Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture

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Background. The chicken is the most abundant food animal in the world. However, despite its importance, the chicken gut microbiome remains largely undefined. Here, we exploit culture-independent and culture-dependent approaches to reveal extensive taxonomic diversity within complex microbial community.

Results. We performed metagenomic sequencing of fifty chicken faecal samples from two breeds and analysed these, alongside all (n=582) relevant publicly available chicken metagenomes, to cluster over 20 million non-redundant genes and to construct over 5,500 metagenome-assembled bacterial genomes. In addition, we recovered nearly 600 bacteriophage genomes. This represents the most comprehensive view of taxonomic diversity within the chicken gut microbiome to date, encompassing hundreds of novel candidate bacterial genera and species. To provide a stable, clear and memorable nomenclature for novel species, we devised a scalable combinatorial system for the creation of hundreds of well-formed Latin binomials. We cultured and genome-sequenced bacterial isolates from chicken faeces, documenting over forty novel species, together with three species from the genus *Escherichia*, including the newly named species *Escherichia whittamii*.

Conclusions. Our metagenomic and culture-based analyses provide new insights into the bacterial, archaeal and bacteriophage components of the chicken gut microbiome. The resulting datasets expand the known diversity of the chicken gut microbiome and provide a key resource for future high-resolution taxonomic and functional studies on the chicken gut microbiome.

1 **Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics**
2 **and culture**

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26 **Abstract**

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28 its importance, the chicken gut microbiome remains largely undefined. Here, we exploit
29 culture-independent and culture-dependent approaches to reveal extensive taxonomic
30 diversity within complex microbial community.
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32 breeds and analysed these, alongside all (n=582) relevant publicly available chicken
33 metagenomes, to cluster over 20 million non-redundant genes and to construct over 5,500
34 metagenome-assembled bacterial genomes. In addition, we recovered nearly 600
35 bacteriophage genomes. This represents the most comprehensive view of taxonomic diversity
36 within the chicken gut microbiome to date, encompassing hundreds of novel candidate
37 bacterial genera and species. To provide a stable, clear and memorable nomenclature for
38 novel species, we devised a scalable combinatorial system for the creation of hundreds of
39 well-formed Latin binomials. We cultured and genome-sequenced bacterial isolates from
40 chicken faeces, documenting over forty novel species, together with three species from the
41 genus *Escherichia*, including the newly named species *Escherichia whittamii*.
42 **Conclusions.** Our metagenomic and culture-based analyses provide new insights into the
43 bacterial, archaeal and bacteriophage components of the chicken gut microbiome. The
44 resulting datasets expand the known diversity of the chicken gut microbiome and provide a
45 key resource for future high-resolution taxonomic and functional studies on the chicken gut
46 microbiome.

47 **Introduction**
48 The domestic chicken is the most abundant bird and most abundant food animal on Earth,
49 accounting for a larger fraction of the planet's biomass than all species of wild birds combined
50 (Bennett et al., 2018). Consumption of chicken meat is growing faster than any other type of
51 meat and is seen as a cheaper, healthier, low-carbon alternative to meat from mammalian
52 livestock (Eshel et al., 2014; Willett et al., 2019). Chicken eggs remain a nutritious, affordable
53 food across the globe (Réhault-Godbert et al., 2019).
54   The chicken gastrointestinal tract is home to a complex community of microbes and their
55 genes—the chicken gut microbiome—that underpins links between diet, health and productivity
56 in poultry, as evidenced by the ability of antibiotics to promote growth in chicks (Bedford,
57 2000). This microbial community also acts as a source of pathogens associated with disease in
58 birds or in humans—including *Campylobacter*, *Salmonella*, and *Escherichia coli*—as well as
59 providing a reservoir of antimicrobial resistance genes (Florez-Cuadrado et al., 2018; Jørgensen
60 et al., 2019; Hermans et al., 2012).
61   Previous studies of this community have documented a rich variety of microorganisms
62 (dominated by bacteria, but including viruses, archaea and microbial eukaryotes) and have
63 shown that the taxonomic composition of this community varies with age, breed and disease
64 status (Shang et al., 2018; Rychlik, 2020). However, these earlier efforts have largely relied on
65 analyses of molecular barcodes (in particular short 16S rRNA gene sequences), which fail to
66 provide species-level resolution, are unable to detect viruses and reveal nothing about the
67 genome sequences, population structures or functional repertoires of microbial species (Hillmann
68 et al., 2018).
69   Two strategies have proven productive for exploring taxonomic and functional diversity in
70 complex microbial communities (Almeida et al., 2019; Forster et al., 2019). Culture-independent
71 approaches rely on shotgun metagenomic sequencing of DNA extracted from relevant samples,
72 followed by bioinformatics-based community profiling and analysis (Glendinning et al., 2020;
73 Sergeant et al., 2014). Culture-dependent approaches combine large-scale isolation of
74 microorganisms in pure culture with whole-genome sequencing and phylogenomic analysis
75 (Medvecky et al., 2018). To explore taxonomic novelty in the chicken gut microbiome, we
76 generated phylogenetic profiles to document known and unknown diversity and then exploited
77 culture-dependent and culture-independent approaches to create an unprecedented high-quality
78 reference collection of microbial genes and genomes from the chicken gut, revealing and naming
79 hundreds of new candidate species from this commonplace but important ecological setting.
80
81 **Materials & Methods**
82 **Sample collection and storage**
83 Faecal samples were collected in South-East England from adult Lohmann Brown laying hens
84 and adult Silkie hens in 2018. Birds were housed in a large outdoor run with a substrate of stone
85 chippings and small turf enrichment beds during the day and kept in a coop overnight. They were
86 fed a commercial layer feed, Farmgate Layer pellets and mash (ForFarmers UK Limited,
87 Rougham, Bury St Edmunds), according to the manufacturer's instructions and no antibiotics
88 were used. Faecal sampling was approved by the University of Surrey's NASPA ethics
89 committee.
90   Sixty faecal samples were collected from the Lohmann Brown laying hens and thirty samples
91 from the Silkie hens (six and three samples per day, respectively, for ten days). Freshly
92 evacuated faeces from individual birds were collected in sterile containers and immediately

93   stored at -20 °C. Samples were then transferred to the laboratory for culture or DNA extraction.
94   DNA was extracted using DNeasy PowerSoil kit (Qiagen), following manufacturer's instructions
95   and then stored at -20°C.
96
97   **Sequencing and subsequent workflow**
98   Workflow from this point forward is summarised in Fig. 1.The fifty samples yielding >20 ng
99   DNA were processed according to the Low Input, Transpose Enabled (LITE) library
100   construction pipeline (Perez-Sepulveda et al., 2020) before being subjected to paired-end
101   (2x150bp) metagenomic sequencing on the Illumina Novaseq 6000 platform. Bioinformatics
102   analyses were performed on the Earlham Institute's High Performance Computing cluster and on
103   the Cloud Infrastructure for Microbial Bioinformatics (Connor et al., 2016). Sequences were
104   assessed for quality using FastQC Version 0.11.8 and trimmed using Trimmomatic Version 0.36,
105   configured to a minimum read length of 40, "leading" and "trailing" settings of 3
106   (SLIDINGWINDOW:4:20) (Andrews, ; Bolger et al., 2014). Metagenomic sequences for all
107   samples have been uploaded to the Sequence Read Archive under Bioproject ID PRJNA543206.
108
109   **Reference-based metagenomic analysis**
110   An initial analysis of our chicken faecal sequences using the Kraken 2 taxonomic classifier
111   (Wood et al., 2019) was performed on custom databases representing the domestic chicken
112   genome (GenBank assembly accession GCF_000002315.6) and the food plants *Triticum*
113   *aestivum* (wheat), *Aegilops tauschii* (diploid progenitor of the D genome of hexaploid wheat) and
114   *Glycine max* (soy bean): GenBank assembly accessions GCF_001957025.1, GCA_900519105.1,
115   GCA_000004515.4. Kraken 2 revealed that 8% (±16%) of reads originated from the chicken and
116   at least 19% (±21%) originated from the diet. These sequences were filtered from our dataset and
117   excluded from subsequent analyses by keeping only reads 'Unclassified' by Kraken 2 after
118   comparison with each database in turn.
119   The remaining dataset underwent taxonomic profiling using Kraken 2 against a microbial
120   database built from all complete/representative archaeal, bacterial, fungal, protozoan, viral and
121   UniVec_Core sequences in RefSeq (O'Leary et al., 2016) in January 2020. Bracken (Lu et al.,
122   2017) was used to estimate taxon abundance from the Kraken 2 profiles, accepting only those
123   taxa with ≥1000 assigned reads. Bracken-database files were generated using "bracken-build" on
124   our microbial database and visualised using KronaTools (Ondov et al., 2011).
125
126   **Metagenomic assembly**
127   We searched the NCBI BioProjects database (https://www.ncbi.nlm.nih.gov/bioproject/) in
128   November 2019 with the term "chicken gut microbiome" and then selected nine publicly
129   available projects that contained at least one metagenomic sequence dataset >1GByte in size:
130   PRJEB33338, PRJNA193217, PRJNA291299, PRJNA375762, PRJNA415593, PRJNA417359,
131   PRJEB22062, PRJNA543206, PRJNA417359, PRJNA385038, PRJNA616250. Only four of
132   these studies were linked to research publications at the time of publication (Glendinning et al.,
133   2020; Sergeant et al., 2014; Foster-Nyarko et al., 2020; Luiken et al., 2020)
134   All shotgun metagenomic reads were quality-filtered by removing reads shorter than 70% of
135   the maximum expected read length (100 bp, 250 bp for MiSeq data), an estimated accumulated
136   error >2.5 with a probability of ≥0.01 (Puente-Sánchez et al., 2016) or with an observed
137   accumulated error >2, or >1 ambiguous position to assist assembly. If base quality dropped
138   below 20 in a window of 15 bases at the 3' end, or if the accumulated error exceeded 2, reads

139   were trimmed. All these filter steps are integrated in sdm (Hildebrand et al., 2014). Reads
140   mapping to the chicken genome and diet were removed from the metagenomic data as described
141   previously, classifying reads with Kraken 2 against custom databases built on the
142   aforementioned genomes.
143   Sequence datasets from our fifty samples—together with 582 samples from the selected
144   BioProjects—were assembled using MegaHIT (Li et al., 2016) under the option "--k-list
145   25,43,67,87,101,127". To avoid artefacts that sometimes result from co-assembly of sequences
146   from different samples and different sources, we performed individual assemblies on each
147   sample, with the exception of BioProject PRJNA17359. For that BioProject, as multiple
148   metagenomic samples had been sourced from different tissues of the same individual bird, we
149   co-assembled reads from the 120 BioSamples from that project.
150
151   **Bacteriophage identification and characterisation**
152   Scaffold sequences from the MegaHIT assemblies of our fifty samples that were ≥10kb were
153   analysed with VirSorter v1.0.5 with the "-db 2" option to identify viral genomes (Roux et al.,
154   2015). VirSorter Category 1 and 2 scaffold sequences were collapsed at 95% nucleotide identity
155   over 70% of the sequence length using CD-Hit Est v4.6.1 (Fu et al., 2012). Classification of
156   bacteriophage sequences relied on nucleotide searches using BLASTN against the NCBI NT
157   database (Completed April 2020) and protein searches using Kaiju Version 1.7.3 against the
158   RefSeq database (Completed April 2020) (Menzel et al., 2016). Only bacteriophage genomes
159   with BLASTN hit E-Value <0.05, percentage identity >70% and query covering >50% were
160   selected as reliable hits.
161   A taxonomic assignment was drawn from the highest scoring BLASTN (or in rare cases
162   BLASTP) hit ranked by query cover and percentage ID. Synteny between predicted coliphages
163   and their respective reference genomes were visualised using EasyFig (Sullivan et al., 2011).
164   *Escherichia* bacteriophage coverage per sample was determined using Anvi'o v6.1 (Eren et al.,
165   2015) using default parameters and visualised in R using the Pheatmap package
166   (https://www.rdocumentation.org/packages/pheatmap). Remaining viral genomes were filtered
167   for completeness, retaining those that were circular and encoded a complete terminase gene (as
168   predicted by VirSorter). Taxonomic assignments to family were performed on viral genomes
169   using Demovir (https://github.com/feargalr/Demovir).
170
171   **Gene catalogue**
172   Complete genes identified by Prodigal v2.6.1 (Hyatt et al., 2010) were clustered at 95%
173   nucleotide identity using CD-HIT-Est v4.6.1 (Fu et al., 2012). Incomplete genes were then
174   mapped to this complete gene list using Bowtie2 v 2.3.4.1 (Langmead & Salzberg, 2012) and
175   any mapping at 95% nucleotide identity were incorporated into the relevant gene clusters.
176   Finally, genes representing the forty conserved marker genes defined by Mende *et al* (Mende et
177   al., 2013) were clustered separately and then merged with the existing set of gene clusters. We
178   thus obtained a gene catalogue of >20 million genes, defined as non-redundant at 95% average
179   nucleotide identity. The final gene catalogue was uploaded to FigShare
180   (https://doi.org/10.6084/m9.figshare.13116809.v1)
181
182   **Abundance estimates of contigs and genes**
183   Prodigal (Hyatt et al., 2010) was applied in metagenome-mode to all contigs from the MegaHIT
184   assemblies. Unfiltered reads from each sample were mapped against their respective assembly to

185 provide an estimate of contig and gene abundance using Bowtie2 (Langmead & Salzberg, 2012)
186 with the options "--no-unal--end-to-end -score-min L, -0.6,-0.6". Samtools 1.3.1 was used to sort
187 and index all resulting Bam files (Li et al., 2009). Only reads with mapping quality >20, >95%
188 nucleotide identity and >75% overall alignment length were retained. BEDTools v2.21.0
189 (Quinlan, 2014) was used to create depth profiles from the Bam files. These depth profiles were
190 then translated with rdCover (https://github.com/hildebra/rdCover) into average coverage (in a
191 50 bp window) per contig or per gene predicted from each contig. Bam files were translated to
192 abundances using the "jgi_summarize_bam_contig_depths" script from the MetaBAT 2 package
193 (Kang et al., 2019).
194   Gene abundances were linked to their respective gene clusters and originating samples.
195 Redundant genes representing the same orthologue were removed.
196
197 **Binning**
198 We identified metagenomic species (MGSs) using the combinatorial approach described by
199 Hildebrand *et al* (Hildebrand et al., 2019), incorporating single-assembly binning in the creation
200 of metagenome-assembled genomes (MAGs), gene catalogue binning in the creation of canopy
201 clusters (Nielsen et al., 2014) and hierarchical clustering of candidate genes using the R function
202 hclust, method = complete. To start with, we used MetaBAT 2 v2.15 (Kang et al., 2019) to bin
203 contigs ≥400bp. These were quality filtered using CheckM v1.0.11 (Parks et al., 2015) to obtain
204 5,695 bins at >80% completeness and <5% contamination.
205   Species-level clusters were formed using a combination of two distinct approaches. One
206 approach removed redundancy between samples by pre-clustering bins if ≥30% of their genes
207 overlapped with a higher-quality bin to create a set of pre-MGS bins. Lower-quality bins (>60%
208 completeness and <10% contamination) were also included in the analysis but were not used to
209 form new species clusters. To recover prokaryotic species usually obscured using single-sample
210 assemblies and conventional binning techniques, we refined all species bins into "hcl-clusters"
211 using gene correlations and hierarchical clustering, as described by Hildebrand *et al* (Hildebrand
212 et al., 2019). We chose genes occurring in ≥10% of all associated MAGs as representatives for
213 each pre-MGS bin and used these to fish for additional co-occurring genes from the gene
214 catalogue, using a threshold of >0.75 Pearson correlation and >0.85 spearman rho to identify
215 gene co-occurrences within this core gene set. We then merged MetaBAT 2 bins, canopy bins
216 and co-occurring genes into our species bins. We used the presence of 40 known single-copy
217 marker genes, without duplicates, as a quality criterion in selection of sub-clusters, before
218 extracting the final set of MGS gene representatives using MATAFILER
219 (https://github.com/hildebra/MATAFILER). The final collection of MGS bins (canopy clusters +
220 hcl-clusters) was re-assessed for contamination and completeness using CheckM (Parks et al.,
221 2015), so that we could be confident that each bin represents a single species.
222   A second approach de-replicated all MAGs at 95% average nucleotide identity (ANI)
223 (species-level) and 99% ANI (strain-level) using dRep Version 2.0 (Olm et al., 2017) and only
224 species not identified in approach one were added to the resulting non-redundant species
225 catalogue. The minimum aligned fraction used during ANI genome alignment was 60%. A single
226 representative MAG for each novel species cluster was uploaded to NCBI SRA under BioProject
227 PRJNA543206 and all MAGs generated were uploaded to FigShare
228 (https://doi.org/10.6084/m9.figshare.13116809.v1.). CompareM Version0.1.1
229 (https://github.com/dparks1134/CompareM) was used to calculate average amino acid identity

230   between novel genera. The minimum sequence coverage for reporting an AAI alignment was set
231   to default at 70%.

Taxonomy of metagenomic species

234   **Taxonomy of metagenomic species**
235   We used the Genome Taxonomy Database Toolkit (GTDB-Tk Release 95) to perform taxonomic
236   assignments on strain-level dereplicated MAGs (Chaumeil et al., 2019). In addition, genes from
237   each MGS were analysed through GTDB-Tk (Release 95), proGenomes resource (Mende et al.,
238   2017) and underwent k-mer-based taxonomic profiling using Kraken 2. In assigning taxonomy,
239   we allowed GTDB assignments to take precedence—only when no GTDB taxonomy was
240   available would we adopt taxonomies assigned by ProGenomes and Kraken 2 and, then, only
241   where genus and family assignments from these sources matched. When exploiting the
242   taxonomy assigned according genes from metagenomic species, we applied a least-common-
243   ancestor approach to unplaced taxa at higher taxonomic levels. Species distribution analyses
244   were conducted using the Vegan package in R (R-Core-Team., 2018), before visualisation using
245   ggplot2 (Wickham, 2016) and Pheatmap R packages
246   (https://www.rdocumentation.org/packages/pheatmap). Pan-genome analysis was conducted
247   using Roary v3.11.2 and visualised using the roary2svg.pl script (Page et al., 2015). Comparison
248   of our derived metagenomes with those of Glendinning et al. (Glendinning et al., 2020) was
249   performed at 95% ANI using dRep and visualised using web-tool BioVenn (Hulsen et al., 2008).

251   **Bacterial culture**
252   To estimate species richness and diversity, the Phyloseq package of R (R-Core-Team., 2018) was
253   applied to the output from Bracken (Lu et al., 2017) on all of our chicken faecal metagenomic
254   datasets. The six faecal samples that showed highest species richness and taxonomic diversity
255   were selected for culture-based studies. Frozen faecal samples were thawed, vortexed and two
256   0.5g aliquots (once processed aerobically, the other anaerobically) from each sample were
257   suspended in 5ml PBS. Each aliquot was vortexed until homogenised, before performing serial
258   dilutions in duplicate down to 1×10^{-5}. Processing of samples for aerobic and anaerobic culture
259   was identical, except that, for anaerobic culture, all culture media, diluent and consumables were
260   pre-reduced to anaerobic conditions for at least 24 hours before faecal samples were processed in
261   a Whitley A95TG workstation.
262   For dilutions $10^{-3} – 10^5$, 200µl was plated directly on to a set of three agar plates for each
263   culture medium (Brain Heart Infusion, Colombia Blood Agar, Yeast extract, casitone and fatty
264   acid) with or without vancomycin supplementation at a concentration of 6µg/ml (Table S1).
265   Cultures were incubated at 37°C for 72 hours in their respective conditions before assessment of
266   colony growth. Well-isolated colonies were picked according to colonial morphotype distinctive
267   in colour, shape and size, before being re-streaked on to the growth medium from which they
268   were sourced to confirm purity. Individual colonies were subsequently used to inoculate 2ml of
269   broth based on the source culture medium, incubated at 37°C for a further 24 hours before
270   bacterial DNA extraction. All isolates were archived at -80°C in glycerol at 20% concentration.

271

272   **Genome sequencing and analysis**
273   Genomic DNA was extracted using a DNeasy UltraClean DNA isolation kit according to the
274   manufacturer's instructions (Qiagen, Hilden, Germany). DNA was quantified using a Qubit®
275   fluorometer (Invitrogen, CA, USA) high-sensitivity assay, before dilution to the required

276 concentration in RNase-free water and purification on AMPure XP beads (Beckman Coulter).
277 Sequencing libraries were prepared from 0.5ng/µl of RNA free genomic DNA. A total of 282
278 isolates were included for genomic sequencing using the Nextera-XT DNA sample preparation
279 kit (Illumina) and whole-genome sequencing performed using the Illumina NextSeq sequencing
280 platform, generating paired-end reads (2 x 150bp).
281   Paired-end reads were quality-assessed and trimmed using FastQC and Trimmomatic as
282 described above. Trimmed reads were assembled into scaffolds using SPAdes version 3.13.1
283 (Bankevich et al., 2012). Scaffolds shorter than 500 bp were discarded from analysis. Genome
284 contamination and completeness was assessed using CheckM version 1.0.13. To confirm
285 assembly quality, only genomes conforming to all the following criteria were included in further
286 analysis: (i) scaffold N50 of >20 kbp (ii) 90% of assembled bases at > 5x read coverage (iii)
287 completeness of > 95% (iv) contamination of < 5% (v) complete 16S rRNA gene sequence.
288
289 **Genome sequence taxonomic assignment**
290 Barrnap Version 0.9 (https://github.com/tseemann/barrnap) was applied to all genomes that
291 passed the quality filters to extract full-length 16S rRNA gene sequences. These were then
292 compared to NCBI 16S rRNA gene sequences from RefSeq genomes using the NCBI's web-
293 based BLASTN facility (Altschul et al., 1990). 16S rRNA gene sequences that showed an
294 identity of <98.7% to known sequences were assigned to novel species, using the conservative
295 approach in proposed minimal standards (Chun et al., 2018). We used ReferenceSeeker Version
296 1.6.2 (Schwengers et al., 2019) to determine average nucleotide identity (ANI) and conserved
297 DNA values compared to RefSeq bacterial genomes (Completed March 2020) (O'Leary et al.,
298 2016). Genomes that showed ANI ≤95% and conserved DNA ≤69% to the closest relative were
299 designated novel species. The Genome Taxonomy Database Toolkit (GTDB-Tk Release 89) was
300 used to perform taxonomic assignments on isolate genomes (Chaumeil et al., 2019). Genomes
301 were clustered at 95% and 99% ANI before selection of a single representative isolate per
302 species using dRep (Olm et al., 2017). Where a genome previously designated as novel clustered
303 with a genome of assigned taxonomy, this taxonomy was then applied to the previously
304 designated 'novel' genome. Final taxonomic assignments were based on genome-based ANI
305 values derived from RefSeq and GTDB – with GTDB assignments taking precedence. A single
306 representative genome for each novel or renamed species cluster was uploaded to NCBI SRA
307 under BioProject PRJNA543206 and all genomes alongside respective 16S rRNA gene
308 sequences generated were uploaded to FigShare (https://doi.org/10.6084/m9.figshare.13234556).
309
310 **Phylogenetic analysis**
311 For phylogenetic analysis of all MGS and genome sequenced isolates we used PhyloPhlAn
312 v3.0.58 (Asnicar et al., 2020) with the "diversity high" and a proteome input predicted from all
313 genome sequences using Prodigal v2.6.1 (Hyatt et al., 2010). Diamond v0.9.34 (Buchfink et al.,
314 2015) was used to perform a search against 400 universal PhyloPhlAn markers. MAFFT v.7.271
315 (Katoh et al., 2002) was used to perform multiple sequence alignment before refinement with
316 trimAl v.1.4 (Capella-Gutiérrez et al., 2009) and reconstruction into trees using FastTree v2.1
317 and RAxML v. 8.2.12 (Price et al., 2010; Stamatakis, 2014). All trees were visualised used the
318 online iTOLv1.4 platform for visualisation and manual annotation (Letunic & Bork, 2016). Trees
319 were scrutinised to confirm that species and genera were monophyletic. Phylogeny for all
320 cultured genomes unassigned at species level was confirmed as previously described against all
321 available reference proteomes of that respective genus downloaded from NCBI.

