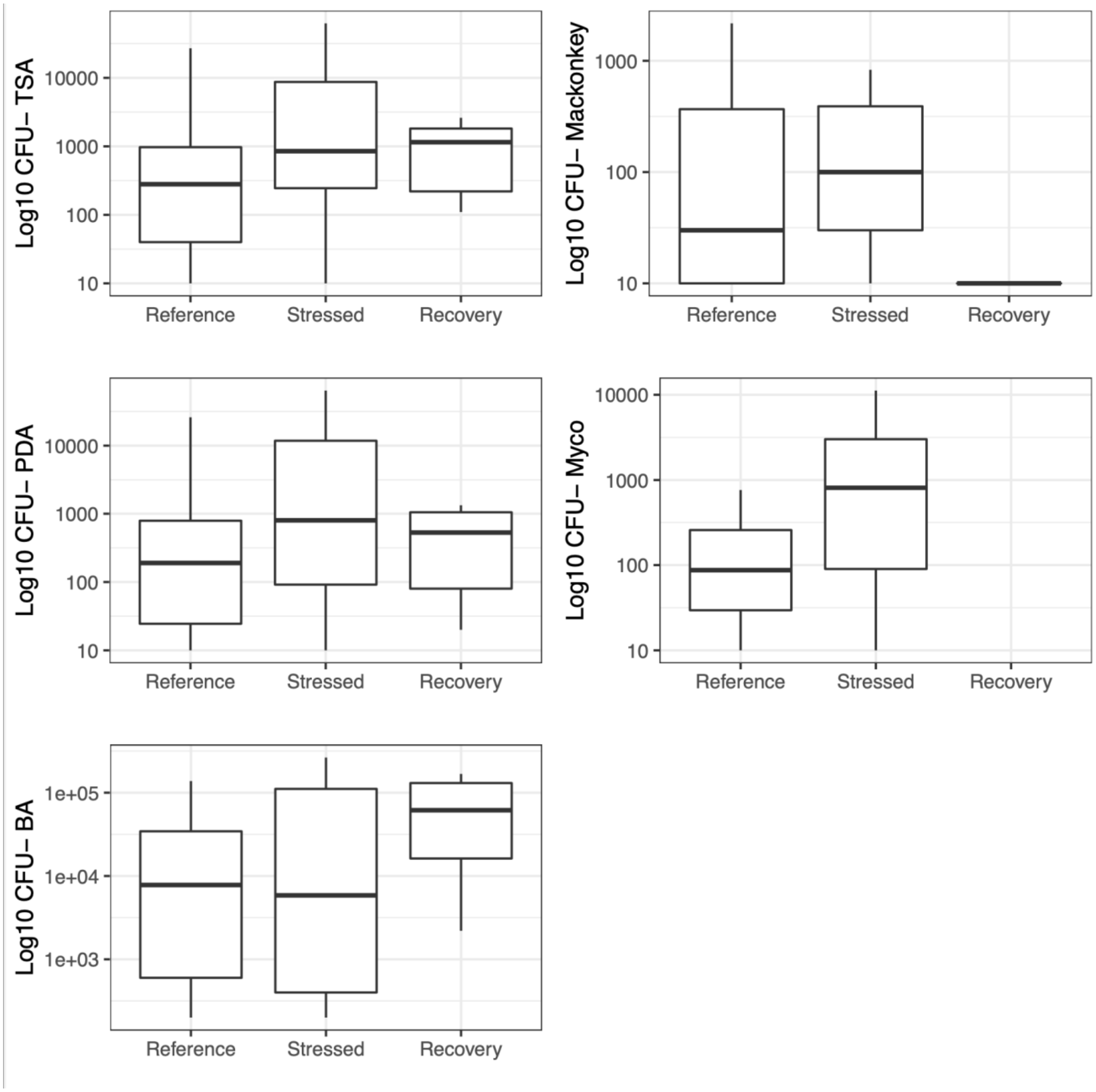

Fig. S2. Box-and-whisker plots of the log$_{10}$ abundance of culturable microorganisms in cloacal samples from captive house sparrows exposed to a chronic mild stress protocol (Stressed, n=20), recovering from chronic mild stress exposure (Recovery, n=5), or not stressed (Reference, n=20). A) TSA= Trypticase Soy Agar, B) MacConkey = MacConkey Agar, C) PDA= Potato Dextrose Agar, D) BA= Sheep's Blood Agar, E) Myco.= Mycosel™ Agar. Microorganisms were cultivated under aerobic conditions except for those on Sheep's Blood Agar. See methods for incubation temperatures and durations.