322   To investigate the phylogenetic placement of cultured isolates designated as *Escherichia*
323   *marmotae* and *Escherichia* sp001660175 by GTDB, we constructed a core genome phylogenetic
324   tree. The genomes from cultured isolates were compared to genomes representing the full
325   diversity of the genus *Escherichia*. Three *Salmonella* genomes were included as an outgroup.
326   The genome sequences were aligned using Mugsy (Angiuoli & Salzberg, 2011), and alignment
327   blocks conserved across all genomes were concatenated to produce a core genome alignment. A
328   phylogenetic tree was constructed by maximum likelihood with 100 rapid bootstrap replicates,
329   using the general time reversible model of nucleotide substitution with gamma correction for rate
330   heterogeneity, as implemented in RAxML version 8.2.12 (Stamatakis, 2014).
331
332   **Results**
333   **Reference-based profiling documents novel diversity**
334   We collected faecal samples from fifty chickens reared in the UK belonging to two breeds:
335   Lohman Browns (n=30) and Silkies (n=20). Short-read sequencing of fifty faecal samples
336   generated a metagenomic dataset in excess of a billion paired-end reads or three hundred billion
337   base pairs (Table S2).
338   We initially analysed the faecal samples using the k-mer-based program Kraken 2, followed
339   by refined phylogenetic analysis using the allied program Bracken (Lu et al., 2017) (Table S3).
340   Unsurprisingly, these programs assigned sequence reads from the faecal samples to all three
341   domains of life, as well as to viruses (Table S4), although relative abundance assignments show
342   that bacteria predominate in this environment. Sequences were assigned to a wide range of
343   bacterial phyla, including the three expected as predominant in the vertebrate gut (Bacteroidetes,
344   Firmicutes, Proteobacteria), but also including over twenty additional phyla. Searches of the
345   PubMed database with each phylum name and the term "chicken" reveal that round half of these
346   have been previously documented in the chicken gut. However, at least a dozen appear to be
347   novel in this setting, including the *Aquificae, Balneolaeota, Calditrichaeota, Chlorobi,*
348   *Dictyoglomi, Fibrobacteres, Gemmatimonadetes, Ignavibacteriae, Kiritimatiellaeota,*
349   *Lentisphaerae, Nitrospirae,* and the *Thermodesulfobacteria*.
350   When we rank-ordered the species identified by Bracken according to maximum abundance
351   in any one sample, we found, as expected, that species from the family *Lactobacillaceae*
352   dominated among the top twenty most abundant organisms. However, we found that two species
353   of *Escherichia— Escherichia coli* and *Escherichia marmotae*—accounted for ≥ 5% of reads in
354   nearly half of the samples (23/50) and in two samples, accounted for more than 50%. Such
355   monodominance of the gut microbiome by bacterial species has been described in diseased
356   humans (Hildebrand et al., 2019; Ravi et al., 2019), but is surprising in the context of poultry
357   reported as apparently healthy by their handlers. We also noted a high relative abundance of the
358   recently described chicken pathogen *Gallibacterium anatis* (Narasinakuppe Krishnegowda et al.,
359   2020) in most birds (with five birds showing >5% reads assigned to this organism), despite their
360   healthy status. Similarly, *Fusobacterium mortiferum*— an opportunistic pathogen of humans
361   (Almohaya et al., 2020)—accounted for >10% of sequences in ten birds, corroborating a recent
362   report of high abundance of 16S rRNA gene sequences from this organism obtained from the
363   chicken caecum (Kollarcikova et al., 2019).
364   Bracken assigned sequences to over a hundred bacteriophage genomes, predominately
365   phages infecting members of the *Enterobacteriaceae* assigned to the families *Myoviridae* and
366   *Podoviridae*. Particularly noteworthy was the high abundance of reads in some samples from two
367   distinct bacteriophages that prey on *E. coli*: phiEcoM-GJ1—a lytic bacteriophage isolated in

368 Canada from pig sewage (Jamalludeen et al., 2008)—which accounted for 6.7% reads in a single
369 sample and phAPEC8—a lytic bacteriophage with a large 147kb genome, isolated from a
370 Belgian poultry farm—which accounted for 10% of reads in a single sample and for >1% of
371 reads in three others (Tsonos et al., 2012).
372   Although these k-mer-based analyses can provide interesting insights into taxonomic
373 diversity within the chicken gut, we quickly realised that they provide an incomplete and
374 misleading picture of this important microbiome for several reasons: (1) they often report the
375 presence of highly implausible organisms—for example, Kraken 2 reported the presence of
376 human pathogens such as *Shigella flexneri* and *Plasmodium falciparum* that are simply not
377 credible in this context on clinical grounds; (2) as with studies on 16S rRNA gene sequences,
378 they fail to provide genomic data or insights into the functional diversity or population structure
379 of the microbial species that they identify and; (3) they rely on a reference database and so can
380 only report previously known organisms and can never uncover "unknown unknowns".
381   The scale of the problem of unknown diversity is clear from the observation that nearly three
382 quarters (73%) of sequence reads from our chicken samples cannot be confidently classified by
383 Kraken 2 to species level and more than half of the reads (54%) cannot be classified at all and
384 are simply designated as "Unassigned". We therefore sought to extend our understanding of this
385 community through two powerful reference-free approaches: assembly-based metagenome
386 analyses and high-throughput culture.
387
388 **Metagenomic assembly uncovers a wealth of viral diversity**
389 Assembly of metagenomic sequences is a reference-free approach that involves aligning and
390 merging short sequence reads into long contiguous sequences (contigs), which can then be
391 ordered into larger scaffolds that include sequence gaps.
392   To confirm the presence of bacteriophages inferred through the reference-based analysis and
393 to identify novel viral genomes, we assembled sequence reads from our fifty chicken faecal
394 samples into scaffolds. Scaffold sequences ≥10kb were analysed with VirSorter—a program
395 designed to detect viral signals in microbial sequence data to find novel viruses (Roux et al.,
396 2015).
397   VirSorter identified 184 of our chicken faecal scaffolds as Category 1 ("most confident")
398 bacteriophage sequences and identified an additional 1,840 scaffolds as Category 2 ("likely")
399 bacteriophage sequences. This was de-replicated to 1,455 genomes using similarity thresholds of
400 95% ANI over 70% of the genome (Table S5). BLASTN analysis revealed only ten of these
401 bacteriophage genomes showed high similarity (percentage identity > 70%; query covering >
402 50%) to known phages at the nucleotide level (Table S6). These included close relatives of the
403 two phages (phiEcoM-GJ1 and phAPEC8) found highly abundant in the Bracken analyses (Fig.
404 2). Interestingly, more than one genus of coliphage (e.g. *Jilinvirus, Phapecoctavirus,* or
405 *Gamaleyavirus*) was often detected in the same sample, along with an abundance of reads from
406 their predicted prey (*Escherichia*) suggesting interesting dynamics in phage-host and phage-
407 phage interactions (Fig. 3; Table S7).
408   Of the remaining 1,445 unclassified bacteriophage genomes, nearly 600 encoded either an
409 obvious terminase region or were circular and as such were suggested as being near-complete.
410 Classification of these genomes revealed all genomes were predicted to belong to the order
411 *Caudovirales* of tailed phages, with the majority belonging to the family *Siphoviridae* (n=429),
412 but we also found representatives from the *Myoviridae* (n=87) and *Podoviridae* (n=27), plus
413 some bacteriophages unclassified at family level (n=28) (Table S8).

414
415   **Remarkable microbial genome diversity in the chicken gut**
416   Next, we subjected our samples to computational binning—a process of grouping
417   contigs/scaffolds on the basis of sequence composition and depth of coverage into discrete
418   population bins representing metagenome-assembled genomes (MAGs). However, to carry out a
419   definitive survey of bacterial and archaeal diversity in the chicken gut microbiome—in addition
420   to analysing the fifty faecal samples mentioned and before we started the binning—we retrieved
421   all publicly available chicken gut metagenomic datasets, to create an expansive dataset
422   representing >630 samples, drawn from ten studies and twelve countries (Belgium, China,
423   France, Germany, Italy, Malaysia, Netherlands, Poland, Spain, The Gambia, UK, USA) (Figure
424   S1a/S1b; Table S9).
425   Sequence assembly and binning on all these samples generated 5,595 MAGs that passed our
426   quality threshold of ≥80% completion and ≤5% contamination (Figure S1c). Of these 3,131
427   could be considered high-quality draft genomes, with >90% completion and <5% contamination,
428   as judged by recently published criteria (Table S10) (Bowers et al., 2017). Genome sizes of the
429   MAGs ranged from ~0.5 to 6.4 Mbp, while GC content ranged from 24% to 73%.
430   Then, we grouped the MAGs into metagenomic species (MGSs). Initially, this involved de-
431   replicating MAGs at the widely accepted 95% average nucleotide identity (ANI) for defining
432   bacterial and archaeal species and 99% ANI for defining bacterial and archaeal strains (Jain et
433   al., 2018; Luo et al., 2014). De-replication of MAGs at 95% ANI resulted in 846 clusters
434   representing bacterial and archaeal species, while de-replication at 99% ANI resulted in 2182
435   clusters, representing strains. However, to improve recovery of MAGs, MGSs and associated
436   gene sets, we used gene correlations to identify species-representative genes and then applied
437   hierarchical clustering to co-occurring genes across the samples. This allowed us to identify
438   additional genes from the core genome of a species, even when they show divergent nucleotide
439   compositions (such as genes from genomic islands and plasmids) (Hildebrand et al., 2019).
440   Similarly, using canopy clustering (Nielsen et al., 2014), we could identify commonly occurring
441   species of low abundance. Using these approaches, we were able to identify an additional seven
442   MGSs (Table S11). These MGS were prevalent at >1x coverage in 53% of all analysed samples
443   spanning at least 4 different BioProjects.
444   Analysis of bacterial metagenomic species, primarily using the Genome Taxonomy Database
445   (GTDB) taxonomy (Parks et al., 2020), confirmed and extended the taxonomic novelty
446   uncovered by reference-based community profiling (Fig. 4), recovering species spanning
447   nineteen of the bacterial phyla defined by GTDB (Table S12). These include *Cyanobacteria* (12
448   species, 32 strains); *Deferribacterota* (1 species, 1 strain) *Synergistota* (2 species; 5 strains) and
449   the *Verrucomicrobiota* (7 species; 8 strains).
450   Of the 853 de-replicated bacterial metagenomic species, 321 represented previously
451   delineated species catalogued in publicly available databases (Table S13). Following direct
452   comparison, a further 165 metagenomic species had been previously identified by Glendinning *et*
453   *al* (Glendinning et al., 2020), with these sequences not currently available in public archives.
454   However, only 158 of our metagenomic species possess validly published names based on Latin
455   binomials.
456   We performed a search of PubMed with the species name and "chicken", leaving aside the 33
457   species named by Glendinning *et al* (Glendinning et al., 2020). This suggested that our study
458   provides the first-evidence-in-chickens for the majority (81/125) of these species (Table S14).
459   Examples include: *Jeotgalicoccus halophilus,* first isolated from the traditional fermented

460   seafood, Jeotgal (Yoon et al., 2003) and present in 197 chicken samples; *Aliicoccus persicus*,
461   first isolated from a hypersaline lake (Amoozegar et al., 2014) and present in 241 chicken
462   samples; and *Bacteroides reticulotermitis,* first isolated from the gut of a termite (Sakamoto &
463   Ohkuma, 2013) and present in 39 chicken samples.
464   We found that 310 of our metagenomic species could be assigned a taxonomy only at the
465   level of genus and so represent novel candidate species. A further 56 species could be assigned a
466   taxonomy only at the level of family and, after AAI clustering at 60%, were assigned to 36 novel
467   candidate genera. One candidate bacterial species could be assigned a taxonomy only at the level
468   of order (*Oscillospirales*) and so represent a new family.
469   Three MAGs were assigned to the domain Archaea. One represents the species
470   *Methanobrevibacter woesei*—which is already known to inhabit the chicken gut (Saengkerdsub
471   et al., 2007)—while the other two represent novel species within the genera
472   *Methanocorpusculum* and UBA71.
473
474   **Linnaean binomials for hundreds of new candidate species**
475   Linnaeus first proposed the assignment of Latin binomials to provide a universal nomenclature
476   for biological species (Linnaeus, 1759). The International Code of Nomenclature of Prokaryotes
477   (ICNP) sets the rules for naming prokaryotic species (Parker et al., 2019), but currently precludes
478   the valid publication of names of uncultivated organisms, represented by MAGs or other
479   sequences. Furthermore, high-throughput generation of MAGs and of sequence-based
480   taxonomies for bacteria, such as the GTDB (Parks et al., 2020) is often assumed to preclude the
481   detailed attention usually given to one-by-one construction of Linnaean binomials. As a result,
482   most uncultured taxa, as well as many taxa defined on sequence-based criteria, have been
483   assigned unstable, confusing and hard to-remember alphanumerical identifiers.
484   To provide a stable, clear and memorable nomenclature for novel and/or previously unnamed
485   bacterial and archaeal species from the chicken gut, we exploited the provision within the ICNP
486   for naming uncultivated taxa via *Candidatus* assignments, which, although provisional, provide
487   the scientific community with well-formed Latin binomials (Oren, 2017; Oren et al., 2020).
488   However, this prompted us into an unprecedented effort to create hundreds of new names for the
489   purpose of this single research study—an effort that required us to devise a scalable
490   combinatorial system for the creation of binomials. Here, we made extensive combinatorial use
491   of several dozen Latin and Greek roots pertaining to poultry (*avi-, galli-, pulli-, alektryo, ptero,*
492   *kotto-, ornitho-*), intestines (*intestini- entero-*), faeces (*faec-, kakke, merd-, kopro-, excrement-*)
493   or microbial life *(-monas, -bacterium, -microbium, -coccus, -bacillus, -bium, -cola)*—twinned
494   with addition of these roots (singly or in tandem) and/or prefixes (*allo, hetero, meta-, para-,*
495   *crypto-*) to existing genus names—to create over 150 *Candidatus* genus names. For genera with
496   alphanumeric designations in GTDB Release 05-RS95 (Parks et al., 2020) known to occur also
497   in gut microbiomes of other animals, we adopted a similar combinatorial approach, but avoided
498   roots pertaining to poultry and stuck instead with combinations that simply meant "gut or faecal
499   microbe", e.g *Fimicola, Caccocola*. An additional source of diversity stemmed from repetitive
500   use of around forty *Candidatus* species epithets built from similar roots, which when combined
501   with genus names gave us a total of over 650 distinctive binomials for new *Candidatus* species
502   (Table 1, Table S15).
503
504   **Taxonomic diversity of cultured bacterial isolates**

505   To extend our metagenomics analyses, we applied culture-based methods to six faecal samples
506   that appeared species-rich in Kraken 2 analyses and in so doing obtained 282 isolates from
507   aerobic culture (~80% of isolates) and anaerobic culture (~20% of isolates) (Table S16). All
508   isolates underwent genome sequencing on the Illumina platform and phylogenetic analysis to
509   enable taxonomic assignment. The resulting chicken gut culture collection was found to contain
510   56 genera, 93 species and 162 strains drawn from five phyla. These included thirty novel species,
511   with all novel species confirmed to originate from a monophyletic group through phylogenetic
512   analysis against all available reference genomes of their respective genus (Figure S2). Curiously,
513   there was no overlap between the species that we obtained and those reported by Medvecky *et al*
514   (Medvecky et al., 2018), suggesting that we are far from exhausting the set of species that can be
515   cultured from this habitat. As with the metagenomic species, all novel or previously unnamed
516   genera and species from cultured isolates were assigned Linnaean binomials (Table 2; Table
517   S17). Species-level ANI clustering of all MAGs and all cultured isolates according to phylum is
518   provided in Figure S4.
519   Interestingly, alongside ten cultured isolates of the well-characterised species *Escherichia*
520   *coli,* we recovered three isolates from *Escherichia marmotae* (a species recently described in
521   Himalayan marmots (Liu et al., 2015)). As previously reported, the *E. marmotae* strains cluster
522   closely with the *Escherichia* Clade V (Liu et al., 2019; Walk, 2015), so all members of this clade
523   should be considered members of this species (Fig. 5, Table S18). Further analysis of the GTDB
524   species designated *Escherichia* sp001660175
525   (https://gtdb.ecogenomic.org/searches?s=al&q=sp001660175) confirmed that this species forms
526   a monophyletic lineage that corresponds to Clade II, among the cryptic environmental clades
527   described by Whittam and his colleagues (Walk et al., 2009), which was subsequently
528   documented in birds (Clermont et al., 2011). As Clade II is comparable in divergence to the other
529   *Escherichia* spp. and cryptic clades, we have therefore assigned the Linnaean binomial
530   *Escherichia whittamii* to designate a new species (Table 2), honouring the outstanding
531   contribution of Thomas S. Whittam to the study of *Escherichia* spp. (Walk & Feng, 2011).
532   We found that only sixteen species were common to our cultured isolates and our MGS.
533   Subsequent sequence mapping allowed us to detect a further two cultured species at ≥1x
534   coverage in at least one metagenomic sample (Fig. 6a; Table S19). The genomes from cultured
535   isolates were on average 20% larger than the corresponding MAG sequences retrieved from the
536   same source sample (Table S20), which is in line with the completeness threshold of 80% we
537   adopted in quality assurance of the MAGs. However, when we performed detailed gene content
538   analyses on three abundant species in both cultured and metagenomic datasets —*Lactobacillus*
539   *reuteri* (with the synonym *Limosilactobacillus reuteri), Escherichia coli* (including the synonym
540   *Escherichia flexneri*) and *Enterococcus faecium*—we found that >99% of the genes from the
541   core genomes and nearly half of the genes in the accessory genomes of cultured species were
542   represented in at least one MAG. These observations suggest that our high-quality MAGs are
543   sufficiently complete to warrant *Candidatus* names.
544   We analysed our chicken faecal metagenomes with a Kraken 2 database derived from
545   genomes representing our candidate metagenomic and cultured species, this yielded a
546   considerable improvement in the number of reads that can be classified through rapid
547   phylogenetic profiling (Fig. 6b).
548
549   **Distribution of microbial species**

550 An analysis of the distribution of 820 MGSs across the entire metagenomic dataset revealed
551 marked variation between samples, with not a single species present at ≥1x coverage in all
552 samples and only 39 species present in >90% of samples— although 441 species were present in
553 >50% of samples at ≥1x coverage (Table S21). At ≥1x coverage, co-occurrence of nearly 300
554 species (n=295) was identified across all 10 BioProjects (Fig. 7a), with no species identified in
555 all BioProjects at ≥10x coverage (Fig. 7b). Focusing on samples from distinct sites, we found no
556 species present in all faecal samples at >1x coverage and only two species were found in all
557 caecal samples at >1x coverage: both of them newly named in this study: *Paraprevotella*
558 *stercoravium* and *Blautia pullistercoris* (the latter identified but not named by Glendinning et al.
559 2020 (Glendinning et al., 2020). These findings rule out the concept of a core chicken gut
560 microbiome. Studies on the human gut microbiome provide a useful comparison in that, in a
561 recent study, only fourteen genera were found to be shared across 95% of samples from the
562 human gut (Falony et al., 2016).
563   Among the species with high coverage, frequency is clearly linked to Bioproject. Although
564 species quantification curves showed that the number of species identified increased rapidly with
565 the number of samples, species discovery appeared to plateau at approximately 230 species after
566 including only 50 metagenomes (Figure S2a). Only two species appeared to be restricted (at ≥1x
567 coverage) to just a single sample: *Aliarcobacter thereius* and *Candidatus* Avibacteroides
568 faecavium. Correlation clustering confirmed structure in the data linked to BioProject (Figure
569 S2b) —for example, the BioProject from the study by Glendinning *et al* (Glendinning et al.,
570 2020) clearly shows enhancement of clostridial species compared to other BioProjects, which
571 reflects the fact that samples in that study were sourced from chicks with no post-hatching
572 contact with an adult bird. However, the BioSamples do not appear to cluster by country (Figure
573 S2c) and show only limited clustering by sample site (Figure S2d). Unfortunately, there is
574 insufficient metadata for other potentially important factors, such as breed, age or diet to draw
575 conclusions on how these might influence clustering.
576
577 **Discussion**
578 Given the dominance of chickens in the planetary biomass, the chicken gut microbiome ranks as
579 one of the most abundant microbial communities on the planet. Here, we have exploited two
580 complementary approaches—metagenomics and culture—to create an extensive catalogue of
581 genes, genomes and isolates from this important ecosystem. Our work illustrates the value of
582 combining culture-dependent and culture-independent approaches in analysing microbiomes.
583   We have clearly demonstrated the advantages of shotgun metagenomic sequencing, when
584 applied to the chicken gut microbiome, providing catalogues of genes and genome sequences
585 that takes us well beyond what can be achieved using 16S ribosomal RNA gene sequences.
586 Similarly, the current study is much wider in scope than the previous study by Glendinning and
587 colleagues (Glendinning et al., 2020), not just including analyses of viral genomes and cultured
588 isolates, while also incorporating MAGs built from data not just from that study but from all
589 publicly available metagenomic datasets. Furthermore, the limited overlap between bacterial
590 species represented among our cultured isolates and in our MGS reinforces the utility of the
591 combined approach. Nonetheless, the substantial co-linearity between genomes obtained by the
592 two approaches—and with those from another similar metagenomic study (Glendinning et al.,
593 2020)—confirms the reliability of our binning approaches.
594   We were surprised to find such a remarkable phylogenetic diversity within this commonplace
595 livestock ecosystem—diversity that rivals that associated with the human gut. Our work has

596   more than doubled the number of bacterial species known to reside in the chicken gut and has
597   resulted in the creation of an unprecedented number of new *Candidatus* species. By including
598   well-formed Latin binomials with the genomes we have uploaded into public repositories, we
599   have ensured that the new proposed names and associated sequences will be integrated into
600   commonly used online taxonomies and databases and will provide a stable taxonomic
601   nomenclature for future studies. In addition, we have provided proof-of-principle for a scalable
602   approach to Linnaean nomenclature that could be applied to species recovered from other
603   metagenomic assembly projects.
604   Given that we did not recover by culture some of the organisms that appear most abundant by
605   metagenomics, there is clearly scope for additional culture-based investigations, using a wider
606   range of cultural conditions—perhaps drawing on the precedent of the Human Microbiome
607   Project to create and target a list of the "most-wanted-for-culture" organisms documented by
608   metagenomics (Fodor et al., 2012). The fact that novel metagenomic species are still being
609   recovered from human gut datasets that include tens of thousands of metagenomes (Almeida et
610   al., 2019)—twinned with the promise of novel long-read and proximity-capture approaches to
611   metagenome analyses(Stewart et al., 2018)—make it clear that our attempts here to analyse all
612   currently available chicken gut metagenomes provide far from the last word on microbial
613   diversity in this abundant and important ecosystem. Nonetheless, the availability of so many
614   novel genes, genome and species represents a substantial step forward.
615
616   **Conclusions**
617   The extensive catalogue of genes, genomes and isolates we have created here substantially
618   improves the coverage of the chicken gut microbiome in the public databases and will make it
619   possible to profile sequences from the chicken gut much more rapidly, easily and
620   comprehensively, providing a valuable resource that lays the ground-work for future comparative
621   and intervention studies. This study also sets a provocative precedent—relevant not just to
622   animal microbiomes, but to studies on all microbiomes—assigning well-formed Latin binomials
623   to hundreds of metagenomic species in a scalable alternative to the automated use of bland,
624   unstable, user-unfriendly alphanumerical designations. Drawing on the precedent set by the
625   current study, we have recently extended this approach to encompass creation of more than a
626   million new names for Bacteria and Archaea (Pallen et al., 2020). Thus, the time is now ripe to
627   bring Linnaeus right into the heart of microbiome studies.
628
629   **Acknowledgements**
630   The authors thank the farmers for collecting the chicken faecal samples for the study.
631
632   **Citation markers for Table 2 to ensure all references included in bibliography (to be**
633   **removed during manuscript preparation)**
634   (Chaumeil et al., 2019; Parks et al., 2020)
635   (Clermont et al., 2011; Gangiredla et al., 2018)
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640
641

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966
967

Protologues for new *Candidatus* taxa identified from metagenomic analysis of chicken gut samples

2
3 **Description of *Candidatus* Acetatifactor stercoripullorum sp. nov.**
4 *Candidatus* Acetatifactor stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
5 masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
6
7 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
9 assigned the MAG ID CHK195-6426 and which is available via NCBI BioSample
10 SAMN15816622. The GC content of the type genome is 48.46% and the genome length is 3.1
11 Mbp.
12
13
14 **Description of *Candidatus* Acinetobacter avistercoris sp. nov.**
15 *Candidatus* Acinetobacter avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
16 dung; N.L. gen. n. *avistercoris* of bird faeces)
17
18 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
19 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
20 assigned the MAG ID 5402 and which is available via NCBI BioSample SAMN15816735. The
21 GC content of the type genome is 38.29% and the genome length is 3.9 Mbp.
22
23
24 **Description of *Candidatus* Acutalibacter ornithocaccae sp. nov.**
25 *Candidatus* Acutalibacter ornithocaccae (or.ni.tho.cac'cae. Gr. masc. or fem. n. *ornis, ornithos*
26 bird Gr. fem. n. *kakke* faeces; N.L. gen. n. *ornithocaccae* of bird faeces)
27
28 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
29 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
30 assigned the MAG ID ChiBcolR8-3208 and which is available via NCBI BioSample
31 SAMN15816822. This is a new name for the alphanumeric GTDB species sp000435395. The
32 GC content of the type genome is 62.02% and the genome length is 2.1 Mbp.
33
34
35 **Description of *Candidatus* Acutalibacter pullicola sp. nov.**
36 *Candidatus* Acutalibacter pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
37 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
38
39 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
40 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
41 assigned the MAG ID CHK185-1770 and which is available via NCBI BioSample
42 SAMN15816590. The GC content of the type genome is 58.43% and the genome length is 2.1
43 Mbp.
44
45
46 **Description of *Candidatus* Acutalibacter pullistercoris sp. nov.**

47 *Candidatus* Acutalibacter pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
48 neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
49
50 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
51 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
52 assigned the MAG ID 1282 and which is available via NCBI BioSample SAMN15816718. The
53 GC content of the type genome is 63.65% and the genome length is 2.0 Mbp.
54
55
56 **Description of *Candidatus* Acutalibacter stercoravium sp. nov.**
57 *Candidatus* Acutalibacter stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
58 bird; N.L. gen. n. *stercoravium* of bird faeces)
59
60 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
61 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
62 assigned the MAG ID ChiBcolR1-495 and which is available via NCBI BioSample
63 SAMN15816868. This is a new name for the alphanumeric GTDB species sp900543555. The
64 GC content of the type genome is 60.31% and the genome length is 2.0 Mbp.
65
66
67 **Description of *Candidatus* Acutalibacter stercorigallinarum sp. nov.**
68 *Candidatus* Acutalibacter stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
69 fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
70
71 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
72 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
73 assigned the MAG ID ChiGjej2B2-2649 and which is available via NCBI BioSample
74 SAMN15816629. The GC content of the type genome is 63.77% and the genome length is 2.1
75 Mbp.
76
77
78 **Description of *Candidatus* Agathobaculum intestinigallinarum sp. nov.**
79 *Candidatus* Agathobaculum intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum*
80 gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
81
82 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
83 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
84 assigned the MAG ID ChiGjej6B6-20540 and which is available via NCBI BioSample
85 SAMN15816816. This is a new name for the alphanumeric GTDB species sp900555465. The
86 GC content of the type genome is 60.79% and the genome length is 2.0 Mbp.
87
88
89 **Description of *Candidatus* Agathobaculum intestinipullorum sp. nov.**
90 *Candidatus* Agathobaculum intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut;
91 L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

93   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
94   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
95   assigned the MAG ID ChiBcec16-9926 and which is available via NCBI BioSample
96   SAMN15816670. The GC content of the type genome is 57.76% and the genome length is 1.9
97   Mbp.
98
99
100 **Description of *Candidatus* Agathobaculum merdavium sp. nov.**
101 *Candidatus* Agathobaculum merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
102 bird; N.L. gen. n. *merdavium* of bird faeces)
103
104 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
105 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
106 assigned the MAG ID ChiBcec15-6302 and which is available via NCBI BioSample
107 SAMN15816712. The GC content of the type genome is 57.98% and the genome length is 2.0
108 Mbp.
109
110
111 **Description of *Candidatus* Agathobaculum merdigallinarum sp. nov.**
112 *Candidatus* Agathobaculum merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L.
113 fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
114
115 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
116 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
117 assigned the MAG ID ChiSjej1B19-3834 and which is available via NCBI BioSample
118 SAMN15816715. The GC content of the type genome is 57.98% and the genome length is 2.0
119 Mbp.
120
121
122 **Description of *Candidatus* Agathobaculum merdipullorum sp. nov.**
123 *Candidatus* Agathobaculum merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc.
124 n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
125
126 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
127 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
128 assigned the MAG ID CHK149-1869 and which is available via NCBI BioSample
129 SAMN15816722. The GC content of the type genome is 56.28% and the genome length is 1.7
130 Mbp.
131
132
133 **Description of *Candidatus* Agathobaculum pullicola sp. nov.**
134 *Candidatus* Agathobaculum pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -
135 *cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
136
137 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
138 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

139 assigned the MAG ID 2940 and which is available via NCBI BioSample SAMN15816725. The
140 GC content of the type genome is 54.80% and the genome length is 2.0 Mbp.
141
142
143 **Description of *Candidatus* Agathobaculum pullistercoris sp. nov.**
144 *Candidatus* Agathobaculum pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken;
145 L. neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
146
147 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
148 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
149 assigned the MAG ID CHK180-9785 and which is available via NCBI BioSample
150 SAMN15816619. The GC content of the type genome is 58.01% and the genome length is 2.3
151 Mbp.
152
153
154 **Description of *Candidatus* Agathobaculum stercoravium sp. nov.**
155 *Candidatus* Agathobaculum stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n.
156 *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
157
158 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
159 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
160 assigned the MAG ID ChiW21-6059 and which is available via NCBI BioSample
161 SAMN15816625. The GC content of the type genome is 59.83% and the genome length is 2.3
162 Mbp.
163
164
165 **Description of *Candidatus* Agrococcus pullicola sp. nov.**
166 *Candidatus* Agrococcus pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
167 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
168
169 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
170 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
171 assigned the MAG ID ChiGjej1B1-98 and which is available via NCBI BioSample
172 SAMN15816710. The GC content of the type genome is 63.86% and the genome length is 3.0
173 Mbp.
174
175
176 **Description of *Candidatus* Akkermansia intestinavium sp. nov.**
177 *Candidatus* Akkermansia intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
178 *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
179
180 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
181 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
182 assigned the MAG ID ChiGjej6B6-8097 and which is available via NCBI BioSample
183 SAMN15816856. This is a new name for the alphanumeric GTDB species sp900548895. The
184 GC content of the type genome is 65.09% and the genome length is 2.2 Mbp.

186
187 **Description of *Candidatus* Akkermansia intestinigallinarum sp. nov.**
188 *Candidatus* Akkermansia intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
189 L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
190
191 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
192 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
193 assigned the MAG ID 14975 and which is available via NCBI BioSample SAMN15816742. The
194 GC content of the type genome is 63.40% and the genome length is 2.1 Mbp.
195
196
197 **Description of *Candidatus* Alectryobacillus gen. nov.**
198 *Candidatus* Alectryobacillus (A.lec.try.o.ba.cil'lus. Gr. neut. n. *alektryon* chicken; L. masc. n.
199 *bacillus* a rod; N.L. masc. n. *Alectryobacillus* a bacillus found in poultry)
200
201 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
202 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
203 species *Alectryobacillus merdavium*. This genus has been assigned by GTDB-Tk v1.3.0 working
204 on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RFN20* and to
205 the family *CAG-826*.
206
207
208 **Description of *Candidatus* Alectryobacillus merdavium sp. nov.**
209 *Candidatus* Alectryobacillus merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
210 bird; N.L. gen. n. *merdavium* of bird faeces)
211
212 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
213 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
214 assigned the MAG ID 13038 and which is available via NCBI BioSample SAMN15816966. The
215 GC content of the type genome is 27.10% and the genome length is 1.2 Mbp.
216
217
218 **Description of *Candidatus* Alectryocaccobium gen. nov.**
219 *Candidatus* Alectryocaccobium (A.lec.try.o.cac.co'bi.um. Gr. neut. n. *alektryon* chicken; Gr.
220 fem. n. *kakke* faeces; Gr. masc. n. *bios* life; N.L. neut. n. *Alectryocaccobium* A life form found in
221 chicken faceces)
222
223 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
224 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
225 species *Alectryocaccobium stercorigallinarum*. This genus has been assigned by GTDB-Tk
226 v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the
227 order *Lachnospirales* and to the family *Lachnospiraceae*.
228
229
230 **Description of *Candidatus* Alectryocaccobium stercorigallinarum sp. nov.**

231 *Candidatus* Alectryocaccobium stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus*
232 dung; L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
233
234 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
235 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
236 assigned the MAG ID ChiGjej2B2-785 and which is available via NCBI BioSample
237 SAMN15816998. The GC content of the type genome is 46.32% and the genome length is 1.5
238 Mbp.
239
240
241 **Description of *Candidatus* Alectryocaccomicrobium gen. nov.**
242 *Candidatus* Alectryocaccomicrobium (A.lec.try.o.cac.co.mi.cro'bi.um. Gr. neut. n. *alektryon*
243 chicken; Gr. fem. n. *kakke* faeces; N.L. neut. n. *microbium* a microbe; N.L. neut. n.
244 *Alectryocaccomicrobium* A microbe found in chicken faceces)
245
246 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
247 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
248 species *Alectryocaccomicrobium excrementavium*. This genus has been assigned by GTDB-Tk
249 v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the
250 order *Christensenellales* and to the family *CAG-74*.
251
252
253 **Description of *Candidatus* Alectryocaccomicrobium excrementavium sp. nov.**
254 *Candidatus* Alectryocaccomicrobium excrementavium (ex.cre.ment.a'vi.um. L. neut. n.
255 *excrementum* excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
256
257 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
258 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
259 assigned the MAG ID 13766 and which is available via NCBI BioSample SAMN15816965. The
260 GC content of the type genome is 59.90% and the genome length is 3.0 Mbp.
261
262
263 **Description of *Candidatus* Alistipes avicola sp. nov.**
264 *Candidatus* Alistipes avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. -*cola* inhabitant of; N.L. n.
265 *avicola* inhabitant of birds)
266
267 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
268 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
269 assigned the MAG ID CHK169-11906 and which is available via NCBI BioSample
270 SAMN15816659. The GC content of the type genome is 53.79% and the genome length is 1.6
271 Mbp.
272
273
274 **Description of *Candidatus* Alistipes avistercoris sp. nov.**
275 *Candidatus* Alistipes avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung;
276 N.L. gen. n. *avistercoris* of bird faeces)

277
278   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
279   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
280   assigned the MAG ID 653 and which is available via NCBI BioSample SAMN15816855. This is
281   a new name for the alphanumeric GTDB species sp000434235. The GC content of the type
282   genome is 62.33% and the genome length is 2.4 Mbp.
283
284
285   **Description of *Candidatus* Alistipes cottocaccae sp. nov.**
286   *Candidatus* Alistipes cottocaccae (cot.to.cac'cae. Gr. masc. n. *kottos* chicken Gr. fem. n. *kakke*
287   faeces; N.L. gen. n. *cottocaccae* of chicken faeces)
288
289   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
290   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
291   assigned the MAG ID ChiBcec16-1783 and which is available via NCBI BioSample
292   SAMN15816853. This is a new name for the alphanumeric GTDB species sp002161445. The
293   GC content of the type genome is 60.94% and the genome length is 2.4 Mbp.
294
295
296   **Description of *Candidatus* Alistipes excrementavium sp. nov.**
297   *Candidatus* Alistipes excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum* excrement;
298   L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
299
300   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
301   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
302   assigned the MAG ID CHK15-232 and which is available via NCBI BioSample
303   SAMN15816809. This is a new name for the alphanumeric GTDB species sp900021155. The
304   GC content of the type genome is 61.18% and the genome length is 2.2 Mbp.
305
306
307   **Description of *Candidatus* Alistipes excrementigallinarum sp. nov.**
308   *Candidatus* Alistipes excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum*
309   excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)
310
311   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
312   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
313   assigned the MAG ID CHK106-249 and which is available via NCBI BioSample
314   SAMN15816875. The GC content of the type genome is 63.33% and the genome length is 2.3
315   Mbp.
316
317
318   **Description of *Candidatus* Alistipes excrementipullorum sp. nov.**
319   *Candidatus* Alistipes excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
320   excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
321   chicken excrement)
322

323 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
324 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
325 assigned the MAG ID ChiHjej8B7-9065 and which is available via NCBI BioSample
326 SAMN15816799. This is a new name for the alphanumeric GTDB species. The GC content of
327 the type genome is 56.25% and the genome length is 1.7 Mbp.
328
329
330 **Description of *Candidatus* Alistipes faecavium sp. nov.**
331 *Candidatus* Alistipes faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n. *avis*
332 bird; N.L. gen. n. *faecavium* of bird faeces)
333
334 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
335 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
336 assigned the MAG ID ChiGjej2B2-19477 and which is available via NCBI BioSample
337 SAMN15816800. The GC content of the type genome is 62.24% and the genome length is 2.3
338 Mbp.
339
340
341 **Description of *Candidatus* Alistipes faecigallinarum sp. nov.**
342 *Candidatus* Alistipes faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
343 fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of chicken faeces)
344
345 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
346 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
347 assigned the MAG ID 6451 and which is available via NCBI BioSample SAMN15816915. The
348 GC content of the type genome is 61.37% and the genome length is 2.2 Mbp.
349
350
351 **Description of *Candidatus* Alistipes intestinigallinarum sp. nov.**
352 *Candidatus* Alistipes intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut; L.
353 fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
354
355 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
356 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
357 assigned the MAG ID 5134 and which is available via NCBI BioSample SAMN15816708. The
358 GC content of the type genome is 59.58% and the genome length is 2.7 Mbp.
359
360
361 **Description of *Candidatus* Alistipes intestinipullorum sp. nov.**
362 *Candidatus* Alistipes intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc.
363 n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
364
365 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
366 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
367 assigned the MAG ID ChiGjej2B2-5998 and which is available via NCBI BioSample

368 SAMN15816759. The GC content of the type genome is 59.58% and the genome length is 2.3
369 Mbp.
370
371
372 **Description of *Candidatus* Alistipes merdavium sp. nov.**
373 *Candidatus* Alistipes merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
374 N.L. gen. n. *merdavium* of bird faeces)
375
376 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
377 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
378 assigned the MAG ID ChiBcolR5-1230 and which is available via NCBI BioSample
379 SAMN15816813. This is a new name for the alphanumeric GTDB species sp900544265. The
380 GC content of the type genome is 63.44% and the genome length is 2.2 Mbp.
381
382
383 **Description of *Candidatus* Alistipes merdigallinarum sp. nov.**
384 *Candidatus* Alistipes merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem. n.
385 *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
386
387 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
388 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
389 assigned the MAG ID 2432 and which is available via NCBI BioSample SAMN15816893.
390 Although GTDB has assigned this species to the genus it calls Alistipes_A , this genus
391 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
392 have used the current validly published name for the genus. The GC content of the type genome
393 is 49.96% and the genome length is 2.2 Mbp.
394
395
396 **Description of *Candidatus* Alistipes merdipullorum sp. nov.**
397 *Candidatus* Alistipes merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
398 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
399
400 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
401 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
402 assigned the MAG ID ChiHjej9B8-3741 and which is available via NCBI BioSample
403 SAMN15816807. This is a new name for the alphanumeric GTDB species sp900546065. The
404 GC content of the type genome is 57.66% and the genome length is 2.3 Mbp.
405
406
407 **Description of *Candidatus* Alistipes pullicola sp. nov.**
408 *Candidatus* Alistipes pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
409 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
410
411 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
412 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
413 assigned the MAG ID ChiHjej10B9-11434 and which is available via NCBI BioSample

414   SAMN15816929. This is a new name for the alphanumeric GTDB species sp900546005.
415   Although GTDB has assigned this species to the genus it calls Alistipes_A , this genus
416   designation cannot be incorporated into a well-formed binomial, so in naming this species, we
417   have used the current validly published name for the genus. The GC content of the type genome
418   is 52.02% and the genome length is 1.9 Mbp.
419
420
421   **Description of *Candidatus* Alistipes pullistercoris sp. nov.**
422   *Candidatus* Alistipes pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L. neut.
423   n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
424
425   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
426   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
427   assigned the MAG ID 3244 and which is available via NCBI BioSample SAMN15816930. This
428   is a new name for the alphanumeric GTDB species sp900240235. Although GTDB has assigned
429   this species to the genus it calls Alistipes_A , this genus designation cannot be incorporated into
430   a well-formed binomial, so in naming this species, we have used the current validly published
431   name for the genus. The GC content of the type genome is 56.88% and the genome length is 2.0
432   Mbp.
433
434
435   **Description of *Candidatus* Alistipes stercoravium sp. nov.**
436   *Candidatus* Alistipes stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis* bird;
437   N.L. gen. n. *stercoravium* of bird faeces)
438
439   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
440   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
441   assigned the MAG ID ChiHjej8B7-9257 and which is available via NCBI BioSample
442   SAMN15816640. The GC content of the type genome is 61.39% and the genome length is 2.0
443   Mbp.
444
445
446   **Description of *Candidatus* Alistipes stercorigallinarum sp. nov.**
447   *Candidatus* Alistipes stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L. fem.
448   n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
449
450   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
451   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
452   assigned the MAG ID ChiHcolR4-13572 and which is available via NCBI BioSample
453   SAMN15816817. This is a new name for the alphanumeric GTDB species sp900542505. The
454   GC content of the type genome is 62.42% and the genome length is 2.2 Mbp.
455
456
457   **Description of *Candidatus* Alistipes stercoripullorum sp. nov.**
458   *Candidatus* Alistipes stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n.
459   *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)

460
461 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
462 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
463 assigned the MAG ID ChiBcec8-6454 and which is available via NCBI BioSample
464 SAMN15816818. This is a new name for the alphanumeric GTDB species sp006542685. The
465 GC content of the type genome is 62.87% and the genome length is 2.4 Mbp.
466
467
468 **Description of *Candidatus* Anaerobiospirillum merdipullorum sp. nov.**
469 *Candidatus* Anaerobiospirillum merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L.
470 masc. n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
471
472 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
473 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
474 assigned the MAG ID 687 and which is available via NCBI BioSample SAMN15816911.
475 Although GTDB has assigned this species to the genus it calls Anaerobiospirillum_A , this genus
476 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
477 have used the current validly published name for the genus. The GC content of the type genome
478 is 49.84% and the genome length is 2.0 Mbp.
479
480
481 **Description of *Candidatus* Anaerobiospirillum pullicola sp. nov.**
482 *Candidatus* Anaerobiospirillum pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L.
483 suff. *-cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
484
485 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
486 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
487 assigned the MAG ID 378 and which is available via NCBI BioSample SAMN15816727. The
488 GC content of the type genome is 52.37% and the genome length is 3.9 Mbp.
489
490
491 **Description of *Candidatus* Anaerobiospirillum pullistercoris sp. nov.**
492 *Candidatus* Anaerobiospirillum pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young
493 chicken; L. neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
494
495 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
496 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
497 assigned the MAG ID USASDec5-558 and which is available via NCBI BioSample
498 SAMN15816730. The GC content of the type genome is 49.01% and the genome length is 3.3
499 Mbp.
500
501
502 **Description of *Candidatus* Anaerobiospirillum stercoravium sp. nov.**
503 *Candidatus* Anaerobiospirillum stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem.
504 n. *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
505

506 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
507 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
508 assigned the MAG ID USASDcec2-551 and which is available via NCBI BioSample
509 SAMN15816778. The GC content of the type genome is 56.27% and the genome length is 2.9
510 Mbp.
511
512
513 **Description of *Candidatus* Anaerobutyricum avicola sp. nov.**
514 *Candidatus* Anaerobutyricum avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. -*cola* inhabitant of;
515 N.L. n. *avicola* inhabitant of birds)
516
517 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
518 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
519 assigned the MAG ID ChiSxjej6B18-9268 and which is available via NCBI BioSample
520 SAMN15816760. The GC content of the type genome is 50.20% and the genome length is 2.5
521 Mbp.
522
523
524 **Description of *Candidatus* Anaerobutyricum faecale sp. nov.**
525 *Candidatus* Anaerobutyricum faecale (fae.ca'le. L. neut. adj. *faecale* of faeces)
526
527 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
528 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
529 assigned the MAG ID CHK182-24705 and which is available via NCBI BioSample
530 SAMN15816814. This is a new name for the alphanumeric GTDB species sp002161065. The
531 GC content of the type genome is 48.07% and the genome length is 2.8 Mbp.
532
533
534 **Description of *Candidatus* Anaerobutyricum stercoripullorum sp. nov.**
535 *Candidatus* Anaerobutyricum stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
536 masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
537
538 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
539 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
540 assigned the MAG ID ChiSxjej3B15-1167 and which is available via NCBI BioSample
541 SAMN15816729. The GC content of the type genome is 52.36% and the genome length is 2.3
542 Mbp.
543
544
545 **Description of *Candidatus* Anaerobutyricum stercoris sp. nov.**
546 *Candidatus* Anaerobutyricum stercoris (ster'co.ris. L. gen. n. *stercoris* of dung, excrement)
547
548 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
549 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
550 assigned the MAG ID CHK179-28034 and which is available via NCBI BioSample

551 SAMN15816848. This is a new name for the alphanumeric GTDB species sp900016875. The
552 GC content of the type genome is 47.36% and the genome length is 3.0 Mbp.
553
554
555 **Description of *Candidatus* Anaerofilum excrementigallinarum sp. nov.**
556 *Candidatus* Anaerofilum excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
557 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
558 excrement)
559
560 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
561 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
562 assigned the MAG ID 3951 and which is available via NCBI BioSample SAMN15816720. The
563 GC content of the type genome is 61.37% and the genome length is 2.5 Mbp.
564
565
566 **Description of *Candidatus* Anaerofilum faecale sp. nov.**
567 *Candidatus* Anaerofilum faecale (fae.ca'le. L. neut. adj. *faecale* of faeces)
568
569 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
570 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
571 assigned the MAG ID ChiGjej6B6-374 and which is available via NCBI BioSample
572 SAMN15816865. This is a new name for the alphanumeric GTDB species sp002160015. The
573 GC content of the type genome is 63.11% and the genome length is 2.3 Mbp.
574
575
576 **Description of *Candidatus* Anaeromassilibacillus stercoravium sp. nov.**
577 *Candidatus* Anaeromassilibacillus stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L.
578 fem. n. *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
579
580 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
581 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
582 assigned the MAG ID ChiSjej5B23-4625 and which is available via NCBI BioSample
583 SAMN15816824. This is a new name for the alphanumeric GTDB species sp002159845. The
584 GC content of the type genome is 54.17% and the genome length is 2.2 Mbp.
585
586
587 **Description of *Candidatus* Anaerostipes avicola sp. nov.**
588 *Candidatus* Anaerostipes avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L.
589 n. *avicola* inhabitant of birds)
590
591 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
592 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
593 assigned the MAG ID CHK189-27985 and which is available via NCBI BioSample
594 SAMN15816576. The GC content of the type genome is 43.22% and the genome length is 2.5
595 Mbp.
596

597

Description of *Candidatus* Anaerostipes avistercoris sp. nov.

Candidatus Anaerostipes avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
dung; N.L. gen. n. *avistercoris* of bird faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with
genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
assigned the MAG ID ChiSjej3B21-8574 and which is available via NCBI BioSample
SAMN15816634. The GC content of the type genome is 44.43% and the genome length is 2.6
Mbp.

Description of *Candidatus* Anaerostipes excrementavium sp. nov.

Candidatus Anaerostipes excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with
genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
assigned the MAG ID CHK191-13928 and which is available via NCBI BioSample
SAMN15816615. The GC content of the type genome is 41.56% and the genome length is 2.7
Mbp.

Description of *Candidatus* Anaerotignum merdipullorum sp. nov.

Candidatus Anaerotignum merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc.
n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with
genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
assigned the MAG ID CHK190-6203 and which is available via NCBI BioSample
SAMN15816613. The GC content of the type genome is 44.75% and the genome length is 2.2
Mbp.

Description of *Candidatus* Anaerotruncus excrementipullorum sp. nov.

Candidatus Anaerotruncus excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
excrementum excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
young chicken excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with
genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
assigned the MAG ID CHK188-5543 and which is available via NCBI BioSample
SAMN15816616. The GC content of the type genome is 64.05% and the genome length is 1.9
Mbp.