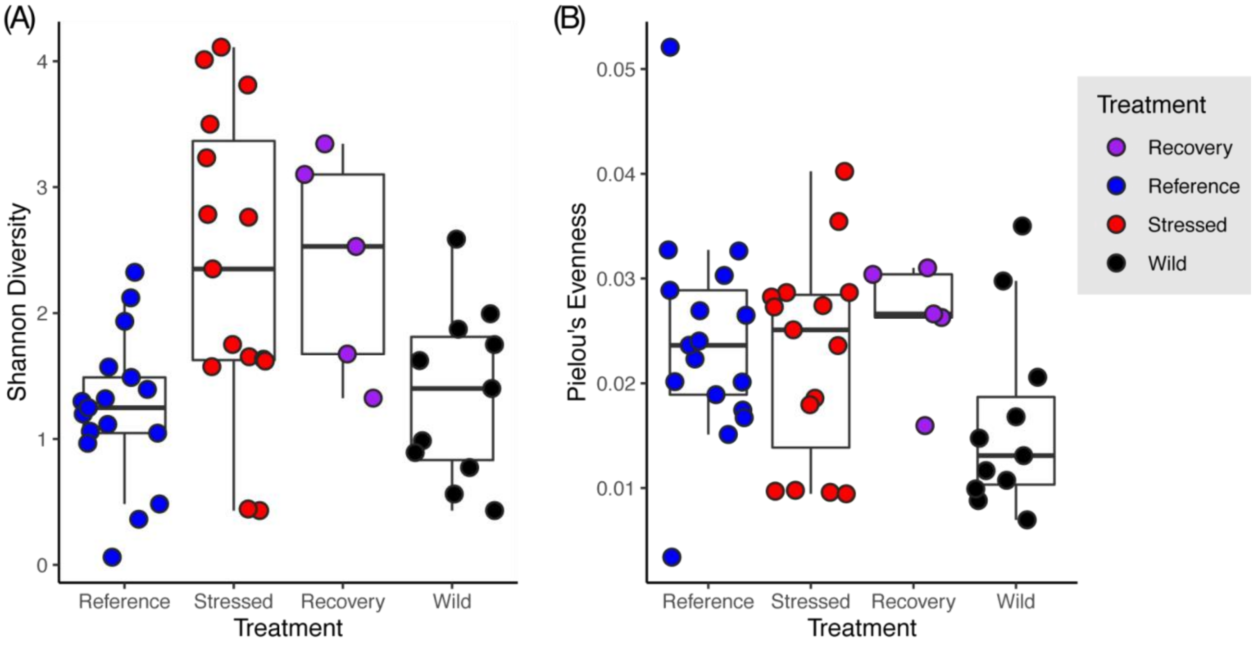

Fig. S3. Box-and-whisker plots of bacterial Shannon Diversity (A) and Pielou's Evenness (B) from house sparrow cloacae samples as determined by 16S rRNA marker gene sequencing. Individuals were either wild-caught and exposed to a chronic mild stress protocol (Stressed, n=15), wild-caught and recovering from chronic mild stress exposure (Recovery, n=5), wild-caught captive but not exposed to the stress protocol (Reference, n=17), or caught and immediately sampled without captivity (Wild, n=11). Boxes are the 25th and 75th quartiles, the black line is the median, and dots represent each of the 48 samples.

Table S1. Sample sizes used in analyses.

	Original Sample Size	Samples used for cultivation-dependent analyses*	Sampled with 16S rRNA gene amplicons	Samples used in 16S data analyses	Sampled with ITS rRNA gene amplicons	Samples used in ITS data analyses
Tx (Overall)						
Reference	20	20	17	17	0	0
Stressed	20	20	18	15	0	0
Recovery	6	5	5	5	0	0
Wild (NoTx)	11	NA	11	11	3	3
Overall Totals	57	45	51	48	3	3
Tx (Weekly)						
Reference Week 0	6	6	6	6	0	0
Stressed Week 1	6	6	6	5	0	0
Reference Week 2	6	5	5	5	0	0
Stressed Week 2	6	6	6	5	0	0
Stressed Week 3	8	8	6	5	0	0
Reference Week 4	**8**	**8**	**6**	**6**	**0**	**0**
Recovery	6	**5**	5	**5**	0	**0**
Wild (NoTx)	11	**NA**	11	**11**	3	**3**
Overall Totals	57	**45**	51	**48**	3	**3**

* One bird was removed due to antibiotic treatment administered during captivity

Table S2. Isolates cultivated on Mycosel™ Agar from cloacal swabs and identified to species via sequencing of the ITS1-5.8S-ITS2 rRNA gene fragment.