643   **Description of *Candidatus* Aphodenecus gen. nov.**
644   *Candidatus* Aphodenecus (Aph.o.d.en.e'cus. Gr. fem. n. *aphodos* dung; Gr. masc. *enoikos*
645   inhabitant; N.L. masc. n. *Aphodenecus* a microbe associated with faeces)
646
647   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
648   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
649   species *Aphodenecus pullistercoris*. This is a name for the alphanumeric GTDB genus Spiro-01.
650   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
651   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Sphaerochaetales* and to the family
652   *Sphaerochaetaceae.*
653
654
655   **Description of *Candidatus* Aphodenecus pullistercoris sp. nov.**
656   *Candidatus* Aphodenecus pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
657   neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
658
659   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
660   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
661   assigned the MAG ID 11167 and which is available via NCBI BioSample SAMN15817123. The
662   GC content of the type genome is 59.34% and the genome length is 2.0 Mbp.
663
664
665   **Description of *Candidatus* Aphodocola gen. nov.**
666   *Candidatus* Aphodocola (Aph.o.do'co.la. Gr. fem. n. *aphodos* dung; L. suff. *-cola* inhabitant of;
667   N.L. fem. n. *Aphodocola* a microbe associated with faeces)
668
669   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
670   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
671   species *Aphodocola excrementigallinarum*. This is a name for the alphanumeric GTDB genus
672   CAG-594. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
673   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-433.*
674
675
676   **Description of *Candidatus* Aphodocola excrementigallinarum sp. nov.**
677   *Candidatus* Aphodocola excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
678   *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
679   excrement)
680
681   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
682   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
683   assigned the MAG ID CHK193-30670 and which is available via NCBI BioSample
684   SAMN15817049. The GC content of the type genome is 27.74% and the genome length is 1.2
685   Mbp.
686
687
688   **Description of *Candidatus* Aphodomonas gen. nov.**

689 *Candidatus* Aphodomonas (Aph.o.d.omo'nas. Gr. fem. n. *aphodos* dung; L. fem. n. *monas* a
690 monad; N.L. fem. n. *Aphodomonas* a microbe associated with faeces)
691
692 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
693 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
694 species *Aphodomonas merdavium*. This is a name for the alphanumeric GTDB genus SFFS01.
695 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
696 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family *CAG-*
697 *74.*
698
699
700 **Description of *Candidatus* Aphodomonas merdavium sp. nov.**
701 *Candidatus* Aphodomonas merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
702 bird; N.L. gen. n. *merdavium* of bird faeces)
703
704 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
705 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
706 assigned the MAG ID ChiGjej2B2-35035 and which is available via NCBI BioSample
707 SAMN15817117. The GC content of the type genome is 59.45% and the genome length is 2.1
708 Mbp.
709
710
711 **Description of *Candidatus* Aphodomorpha gen. nov.**
712 *Candidatus* Aphodomorpha (Aph.o.d.o.mor'pha. Gr. fem. n. *aphodos* dung; Gr. fem. n. *morphe* a
713 form, shape; N.L. fem. n. *Aphodomorpha* a microbe associated with faeces)
714
715 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
716 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
717 species *Aphodomorpha intestinavium*. This is a name for the alphanumeric GTDB genus
718 UMGS1241. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
719 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family
720 *CAG-138.*
721
722
723 **Description of *Candidatus* Aphodomorpha intestinavium sp. nov.**
724 *Candidatus* Aphodomorpha intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem.
725 n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
726
727 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
728 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
729 assigned the MAG ID ChiGjej2B2-16831 and which is available via NCBI BioSample
730 SAMN15817204. This is a new name for the alphanumeric GTDB species sp900550525. The
731 GC content of the type genome is 68.13% and the genome length is 1.6 Mbp.
732
733
734 **Description of *Candidatus* Aphodoplasma gen. nov.**

735 *Candidatus* Aphodoplasma (Aph.o.d.o.plas'ma. Gr. fem. n. *aphodos* dung; Gr. neut. n. *plasma* a
736 form; N.L. neut. n. *Aphodoplasma* a microbe associated with faeces)
737
738 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
739 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
740 species *Aphodoplasma excrementigallinarum*. This is a name for the alphanumeric GTDB genus
741 UMGS1253. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
742 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Monoglobales_A* and to the family
743 *UMGS1253*.
744
745
746 **Description of *Candidatus* Aphodoplasma excrementigallinarum sp. nov.**
747 *Candidatus* Aphodoplasma excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
748 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
749 excrement)
750
751 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
752 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
753 assigned the MAG ID 4920 and which is available via NCBI BioSample SAMN15817155. The
754 GC content of the type genome is 54.59% and the genome length is 1.8 Mbp.
755
756
757 **Description of *Candidatus* Aphodosoma gen. nov.**
758 *Candidatus* Aphodosoma (Aph.o.d.o.so'ma. Gr. fem. n. *aphodos* dung; Gr. neut. n. *soma* a body;
759 N.L. neut. n. *Aphodosoma* a microbe associated with faeces)
760
761 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
762 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
763 species *Aphodosoma intestinipullorum*. This is a name for the alphanumeric GTDB genus
764 SFVR01. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
765 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family
766 *Paludibacteraceae*.
767
768
769 **Description of *Candidatus* Aphodosoma intestinipullorum sp. nov.**
770 *Candidatus* Aphodosoma intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
771 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
772
773 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
774 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
775 assigned the MAG ID 3924 and which is available via NCBI BioSample SAMN15817132. The
776 GC content of the type genome is 52.56% and the genome length is 2.4 Mbp.
777
778
779 **Description of *Candidatus* Aphodousia gen. nov.**

780 *Candidatus* Aphodousia (Aph.o.d.ou'si.a. Gr. fem. n. *aphodos* dung; Gr. fem. n. *ousia* an
781 essence; N.L. fem. n. *Aphodousia* a microbe associated with faeces)
782
783 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
784 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
785 species *Aphodousia faecavium*. This is a name for the alphanumeric GTDB genus CAG-521.
786 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
787 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Burkholderiales* and to the family
788 *Burkholderiaceae.*
789
790
791 **Description of *Candidatus* Aphodousia faecalis sp. nov.**
792 *Candidatus* Aphodousia faecalis (fae.ca'lis. L. fem. adj. *faecalis* of faeces)
793
794 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
795 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
796 assigned the MAG ID ChiW13-1064 and which is available via NCBI BioSample
797 SAMN15817170. This is a new name for the alphanumeric GTDB species sp000437635. The
798 GC content of the type genome is 47.35% and the genome length is 1.7 Mbp.
799
800
801 **Description of *Candidatus* Aphodousia faecavium sp. nov.**
802 *Candidatus* Aphodousia faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
803 *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
804
805 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
806 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
807 assigned the MAG ID 10345 and which is available via NCBI BioSample SAMN15817126. The
808 GC content of the type genome is 48.23% and the genome length is 1.7 Mbp.
809
810
811 **Description of *Candidatus* Aphodousia faecigallinarum sp. nov.**
812 *Candidatus* Aphodousia faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;
813 L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
814
815 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
816 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
817 assigned the MAG ID 7463 and which is available via NCBI BioSample SAMN15817137. The
818 GC content of the type genome is 48.37% and the genome length is 1.5 Mbp.
819
820
821 **Description of *Candidatus* Aphodousia faecipullorum sp. nov.**
822 *Candidatus* Aphodousia faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
823 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
824

825 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
826 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
827 assigned the MAG ID CHK135-12538 and which is available via NCBI BioSample
828 SAMN15817146. The GC content of the type genome is 48.08% and the genome length is 1.8
829 Mbp.
830
831
832 **Description of *Candidatus* Aphodousia gallistercoris sp. nov.**
833 *Candidatus* Aphodousia gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
834 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
835
836 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
837 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
838 assigned the MAG ID CHK121-301 and which is available via NCBI BioSample
839 SAMN15817147. The GC content of the type genome is 52.58% and the genome length is 1.8
840 Mbp.
841
842
843 **Description of *Candidatus* Aphodovivens gen. nov.**
844 *Candidatus* Aphodovivens (Aph.o.d.o.viv'ens. Gr. fem. n. *aphodos* dung; N.L. pres. part. *vivens*
845 living; N.L. fem. n. *Aphodovivens* a microbe associated with faeces)
846
847 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
848 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
849 species *Aphodovivens avicola*. This is a name for the alphanumeric GTDB genus UMGS1293.
850 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
851 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Coriobacteriales* and to the family
852 *Eggerthellaceae*.
853
854
855 **Description of *Candidatus* Aphodovivens avicola sp. nov.**
856 *Candidatus* Aphodovivens avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. -*cola* inhabitant of;
857 N.L. n. *avicola* inhabitant of birds)
858
859 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
860 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
861 assigned the MAG ID ChiGjej6B6-21069 and which is available via NCBI BioSample
862 SAMN15817067. The GC content of the type genome is 65.54% and the genome length is 2.2
863 Mbp.
864
865
866 **Description of *Candidatus* Aphodovivens avistercoris sp. nov.**
867 *Candidatus* Aphodovivens avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
868 dung; N.L. gen. n. *avistercoris* of bird faeces)
869

870 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
871 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
872 assigned the MAG ID ChiGjej5B5-3278 and which is available via NCBI BioSample
873 SAMN15817093. The GC content of the type genome is 66.86% and the genome length is 2.4
874 Mbp.
875
876
877 **Description of *Candidatus* Aphodovivens excrementavium sp. nov.**
878 *Candidatus* Aphodovivens excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
879 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
880
881 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
882 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
883 assigned the MAG ID ChiGjej2B2-30709 and which is available via NCBI BioSample
884 SAMN15817109. The GC content of the type genome is 58.74% and the genome length is 2.1
885 Mbp.
886
887
888 **Description of *Candidatus* Aquabacterium excrementipullorum sp. nov.**
889 *Candidatus* Aquabacterium excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
890 *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
891 young chicken excrement)
892
893 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
894 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
895 assigned the MAG ID ChiHile3-4534 and which is available via NCBI BioSample
896 SAMN15816783. The GC content of the type genome is 67.11% and the genome length is 4.7
897 Mbp.
898
899
900 **Description of *Candidatus* Atopostipes pullistercoris sp. nov.**
901 *Candidatus* Atopostipes pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
902 neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
903
904 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
905 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
906 assigned the MAG ID CHK169-4300 and which is available via NCBI BioSample
907 SAMN15816688. The GC content of the type genome is 34.84% and the genome length is 1.9
908 Mbp.
909
910
911 **Description of *Candidatus* Avacholeplasma gen. nov.**
912 *Candidatus* Avacholeplasma (Av.a.cho.le.plas'ma. L. fem. n. *avis* bird; N.L. neut. n.
913 *Acholeplasma* a genus name; N.L. neut n. *Aviacholeplasma* a genus related to the genus
914 *Acholeplasma* but distinct from it and found in poultry)
915

916   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
917   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
918   species *Avacholeplasma faecigallinarum.* This genus has been assigned by GTDB-Tk v1.3.0
919   working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
920   *Acholeplasmatales* and to the family *Anaeroplasmataceae.*
921
922
923   **Description of *Candidatus* Avacholeplasma faecigallinarum sp. nov.**
924   *Candidatus* Avacholeplasma faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis*
925   excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
926
927   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
928   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
929   assigned the MAG ID 3263 and which is available via NCBI BioSample SAMN15816972. The
930   GC content of the type genome is 29.88% and the genome length is 1.3 Mbp.
931
932
933   **Description of *Candidatus* Avacidaminococcus gen. nov.**
934   *Candidatus* Avacidaminococcus (Av.a.cid.a.mi.no.coc'cus. L. fem. n. *avis* bird; N.L. masc. n.
935   *Acidaminococcus* a genus name; N.L. masc. n. *Avacidaminococcus* a genus related to the genus
936   *Acidaminococcus* but distinct from it and found in poultry)
937
938   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
939   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
940   species *Avacidaminococcus intestinavium.* This genus has been assigned by GTDB-Tk v1.3.0
941   working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
942   *Acidaminococcales* and to the family *Acidaminococcaceae.*
943
944
945   **Description of *Candidatus* Avacidaminococcus intestinavium sp. nov.**
946   *Candidatus* Avacidaminococcus intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L.
947   fem. n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
948
949   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
950   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
951   assigned the MAG ID CHK160-1198 and which is available via NCBI BioSample
952   SAMN15816987. The GC content of the type genome is 37.45% and the genome length is 1.6
953   Mbp.
954
955
956   **Description of *Candidatus* Avamphibacillus gen. nov.**
957   *Candidatus* Avamphibacillus (Av.am.phi.ba.cil'lus. L. fem. n. *avis* bird; N.L. masc. n.
958   *Amphibacillus* a genus name; N.L. masc. n. *Avamphibacillus* a genus related to the genus
959   *Amphibacillus* but distinct from it and found in poultry)
960

961 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
962 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
963 species *Avamphibacillus intestinigallinarum*. This genus has been assigned by GTDB-Tk v1.3.0
964 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
965 *Bacillales* and to the family *Amphibacillaceae*.
966
967
968 **Description of *Candidatus* Avamphibacillus intestinigallinarum sp. nov.**
969 *Candidatus* Avamphibacillus intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum*
970 gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
971
972 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
973 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
974 assigned the MAG ID CHK125-3527 and which is available via NCBI BioSample
975 SAMN15816959. The GC content of the type genome is 36.77% and the genome length is 2.0
976 Mbp.
977
978
979 **Description of *Candidatus* Avanaerovorax gen. nov.**
980 *Candidatus* Avanaerovorax (Av.an.a.e.ro.vo'rax. L. fem. n. *avis* bird; N.L. masc. n. *Anaerovorax*
981 a genus name; N.L. masc. n. *Avanaerovorax* a genus related to the genus *Anaerovorax* but
982 distinct from it and found in poultry)
983
984 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
985 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
986 species *Avanaerovorax faecigallinarum*. This genus has been assigned by GTDB-Tk v1.3.0
987 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
988 *Peptostreptococcales* and to the family *Anaerovoracaceae*.
989
990
991 **Description of *Candidatus* Avanaerovorax faecigallinarum sp. nov.**
992 *Candidatus* Avanaerovorax faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis*
993 excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
994
995 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
996 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
997 assigned the MAG ID Gambia13-1450 and which is available via NCBI BioSample
998 SAMN15816994. The GC content of the type genome is 48.68% and the genome length is 1.8
999 Mbp.
1000
1001
1002 **Description of *Candidatus* Aveggerthella gen. nov.**
1003 *Candidatus* Aveggerthella (Av.eg.ger.thel'la. L. fem. n. *avis* bird; N.L. fem. n. *Eggerthella* a
1004 genus name; N.L. fem. n. *Aveggerthella* a genus related to the genus *Eggerthella* but distinct
1005 from it and found in poultry)
1006

1007 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1008 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1009 species *Avieggerthella excrementigallinarum*. This genus has been assigned by GTDB-Tk v1.3.0
1010 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
1011 *Coriobacteriales* and to the family *Eggerthellaceae*.

1012
1013

1014 **Description of *Candidatus* Aveggerthella excrementigallinarum sp. nov.**
1015 *Candidatus* Aveggerthella excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
1016 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
1017 excrement)

1018
1019 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1020 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1021 assigned the MAG ID ChiGjej4B4-3573 and which is available via NCBI BioSample
1022 SAMN15816976. The GC content of the type genome is 65.93% and the genome length is 2.0
1023 Mbp.

1024
1025

1026 **Description of *Candidatus* Aveggerthella stercoripullorum sp. nov.**
1027 *Candidatus* Aveggerthella stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
1028 masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
1029
1030 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1031 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1032 assigned the MAG ID ChiGjej1B1-2707 and which is available via NCBI BioSample
1033 SAMN15816950. The GC content of the type genome is 61.50% and the genome length is 2.1
1034 Mbp.

1035
1036

1037 **Description of *Candidatus* Avelusimicrobium gen. nov.**
1038 *Candidatus* Avelusimicrobium (Av.e.lu.si.mi.cro'bi.um. L. fem. n. *avis* bird; N.L. neut. n.
1039 *Elusimicrobium* a genus name; N.L. neut. n. *Avelusimicrobium* a genus related to the genus
1040 *Elusimicrobium* but distinct from it and found in poultry)

1041
1042 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1043 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1044 species *Avielusimicrobium excrementipullorum*. This genus has been assigned by GTDB-Tk
1045 v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the
1046 order *Elusimicrobiales* and to the family *Elusimicrobiaceae*.

1047
1048

1049 **Description of *Candidatus* Avelusimicrobium excrementipullorum sp. nov.**
1050 *Candidatus* Avelusimicrobium excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
1051 *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
1052 young chicken excrement)

1053
1054 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1055 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1056 assigned the MAG ID CHK136-6324 and which is available via NCBI BioSample
1057 SAMN15817002. The GC content of the type genome is 53.46% and the genome length is 1.3
1058 Mbp.
1059
1060
1061 **Description of *Candidatus* Avibacteroides gen. nov.**
1062 *Candidatus* Avibacteroides (A.vi.bac.te.ro'i.des. L. fem. n. *avis* bird; N.L. masc. n. *Bacteroides* a
1063 genus name; N.L. masc. n. *Avibacteroides* a genus related to the genus *Bacteroides* but distinct
1064 from it and found in poultry)
1065
1066 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1067 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1068 species *Avibacteroides excrementipullorum.* This genus has been assigned by GTDB-Tk v1.3.0
1069 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
1070 *Bacteroidales* and to the family *Bacteroidaceae.*
1071
1072
1073 **Description of *Candidatus* Avibacteroides avistercoris sp. nov.**
1074 *Candidatus* Avibacteroides avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
1075 dung; N.L. gen. n. *avistercoris* of bird faeces)
1076
1077 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1078 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1079 assigned the MAG ID MalCec1-1739 and which is available via NCBI BioSample
1080 SAMN15816974. The GC content of the type genome is 53.14% and the genome length is 2.2
1081 Mbp.
1082
1083
1084 **Description of *Candidatus* Avibacteroides excrementipullorum sp. nov.**
1085 *Candidatus* Avibacteroides excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
1086 *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
1087 young chicken excrement)
1088
1089 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1090 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1091 assigned the MAG ID ChiHjej12B11-16860 and which is available via NCBI BioSample
1092 SAMN15816958. The GC content of the type genome is 47.79% and the genome length is 2.2
1093 Mbp.
1094
1095
1096 **Description of *Candidatus* Avibacteroides faecavium sp. nov.**
1097 *Candidatus* Avibacteroides faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
1098 *avis* bird; N.L. gen. n. *faecavium* of bird faeces)

1099
1100   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1101   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1102   assigned the MAG ID 3702 and which is available via NCBI BioSample SAMN15816980. The
1103   GC content of the type genome is 55.42% and the genome length is 2.1 Mbp.
1104
1105
1106   **Description of *Candidatus* Avichristensenella gen. nov.**
1107   *Candidatus* Avichristensenella (A.vi.chris.ten.sen.el'la. L. fem. n. *avis* bird; N.L. fem. n.
1108   *Christensenella* a genus name; N.L. fem. n. *Avichristensenella* a genus related to the genus
1109   *Christensenella* but distinct from it and found in poultry)
1110
1111   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1112   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1113   species *Avichristensenella intestinipullorum.* This genus has been assigned by GTDB-Tk v1.3.0
1114   working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
1115   *Christensenellales* and to the family *CAG-74.*
1116
1117
1118   **Description of *Candidatus* Avichristensenella intestinipullorum sp. nov.**
1119   *Candidatus* Avichristensenella intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum*
1120   gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young
1121   chickens)
1122
1123   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1124   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1125   assigned the MAG ID ChiHile30-977 and which is available via NCBI BioSample
1126   SAMN15816947. The GC content of the type genome is 63.80% and the genome length is 2.3
1127   Mbp.
1128
1129
1130   **Description of *Candidatus* Avidehalobacter gen. nov.**
1131   *Candidatus* Avidehalobacter (A.vi.de.ha.lo.bac'ter. L. fem. n. *avis* bird; N.L. masc. n.
1132   *Dehalobacter* a genus name; N.L. masc. n. *Avidehalobacter* a genus related to the genus
1133   *Dehalobacter* but distinct from it and found in poultry)
1134
1135   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1136   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1137   species *Avidehalobacter gallistercoris.* This genus has been assigned by GTDB-Tk v1.3.0
1138   working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
1139   *UBA4068* and to the family *UBA5755.*
1140
1141
1142   **Description of *Candidatus* Avidehalobacter gallistercoris sp. nov.**
1143   *Candidatus* Avidehalobacter gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
1144   *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)

1145
1146 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1147 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1148 assigned the MAG ID 2830 and which is available via NCBI BioSample SAMN15816981. The
1149 GC content of the type genome is 52.20% and the genome length is 1.4 Mbp.
1150
1151
1152 **Description of *Candidatus* Avidesulfovibrio gen. nov.**
1153 *Candidatus* Avidesulfovibrio (A.vi.de.sul.fo.vi'bri.o. L. fem. n. *avis* bird; N.L. masc. n.
1154 *Desulfovibrio* a genus name; N.L. masc. n. *Avidesulfovibrio* a genus related to the genus
1155 *Desulfovibrio* but distinct from it and found in poultry)
1156
1157 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1158 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1159 species *Avidesulfovibrio excrementigallinarum.* This genus has been assigned by GTDB-Tk
1160 v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the
1161 order *Desulfovibrionales* and to the family *Desulfovibrionaceae*.
1162
1163
1164 **Description of *Candidatus* Avidesulfovibrio excrementigallinarum sp. nov.**
1165 *Candidatus* Avidesulfovibrio excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
1166 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
1167 excrement)
1168
1169 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1170 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1171 assigned the MAG ID ChiHcec4-2777 and which is available via NCBI BioSample
1172 SAMN15816982. The GC content of the type genome is 60.70% and the genome length is 2.2
1173 Mbp.
1174
1175
1176 **Description of *Candidatus* Avigastranaerophilus gen. nov.**
1177 *Candidatus* Avigastranaerophilus (A.vi.gastr.an.a.e.ro'phi.lus. L. fem. n. *avis* bird; N.L. masc. n.
1178 *Gastranaerophilus* a genus name; N.L. masc. n. *Avigastranaerophilus* a genus related to the
1179 genus *Gastranaerophilus* but distinct from it and found in poultry)
1180
1181 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1182 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1183 species *Avigastranaerophilus faecigallinarum.* This genus has been assigned by GTDB-Tk
1184 v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the
1185 order *Gastranaerophilales* and to the family *Gastranaerophilaceae*.
1186
1187
1188 **Description of *Candidatus* Avigastranaerophilus faecigallinarum sp. nov.**
1189 *Candidatus* Avigastranaerophilus faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis*
1190 excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

1191
1192   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1193   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1194   assigned the MAG ID 5572 and which is available via NCBI BioSample SAMN15816968. The
1195   GC content of the type genome is 29.33% and the genome length is 2.2 Mbp.
1196
1197

1198   **Description of *Candidatus* Avilachnospira gen. nov.**
1199   *Candidatus* Avilachnospira (A.vi.lach.no.spi'ra. L. fem. n. *avis* bird; N.L. fem. n. *Lachnospira* a
1200   genus name; N.L. fem. n. *Avilachnospira* a genus related to the genus *Lachnospira* but distinct
1201   from it and found in poultry)
1202
1203   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1204   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1205   species *Avilachnospira avistercoris.* This genus has been assigned by GTDB-Tk v1.3.0 working
1206   on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
1207   *Lachnospirales* and to the family *Lachnospiraceae.*
1208
1209

1210   **Description of *Candidatus* Avilachnospira avicola sp. nov.**
1211   *Candidatus* Avilachnospira avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of;
1212   N.L. n. *avicola* inhabitant of birds)
1213
1214   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1215   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1216   assigned the MAG ID ChiHecec3B27-5021 and which is available via NCBI BioSample
1217   SAMN15816990. The GC content of the type genome is 49.15% and the genome length is 1.6
1218   Mbp.
1219
1220

1221   **Description of *Candidatus* Avilachnospira avistercoris sp. nov.**
1222   *Candidatus* Avilachnospira avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
1223   dung; N.L. gen. n. *avistercoris* of bird faeces)
1224
1225   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1226   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1227   assigned the MAG ID ChiGjej5B5-15814 and which is available via NCBI BioSample
1228   SAMN15816991. The GC content of the type genome is 50.02% and the genome length is 1.6
1229   Mbp.
1230
1231
1232   **Description of *Candidatus* Avimonoglobus gen. nov.**
1233   *Candidatus* Avimonoglobus (A.vi.mo.no.glo'bus. L. fem. n. *avis* bird; N.L. masc. n. *Monoglobus*
1234   a genus name; N.L. masc. n. *Avimonoglobus* a genus related to the genus *Monoglobus* but
1235   distinct from it and found in poultry)
1236

1237 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1238 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1239 species *Avimonoglobus intestinipullorum*. This genus has been assigned by GTDB-Tk v1.3.0
1240 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
1241 *Monoglobales_A* and to the family *UBA1381*.

1242
1243

1244 **Description of *Candidatus* Avimonoglobus intestinipullorum sp. nov.**
1245 *Candidatus* Avimonoglobus intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut;
1246 L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

1247
1248 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1249 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1250 assigned the MAG ID ChiSjej4B22-9803 and which is available via NCBI BioSample
1251 SAMN15816985. The GC content of the type genome is 51.95% and the genome length is 1.8
1252 Mbp.

1253
1254

1255 **Description of *Candidatus* Avimuribaculum gen. nov.**
1256 *Candidatus* Avimuribaculum (A.vi.mu.ri.ba'cu.lum. L. fem. n. *avis* bird; N.L. neut. n.
1257 *Muribaculum* a genus name; N.L. neut. n. *Avimuribaculum* a genus related to the genus
1258 *Muribaculum* but distinct from it and found in poultry)

1259
1260 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1261 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1262 species *Avimuribaculum pullicola*. This genus has been assigned by GTDB-Tk v1.3.0 working
1263 on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales*
1264 and to the family *Muribaculaceae*.

1265
1266

1267 **Description of *Candidatus* Avimuribaculum pullicola sp. nov.**
1268 *Candidatus* Avimuribaculum pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -
1269 *cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)

1270
1271 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1272 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1273 assigned the MAG ID ChiHecec3B27-9160 and which is available via NCBI BioSample
1274 SAMN15816969. The GC content of the type genome is 47.58% and the genome length is 2.2
1275 Mbp.

1276
1277

1278 **Description of *Candidatus* Avipropionibacterium gen. nov.**
1279 *Candidatus* Avipropionibacterium (A.vi.pro.pi.o.ni.bac.te'ri.um. L. fem. n. *avis* bird; N.L. neut.
1280 n. *Propionibacterium* a genus name; N.L. neut. n. *Avipropionibacterium* a genus related to the
1281 genus *Propionibacterium* but distinct from it and found in poultry)
1282

1283 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1284 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1285 species *Avipropionibacterium avicola.* This genus has been assigned by GTDB-Tk v1.3.0
1286 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
1287 *Propionibacteriales* and to the family *Propionibacteriaceae.*
1288
1289
1290 **Description of *Candidatus* Avipropionibacterium avicola sp. nov.**
1291 *Candidatus* Avipropionibacterium avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola*
1292 inhabitant of; N.L. n. *avicola* inhabitant of birds)
1293
1294 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1295 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1296 assigned the MAG ID ChiGjej1B1-24693 and which is available via NCBI BioSample
1297 SAMN15816979. The GC content of the type genome is 69.14% and the genome length is 3.2
1298 Mbp.
1299
1300
1301 **Description of *Candidatus* Avirikenella gen. nov.**
1302 *Candidatus* Avirikenella (A.vi.ri.ke.nel'la. L. fem. n. *avis* bird; N.L. fem. n. *Rikenella* a genus
1303 name; N.L. fem. n. *Avirikenella* a genus related to the genus *Rikenella* but distinct from it and
1304 found in poultry)
1305
1306 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1307 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1308 species *Avirikenella pullistercoris.* This genus has been assigned by GTDB-Tk v1.3.0 working
1309 on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales*
1310 and to the family *Rikenellaceae.*
1311
1312
1313 **Description of *Candidatus* Avirikenella pullistercoris sp. nov.**
1314 *Candidatus* Avirikenella pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
1315 neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
1316
1317 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1318 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1319 assigned the MAG ID 9321 and which is available via NCBI BioSample SAMN15816960. The
1320 GC content of the type genome is 41.91% and the genome length is 1.9 Mbp.
1321
1322
1323 **Description of *Candidatus* Avisuccinivibrio gen. nov.**
1324 *Candidatus* Avisuccinivibrio (A.vi.suc.ci.ni.vi'bri.o. L. fem. n. *avis* bird; N.L. masc. n.
1325 *Succinivibrio* a genus name; N.L. masc. n. *Avisuccinivibrio* a genus related to the genus
1326 *Succinivibrio* but distinct from it and found in poultry)
1327

1328 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1329 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1330 species *Avisuccinivibrio stercorigallinarum*. This genus has been assigned by GTDB-Tk v1.3.0
1331 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
1332 *Enterobacterales* and to the family *Succinivibrionaceae*.
1333
1334

1335 **Description of *Candidatus* Avisuccinivibrio pullicola sp. nov.**
1336 *Candidatus* Avisuccinivibrio pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -
1337 *cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
1338
1339 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1340 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1341 assigned the MAG ID 3820 and which is available via NCBI BioSample SAMN15816999. The
1342 GC content of the type genome is 55.94% and the genome length is 2.4 Mbp.
1343
1344

1345 **Description of *Candidatus* Avisuccinivibrio stercorigallinarum sp. nov.**
1346 *Candidatus* Avisuccinivibrio stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung;
1347 L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
1348
1349 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1350 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1351 assigned the MAG ID 17213 and which is available via NCBI BioSample SAMN15817000. The
1352 GC content of the type genome is 54.49% and the genome length is 2.4 Mbp.
1353
1354

1355 **Description of *Candidatus* Avitreponema gen. nov.**
1356 *Candidatus* Avitreponema (A.vi.tre.po.ne'ma. L. fem. n. *avis* bird; N.L. neut. n. *Treponema* a
1357 genus name; N.L. neut. n. *Avitreponema* a genus related to the genus *Treponema* but distinct
1358 from it and found in poultry)
1359
1360 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1361 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1362 species *Avitreponema avistercoris*. This genus has been assigned by GTDB-Tk v1.3.0 working
1363 on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
1364 *Treponematales* and to the family *Treponemataceae*.
1365
1366

1367 **Description of *Candidatus* Avitreponema avistercoris sp. nov.**
1368 *Candidatus* Avitreponema avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
1369 dung; N.L. gen. n. *avistercoris* of bird faeces)
1370
1371 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1372 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

1373   assigned the MAG ID B3-4054 and which is available via NCBI BioSample SAMN15816977.
1374   The GC content of the type genome is 55.36% and the genome length is 1.9 Mbp.
1375
1376
1377   **Description of *Candidatus* Avoscillospira gen. nov.**
1378   *Candidatus* Avoscillospira (Av.os.cil.lo.spi'ra. L. fem. n. *avis* bird; N.L. fem. n. *Oscillospira* a
1379   genus name; N.L. fem. n. *Avoscillospira* a genus related to the genus *Oscillospira* but distinct
1380   from it and found in poultry)
1381
1382   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
1383   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
1384   species *Avioscillospira stercorigallinarum.* This genus has been assigned by GTDB-Tk v1.3.0
1385   working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
1386   *Oscillospirales* and to the family *Oscillospiraceae.*
1387
1388
1389   **Description of *Candidatus* Avoscillospira avicola sp. nov.**
1390   *Candidatus* Avoscillospira avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of;
1391   N.L. n. *avicola* inhabitant of birds)
1392
1393   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1394   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1395   assigned the MAG ID ChiBcec15-4380 and which is available via NCBI BioSample
1396   SAMN15816934. The GC content of the type genome is 61.76% and the genome length is 2.5
1397   Mbp.
1398
1399
1400   **Description of *Candidatus* Avoscillospira avistercoris sp. nov.**
1401   *Candidatus* Avoscillospira avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
1402   dung; N.L. gen. n. *avistercoris* of bird faeces)
1403
1404   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1405   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1406   assigned the MAG ID ChiBcec16-1751 and which is available via NCBI BioSample
1407   SAMN15816964. The GC content of the type genome is 58.00% and the genome length is 2.4
1408   Mbp.
1409
1410
1411   **Description of *Candidatus* Avoscillospira stercorigallinarum sp. nov.**
1412   *Candidatus* Avoscillospira stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
1413   fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
1414
1415   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1416   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1417   assigned the MAG ID ChiSjej2B20-13462 and which is available via NCBI BioSample

1418   SAMN15816948. The GC content of the type genome is 63.01% and the genome length is 2.2
1419   Mbp.
1420
1421
1422   **Description of *Candidatus* Avoscillospira stercoripullorum sp. nov.**
1423   *Candidatus* Avoscillospira stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
1424   masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
1425
1426   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1427   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1428   assigned the MAG ID ChiHjej9B8-7071 and which is available via NCBI BioSample
1429   SAMN15816951. The GC content of the type genome is 60.69% and the genome length is 1.9
1430   Mbp.
1431
1432
1433   **Description of *Candidatus* Bacteroides avicola sp. nov.**
1434   *Candidatus* Bacteroides avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. -*cola* inhabitant of; N.L.
1435   n. *avicola* inhabitant of birds)
1436
1437   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1438   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1439   assigned the MAG ID ChiHjej12B11-9795 and which is available via NCBI BioSample
1440   SAMN15816830. This is a new name for the alphanumeric GTDB species sp002160055. The
1441   GC content of the type genome is 50.12% and the genome length is 3.0 Mbp.
1442
1443
1444   **Description of *Candidatus* Bacteroides intestinavium sp. nov.**
1445   *Candidatus* Bacteroides intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
1446   *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
1447
1448   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1449   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1450   assigned the MAG ID ChiHecec1B25-7008 and which is available via NCBI BioSample
1451   SAMN15816665. The GC content of the type genome is 54.17% and the genome length is 2.6
1452   Mbp.
1453
1454
1455   **Description of *Candidatus* Bacteroides intestinigallinarum sp. nov.**
1456   *Candidatus* Bacteroides intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
1457   L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
1458
1459   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1460   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1461   assigned the MAG ID 2926 and which is available via NCBI BioSample SAMN15816831. This
1462   is a new name for the alphanumeric GTDB species sp003463205. The GC content of the type
1463   genome is 41.82% and the genome length is 5.8 Mbp.

1464
1465
1466 **Description of *Candidatus* Bacteroides intestinipullorum sp. nov.**
1467 *Candidatus* Bacteroides intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
1468 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
1469
1470 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1471 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1472 assigned the MAG ID B3-3758 and which is available via NCBI BioSample SAMN15816671.
1473 The GC content of the type genome is 53.99% and the genome length is 2.7 Mbp.
1474
1475
1476 **Description of *Candidatus* Bacteroides merdavium sp. nov.**
1477 *Candidatus* Bacteroides merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
1478 N.L. gen. n. *merdavium* of bird faeces)
1479
1480 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1481 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1482 assigned the MAG ID CHK118-2852 and which is available via NCBI BioSample
1483 SAMN15816687. The GC content of the type genome is 49.76% and the genome length is 2.9
1484 Mbp.
1485
1486
1487 **Description of *Candidatus* Bacteroides merdigallinarum sp. nov.**
1488 *Candidatus* Bacteroides merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
1489 n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
1490
1491 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1492 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1493 assigned the MAG ID ChiHjej9B8-1298 and which is available via NCBI BioSample
1494 SAMN15816694. The GC content of the type genome is 54.52% and the genome length is 2.7
1495 Mbp.
1496
1497
1498 **Description of *Candidatus* Bacteroides merdipullorum sp. nov.**
1499 *Candidatus* Bacteroides merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
1500 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
1501
1502 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1503 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1504 assigned the MAG ID ChiHjej12B11-24981 and which is available via NCBI BioSample
1505 SAMN15816699. The GC content of the type genome is 53.73% and the genome length is 2.5
1506 Mbp.
1507
1508
1509 **Description of *Candidatus* Bacteroides pullicola sp. nov.**

1510   *Candidatus* Bacteroides pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
1511   inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
1512
1513   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1514   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1515   assigned the MAG ID Gambia2-208 and which is available via NCBI BioSample
1516   SAMN15816704. The GC content of the type genome is 55.18% and the genome length is 2.7
1517   Mbp.
1518
1519
1520   **Description of *Candidatus* Bariatricus faecipullorum sp. nov.**
1521   *Candidatus* Bariatricus faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
1522   masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
1523
1524   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1525   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1526   assigned the MAG ID 9095 and which is available via NCBI BioSample SAMN15816662. The
1527   GC content of the type genome is 51.54% and the genome length is 2.5 Mbp.
1528
1529
1530   **Description of *Candidatus* Barnesiella excrementavium sp. nov.**
1531   *Candidatus* Barnesiella excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
1532   excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
1533
1534   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1535   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1536   assigned the MAG ID 4398 and which is available via NCBI BioSample SAMN15816714. The
1537   GC content of the type genome is 52.73% and the genome length is 2.7 Mbp.
1538
1539
1540   **Description of *Candidatus* Barnesiella excrementigallinarum sp. nov.**
1541   *Candidatus* Barnesiella excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
1542   *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
1543   excrement)
1544
1545   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1546   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1547   assigned the MAG ID CHK169-14362 and which is available via NCBI BioSample
1548   SAMN15816739. The GC content of the type genome is 47.04% and the genome length is 2.6
1549   Mbp.
1550
1551
1552   **Description of *Candidatus* Barnesiella excrementipullorum sp. nov.**
1553   *Candidatus* Barnesiella excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
1554   excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
1555   chicken excrement)

1556

1557 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1558 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1559 assigned the MAG ID ChiHjej12B11-16260 and which is available via NCBI BioSample
1560 SAMN15816862. This is a new name for the alphanumeric GTDB species sp900542255. The
1561 GC content of the type genome is 50.69% and the genome length is 2.1 Mbp.

1562
1563

1564 **Description of *Candidatus* Barnesiella merdigallinarum sp. nov.**
1565 *Candidatus* Barnesiella merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
1566 n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)

1567
1568 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1569 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1570 assigned the MAG ID CHK136-6590 and which is available via NCBI BioSample
1571 SAMN15816819. This is a new name for the alphanumeric GTDB species sp002159975. The
1572 GC content of the type genome is 54.15% and the genome length is 2.7 Mbp.

1573
1574

1575 **Description of *Candidatus* Barnesiella merdipullorum sp. nov.**
1576 *Candidatus* Barnesiella merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
1577 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)

1578
1579 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1580 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1581 assigned the MAG ID 5648 and which is available via NCBI BioSample SAMN15816849. This
1582 is a new name for the alphanumeric GTDB species sp002161555. The GC content of the type
1583 genome is 52.62% and the genome length is 2.6 Mbp.

1584
1585

1586 **Description of *Candidatus* Bilophila faecipullorum sp. nov.**
1587 *Candidatus* Bilophila faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
1588 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

1589
1590 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1591 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1592 assigned the MAG ID ChiSxjej5B17-1746 and which is available via NCBI BioSample
1593 SAMN15816754. The GC content of the type genome is 63.22% and the genome length is 2.8
1594 Mbp.

1595
1596

1597 **Description of *Candidatus* Blautia avicola sp. nov.**
1598 *Candidatus* Blautia avicola (a.vi.co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L. n.
1599 *avicola* inhabitant of birds)

1600

1601   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1602   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1603   assigned the MAG ID ChiBcec6-4105 and which is available via NCBI BioSample
1604   SAMN15816794. The GC content of the type genome is 46.40% and the genome length is 3.1
1605   Mbp.
1606
1607
1608   **Description of *Candidatus* Blautia avistercoris sp. nov.**
1609   *Candidatus* Blautia avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung;
1610   N.L. gen. n. *avistercoris* of bird faeces)
1611
1612   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1613   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1614   assigned the MAG ID 5548 and which is available via NCBI BioSample SAMN15816924. This
1615   is a new name for the alphanumeric GTDB species sp002159835. Although GTDB has assigned
1616   this species to the genus it calls Blautia_A , this genus designation cannot be incorporated into a
1617   well-formed binomial, so in naming this species, we have used the current validly published
1618   name for the genus. The GC content of the type genome is 45.38% and the genome length is 2.5
1619   Mbp.
1620
1621
1622   **Description of *Candidatus* Blautia excrementigallinarum sp. nov.**
1623   *Candidatus* Blautia excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum*
1624   excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)
1625
1626   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1627   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1628   assigned the MAG ID ChiSjej6B24-370 and which is available via NCBI BioSample
1629   SAMN15816894. Although GTDB has assigned this species to the genus it calls Blautia_A , this
1630   genus designation cannot be incorporated into a well-formed binomial, so in naming this species,
1631   we have used the current validly published name for the genus. The GC content of the type
1632   genome is 49.44% and the genome length is 2.3 Mbp.
1633
1634
1635   **Description of *Candidatus* Blautia excrementipullorum sp. nov.**
1636   *Candidatus* Blautia excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
1637   excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
1638   chicken excrement)
1639
1640   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1641   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1642   assigned the MAG ID CHK197-7439 and which is available via NCBI BioSample
1643   SAMN15816885. Although GTDB has assigned this species to the genus it calls Blautia_A , this
1644   genus designation cannot be incorporated into a well-formed binomial, so in naming this species,
1645   we have used the current validly published name for the genus. The GC content of the type
1646   genome is 46.79% and the genome length is 3.3 Mbp.

1647
1648
1649 **Description of *Candidatus* Blautia faecavium sp. nov.**
1650 *Candidatus* Blautia faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n. *avis*
1651 bird; N.L. gen. n. *faecavium* of bird faeces)
1652
1653 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1654 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1655 assigned the MAG ID ChiSjej1B19-5720 and which is available via NCBI BioSample
1656 SAMN15816886. Although GTDB has assigned this species to the genus it calls Blautia_A , this
1657 genus designation cannot be incorporated into a well-formed binomial, so in naming this species,
1658 we have used the current validly published name for the genus. The GC content of the type
1659 genome is 45.35% and the genome length is 3.5 Mbp.
1660
1661
1662 **Description of *Candidatus* Blautia faecigallinarum sp. nov.**
1663 *Candidatus* Blautia faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
1664 fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
1665
1666 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1667 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1668 assigned the MAG ID 14324 and which is available via NCBI BioSample SAMN15816901.
1669 Although GTDB has assigned this species to the genus it calls Blautia_A , this genus designation
1670 cannot be incorporated into a well-formed binomial, so in naming this species, we have used the
1671 current validly published name for the genus. The GC content of the type genome is 48.52% and
1672 the genome length is 2.9 Mbp.
1673
1674
1675 **Description of *Candidatus* Blautia faecipullorum sp. nov.**
1676 *Candidatus* Blautia faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L. masc.
1677 n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
1678
1679 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1680 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1681 assigned the MAG ID ChiSxjej6B18-2004 and which is available via NCBI BioSample
1682 SAMN15816906. Although GTDB has assigned this species to the genus it calls Blautia_A , this
1683 genus designation cannot be incorporated into a well-formed binomial, so in naming this species,
1684 we have used the current validly published name for the genus. The GC content of the type
1685 genome is 48.18% and the genome length is 3.5 Mbp.
1686
1687
1688 **Description of *Candidatus* Blautia gallistercoris sp. nov.**
1689 *Candidatus* Blautia gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n. *stercus*
1690 dung; N.L. gen. n. *gallistercoris* of chicken faeces)
1691

1692 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1693 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1694 assigned the MAG ID ChiSjej1B19-8411 and which is available via NCBI BioSample
1695 SAMN15816925. This is a new name for the alphanumeric GTDB species sp900542045.
1696 Although GTDB has assigned this species to the genus it calls Blautia_A , this genus designation
1697 cannot be incorporated into a well-formed binomial, so in naming this species, we have used the
1698 current validly published name for the genus. The GC content of the type genome is 48.96% and
1699 the genome length is 2.8 Mbp.
1700
1701

1702 **Description of *Candidatus* Blautia intestinavium sp. nov.**
1703 *Candidatus* Blautia intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n. *avis*
1704 bird; N.L. gen. n. *intestinavium* of the gut of birds)
1705
1706 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1707 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1708 assigned the MAG ID CHK186-553 and which is available via NCBI BioSample
1709 SAMN15816890. Although GTDB has assigned this species to the genus it calls Blautia_A , this
1710 genus designation cannot be incorporated into a well-formed binomial, so in naming this species,
1711 we have used the current validly published name for the genus. The GC content of the type
1712 genome is 47.27% and the genome length is 2.8 Mbp.
1713
1714

1715 **Description of *Candidatus* Blautia intestinigallinarum sp. nov.**
1716 *Candidatus* Blautia intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut; L.
1717 fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
1718
1719 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1720 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1721 assigned the MAG ID CHK186-9876 and which is available via NCBI BioSample
1722 SAMN15816891. Although GTDB has assigned this species to the genus it calls Blautia_A , this
1723 genus designation cannot be incorporated into a well-formed binomial, so in naming this species,
1724 we have used the current validly published name for the genus. The GC content of the type
1725 genome is 46.77% and the genome length is 2.7 Mbp.
1726
1727

1728 **Description of *Candidatus* Blautia intestinipullorum sp. nov.**
1729 *Candidatus* Blautia intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc.
1730 n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
1731
1732 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1733 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1734 assigned the MAG ID ChiW16-4312 and which is available via NCBI BioSample
1735 SAMN15816892. Although GTDB has assigned this species to the genus it calls Blautia_A , this
1736 genus designation cannot be incorporated into a well-formed binomial, so in naming this species,

1737 we have used the current validly published name for the genus. The GC content of the type
1738 genome is 47.05% and the genome length is 2.4 Mbp.
1739
1740
1741 **Description of *Candidatus* Blautia merdavium sp. nov.**
1742 *Candidatus* Blautia merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird; N.L.
1743 gen. n. *merdavium* of bird faeces)
1744
1745 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1746 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1747 assigned the MAG ID ChiBcec2-3848 and which is available via NCBI BioSample
1748 SAMN15816633. The GC content of the type genome is 48.60% and the genome length is 3.3
1749 Mbp.
1750
1751
1752 **Description of *Candidatus* Blautia merdigallinarum sp. nov.**
1753 *Candidatus* Blautia merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem. n.
1754 *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
1755
1756 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1757 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1758 assigned the MAG ID ChiSxjej6B18-287 and which is available via NCBI BioSample
1759 SAMN15816815. This is a new name for the alphanumeric GTDB species sp900543715. The
1760 GC content of the type genome is 45.18% and the genome length is 3.3 Mbp.
1761
1762
1763 **Description of *Candidatus* Blautia merdipullorum sp. nov.**
1764 *Candidatus* Blautia merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
1765 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
1766
1767 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1768 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1769 assigned the MAG ID 17058 and which is available via NCBI BioSample SAMN15816655. The
1770 GC content of the type genome is 45.05% and the genome length is 3.2 Mbp.
1771
1772
1773 **Description of *Candidatus* Blautia ornithocaccae sp. nov.**
1774 *Candidatus* Blautia ornithocaccae (or.ni.tho.cac'cae. Gr. masc. or fem. n. *ornis, ornithos* bird Gr.
1775 fem. n. *kakke* faeces; N.L. gen. n. *ornithocaccae* of bird faeces)
1776
1777 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1778 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1779 assigned the MAG ID ChiBcec1-3711 and which is available via NCBI BioSample
1780 SAMN15816880. This is a new name for the alphanumeric GTDB species sp002161285. The
1781 GC content of the type genome is 44.79% and the genome length is 3.1 Mbp.
1782

1783
1784 **Description of *Candidatus* Blautia pullicola sp. nov.**
1785 *Candidatus* Blautia pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -*cola*
1786 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
1787
1788 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1789 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1790 assigned the MAG ID 1068 and which is available via NCBI BioSample SAMN15816689. The
1791 GC content of the type genome is 45.62% and the genome length is 3.0 Mbp.
1792
1793
1794 **Description of *Candidatus* Blautia pullistercoris sp. nov.**
1795 *Candidatus* Blautia pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L. neut. n.
1796 *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
1797
1798 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1799 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1800 assigned the MAG ID ChiHjej12B11-1927 and which is available via NCBI BioSample
1801 SAMN15816618. The GC content of the type genome is 45.73% and the genome length is 3.2
1802 Mbp.
1803
1804
1805 **Description of *Candidatus* Blautia stercoravium sp. nov.**
1806 *Candidatus* Blautia stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis* bird;
1807 N.L. gen. n. *stercoravium* of bird faeces)
1808
1809 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1810 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1811 assigned the MAG ID 3268 and which is available via NCBI BioSample SAMN15816738. The
1812 GC content of the type genome is 44.17% and the genome length is 2.7 Mbp.
1813
1814
1815 **Description of *Candidatus* Blautia stercorigallinarum sp. nov.**
1816 *Candidatus* Blautia stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L. fem.
1817 n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
1818
1819 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1820 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1821 assigned the MAG ID CHK195-9823 and which is available via NCBI BioSample
1822 SAMN15816627. The GC content of the type genome is 45.83% and the genome length is 3.1
1823 Mbp.
1824
1825
1826 **Description of *Candidatus* Blautia stercoripullorum sp. nov.**
1827 *Candidatus* Blautia stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n.
1828 *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)

1829
1830 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1831 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1832 assigned the MAG ID ChiW19-6364 and which is available via NCBI BioSample
1833 SAMN15816793. The GC content of the type genome is 44.78% and the genome length is 3.1
1834 Mbp.
1835
1836
1837 **Description of *Candidatus* Borkfalkia avicola sp. nov.**
1838 *Candidatus* Borkfalkia avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L.
1839 n. *avicola* inhabitant of birds)
1840
1841 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1842 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1843 assigned the MAG ID CHK192-19661 and which is available via NCBI BioSample
1844 SAMN15816606. The GC content of the type genome is 58.92% and the genome length is 1.7
1845 Mbp.
1846
1847
1848 **Description of *Candidatus* Borkfalkia avistercoris sp. nov.**
1849 *Candidatus* Borkfalkia avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung;
1850 N.L. gen. n. *avistercoris* of bird faeces)
1851
1852 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1853 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1854 assigned the MAG ID CHK187-5294 and which is available via NCBI BioSample
1855 SAMN15816607. The GC content of the type genome is 53.99% and the genome length is 1.7
1856 Mbp.
1857
1858
1859 **Description of *Candidatus* Borkfalkia excrementavium sp. nov.**
1860 *Candidatus* Borkfalkia excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
1861 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
1862
1863 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1864 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1865 assigned the MAG ID CHK199-9574 and which is available via NCBI BioSample
1866 SAMN15816608. The GC content of the type genome is 52.76% and the genome length is 1.6
1867 Mbp.
1868
1869
1870 **Description of *Candidatus* Borkfalkia excrementigallinarum sp. nov.**
1871 *Candidatus* Borkfalkia excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
1872 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
1873 excrement)
1874

1875   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1876   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1877   assigned the MAG ID 1345 and which is available via NCBI BioSample SAMN15816609. The
1878   GC content of the type genome is 53.42% and the genome length is 1.9 Mbp.
1879
1880
1881   **Description of *Candidatus* Borkfalkia excrementipullorum sp. nov.**
1882   *Candidatus* Borkfalkia excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
1883   excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
1884   chicken excrement)
1885
1886   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1887   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1888   assigned the MAG ID CHK192-2667 and which is available via NCBI BioSample
1889   SAMN15816611. The GC content of the type genome is 55.63% and the genome length is 1.6
1890   Mbp.
1891
1892
1893   **Description of *Candidatus* Borkfalkia faecavium sp. nov.**
1894   *Candidatus* Borkfalkia faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n. *avis*
1895   bird; N.L. gen. n. *faecavium* of bird faeces)
1896
1897   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1898   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1899   assigned the MAG ID 2189 and which is available via NCBI BioSample SAMN15816731. The
1900   GC content of the type genome is 58.98% and the genome length is 1.7 Mbp.
1901
1902
1903   **Description of *Candidatus* Borkfalkia faecigallinarum sp. nov.**
1904   *Candidatus* Borkfalkia faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
1905   fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
1906
1907   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1908   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1909   assigned the MAG ID 26628 and which is available via NCBI BioSample SAMN15816617. The
1910   GC content of the type genome is 62.49% and the genome length is 1.6 Mbp.
1911
1912
1913   **Description of *Candidatus* Borkfalkia faecipullorum sp. nov.**
1914   *Candidatus* Borkfalkia faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
1915   masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
1916
1917   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1918   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1919   assigned the MAG ID 811 and which is available via NCBI BioSample SAMN15816621. The
1920   GC content of the type genome is 54.29% and the genome length is 1.9 Mbp.