Strain	**Treatment**	**Host Sex**	**Accession Match**	**Species**	**% match**	**GenBank Sequence**
R01	Stressed	Male	AB305093.1	*Candida albicans*	99	MW408203
R04	Reference	Female	AB305093.1	*Candida albicans*	99	MW408205
R05	Stressed	Male	AB305093.1	*Candida albicans*	99	MW408206
R07	Stressed	Female	L28817.1	*Candida albicans*	99	MW408208
R08	Reference	Male	L28817.1	*Candida albicans*	99	MW408209

Table S3. Accession numbers (OTU IDs) of the top twenty OTUs that were most important for discriminating treatment categories as determined by the random forest model and their corresponding Figure 4 labels.

OTU_ID	**Label**
AB365066.1.1533	Acinetobacter 1,
EF517956.1.1666	Acinetobacter 2,
JN082536.1.1536	Acinetobacter 3,
EU559331.1.1470	Campylobacter,
FJ192638.1.1515	Catellicoccus 1,
KF799139.1.1524	Catellicoccus 2,
JPLY01000001.145690.147219	Chryseobacterium,
DQ798456.1.1292	Collinsella,
EU999001.1.1609	Comamonas,
CCPS01000022.154.1916	Escherichia-Shigella,
AF197125.1.1555	Lactobacillus 1,
KF178310.1.1559	Lactobacillus 2,
CP015906.2140419.2141977	Lactococcus,
CP012201.3677670.3679209	Massilia,
KJ161326.1.1708	Pseudomonas 1,
KJ535378.1.1545	Pseudomonas 2,
AYTB01000002.62877.64412	Rummeliibacillus,
KF625184.1.1787	Romboutsia,
CDMW01000001.16532.18068	Streptococcus,
AMYT01000015.54.1603	Enterococcaceae

Supplementary Materials and Methods

Probable endotoxin (LPS)-producing taxa annotations:

Taxa were manually assigned as “Probable_LPS-producers,” “Not probable_LPS-producers” or “Unknown” based on phyla-level taxonomic information per the review by Sutcliffe 2010 for phyla where LPS biosynthetic genes were detected.

For taxa where there was ambiguity, either because of unusual cell wall components, differing information about staining behavior versus outer membrane components, lack of coverage in this review, or a lack of information from cultivated representatives, we made the following annotations:

- Armatimonadetes are listed as probable LPS-producers based on the genetic evidence that they have been speculated to have a diderm cell envelope (Hu et al. 2014)
- Members of the Firmicutes are listed as non-LPS-producers, with the exception of those in the class Negativicutes, which were listed as LPS-producers per Antunes et al. (2016).
- Planctomycetes are listed as LPS-producers per Boedeker et al. (2017).
- Tenericutes are listed as non LPS-producers per Shimizu (2016).
- Spirochaetes are listed as “unknown” as there is considerable variety within the phylum per Sutcliffe (2010).
- Epsilonbacteraeota are listed as LPS-producers per Waite et al. (2017).
- Verrucomicrobia are listed as LPS-producers as inferred from cell architecture of gram negatives (Salguero et al. 2019).
- WPS-2, Dependentiae, and FBP are listed as “unknown” because of the lack of information from cultivated representatives.

	Taxon	**Probable_LPS-producer**
1	D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteriia;D_3__Acidobacteriales;D_4__Acidobacteriaceae(Subgroup1)	Yes
2	D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteriia;D_3__Acidobacteriales;D_4__uncultured	Yes
3	D_0__Bacteria;D_1__Acidobacteria;D_2__Acidobacteriia;D_3__Solibacterales;D_4__Solibacteraceae(Subgroup3)	Yes
4	D_0__Bacteria;D_1__Acidobacteria;D_2__Blastocatellia(Subgroup4);D_3__Blastocatellales;D_4__Blastocatellaceae	Yes
5	D_0__Bacteria;D_1__Acidobacteria;D_2__Holophagae;D_3__Subgroup 7;Ambiguous_taxa	Yes
6	D_0__Bacteria;D_1__Acidobacteria;D_2__Thermoanaerobaculia;D_3__Thermoanaerobaculales;D_4__Thermoanaerobaculaceae	Yes