1921
1922
1923 **Description of *Candidatus* Borkfalkia stercoripullorum sp. nov.**
1924 *Candidatus* Borkfalkia stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc.
1925 n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
1926
1927 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1928 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1929 assigned the MAG ID CHK196-13738 and which is available via NCBI BioSample
1930 SAMN15816588. The GC content of the type genome is 55.22% and the genome length is 1.8
1931 Mbp.
1932
1933
1934 **Description of *Candidatus* Brachybacterium intestinipullorum sp. nov.**
1935 *Candidatus* Brachybacterium intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut;
1936 L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
1937
1938 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1939 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1940 assigned the MAG ID CHK130-7132 and which is available via NCBI BioSample
1941 SAMN15816812. This is a new name for the alphanumeric GTDB species sp003711805. The
1942 GC content of the type genome is 72.59% and the genome length is 3.5 Mbp.
1943
1944
1945 **Description of *Candidatus* Brachybacterium merdavium sp. nov.**
1946 *Candidatus* Brachybacterium merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
1947 bird; N.L. gen. n. *merdavium* of bird faeces)
1948
1949 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1950 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1951 assigned the MAG ID ChiHjej13B12-24818 and which is available via NCBI BioSample
1952 SAMN15816666. The GC content of the type genome is 70.22% and the genome length is 3.7
1953 Mbp.
1954
1955
1956 **Description of *Candidatus* Brachybacterium merdigallinarum sp. nov.**
1957 *Candidatus* Brachybacterium merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L.
1958 fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
1959
1960 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1961 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1962 assigned the MAG ID ChiHjej13B12-7362 and which is available via NCBI BioSample
1963 SAMN15816717. The GC content of the type genome is 71.16% and the genome length is 3.1
1964 Mbp.
1965
1966

1967 **Description of *Candidatus* Brevibacterium intestinavium sp. nov.**
1968 *Candidatus* Brevibacterium intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
1969 *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
1970
1971 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1972 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1973 assigned the MAG ID 5295 and which is available via NCBI BioSample SAMN15816668. The
1974 GC content of the type genome is 66.76% and the genome length is 3.2 Mbp.
1975
1976
1977 **Description of *Candidatus* Brevibacterium intestinigallinarum sp. nov.**
1978 *Candidatus* Brevibacterium intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum*
1979 gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
1980
1981 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1982 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1983 assigned the MAG ID CHK132-2174 and which is available via NCBI BioSample
1984 SAMN15816673. The GC content of the type genome is 70.54% and the genome length is 2.7
1985 Mbp.
1986
1987
1988 **Description of *Candidatus* Butyricicoccus avicola sp. nov.**
1989 *Candidatus* Butyricicoccus avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of;
1990 N.L. n. *avicola* inhabitant of birds)
1991
1992 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
1993 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
1994 assigned the MAG ID ChiSjej6B24-14740 and which is available via NCBI BioSample
1995 SAMN15816587. The GC content of the type genome is 59.67% and the genome length is 2.0
1996 Mbp.
1997
1998
1999 **Description of *Candidatus* Butyricicoccus avistercoris sp. nov.**
2000 *Candidatus* Butyricicoccus avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
2001 dung; N.L. gen. n. *avistercoris* of bird faeces)
2002
2003 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2004 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2005 assigned the MAG ID CHK193-4272 and which is available via NCBI BioSample
2006 SAMN15816626. The GC content of the type genome is 35.60% and the genome length is 2.0
2007 Mbp.
2008
2009
2010 **Description of *Candidatus* Butyricicoccus stercorigallinarum sp. nov.**
2011 *Candidatus* Butyricicoccus stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung;
2012 L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)

2013

2014 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2015 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2016 assigned the MAG ID ChiHecec2B26-12929 and which is available via NCBI BioSample
2017 SAMN15816912. Although GTDB has assigned this species to the genus it calls
2018 Butyricicoccus_A , this genus designation cannot be incorporated into a well-formed binomial,
2019 so in naming this species, we have used the current validly published name for the genus. The
2020 GC content of the type genome is 62.06% and the genome length is 2.1 Mbp.

2021

2022

2023 **Description of *Candidatus* Butyricimonas faecavium sp. nov.**
2024 *Candidatus* Butyricimonas faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
2025 *avis* bird; N.L. gen. n. *faecavium* of bird faeces)

2026

2027 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2028 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2029 assigned the MAG ID CHK27-1272 and which is available via NCBI BioSample
2030 SAMN15816676. The GC content of the type genome is 40.60% and the genome length is 3.6
2031 Mbp.

2032

2033

2034 **Description of *Candidatus* Caccalectryoclostridium gen. nov.**
2035 *Candidatus* Caccalectryoclostridium (Cacc.a.lec.try.o.clos.tri'di.um. Gr. fem. n. *kakke* faeces; Gr.
2036 neut. n. *alektryon* chicken; N.L. neut. n. *Clostridium* a genus name; N.L. neut. n.
2037 *Caccalectryoclostridium* a genus related to the genus *Clostridium* but distinct from it and found
2038 in poultry faeces)

2039

2040 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2041 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2042 species *Caccalectryoclostridium excrementigallinarum.* This genus has been assigned by GTDB-
2043 Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the
2044 order *Christensenellales* and to the family *UBA3700.*

2045

2046

2047 **Description of *Candidatus* Caccalectryoclostridium excrementigallinarum sp. nov.**
2048 *Candidatus* Caccalectryoclostridium excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut.
2049 n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
2050 excrement)

2051

2052 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2053 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2054 assigned the MAG ID 9366 and which is available via NCBI BioSample SAMN15816988. The
2055 GC content of the type genome is 54.72% and the genome length is 1.5 Mbp.

2056

2057

2058 **Description of *Candidatus* Caccenecus gen. nov.**

2059 *Candidatus* Caccenecus (Caccen.e'cus. Gr. fem. n. *kakke* dung; Gr. masc. *enoikos* inhabitant;
2060 N.L. masc. n. *Caccenecus* a microbe associated with faeces)
2061
2062 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2063 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2064 species *Caccenecus avistercoris*. This is a name for the alphanumeric GTDB genus CAG-776.
2065 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
2066 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-1000.*
2067
2068
2069 **Description of *Candidatus* Caccenecus avistercoris sp. nov.**
2070 *Candidatus* Caccenecus avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung;
2071 N.L. gen. n. *avistercoris* of bird faeces)
2072
2073 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2074 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2075 assigned the MAG ID CHK193-13418 and which is available via NCBI BioSample
2076 SAMN15817030. The GC content of the type genome is 28.47% and the genome length is 1.3
2077 Mbp.
2078
2079
2080 **Description of *Candidatus* Caccocola gen. nov.**
2081 *Candidatus* Caccocola (Cacc.o.co'la. Gr. fem. n. *kakke* dung; L. suff. -*cola* inhabitant of; N.L.
2082 fem. n. *Caccocola* a microbe associated with faeces)
2083
2084 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2085 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2086 species *Caccocola faecigallinarum*. This is a name for the alphanumeric GTDB genus An23.
2087 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
2088 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Synergistales* and to the family
2089 *Synergistaceae.*
2090
2091
2092 **Description of *Candidatus* Caccocola faecigallinarum sp. nov.**
2093 *Candidatus* Caccocola faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
2094 fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
2095
2096 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2097 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2098 assigned the MAG ID ChiHjej11B10-3130 and which is available via NCBI BioSample
2099 SAMN15817215. This is a new name for the alphanumeric GTDB species sp900544635. The
2100 GC content of the type genome is 60.31% and the genome length is 2.3 Mbp.
2101
2102
2103 **Description of *Candidatus* Caccocola faecipullorum sp. nov.**

2104 *Candidatus* Caccocola faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
2105 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
2106
2107 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2108 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2109 assigned the MAG ID ChiHcec3-7374 and which is available via NCBI BioSample
2110 SAMN15817103. The GC content of the type genome is 59.08% and the genome length is 2.2
2111 Mbp.
2112
2113
2114 **Description of *Candidatus* Caccomonas gen. nov.**
2115 *Candidatus* Caccomonas (Cacc.omo'nas. Gr. fem. n. *kakke* dung; L. fem. n. *monas* a monad;
2116 N.L. fem. n. *Caccomonas* a microbe associated with faeces)
2117
2118 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2119 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2120 species *Caccomonas pullistercoris*. This is a name for the alphanumeric GTDB genus CAG-617.
2121 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
2122 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family
2123 *Bacteroidaceae.*
2124
2125
2126 **Description of *Candidatus* Caccomonas pullistercoris sp. nov.**
2127 *Candidatus* Caccomonas pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
2128 neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
2129
2130 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2131 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2132 assigned the MAG ID 5345 and which is available via NCBI BioSample SAMN15817152. The
2133 GC content of the type genome is 59.45% and the genome length is 2.2 Mbp.
2134
2135
2136 **Description of *Candidatus* Caccomorpha gen. nov.**
2137 *Candidatus* Caccomorpha (Cacc.o.mor'pha. Gr. fem. n. *kakke* dung; Gr. fem. n. *morphe* a form,
2138 shape; N.L. fem. n. *Caccomorpha* a microbe associated with faeces)
2139
2140 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2141 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2142 species *Caccomorpha excrementavium*. This is a name for the alphanumeric GTDB genus
2143 SZUA-448. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
2144 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
2145 *Lachnospiraceae.*
2146
2147
2148 **Description of *Candidatus* Caccomorpha excrementavium sp. nov.**

2149 *Candidatus* Caccomorpha excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
2150 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
2151
2152 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2153 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2154 assigned the MAG ID 1999 and which is available via NCBI BioSample SAMN15817145. The
2155 GC content of the type genome is 50.75% and the genome length is 2.7 Mbp.
2156
2157
2158 **Description of *Candidatus* Caccoplasma gen. nov.**
2159 *Candidatus* Caccoplasma (Cacc.o.plas'ma. Gr. fem. n. *kakke* dung; Gr. neut. n. *plasma* a form;
2160 N.L. neut. n. *Caccoplasma* a microbe associated with faeces)
2161
2162 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2163 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2164 species *Caccoplasma merdavium*. This is a name for the alphanumeric GTDB genus UBA11471.
2165 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
2166 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family
2167 *UBA11471.*
2168
2169
2170 **Description of *Candidatus* Caccoplasma intestinavium sp. nov.**
2171 *Candidatus* Caccoplasma intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
2172 *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
2173
2174 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2175 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2176 assigned the MAG ID 21143 and which is available via NCBI BioSample SAMN15817187. This
2177 is a new name for the alphanumeric GTDB species sp000434215. The GC content of the type
2178 genome is 45.83% and the genome length is 2.4 Mbp.
2179
2180
2181 **Description of *Candidatus* Caccoplasma merdavium sp. nov.**
2182 *Candidatus* Caccoplasma merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
2183 bird; N.L. gen. n. *merdavium* of bird faeces)
2184
2185 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2186 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2187 assigned the MAG ID 6821 and which is available via NCBI BioSample SAMN15817190. This
2188 is a new name for the alphanumeric GTDB species sp900542765. The GC content of the type
2189 genome is 52.79% and the genome length is 2.4 Mbp.
2190
2191
2192 **Description of *Candidatus* Caccoplasma merdipullorum sp. nov.**
2193 *Candidatus* Caccoplasma merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
2194 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)

2195

2196 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2197 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2198 assigned the MAG ID G3-4614 and which is available via NCBI BioSample SAMN15817135.
2199 The GC content of the type genome is 46.70% and the genome length is 2.0 Mbp.

2200

2201

2202 **Description of *Candidatus* Caccopulliclostridium gen. nov.**
2203 *Candidatus* Caccopulliclostridium (Cac.co.pul.li.clos.tri'di.um. Gr. fem. n. *kakke* faeces; L. masc.
2204 n. *pullus* a young chicken; N.L. neut. n. *Clostridium* a genus name; N.L. neut. n.
2205 *Caccopulliclostridium* a genus related to the genus *Clostridium* but distinct from it and found in
2206 poultry faeces)

2207

2208 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2209 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2210 species *Caccopulliclostridium gallistercoris*. This genus was identified but not named by
2211 Glendinning et al. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release
2212 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *4C28d-15* and to the family
2213 *UBA1242*.

2214

2215

2216 **Description of *Candidatus* Caccopulliclostridium gallistercoris sp. nov.**
2217 *Candidatus* Caccopulliclostridium gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L.
2218 neut. n. *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)

2219

2220 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2221 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2222 assigned the MAG ID CHK186-9395 and which is available via NCBI BioSample
2223 SAMN15816943. The GC content of the type genome is 35.40% and the genome length is 1.0
2224 Mbp.

2225

2226

2227 **Description of *Candidatus* Caccosoma gen. nov.**
2228 *Candidatus* Caccosoma (Cacc.o.so'ma. Gr. fem. n. *kakke* dung; Gr. neut. n. *soma* a body; N.L.
2229 neut. n. *Caccosoma* a microbe associated with faeces)

2230

2231 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2232 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2233 species *Caccosoma faecigallinarum*. This is a name for the alphanumeric GTDB genus CAG-
2234 631. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
2235 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RFN20* and to the family *CAG-631*.

2236

2237

2238 **Description of *Candidatus* Caccosoma faecigallinarum sp. nov.**
2239 *Candidatus* Caccosoma faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
2240 fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

2241
2242   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2243   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2244   assigned the MAG ID 14508 and which is available via NCBI BioSample SAMN15817185. This
2245   is a new name for the alphanumeric GTDB species sp000433015. The GC content of the type
2246   genome is 30.38% and the genome length is 1.3 Mbp.
2247
2248
2249   **Description of *Candidatus* Caccousia gen. nov.**
2250   *Candidatus* Caccousia (Cacc.ou'si.a. Gr. fem. n. *kakke* dung; Gr. fem. n. *ousia* an essence; N.L.
2251   fem. n. *Caccousia* a microbe associated with faeces)
2252
2253   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2254   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2255   species *Caccousia avicola*. This is a name for the alphanumeric GTDB genus An200. This genus
2256   has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al.,
2257   2019; Parks et al., 2020) to the order *Oscillospirales* and to the family *Acutalibacteraceae.*
2258
2259
2260   **Description of *Candidatus* Caccousia avicola sp. nov.**
2261   *Candidatus* Caccousia avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L. n.
2262   *avicola* inhabitant of birds)
2263
2264   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2265   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2266   assigned the MAG ID ChiSxjej1B13-7958 and which is available via NCBI BioSample
2267   SAMN15817070. The GC content of the type genome is 58.28% and the genome length is 2.2
2268   Mbp.
2269
2270
2271   **Description of *Candidatus* Caccousia avistercoris sp. nov.**
2272   *Candidatus* Caccousia avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung;
2273   N.L. gen. n. *avistercoris* of bird faeces)
2274
2275   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2276   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2277   assigned the MAG ID 3024 and which is available via NCBI BioSample SAMN15817047. The
2278   GC content of the type genome is 60.88% and the genome length is 2.6 Mbp.
2279
2280
2281   **Description of *Candidatus* Caccousia stercoris sp. nov.**
2282   *Candidatus* Caccousia stercoris (ster'co.ris. L. gen. n. *stercoris* of dung, excrement)
2283
2284   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2285   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2286   assigned the MAG ID 6086 and which is available via NCBI BioSample SAMN15817184. This

2287   is a new name for the alphanumeric GTDB species sp002160025. The GC content of the type
2288   genome is 56.84% and the genome length is 2.3 Mbp.
2289
2290
2291   **Description of *Candidatus* Caccovicinus gen. nov.**
2292   *Candidatus* Caccovicinus (Cacc.o.vic.in'us. Gr. fem. n. *kakke* dung; L. masc. n. *vicinus* a
2293   neighbour; N.L. masc. n. *Caccovicinus* a microbe associated with faeces)
2294
2295   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2296   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2297   species *Caccovicinus merdipullorum*. This is a name for the alphanumeric GTDB genus
2298   UMGS1370. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
2299   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
2300   *Lachnospiraceae.*
2301
2302
2303   **Description of *Candidatus* Caccovicinus merdipullorum sp. nov.**
2304   *Candidatus* Caccovicinus merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
2305   *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
2306
2307   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2308   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2309   assigned the MAG ID CHK198_11255 and which is available via NCBI BioSample
2310   SAMN15817041. The GC content of the type genome is 50.44% and the genome length is 3.0
2311   Mbp.
2312
2313
2314   **Description of *Candidatus* Caccovivens gen. nov.**
2315   *Candidatus* Caccovivens (Cacc.o.viv'ens. Gr. fem. n. *kakke* dung; N.L. pres. part. *vivens* living;
2316   N.L. fem. n. *Caccovivens* a microbe associated with faeces)
2317
2318   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2319   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2320   species *Caccovivens faecavium*. This is a name for the alphanumeric GTDB genus UBA11517.
2321   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
2322   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family
2323   *UBA1242.*
2324
2325
2326   **Description of *Candidatus* Caccovivens faecavium sp. nov.**
2327   *Candidatus* Caccovivens faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
2328   *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
2329
2330   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2331   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2332   assigned the MAG ID ChiW6-1002 and which is available via NCBI BioSample

2333 SAMN15817119. The GC content of the type genome is 34.22% and the genome length is 1.1
2334 Mbp.
2335
2336
2337 **Description of *Candidatus* Cellulosilyticum pullistercoris sp. nov.**
2338 *Candidatus* Cellulosilyticum pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken;
2339 L. neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
2340
2341 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2342 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2343 assigned the MAG ID B5-657 and which is available via NCBI BioSample SAMN15816752.
2344 The GC content of the type genome is 33.78% and the genome length is 2.3 Mbp.
2345
2346
2347 **Description of *Candidatus* Choladocola gen. nov.**
2348 *Candidatus* Choladocola (Cho.lad.o.co'la. Gr. fem. n. *cholas* guts; L. suff. *-cola* inhabitant of;
2349 N.L. fem. n. *Choladocola* a microbe associated with the intestines)
2350
2351 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2352 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2353 species *Choladocola avistercoris*. This is a name for the alphanumeric GTDB genus UBA7182.
2354 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
2355 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
2356 *Lachnospiraceae.*
2357
2358
2359 **Description of *Candidatus* Choladocola avistercoris sp. nov.**
2360 *Candidatus* Choladocola avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
2361 dung; N.L. gen. n. *avistercoris* of bird faeces)
2362
2363 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2364 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2365 assigned the MAG ID ChiBcec18-1958 and which is available via NCBI BioSample
2366 SAMN15817180. This is a new name for the alphanumeric GTDB species sp002160135. The
2367 GC content of the type genome is 50.79% and the genome length is 2.4 Mbp.
2368
2369
2370 **Description of *Candidatus* Choladousia gen. nov.**
2371 *Candidatus* Choladousia (Cho.lad.ou'si.a. Gr. fem. n. *cholas* guts; Gr. fem. n. *ousia* an essence;
2372 N.L. fem. n. *Choladousia* a microbe associated with the intestines)
2373
2374 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2375 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2376 species *Choladousia intestinavium*. This is a name for the alphanumeric GTDB genus UBA7160.
2377 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95

2378 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
2379 *Lachnospiraceae.*
2380
2381
2382 **Description of *Candidatus* Choladousia intestinavium sp. nov.**
2383 *Candidatus* Choladousia intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
2384 *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
2385
2386 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2387 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2388 assigned the MAG ID ChiSjej4B22-8148 and which is available via NCBI BioSample
2389 SAMN15817012. The GC content of the type genome is 49.57% and the genome length is 2.9
2390 Mbp.
2391
2392
2393 **Description of *Candidatus* Choladousia intestinigallinarum sp. nov.**
2394 *Candidatus* Choladousia intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
2395 L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
2396
2397 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2398 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2399 assigned the MAG ID ChiBcec11-13528 and which is available via NCBI BioSample
2400 SAMN15817065. The GC content of the type genome is 48.69% and the genome length is 3.1
2401 Mbp.
2402
2403
2404 **Description of *Candidatus* Choladousia intestinipullorum sp. nov.**
2405 *Candidatus* Choladousia intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
2406 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
2407
2408 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2409 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2410 assigned the MAG ID ChiSjej5B23-16397 and which is available via NCBI BioSample
2411 SAMN15817078. The GC content of the type genome is 50.54% and the genome length is 2.2
2412 Mbp.
2413
2414
2415 **Description of *Candidatus* Collinsella stercoripullorum sp. nov.**
2416 *Candidatus* Collinsella stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc.
2417 n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
2418
2419 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2420 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2421 assigned the MAG ID ChiGjej6B6-20822 and which is available via NCBI BioSample
2422 SAMN15816681. The GC content of the type genome is 68.61% and the genome length is 2.3
2423 Mbp.

2424
2425
2426 **Description of *Candidatus* Companilactobacillus pullicola sp. nov.**
2427 *Candidatus* Companilactobacillus pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L.
2428 suff. -*cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
2429
2430 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2431 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2432 assigned the MAG ID 3204 and which is available via NCBI BioSample SAMN15816700. The
2433 GC content of the type genome is 35.87% and the genome length is 2.9 Mbp.
2434
2435
2436 **Description of *Candidatus* Coprenecus gen. nov.**
2437 *Candidatus* Coprenecus (Copr.en.e'cus. Gr. fem. n. *kopros* dung; Gr. masc. *enoikos* inhabitant;
2438 N.L. masc. n. *Coprenecus* a microbe associated with faeces)
2439
2440 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2441 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2442 species *Coprenecus pullicola*. This is a name for the alphanumeric GTDB genus CAG-831. This
2443 genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
2444 al., 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family *UBA932*.
2445
2446
2447 **Description of *Candidatus* Coprenecus avistercoris sp. nov.**
2448 *Candidatus* Coprenecus avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung;
2449 N.L. gen. n. *avistercoris* of bird faeces)
2450
2451 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2452 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2453 assigned the MAG ID ChiHjej13B12-12457 and which is available via NCBI BioSample
2454 SAMN15817175. This is a new name for the alphanumeric GTDB species sp000432775. The
2455 GC content of the type genome is 56.44% and the genome length is 2.0 Mbp.
2456
2457
2458 **Description of *Candidatus* Coprenecus merdigallinarum sp. nov.**
2459 *Candidatus* Coprenecus merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
2460 n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
2461
2462 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2463 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2464 assigned the MAG ID ChiHecolR1B25-18470 and which is available via NCBI BioSample
2465 SAMN15817066. The GC content of the type genome is 55.94% and the genome length is 2.2
2466 Mbp.
2467
2468
2469 **Description of *Candidatus* Coprenecus merdipullorum sp. nov.**

2470   *Candidatus* Coprenecus merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
2471   *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
2472
2473   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2474   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2475   assigned the MAG ID Gambia11-1358 and which is available via NCBI BioSample
2476   SAMN15817068. The GC content of the type genome is 54.29% and the genome length is 2.1
2477   Mbp.
2478
2479
2480   **Description of *Candidatus* Coprenecus pullicola sp. nov.**
2481   *Candidatus* Coprenecus pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
2482   inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
2483
2484   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2485   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2486   assigned the MAG ID ChiHjej9B8-15444 and which is available via NCBI BioSample
2487   SAMN15817077. The GC content of the type genome is 52.53% and the genome length is 2.1
2488   Mbp.
2489
2490
2491   **Description of *Candidatus* Coprenecus pullistercoris sp. nov.**
2492   *Candidatus* Coprenecus pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
2493   neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
2494
2495   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2496   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2497   assigned the MAG ID Gambia18-42 and which is available via NCBI BioSample
2498   SAMN15817084. The GC content of the type genome is 52.64% and the genome length is 2.0
2499   Mbp.
2500
2501
2502   **Description of *Candidatus* Coprenecus stercoravium sp. nov.**
2503   *Candidatus* Coprenecus stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
2504   bird; N.L. gen. n. *stercoravium* of bird faeces)
2505
2506   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2507   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2508   assigned the MAG ID Gambia16-554 and which is available via NCBI BioSample
2509   SAMN15817085. The GC content of the type genome is 51.84% and the genome length is 1.8
2510   Mbp.
2511
2512
2513   **Description of *Candidatus* Coprenecus stercorigallinarum sp. nov.**
2514   *Candidatus* Coprenecus stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
2515   fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)

2516
2517 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2518 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2519 assigned the MAG ID 3382 and which is available via NCBI BioSample SAMN15817086. The
2520 GC content of the type genome is 53.66% and the genome length is 2.1 Mbp.
2521
2522
2523 **Description of *Candidatus* Coprenecus stercoripullorum sp. nov.**
2524 *Candidatus* Coprenecus stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc.
2525 n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
2526
2527 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2528 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2529 assigned the MAG ID 7141 and which is available via NCBI BioSample SAMN15817115. The
2530 GC content of the type genome is 50.92% and the genome length is 1.7 Mbp.
2531
2532
2533 **Description of *Candidatus* Coprocola gen. nov.**
2534 *Candidatus* Coprocola (Copr.o.co'la. Gr. fem. n. *kopros* dung; L. suff. -*cola* inhabitant of; N.L.
2535 fem. n. *Coprocola* a microbe associated with faeces)
2536
2537 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2538 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2539 species *Coprocola pullicola*. This is a name for the alphanumeric GTDB genus ASF356. This
2540 genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
2541 al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family *Anaerotignaceae.*
2542
2543
2544 **Description of *Candidatus* Coprocola pullicola sp. nov.**
2545 *Candidatus* Coprocola pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -*cola*
2546 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
2547
2548 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2549 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2550 assigned the MAG ID CHK193-15662 and which is available via NCBI BioSample
2551 SAMN15817043. The GC content of the type genome is 33.91% and the genome length is 3.0
2552 Mbp.
2553
2554
2555 **Description of *Candidatus* Copromonas gen. nov.**
2556 *Candidatus* Copromonas (Copr.omo'nas. Gr. fem. n. *kopros* dung; L. fem. n. *monas* a monad;
2557 N.L. fem. n. *Copromonas* a microbe associated with faeces)
2558
2559 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2560 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2561 species *Copromonas avistercoris*. This is a name for the alphanumeric GTDB genus CAG-81.