7	D_0__Bacteria;D_1__Actinobacteria;D_2__Acidimicrobiia;D_3__IMCC26256;Ambiguous_taxa	No
8	D_0__Bacteria;D_1__Actinobacteria;D_2__Acidimicrobiia;D_3__Microtrichales;D_4__Iamiaceae	No
9	D_0__Bacteria;D_1__Actinobacteria;D_2__Acidimicrobiia;D_3__Microtrichales;D_4__Ilumatobacteraceae	No
10	D_0__Bacteria;D_1__Actinobacteria;D_2__Acidimicrobiia;D_3__uncultured;Ambiguous_taxa	No
11	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Actinomycetales;D_4__Actinomycetaceae	No
12	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Bifidobacteriales;D_4__Bifidobacteriaceae	No
13	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Corynebacteriales;D_4__Corynebacteriaceae	No
14	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Corynebacteriales;D_4__Dietziaceae	No
15	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Corynebacteriales;D_4__Mycobacteriaceae	No
16	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Corynebacteriales;D_4__Nocardiaceae	No
17	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;D_4__Frankiaceae	No
18	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;D_4__Geodermatophilaceae	No
19	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;D_4__uncultured	No
20	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Frankiales;NA	No
21	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Kineosporiales;D_4__Kineosporiaceae	No
22	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Beutenbergiaceae	No
23	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Bogoriellaceae	No
24	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Brevibacteriaceae	No

25	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Cellulomonadaceae	No
26	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Dermabacteraceae	No
27	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Dermatophilaceae	No
28	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Intrasporangiaceae	No
29	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Microbacteriaceae	No
30	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Micrococcaceae	No
31	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Ruaniaceae	No
32	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;NA	No
33	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Propionibacteriales;D_4__Nocardioidaceae	No
34	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Propionibacteriales;D_4__Propionibacteriaceae	No
35	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Pseudonocardiales;D_4__Pseudonocardiaceae	No
36	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Streptomycetales;D_4__Streptomycetaceae	No
37	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Streptosporangiales;D_4__Nocardiopsaceae	No
38	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Coriobacteriaceae	No
39	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae	No
40	D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Gaiellales;D_4__uncultured	No
41	D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__67-14	No
42	D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;D_4__Solirubrobacteraceae	No

43	D_0__Bacteria;D_1__Actinobacteria;D_2__Thermoleophilia;D_3__Solirubrobacterales;NA	No
44	D_0__Bacteria;D_1__Armatimonadetes;D_2__uncultured;D_3__unculturedbacterium;D_4__unculturedbacterium	Yes
45	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Bacteroidaceae	Yes
46	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Dysgonomonadaceae	Yes
47	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Muribaculaceae	Yes
48	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Paludibacteraceae	Yes
49	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Prevotellaceae	Yes
50	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Tannerellaceae	Yes
51	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Chitinophagales;D_4__Chitinophagaceae	Yes
52	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Cytophagales;D_4__Hymenobacteraceae	Yes
53	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Cytophagales;D_4__Microscillaceae	Yes
54	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Cytophagales;D_4__Spirosomaceae	Yes
55	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Flavobacteriales;D_4__Flavobacteriaceae	Yes
56	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Flavobacteriales;D_4__Weeksellaceae	Yes
57	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Sphingobacteriales;D_4__env.OPS17	Yes
58	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Sphingobacteriales;D_4__Sphingobacteriaceae	Yes
59	D_0__Bacteria;D_1__Bacteroidetes;D_2__Rhodothermia;D_3__Rhodothermales;D_4__Rhodothermaceae	Yes
60	D_0__Bacteria;D_1__Chlamydiae;D_2__Chlamydiae;D_3__Chlamydiales;D_4__Simkaniaceae	Yes

61	D_0__Bacteria;D_1__Chloroflexi;D_2__Anaerolineae;D_3__RBG-13-54-9;Ambiguous_taxa	No
62	D_0__Bacteria;D_1__Chloroflexi;D_2__Chloroflexia;D_3__Chloroflexales;D_4__Chloroflexaceae	No
63	D_0__Bacteria;D_1__Chloroflexi;D_2__Gitt-GS-136;D_3__unculturedbacterium;D_4__unculturedbacterium	No
64	D_0__Bacteria;D_1__Chloroflexi;D_2__KD4-96;D_3__unculturedbacterium;D_4__unculturedbacterium	No
65	D_0__Bacteria;D_1__Cyanobacteria;D_2__Sericytochromatia;Ambiguous_taxa;Ambiguous_taxa	Yes
66	D_0__Bacteria;D_1__Deinococcus-Thermus;D_2__Deinococci;D_3__Deinococcales;D_4__Deinococcaceae	No
67	D_0__Bacteria;D_1__Deinococcus-Thermus;D_2__Deinococci;D_3__Deinococcales;D_4__Trueperaceae	No
68	D_0__Bacteria;D_1__Dependentiae;D_2__Babeliae;D_3__Babeliales;D_4__Vermiphilaceae	Unknown
69	D_0__Bacteria;D_1__Epsilonbacteraeota;D_2__Campylobacteria;D_3__Campylobacterales;D_4__Campylobacteraceae	Yes
70	D_0__Bacteria;D_1__Epsilonbacteraeota;D_2__Campylobacteria;D_3__Campylobacterales;D_4__Helicobacteraceae	Yes
71	D_0__Bacteria;D_1__FBP;Ambiguous_taxa;Ambiguous_taxa;Ambiguous_taxa	Unknown
72	D_0__Bacteria;D_1__FBP;D_2__unculturedbacterium;D_3__unculturedbacterium;D_4__unculturedbacterium	Unknown
73	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Alicyclobacillaceae	No
74	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Bacillaceae	No
75	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__FamilyXI	No
76	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Paenibacillaceae	No
77	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Planococcaceae	No
78	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Staphylococcaceae	No

79	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Aerococcaceae	No
80	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Carnobacteriaceae	No
81	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Enterococcaceae	No
82	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Lactobacillaceae	No
83	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Leuconostocaceae	No
84	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Streptococcaceae	No
85	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae1	No
86	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Eubacteriaceae	No
87	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__FamilyXI	No
88	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae	No
89	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae	No
90	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptostreptococcaceae	No
91	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae	No
92	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae	No
93	D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__Acidaminococcaceae	Yes
94	D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__Veillonellaceae	Yes
95	D_0__Bacteria;D_1__Fusobacteria;D_2__Fusobacteriia;D_3__Fusobacteriales;D_4__Fusobacteriaceae	Yes
96	D_0__Bacteria;D_1__Fusobacteria;D_2__Fusobacteriia;D_3__Fusobacteriales;D_4__Leptotrichiaceae	Yes

97	D_0__Bacteria;D_1__Gemmatimonadetes;D_2__Gemmatimonadetes;D_3__Gemmatimonadales;D_4__Gemmatimonadaceae	Yes
98	D_0__Bacteria;D_1__Planctomycetes;D_2__Planctomycetacia;D_3__Isosphaerales;D_4__Isosphaeraceae	Yes
99	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Acetobacterales;D_4__Acetobacteraceae	Yes
100	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Azospirillales;D_4__Azospirillaceae	Yes
101	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Caulobacterales;D_4__Caulobacteraceae	Yes
102	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Elsterales;D_4__uncultured	Yes
103	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Micavibrionales;D_4__Micavibrionaceae	Yes
104	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Beijerinckiaceae	Yes
105	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Devosiaceae	Yes
106	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Hyphomicrobiaceae	Yes
107	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__KF-JG30-B3	Yes
108	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Methyloligellaceae	Yes
109	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Rhizobiaceae	Yes
110	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__RhizobialesIncertaeSedis	Yes
111	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Xanthobacteraceae	Yes
112	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhodobacterales;D_4__Rhodobacteraceae	Yes
113	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__Anaplasmataceae	Yes
114	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Sphingomonadales;D_4__Sphingomonadaceae	Yes

115	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;NA;NA	Yes
116	D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Bdellovibrionales;D_4__Bdellovibrionaceae	Yes
117	D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__BIrii41	Yes
118	D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__Haliangiaceae	Yes
119	D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;D_4__Polyangiaceae	Yes
120	D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Myxococcales;NA	Yes
121	D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Oligoflexales;D_4__Oligoflexaceae	Yes
122	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Aeromonadales;D_4__Aeromonadaceae	Yes
123	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Alteromonadaceae	Yes
124	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Psychromonadaceae	Yes
125	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Alteromonadales;D_4__Shewanellaceae	Yes
126	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Betaproteobacteriales;D_4__Burkholderiaceae	Yes
127	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Betaproteobacteriales;D_4__Chromobacteriaceae	Yes
128	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Betaproteobacteriales;D_4__Methylophilaceae	Yes
129	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Betaproteobacteriales;D_4__Neisseriaceae	Yes
130	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Betaproteobacteriales;D_4__Rhodocyclaceae	Yes
131	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Betaproteobacteriales;D_4__SC-I-84	Yes
132	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Cardiobacteriales;D_4__Wohlfahrtiimonadaceae	Yes