2562 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
2563 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
2564 *Lachnospiraceae.*
2565
2566
2567 **Description of *Candidatus* Copromonas avistercoris sp. nov.**
2568 *Candidatus* Copromonas avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
2569 dung; N.L. gen. n. *avistercoris* of bird faeces)
2570
2571 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2572 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2573 assigned the MAG ID ChiSjej3B21-5768 and which is available via NCBI BioSample
2574 SAMN15817005. The GC content of the type genome is 52.88% and the genome length is 2.2
2575 Mbp.
2576
2577
2578 **Description of *Candidatus* Copromonas faecavium sp. nov.**
2579 *Candidatus* Copromonas faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
2580 *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
2581
2582 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2583 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2584 assigned the MAG ID CHK180-2868 and which is available via NCBI BioSample
2585 SAMN15817009. The GC content of the type genome is 50.20% and the genome length is 2.7
2586 Mbp.
2587
2588
2589 **Description of *Candidatus* Copromorpha gen. nov.**
2590 *Candidatus* Copromorpha (Copr.o.mor'pha. Gr. fem. n. *kopros* dung; Gr. fem. n. *morphe* a form,
2591 shape; N.L. fem. n. *Copromorpha* a microbe associated with faeces)
2592
2593 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2594 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2595 species *Copromorpha excrementavium*. This is a name for the alphanumeric GTDB genus
2596 UBA1191. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
2597 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Peptostreptococcales* and to the
2598 family *Anaerovoracaceae.*
2599
2600
2601 **Description of *Candidatus* Copromorpha excrementavium sp. nov.**
2602 *Candidatus* Copromorpha excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
2603 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
2604
2605 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2606 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2607 assigned the MAG ID CHK176-22527 and which is available via NCBI BioSample

2608 SAMN15817193. This is a new name for the alphanumeric GTDB species sp900542385. The
2609 GC content of the type genome is 42.88% and the genome length is 1.8 Mbp.
2610
2611
2612 **Description of *Candidatus* Copromorpha excrementigallinarum sp. nov.**
2613 *Candidatus* Copromorpha excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
2614 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
2615 excrement)
2616
2617 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2618 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2619 assigned the MAG ID ChiHcec3-6078 and which is available via NCBI BioSample
2620 SAMN15817131. The GC content of the type genome is 48.15% and the genome length is 2.0
2621 Mbp.
2622
2623
2624 **Description of *Candidatus* Copromorpha excrementipullorum sp. nov.**
2625 *Candidatus* Copromorpha excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
2626 *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
2627 young chicken excrement)
2628
2629 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2630 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2631 assigned the MAG ID ChiSjej4B22-8349 and which is available via NCBI BioSample
2632 SAMN15817205. This is a new name for the alphanumeric GTDB species sp900543485. The
2633 GC content of the type genome is 49.77% and the genome length is 1.9 Mbp.
2634
2635
2636 **Description of *Candidatus* Coproplasma gen. nov.**
2637 *Candidatus* Coproplasma (Copr.o.plas'ma. Gr. fem. n. *kopros* dung; Gr. neut. n. *plasma* a form;
2638 N.L. neut. n. *Coproplasma* a microbe associated with faeces)
2639
2640 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2641 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2642 species *Coproplasma stercoravium*. This is a name for the alphanumeric GTDB genus
2643 UBA11940. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
2644 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family
2645 *Borkfalkiaceae*.
2646
2647
2648 **Description of *Candidatus* Coproplasma avicola sp. nov.**
2649 *Candidatus* Coproplasma avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of;
2650 N.L. n. *avicola* inhabitant of birds)
2651
2652 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2653 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

2654   assigned the MAG ID ChiW16-3235 and which is available via NCBI BioSample
2655   SAMN15817075. The GC content of the type genome is 51.11% and the genome length is 1.5
2656   Mbp.
2657
2658
2659   **Description of *Candidatus* Coproplasma avistercoris sp. nov.**
2660   *Candidatus* Coproplasma avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
2661   dung; N.L. gen. n. *avistercoris* of bird faeces)
2662
2663   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2664   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2665   assigned the MAG ID ChiW7-3743 and which is available via NCBI BioSample
2666   SAMN15817023. The GC content of the type genome is 56.32% and the genome length is 1.4
2667   Mbp.
2668
2669
2670   **Description of *Candidatus* Coproplasma excrementavium sp. nov.**
2671   *Candidatus* Coproplasma excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
2672   excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
2673
2674   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2675   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2676   assigned the MAG ID CHK179-18245 and which is available via NCBI BioSample
2677   SAMN15817045. The GC content of the type genome is 50.26% and the genome length is 1.4
2678   Mbp.
2679
2680
2681   **Description of *Candidatus* Coproplasma excrementigallinarum sp. nov.**
2682   *Candidatus* Coproplasma excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
2683   *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
2684   excrement)
2685
2686   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2687   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2688   assigned the MAG ID CHK195-12923 and which is available via NCBI BioSample
2689   SAMN15817050. The GC content of the type genome is 50.00% and the genome length is 1.4
2690   Mbp.
2691
2692
2693   **Description of *Candidatus* Coproplasma excrementipullorum sp. nov.**
2694   *Candidatus* Coproplasma excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
2695   excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
2696   chicken excrement)
2697
2698   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2699   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

2700   assigned the MAG ID 10570 and which is available via NCBI BioSample SAMN15817148. The
2701   GC content of the type genome is 51.24% and the genome length is 1.7 Mbp.
2702
2703
2704   **Description of *Candidatus* Coproplasma stercoravium sp. nov.**
2705   *Candidatus* Coproplasma stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
2706   bird; N.L. gen. n. *stercoravium* of bird faeces)
2707
2708   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2709   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2710   assigned the MAG ID CHK180-19203 and which is available via NCBI BioSample
2711   SAMN15817006. The GC content of the type genome is 51.86% and the genome length is 1.6
2712   Mbp.
2713
2714
2715   **Description of *Candidatus* Coproplasma stercorigallinarum sp. nov.**
2716   *Candidatus* Coproplasma stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
2717   fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
2718
2719   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2720   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2721   assigned the MAG ID CHK191-24566 and which is available via NCBI BioSample
2722   SAMN15817171. This is a new name for the alphanumeric GTDB species sp900549005. The
2723   GC content of the type genome is 51.83% and the genome length is 1.6 Mbp.
2724
2725
2726   **Description of *Candidatus* Coproplasma stercoripullorum sp. nov.**
2727   *Candidatus* Coproplasma stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
2728   masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)
2729
2730   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2731   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2732   assigned the MAG ID ChiW25-3613 and which is available via NCBI BioSample
2733   SAMN15817071. The GC content of the type genome is 51.17% and the genome length is 1.7
2734   Mbp.
2735
2736
2737   **Description of *Candidatus* Coprosoma gen. nov.**
2738   *Candidatus* Coprosoma (Copr.o.so'ma. Gr. fem. n. *kopros* dung; Gr. neut. n. *soma* a body; N.L.
2739   neut. n. *Coprosoma* a microbe associated with faeces)
2740
2741   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2742   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2743   species *Coprosoma intestinipullorum*. This is a name for the alphanumeric GTDB genus CAG-
2744   822. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
2745   (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-822*.

2746
2747
2748 **Description of *Candidatus* Coprosoma intestinipullorum sp. nov.**
2749 *Candidatus* Coprosoma intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
2750 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
2751
2752 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2753 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2754 assigned the MAG ID CHK147-3167 and which is available via NCBI BioSample
2755 SAMN15817008. The GC content of the type genome is 31.20% and the genome length is 1.3
2756 Mbp.
2757
2758
2759 **Description of *Candidatus* Coprousia gen. nov.**
2760 *Candidatus* Coprousia (Copr.ou'si.a. Gr. fem. n. *kopros* dung; Gr. fem. n. *ousia* an essence; N.L.
2761 fem. n. *Coprousia* a microbe associated with faeces)
2762
2763 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2764 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2765 species *Coprousia avicola*. This is a name for the alphanumeric GTDB genus An7. This genus
2766 has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al.,
2767 2019; Parks et al., 2020) to the order *Coriobacteriales* and to the family *Coriobacteriaceae.*
2768
2769
2770 **Description of *Candidatus* Coprousia avicola sp. nov.**
2771 *Candidatus* Coprousia avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L. n.
2772 *avicola* inhabitant of birds)
2773
2774 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2775 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2776 assigned the MAG ID ChiHjej11B10-5566 and which is available via NCBI BioSample
2777 SAMN15817195. This is a new name for the alphanumeric GTDB species sp002159765. The
2778 GC content of the type genome is 65.47% and the genome length is 2.4 Mbp.
2779
2780
2781 **Description of *Candidatus* Coprovicinus gen. nov.**
2782 *Candidatus* Coprovicinus (Copr.o.vic.in'us. Gr. fem. n. *kopros* dung; L. masc. n. *vicinus* a
2783 neighbour; N.L. masc. n. *Coprovicinus* a microbe associated with faeces)
2784
2785 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
2786 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
2787 species *Coprovicinus avistercoris*. This is a name for the alphanumeric GTDB genus
2788 UMGS1418. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
2789 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Coriobacteriales* and to the family
2790 *Atopobiaceae.*
2791

2792

2793 **Description of *Candidatus* Coprovicinus avistercoris sp. nov.**

2794 *Candidatus* Coprovicinus avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*

2795 dung; N.L. gen. n. *avistercoris* of bird faeces)

2796

2797 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

2798 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

2799 assigned the MAG ID ChiHjej12B11-29160 and which is available via NCBI BioSample

2800 SAMN15817198. This is a new name for the alphanumeric GTDB species sp900551595. The

2801 GC content of the type genome is 49.51% and the genome length is 1.7 Mbp.

2802

2803

2804 **Description of *Candidatus* Coprovivens gen. nov.**

2805 *Candidatus* Coprovivens (Copr.o.viv'ens. Gr. fem. n. *kopros* dung; N.L. pres. part. *vivens* living;

2806 N.L. fem. n. *Coprovivens* a microbe associated with faeces)

2807

2808 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with

2809 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type

2810 species *Coprovivens excrementavium*. This is a name for the alphanumeric GTDB genus

2811 UBA11963. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-

2812 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-1000*.

2813

2814

2815 **Description of *Candidatus* Coprovivens excrementavium sp. nov.**

2816 *Candidatus* Coprovivens excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*

2817 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)

2818

2819 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

2820 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

2821 assigned the MAG ID 3297 and which is available via NCBI BioSample SAMN15817083. The

2822 GC content of the type genome is 28.25% and the genome length is 2.2 Mbp.

2823

2824

2825 **Description of *Candidatus* Corynebacterium avicola sp. nov.**

2826 *Candidatus* Corynebacterium avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of;

2827 N.L. n. *avicola* inhabitant of birds)

2828

2829 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

2830 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

2831 assigned the MAG ID CHK32-1732 and which is available via NCBI BioSample

2832 SAMN15816750. The GC content of the type genome is 66.95% and the genome length is 3.1

2833 Mbp.

2834

2835

2836 **Description of *Candidatus* Corynebacterium faecigallinarum sp. nov.**

2837 *Candidatus* Corynebacterium faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis*
2838 excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
2839
2840 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2841 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2842 assigned the MAG ID ChiHjej13B12-4958 and which is available via NCBI BioSample
2843 SAMN15816631. The GC content of the type genome is 66.91% and the genome length is 2.8
2844 Mbp.
2845
2846
2847 **Description of *Candidatus* Corynebacterium faecipullorum sp. nov.**
2848 *Candidatus* Corynebacterium faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement;
2849 L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
2850
2851 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2852 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2853 assigned the MAG ID 913 and which is available via NCBI BioSample SAMN15816858. This is
2854 a new name for the alphanumeric GTDB species sp001836165. The GC content of the type
2855 genome is 61.16% and the genome length is 2.1 Mbp.
2856
2857
2858 **Description of *Candidatus* Corynebacterium gallistercoris sp. nov.**
2859 *Candidatus* Corynebacterium gallistercoris (gal.li.ster'co.ris. L. masc. n. *gallus* chicken; L. neut.
2860 n. *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
2861
2862 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2863 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2864 assigned the MAG ID 4376 and which is available via NCBI BioSample SAMN15816747. The
2865 GC content of the type genome is 62.96% and the genome length is 2.0 Mbp.
2866
2867
2868 **Description of *Candidatus* Corynebacterium intestinavium sp. nov.**
2869 *Candidatus* Corynebacterium intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem.
2870 n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
2871
2872 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2873 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2874 assigned the MAG ID 5925 and which is available via NCBI BioSample SAMN15816787. The
2875 GC content of the type genome is 65.59% and the genome length is 1.9 Mbp.
2876
2877
2878 **Description of *Candidatus* Cottocaccamicrobium gen. nov.**
2879 *Candidatus* Cottocaccamicrobium (Cot.to.cac.co.mi.cro'bi.um. Gr. masc. n. *kottos* chicken; Gr.
2880 fem. n. *kakke* faeces; N.L. neut. n. *microbium* a microbe; N.L. neut. n. *Cottocaccamicrobium* a
2881 microbe asociated with chicken faeces)
2882

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type species *Cottocaccamicrobium excrementipullorum.* This genus was identified but not named by Glendinning et al. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family *Lachnospiraceae.*

Description of *Candidatus* Cottocaccamicrobium excrementipullorum sp. nov.
Candidatus Cottocaccamicrobium excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young chicken excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK179-5732 and which is available via NCBI BioSample SAMN15816932. The GC content of the type genome is 47.54% and the genome length is 3.4 Mbp.

Description of *Candidatus* Cryptobacteroides gen. nov.
Candidatus Cryptobacteroides (Cryp.to.bac.te.ro'i.des. Gr. masc. adj. *kryptos* hidden; N.L. masc. n. *Bacteroides* a genus name; N.L. masc. n. *Cryptobacteroides* a genus related to the genus *Bacteroides* but distinct from it)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type species *Cryptobacteroides avicola*. This is a name for the alphanumeric GTDB genus RC9. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family *UBA932*.

Description of *Candidatus* Cryptobacteroides avicola sp. nov.
Candidatus Cryptobacteroides avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L. n. *avicola* inhabitant of birds)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID G3-8215 and which is available via NCBI BioSample SAMN15817056. The GC content of the type genome is 49.81% and the genome length is 2.6 Mbp.

Description of *Candidatus* Cryptobacteroides avistercoris sp. nov.
Candidatus Cryptobacteroides avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung; N.L. gen. n. *avistercoris* of bird faeces)

2929 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2930 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2931 assigned the MAG ID B3-1481 and which is available via NCBI BioSample SAMN15817057.
2932 The GC content of the type genome is 59.28% and the genome length is 1.6 Mbp.

2933
2934

2935 **Description of *Candidatus* Cryptobacteroides excrementavium sp. nov.**
2936 *Candidatus* Cryptobacteroides excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
2937 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)

2938

2939 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2940 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2941 assigned the MAG ID B2-16538 and which is available via NCBI BioSample SAMN15817059.
2942 The GC content of the type genome is 50.29% and the genome length is 2.1 Mbp.

2943
2944

2945 **Description of *Candidatus* Cryptobacteroides excrementigallinarum sp. nov.**
2946 *Candidatus* Cryptobacteroides excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
2947 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
2948 excrement)

2949

2950 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2951 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2952 assigned the MAG ID ChiHecolR1B25-7735 and which is available via NCBI BioSample
2953 SAMN15817167. This is a new name for the alphanumeric GTDB species sp900543205. The
2954 GC content of the type genome is 57.80% and the genome length is 1.8 Mbp.

2955
2956

2957 **Description of *Candidatus* Cryptobacteroides excrementipullorum sp. nov.**
2958 *Candidatus* Cryptobacteroides excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
2959 *excrementum* excrement; L. masc. gen.pl. n. *pullorum* of young chickens; N.L. gen. n.
2960 *excrementipullorum* of young chicken excrement)

2961

2962 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2963 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2964 assigned the MAG ID 2478 and which is available via NCBI BioSample SAMN15817061. The
2965 GC content of the type genome is 52.35% and the genome length is 2.5 Mbp.

2966
2967

2968 **Description of *Candidatus* Cryptobacteroides faecavium sp. nov.**
2969 *Candidatus* Cryptobacteroides faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L.
2970 fem. n. *avis* bird; N.L. gen. n. *faecavium* of bird faeces)

2971

2972 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2973 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

2974   assigned the MAG ID B2-22910 and which is available via NCBI BioSample SAMN15817063.
2975   The GC content of the type genome is 52.41% and the genome length is 2.4 Mbp.
2976
2977
2978   **Description of *Candidatus* Cryptobacteroides faecigallinarum sp. nov.**
2979   *Candidatus* Cryptobacteroides faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis*
2980   excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
2981
2982   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2983   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2984   assigned the MAG ID B1-13419 and which is available via NCBI BioSample SAMN15817072.
2985   The GC content of the type genome is 49.87% and the genome length is 2.0 Mbp.
2986
2987
2988   **Description of *Candidatus* Cryptobacteroides faecipullorum sp. nov.**
2989   *Candidatus* Cryptobacteroides faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis*
2990   excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken
2991   faeces)
2992
2993   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
2994   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
2995   assigned the MAG ID B1-15692 and which is available via NCBI BioSample SAMN15817080.
2996   The GC content of the type genome is 49.55% and the genome length is 2.3 Mbp.
2997
2998
2999   **Description of *Candidatus* Cryptobacteroides gallistercoris sp. nov.**
3000   *Candidatus* Cryptobacteroides gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut.
3001   n. *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
3002
3003   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3004   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3005   assigned the MAG ID F1-3629 and which is available via NCBI BioSample SAMN15817088.
3006   The GC content of the type genome is 51.79% and the genome length is 2.0 Mbp.
3007
3008
3009   **Description of *Candidatus* Cryptobacteroides intestinavium sp. nov.**
3010   *Candidatus* Cryptobacteroides intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L.
3011   fem. n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
3012
3013   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3014   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3015   assigned the MAG ID B1-20833 and which is available via NCBI BioSample SAMN15817087.
3016   The GC content of the type genome is 51.51% and the genome length is 2.4 Mbp.
3017
3018
3019   **Description of *Candidatus* Cryptobacteroides intestinigallinarum sp. nov.**

3020 *Candidatus* Cryptobacteroides intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum*
3021 gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
3022
3023 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3024 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3025 assigned the MAG ID B1-3475 and which is available via NCBI BioSample SAMN15817089.
3026 The GC content of the type genome is 49.55% and the genome length is 2.3 Mbp.
3027
3028
3029 **Description of *Candidatus* Cryptobacteroides intestinipullorum sp. nov.**
3030 *Candidatus* Cryptobacteroides intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum*
3031 gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young
3032 chickens)
3033
3034 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3035 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3036 assigned the MAG ID 33258 and which is available via NCBI BioSample SAMN15817090. The
3037 GC content of the type genome is 50.60% and the genome length is 2.4 Mbp.
3038
3039
3040 **Description of *Candidatus* Cryptobacteroides merdavium sp. nov.**
3041 *Candidatus* Cryptobacteroides merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n.
3042 *avis* bird; N.L. gen. n. *merdavium* of bird faeces)
3043
3044 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3045 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3046 assigned the MAG ID D5-748 and which is available via NCBI BioSample SAMN15817104.
3047 The GC content of the type genome is 50.98% and the genome length is 2.5 Mbp.
3048
3049
3050 **Description of *Candidatus* Cryptobacteroides merdigallinarum sp. nov.**
3051 *Candidatus* Cryptobacteroides merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L.
3052 fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
3053
3054 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3055 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3056 assigned the MAG ID 20514 and which is available via NCBI BioSample SAMN15817110. The
3057 GC content of the type genome is 54.69% and the genome length is 2.3 Mbp.
3058
3059
3060 **Description of *Candidatus* Cryptobacteroides merdipullorum sp. nov.**
3061 *Candidatus* Cryptobacteroides merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L.
3062 masc. n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
3063
3064 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3065 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

3066 assigned the MAG ID ChiHecec2B26-709 and which is available via NCBI BioSample
3067 SAMN15817116. The GC content of the type genome is 57.16% and the genome length is 2.0
3068 Mbp.
3069
3070
3071 **Description of *Candidatus* Cryptobacteroides pullicola sp. nov.**
3072 *Candidatus* Cryptobacteroides pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff.
3073 *-cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
3074
3075 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3076 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3077 assigned the MAG ID ChiHecec2B26-3624 and which is available via NCBI BioSample
3078 SAMN15817179. This is a new name for the alphanumeric GTDB species sp001915575. The
3079 GC content of the type genome is 58.01% and the genome length is 1.7 Mbp.
3080
3081
3082 **Description of *Candidatus* Desulfovibrio faecigallinarum sp. nov.**
3083 *Candidatus* Desulfovibrio faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;
3084 L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
3085
3086 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3087 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3088 assigned the MAG ID 8923 and which is available via NCBI BioSample SAMN15816873. This
3089 is a new name for the alphanumeric GTDB species sp002159665. The GC content of the type
3090 genome is 57.29% and the genome length is 2.0 Mbp.
3091
3092
3093 **Description of *Candidatus* Desulfovibrio gallistercoris sp. nov.**
3094 *Candidatus* Desulfovibrio gallistercoris (gal.li.ster'co.ris. L. masc. n. *gallus* chicken; L. neut. n.
3095 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
3096
3097 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3098 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3099 assigned the MAG ID ChiGjej2B2-32749 and which is available via NCBI BioSample
3100 SAMN15816654. The GC content of the type genome is 64.54% and the genome length is 2.8
3101 Mbp.
3102
3103
3104 **Description of *Candidatus* Desulfovibrio intestinavium sp. nov.**
3105 *Candidatus* Desulfovibrio intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
3106 *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
3107
3108 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3109 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3110 assigned the MAG ID 5032 and which is available via NCBI BioSample SAMN15816664. The
3111 GC content of the type genome is 64.60% and the genome length is 2.5 Mbp.

3112
3113
3114 **Description of *Candidatus* Desulfovibrio intestinigallinarum sp. nov.**
3115 *Candidatus* Desulfovibrio intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
3116 L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
3117
3118 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3119 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3120 assigned the MAG ID ChiHecec3B27-2601 and which is available via NCBI BioSample
3121 SAMN15816737. The GC content of the type genome is 61.03% and the genome length is 2.9
3122 Mbp.
3123
3124
3125 **Description of *Candidatus* Desulfovibrio intestinipullorum sp. nov.**
3126 *Candidatus* Desulfovibrio intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
3127 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
3128
3129 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3130 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3131 assigned the MAG ID ChiHecec2B26-446 and which is available via NCBI BioSample
3132 SAMN15816774. The GC content of the type genome is 60.23% and the genome length is 2.8
3133 Mbp.
3134
3135
3136 **Description of *Candidatus* Dietzia intestinigallinarum sp. nov.**
3137 *Candidatus* Dietzia intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut; L.
3138 fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
3139
3140 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3141 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3142 assigned the MAG ID ChiHjej12B11-1528 and which is available via NCBI BioSample
3143 SAMN15816635. The GC content of the type genome is 69.86% and the genome length is 3.9
3144 Mbp.
3145
3146
3147 **Description of *Candidatus* Dietzia intestinipullorum sp. nov.**
3148 *Candidatus* Dietzia intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc.
3149 n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
3150
3151 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3152 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3153 assigned the MAG ID ChiHjej13B12-8321 and which is available via NCBI BioSample
3154 SAMN15816639. The GC content of the type genome is 71.26% and the genome length is 3.0
3155 Mbp.
3156
3157

3158 **Description of *Candidatus* Dietzia merdigallinarum sp. nov.**
3159 *Candidatus* Dietzia merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem. n.
3160 *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
3161
3162 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3163 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3164 assigned the MAG ID ChiHjej8B7-16427 and which is available via NCBI BioSample
3165 SAMN15816758. The GC content of the type genome is 68.76% and the genome length is 3.6
3166 Mbp.
3167
3168
3169 **Description of *Candidatus* Dorea faecigallinarum sp. nov.**
3170 *Candidatus* Dorea faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L. fem.
3171 n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
3172
3173 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3174 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3175 assigned the MAG ID ChiHjej12B11-29902 and which is available via NCBI BioSample
3176 SAMN15816646. The GC content of the type genome is 50.13% and the genome length is 2.0
3177 Mbp.
3178
3179
3180 **Description of *Candidatus* Dorea faecipullorum sp. nov.**
3181 *Candidatus* Dorea faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L. masc. n.
3182 *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
3183
3184 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3185 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3186 assigned the MAG ID ChiGjej2B2-10896 and which is available via NCBI BioSample
3187 SAMN15816847. This is a new name for the alphanumeric GTDB species sp900543315. The
3188 GC content of the type genome is 45.40% and the genome length is 2.3 Mbp.
3189
3190
3191 **Description of *Candidatus* Dorea gallistercoris sp. nov.**
3192 *Candidatus* Dorea gallistercoris (gal.li.ster'co.ris. L. masc. n. *gallus* chicken; L. neut. n. *stercus*
3193 dung; N.L. gen. n. *gallistercoris* of chicken faeces)
3194
3195 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3196 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3197 assigned the MAG ID ChiSxjej1B13-11762 and which is available via NCBI BioSample
3198 SAMN15816753. The GC content of the type genome is 51.71% and the genome length is 2.2
3199 Mbp.
3200
3201
3202 **Description of *Candidatus* Dorea intestinavium sp. nov.**

3203 *Candidatus* Dorea intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n. *avis*
3204 bird; N.L. gen. n. *intestinavium* of the gut of birds)

3205

3206 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3207 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3208 assigned the MAG ID CHK160-14747 and which is available via NCBI BioSample
3209 SAMN15816767. The GC content of the type genome is 35.91% and the genome length is 1.9
3210 Mbp.