133	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Cellvibrionales;D_4__Cellvibrionaceae	Yes
134	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Diplorickettsiales;D_4__Diplorickettsiaceae	Yes
135	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Enterobacteriales;D_4__Enterobacteriaceae	Yes
136	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Legionellales;D_4__Legionellaceae	Yes
137	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Oceanospirillales;D_4__Halomonadaceae	Yes
138	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Oceanospirillales;D_4__Marinomonadaceae	Yes
139	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pasteurellales;D_4__Pasteurellaceae	Yes
140	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae	Yes
141	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Pseudomonadaceae	Yes
142	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Vibrionales;D_4__Vibrionaceae	Yes
143	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Rhodanobacteraceae	Yes
144	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Xanthomonadales;D_4__Xanthomonadaceae	Yes
145	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;NA;NA	Yes
146	D_0__Bacteria;D_1__Spirochaetes;D_2__Spirochaetia;D_3__Spirochaetales;D_4__Spirochaetaceae	Unknown
147	D_0__Bacteria;D_1__Synergistetes;D_2__Synergistia;D_3__Synergistales;D_4__Synergistaceae	Yes
148	D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__Entomoplasmatales;D_4__Spiroplasmataceae	No
149	D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__Mycoplasmatales;D_4__Mycoplasmataceae	No
150	D_0__Bacteria;D_1__Verrucomicrobia;D_2__Verrucomicrobiae;D_3__Chthoniobacterales;D_4__Chthoniobacteraceae	Yes

151	D_0__Bacteria;D_1__Verrucomicrobia;D_2__Verrucomicrobiae;D_3__Verrucomicrobiales;D_4__Akkermansiaceae	Yes
152	D_0__Bacteria;D_1__Verrucomicrobia;D_2__Verrucomicrobiae;D_3__Verrucomicrobiales;D_4__Rubritaleaceae	Yes
153	D_0__Bacteria;D_1__Verrucomicrobia;D_2__Verrucomicrobiae;D_3__Verrucomicrobiales;D_4__Verrucomicrobiaceae	Yes
154	D_0__Bacteria;D_1__WPS-2;Ambiguous_taxa;Ambiguous_taxa;Ambiguous_taxa	Unknown

References:

Antunes, L. C. S., D. Poppleton, A. Klingl, A. Criscuolo, B. Dupuy, C. Brochier-Armanet, C. Beloin, and S. Gribaldo (2016). Phylogenomic analysis supports the ancestral presence of LPS-outer membranes in the Firmicutes. eLife. https://doi.org/10.7554/eLife.14589.00.1

Boedeker, C., M. Schuler, G. Reintjes, O. Jeske, M. C. F. van Teeseling, M. Jogler, P. Rast, D. Borchert, D. P. Devos, M. Kucklick, M. Schaffer, R. Kolter, L. van Niftrik, S. Engelmann, R. Amann, M. Rohde, H. Engelhardt, and C. Jogler (2017). Determining the bacterial cell biology of Planctomycetes. Nature Communications **8**:14853.

Hu Z., Y. Wang, W. Im, S. Wang, G. Zhao, H. Zheng, and X. Quan (2014). The first complete genome sequence of the class Fimbriimonadia in the phylum Armatimonadetes. PLoS One **9**(6): e100794.

Salguero, M. V., M. A. I. Al-Obaide, R. Singh, T. Siepmann, and T. L. Vasylyeva (2019). Dysbiosis of gram-negative gut microbiota and the associated serum lipopolysaccharide exacerbates inflammation in type 2 diabetic patients with chronic kidney disease. Experimental Therapeutic Medicine **18**(5): 3461-3469.

Shimizu, T. (2016). Inflammation-inducing factors of Mycoplasma pneumonia. Frontiers in Microbiology **7**: 414.

Sutcliffe, I. C. (2010). A phylum level perspective on bacterial cell envelope architecture. Trends in Microbiology. **18**(10): P464-470.

Waite, D. W., I. Vanwonterghem, C. Rinke, D. H. Parks, Y. Zhang, K. Takai, S. M. Sievert, J. Simon, B. J. Campbell, T. E. Hanson, T. Woyke, M. G. Klotz, P. Hugenholtz (2017). Comparative genomic analysis of the class Epsilonproteobacteria and proposed reclassification to epsilonbacteraeota (phyl. Nov.) Frontiers in Microbiology. **8**: 682.