3211

3212

3213 **Description of *Candidatus* Dorea intestinigallinarum sp. nov.**
3214 *Candidatus* Dorea intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut; L. fem.
3215 n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)

3216

3217 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3218 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3219 assigned the MAG ID CHK188-17839 and which is available via NCBI BioSample
3220 SAMN15816854. This is a new name for the alphanumeric GTDB species sp000765215. The
3221 GC content of the type genome is 54.58% and the genome length is 2.5 Mbp.

3222

3223

3224 **Description of *Candidatus* Dorea merdavium sp. nov.**
3225 *Candidatus* Dorea merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird; N.L.
3226 gen. n. *merdavium* of bird faeces)

3227

3228 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3229 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3230 assigned the MAG ID ChiSxjej1B13-1060 and which is available via NCBI BioSample
3231 SAMN15816851. This is a new name for the alphanumeric GTDB species sp900312975. The
3232 GC content of the type genome is 53.23% and the genome length is 2.0 Mbp.

3233

3234

3235 **Description of *Candidatus* Dorea stercoravium sp. nov.**
3236 *Candidatus* Dorea stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis* bird;
3237 N.L. gen. n. *stercoravium* of bird faeces)

3238

3239 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3240 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3241 assigned the MAG ID ChiSjej1B19-6982 and which is available via NCBI BioSample
3242 SAMN15816837. This is a new name for the alphanumeric GTDB species sp002160985. The
3243 GC content of the type genome is 55.00% and the genome length is 2.5 Mbp.

3244

3245

3246 **Description of *Candidatus* Duodenibacillus intestinavium sp. nov.**
3247 *Candidatus* Duodenibacillus intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem.
3248 n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)

3249
3250 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3251 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3252 assigned the MAG ID 2430 and which is available via NCBI BioSample SAMN15816841. This
3253 is a new name for the alphanumeric GTDB species sp900538905. The GC content of the type
3254 genome is 55.01% and the genome length is 1.8 Mbp.
3255
3256
3257 **Description of *Candidatus* Duodenibacillus intestinigallinarum sp. nov.**
3258 *Candidatus* Duodenibacillus intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum*
3259 gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
3260
3261 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3262 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3263 assigned the MAG ID CHK1-2119 and which is available via NCBI BioSample
3264 SAMN15816840. This is a new name for the alphanumeric GTDB species sp003472385. The
3265 GC content of the type genome is 56.00% and the genome length is 2.0 Mbp.
3266
3267
3268 **Description of *Candidatus* Egerieenecus gen. nov.**
3269 *Candidatus* Egerieenecus (E.ger.i.een.e'cus. L. fem. n. *egeries* dung; Gr. masc. *enoikos*
3270 inhabitant; N.L. masc. n. *Egerieenecus* a microbe associated with faeces)
3271
3272 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
3273 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
3274 species *Egerieenecus merdigallinarum*. This is a name for the alphanumeric GTDB genus
3275 UMGS1600. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
3276 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family
3277 *CAG-74*.
3278
3279
3280 **Description of *Candidatus* Egerieenecus merdigallinarum sp. nov.**
3281 *Candidatus* Egerieenecus merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
3282 n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
3283
3284 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3285 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3286 assigned the MAG ID ChiSxjej2B14-4419 and which is available via NCBI BioSample
3287 SAMN15817218. This is a new name for the alphanumeric GTDB species sp900553295. The
3288 GC content of the type genome is 60.15% and the genome length is 2.5 Mbp.
3289
3290
3291 **Description of *Candidatus* Egerieicola gen. nov.**
3292 *Candidatus* Egerieicola (E.ger.i.ei.co'la. L. fem. n. *egeries* dung; L. suff. *-cola* inhabitant of; N.L.
3293 fem. n. *Egerieicola* a microbe associated with faeces)
3294

3295 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
3296 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
3297 species *Egerieicola faecale*. This is a name for the alphanumeric GTDB genus UBA1375. This
3298 genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
3299 al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family *Ruminococcaceae*.
3300
3301
3302 **Description of *Candidatus* Egerieicola faecale sp. nov.**
3303 *Candidatus* Egerieicola faecale (fae.ca'le. L. neut. adj. *faecale* of faeces)
3304
3305 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3306 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3307 assigned the MAG ID 4509 and which is available via NCBI BioSample SAMN15817200. This
3308 is a new name for the alphanumeric GTDB species sp002305795. The GC content of the type
3309 genome is 55.66% and the genome length is 1.8 Mbp.
3310
3311
3312 **Description of *Candidatus* Egerieicola pullicola sp. nov.**
3313 *Candidatus* Egerieicola pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -*cola*
3314 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
3315
3316 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3317 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3318 assigned the MAG ID CHK184-25365 and which is available via NCBI BioSample
3319 SAMN15817017. The GC content of the type genome is 52.81% and the genome length is 1.9
3320 Mbp.
3321
3322
3323 **Description of *Candidatus* Egerieimonas gen. nov.**
3324 *Candidatus* Egerieimonas (E.ger.i.eimo'nas. L. fem. n. *egeries* dung; L. fem. n. *monas* a monad;
3325 N.L. fem. n. *Egerieimonas* a microbe associated with faeces)
3326
3327 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
3328 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
3329 species *Egerieimonas intestinavium*. This is a name for the alphanumeric GTDB genus
3330 UMGS1472. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
3331 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
3332 *Lachnospiraceae*.
3333
3334
3335 **Description of *Candidatus* Egerieimonas faecigallinarum sp. nov.**
3336 *Candidatus* Egerieimonas faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;
3337 L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
3338
3339 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3340 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

3341 assigned the MAG ID CHK180-10209 and which is available via NCBI BioSample
3342 SAMN15817015. The GC content of the type genome is 51.75% and the genome length is 2.9
3343 Mbp.
3344
3345

Description of *Candidatus* Egerieimonas intestinavium sp. nov.
3347 *Candidatus* Egerieimonas intestinavium (chicken faeces *intestinum* gut; L. fem. n. *avis* bird;
3348 N.L. gen. n. *intestinavium* of the gut of birds)
3349
3350 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3351 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3352 assigned the MAG ID ChiSxjej1B13-7041 and which is available via NCBI BioSample
3353 SAMN15817079. The GC content of the type genome is 55.23% and the genome length is 2.6
3354 Mbp.
3355
3356

Description of *Candidatus* Egerieisoma gen. nov.
3358 *Candidatus* Egerieisoma (E.ger.i.ei.so'ma. L. fem. n. *egeries* dung; Gr. neut. n. *soma* a body;
3359 N.L. neut. n. *Egerieisoma* a microbe associated with faeces)
3360
3361 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
3362 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
3363 species *Egerieisoma faecipullorum*. This is a name for the alphanumeric GTDB genus
3364 UMGS1537. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
3365 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *UBA1212* and to the family
3366 *UBA1255*.
3367
3368

Description of *Candidatus* Egerieisoma faecipullorum sp. nov.
3370 *Candidatus* Egerieisoma faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
3371 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
3372
3373 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3374 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3375 assigned the MAG ID CHK195-4489 and which is available via NCBI BioSample
3376 SAMN15817230. This is a new name for the alphanumeric GTDB species sp900543695. The
3377 GC content of the type genome is 50.69% and the genome length is 2.0 Mbp.
3378
3379

Description of *Candidatus* Egerieousia gen. nov.
3381 *Candidatus* Egerieousia (E.ger.i.e.ou'si.a. L. fem. n. *egeries* dung; Gr. fem. n. *ousia* an essence;
3382 N.L. fem. n. *Egerieousia* a microbe associated with faeces)
3383
3384 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
3385 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
3386 species *Egerieousia excrementavium*. This is a name for the alphanumeric GTDB genus

3387 UBA1232. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
3388 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family
3389 *UBA932.*
3390
3391
3392 **Description of *Candidatus* Egerieousia excrementavium sp. nov.**
3393 *Candidatus* Egerieousia excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
3394 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
3395
3396 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3397 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3398 assigned the MAG ID 15467 and which is available via NCBI BioSample SAMN15817149. The
3399 GC content of the type genome is 46.96% and the genome length is 1.5 Mbp.
3400
3401
3402 **Description of *Candidatus* Eisenbergiella intestinigallinarum sp. nov.**
3403 *Candidatus* Eisenbergiella intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum*
3404 gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
3405
3406 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3407 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3408 assigned the MAG ID ChiBcec1-1630 and which is available via NCBI BioSample
3409 SAMN15816806. This is a new name for the alphanumeric GTDB species sp900544445. The
3410 GC content of the type genome is 53.15% and the genome length is 3.4 Mbp.
3411
3412
3413 **Description of *Candidatus* Eisenbergiella intestinipullorum sp. nov.**
3414 *Candidatus* Eisenbergiella intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
3415 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
3416
3417 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3418 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3419 assigned the MAG ID CHK177-9469 and which is available via NCBI BioSample
3420 SAMN15816580. The GC content of the type genome is 54.63% and the genome length is 3.5
3421 Mbp.
3422
3423
3424 **Description of *Candidatus* Eisenbergiella merdavium sp. nov.**
3425 *Candidatus* Eisenbergiella merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
3426 bird; N.L. gen. n. *merdavium* of bird faeces)
3427
3428 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3429 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3430 assigned the MAG ID USAMLcec2-132 and which is available via NCBI BioSample
3431 SAMN15816641. The GC content of the type genome is 54.07% and the genome length is 4.2
3432 Mbp.

3433

3434

Description of *Candidatus* Eisenbergiella merdigallinarum sp. nov.

Candidatus Eisenbergiella merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID USAMLcec3-2134 and which is available via NCBI BioSample SAMN15816643. The GC content of the type genome is 57.03% and the genome length is 3.2 Mbp.

Description of *Candidatus* Eisenbergiella merdipullorum sp. nov.

Candidatus Eisenbergiella merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK179-7159 and which is available via NCBI BioSample SAMN15816597. The GC content of the type genome is 51.92% and the genome length is 3.5 Mbp.

Description of *Candidatus* Eisenbergiella pullicola sp. nov.

Candidatus Eisenbergiella pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -*cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK197-24098 and which is available via NCBI BioSample SAMN15816836. This is a new name for the alphanumeric GTDB species sp003343625. The GC content of the type genome is 54.54% and the genome length is 2.6 Mbp.

Description of *Candidatus* Eisenbergiella pullistercoris sp. nov.

Candidatus Eisenbergiella pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L. neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej3B15-24422 and which is available via NCBI BioSample SAMN15816711. The GC content of the type genome is 56.23% and the genome length is 3.3 Mbp.

Description of *Candidatus* Eisenbergiella stercoravium sp. nov.

Candidatus Eisenbergiella stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID USAMLcec4-2206 and which is available via NCBI BioSample SAMN15816624. The GC content of the type genome is 51.92% and the genome length is 3.9 Mbp.

Description of *Candidatus* Eisenbergiella stercorigallinarum sp. nov.

Candidatus Eisenbergiella stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej8B7-25341 and which is available via NCBI BioSample SAMN15816792. The GC content of the type genome is 55.79% and the genome length is 2.8 Mbp.

Description of *Candidatus* Enterenecus gen. nov.

Candidatus Enterenecus (En.ter.en.e'cus. Gr. neut. n. *enteron* the gut; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Enterenecus* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type species *Enterenecus merdae*. This is a name for the alphanumeric GTDB genus UBA9475. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family *Oscillospiraceae.*

Description of *Candidatus* Enterenecus avicola sp. nov.

Candidatus Enterenecus avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L. n. *avicola* inhabitant of birds)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 153 and which is available via NCBI BioSample SAMN15817108. The GC content of the type genome is 60.43% and the genome length is 1.9 Mbp.

Description of *Candidatus* Enterenecus avistercoris sp. nov.

Candidatus Enterenecus avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung; N.L. gen. n. *avistercoris* of bird faeces)

3525

3526 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3527 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3528 assigned the MAG ID ChiSxjej3B15-11837 and which is available via NCBI BioSample
3529 SAMN15817165. The GC content of the type genome is 64.30% and the genome length is 1.5
3530 Mbp.

3531

3532

3533 **Description of *Candidatus* Enterenecus faecium sp. nov.**
3534 *Candidatus* Enterenecus faecium (fae'ci.um. L. fem. n. *faex, faecis* excrement; L. masc. gen.pl. n.
3535 *faecium* of faeces)

3536

3537 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3538 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3539 assigned the MAG ID ChiGjej2B2-12916 and which is available via NCBI BioSample
3540 SAMN15817211. This is a new name for the alphanumeric GTDB species sp002161675. The
3541 GC content of the type genome is 60.00% and the genome length is 2.0 Mbp.

3542

3543

3544 **Description of *Candidatus* Enterenecus merdae sp. nov.**
3545 *Candidatus* Enterenecus merdae (mer'dae. L. gen. n. *merdae* of faeces)

3546

3547 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3548 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3549 assigned the MAG ID ChiHcolR17-2730 and which is available via NCBI BioSample
3550 SAMN15817102. The GC content of the type genome is 63.48% and the genome length is 1.7
3551 Mbp.

3552

3553

3554 **Description of *Candidatus* Enterenecus stercoripullorum sp. nov.**
3555 *Candidatus* Enterenecus stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc.
3556 n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)

3557

3558 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3559 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3560 assigned the MAG ID 3668 and which is available via NCBI BioSample SAMN15817106. The
3561 GC content of the type genome is 60.97% and the genome length is 1.8 Mbp.

3562

3563

3564 **Description of *Candidatus* Enterocloster excrementigallinarum sp. nov.**
3565 *Candidatus* Enterocloster excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
3566 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
3567 excrement)

3568

3569 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3570 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

3571 assigned the MAG ID CHK198-12963 and which is available via NCBI BioSample
3572 SAMN15816811. This is a new name for the alphanumeric GTDB species sp900547035. The
3573 GC content of the type genome is 51.32% and the genome length is 3.1 Mbp.
3574
3575
3576 **Description of *Candidatus* Enterocloster excrementipullorum sp. nov.**
3577 *Candidatus* Enterocloster excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
3578 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
3579 chicken excrement)
3580
3581 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3582 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3583 assigned the MAG ID CHK180-15479 and which is available via NCBI BioSample
3584 SAMN15816584. The GC content of the type genome is 53.85% and the genome length is 2.9
3585 Mbp.
3586
3587
3588 **Description of *Candidatus* Enterocloster faecavium sp. nov.**
3589 *Candidatus* Enterocloster faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
3590 *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
3591
3592 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3593 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3594 assigned the MAG ID CHK188-4685 and which is available via NCBI BioSample
3595 SAMN15816596. The GC content of the type genome is 52.23% and the genome length is 2.8
3596 Mbp.
3597
3598
3599 **Description of *Candidatus* Enterococcus avicola sp. nov.**
3600 *Candidatus* Enterococcus avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of;
3601 N.L. n. *avicola* inhabitant of birds)
3602
3603 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3604 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3605 assigned the MAG ID CHK172-16539 and which is available via NCBI BioSample
3606 SAMN15816900. Although GTDB has assigned this species to the genus it calls Enterococcus_I
3607 , this genus designation cannot be incorporated into a well-formed binomial, so in naming this
3608 species, we have used the current validly published name for the genus. The GC content of the
3609 type genome is 36.87% and the genome length is 2.2 Mbp.
3610
3611
3612 **Description of *Candidatus* Enterococcus stercoravium sp. nov.**
3613 *Candidatus* Enterococcus stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
3614 bird; N.L. gen. n. *stercoravium* of bird faeces)
3615

3616 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3617 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3618 assigned the MAG ID CHK172-14336 and which is available via NCBI BioSample
3619 SAMN15816907. Although GTDB has assigned this species to the genus it calls
3620 Enterococcus_C , this genus designation cannot be incorporated into a well-formed binomial, so
3621 in naming this species, we have used the current validly published name for the genus. The GC
3622 content of the type genome is 44.16% and the genome length is 2.3 Mbp.
3623
3624
3625 **Description of *Candidatus* Enterococcus stercoripullorum sp. nov.**
3626 *Candidatus* Enterococcus stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
3627 masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
3628
3629 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3630 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3631 assigned the MAG ID ChiHjej12B11-924 and which is available via NCBI BioSample
3632 SAMN15816914. Although GTDB has assigned this species to the genus it calls Enterococcus_E
3633 , this genus designation cannot be incorporated into a well-formed binomial, so in naming this
3634 species, we have used the current validly published name for the genus. The GC content of the
3635 type genome is 36.20% and the genome length is 2.3 Mbp.
3636
3637
3638 **Description of *Candidatus* Enterocola gen. nov.**
3639 *Candidatus* Enterocola (En.ter.o.co'la. Gr. neut. n. *enteron* the gut; L. suff. *-cola* inhabitant of;
3640 N.L. fem. n. *Enterocola* a microbe associated with faeces)
3641
3642 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
3643 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
3644 species *Enterocola intestinipullorum*. This is a name for the alphanumeric GTDB genus
3645 RUG163. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
3646 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family
3647 *Paludibacteraceae.*
3648
3649
3650 **Description of *Candidatus* Enterocola intestinipullorum sp. nov.**
3651 *Candidatus* Enterocola intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
3652 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
3653
3654 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3655 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3656 assigned the MAG ID D3-1215 and which is available via NCBI BioSample SAMN15817113.
3657 The GC content of the type genome is 47.46% and the genome length is 1.8 Mbp.
3658
3659
3660 **Description of *Candidatus* Enteromonas gen. nov.**

3661   *Candidatus* Enteromonas (En.ter.omo'nas. Gr. neut. n. *enteron* the gut; L. fem. n. *monas* a
3662   monad; N.L. fem. n. *Enteromonas* a microbe associated with the intestines)
3663
3664   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
3665   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
3666   species *Enteromonas pullistercoris*. This is a name for the alphanumeric GTDB genus UBA733.
3667   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
3668   (Chaumeil et al., 2019; Parks et al., 2020) to the order *RFN20* and to the family *CAG-826*.
3669
3670

3671   **Description of *Candidatus* Enteromonas pullicola sp. nov.**
3672   *Candidatus* Enteromonas pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
3673   inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
3674
3675   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3676   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3677   assigned the MAG ID ChiGjej1B1-22543 and which is available via NCBI BioSample
3678   SAMN15817133. The GC content of the type genome is 57.43% and the genome length is 1.2
3679   Mbp.
3680
3681

3682   **Description of *Candidatus* Enteromonas pullistercoris sp. nov.**
3683   *Candidatus* Enteromonas pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
3684   neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
3685
3686   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3687   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3688   assigned the MAG ID 17113 and which is available via NCBI BioSample SAMN15817142. The
3689   GC content of the type genome is 53.99% and the genome length is 1.4 Mbp.
3690
3691

3692   **Description of *Candidatus* Enterosoma gen. nov.**
3693   *Candidatus* Enterosoma (En.ter.o.so'ma. Gr. neut. n. *enteron* the gut; Gr. neut. n. *soma* a body;
3694   N.L. neut. n. *Enterosoma* a microbe associated with the intestines)
3695
3696   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
3697   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
3698   species *Enterosoma merdigallinarum*. This is a name for the alphanumeric GTDB genus
3699   UBA7642. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
3700   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RFN20* and to the family *CAG-288*.
3701
3702

3703   **Description of *Candidatus* Enterosoma merdigallinarum sp. nov.**
3704   *Candidatus* Enterosoma merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
3705   n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
3706

3707 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3708 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3709 assigned the MAG ID 33044 and which is available via NCBI BioSample SAMN15817141. The
3710 GC content of the type genome is 51.22% and the genome length is 1.4 Mbp.
3711
3712
3713 **Description of *Candidatus* Enterousia gen. nov.**
3714 *Candidatus* Enterousia (En.ter.ou'si.a. Gr. neut. n. *enteron* the gut; Gr. fem. n. *ousia* an essence;
3715 N.L. fem. n. *Enterousia* a microbe associated with the intestines)
3716
3717 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
3718 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
3719 species *Enterousia excrementavium*. This is a name for the alphanumeric GTDB genus Rs-D84.
3720 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
3721 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Rs-D84* and to the family *Rs-D84*.
3722
3723
3724 **Description of *Candidatus* Enterousia avicola sp. nov.**
3725 *Candidatus* Enterousia avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L.
3726 n. *avicola* inhabitant of birds)
3727
3728 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3729 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3730 assigned the MAG ID CHK136-897 and which is available via NCBI BioSample
3731 SAMN15817144. The GC content of the type genome is 39.01% and the genome length is 0.9
3732 Mbp.
3733
3734
3735 **Description of *Candidatus* Enterousia avistercoris sp. nov.**
3736 *Candidatus* Enterousia avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung;
3737 N.L. gen. n. *avistercoris* of bird faeces)
3738
3739 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3740 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3741 assigned the MAG ID 8207 and which is available via NCBI BioSample SAMN15817150. The
3742 GC content of the type genome is 43.79% and the genome length is 0.8 Mbp.
3743
3744
3745 **Description of *Candidatus* Enterousia excrementavium sp. nov.**
3746 *Candidatus* Enterousia excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
3747 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
3748
3749 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3750 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3751 assigned the MAG ID B1-16210 and which is available via NCBI BioSample SAMN15817158.
3752 The GC content of the type genome is 44.26% and the genome length is 0.9 Mbp.

3753
3754
3755 **Description of *Candidatus* Enterousia intestinigallinarum sp. nov.**
3756 *Candidatus* Enterousia intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut; L.
3757 fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
3758
3759 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3760 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3761 assigned the MAG ID ChiGjej3B3-5194 and which is available via NCBI BioSample
3762 SAMN15817183. This is a new name for the alphanumeric GTDB species sp900546185. The
3763 GC content of the type genome is 45.89% and the genome length is 0.9 Mbp.
3764
3765
3766 **Description of *Candidatus* Erysipelatoclostridium merdavium sp. nov.**
3767 *Candidatus* Erysipelatoclostridium merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem.
3768 n. *avis* bird; N.L. gen. n. *merdavium* of bird faeces)
3769
3770 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3771 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3772 assigned the MAG ID ChiGjej1B1-14440 and which is available via NCBI BioSample
3773 SAMN15816860. This is a new name for the alphanumeric GTDB species sp002160495. The
3774 GC content of the type genome is 29.32% and the genome length is 2.6 Mbp.
3775
3776
3777 **Description of *Candidatus* Eubacterium avistercoris sp. nov.**
3778 *Candidatus* Eubacterium avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
3779 dung; N.L. gen. n. *avistercoris* of bird faeces)
3780
3781 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3782 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3783 assigned the MAG ID CHK192-9172 and which is available via NCBI BioSample
3784 SAMN15816888. Although GTDB has assigned this species to the genus it calls Eubacterium_I ,
3785 this genus designation cannot be incorporated into a well-formed binomial, so in naming this
3786 species, we have used the current validly published name for the genus. The GC content of the
3787 type genome is 45.90% and the genome length is 2.6 Mbp.
3788
3789
3790 **Description of *Candidatus* Eubacterium faecale sp. nov.**
3791 *Candidatus* Eubacterium faecale (fae.ca'le. L. neut. adj. *faecale* of faeces)
3792
3793 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3794 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3795 assigned the MAG ID CHK188-16595 and which is available via NCBI BioSample
3796 SAMN15816917. This is a new name for the alphanumeric GTDB species sp000431535.
3797 Although GTDB has assigned this species to the genus it calls Eubacterium_R , this genus
3798 designation cannot be incorporated into a well-formed binomial, so in naming this species, we

3799   have used the current validly published name for the genus. The GC content of the type genome
3800   is 46.56% and the genome length is 1.8 Mbp.
3801
3802
3803   **Description of *Candidatus* Eubacterium faecavium sp. nov.**
3804   *Candidatus* Eubacterium faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
3805   *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
3806
3807   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3808   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3809   assigned the MAG ID ChiHecec3B27-3607 and which is available via NCBI BioSample
3810   SAMN15816921. This is a new name for the alphanumeric GTDB species sp900539845.
3811   Although GTDB has assigned this species to the genus it calls Eubacterium_R , this genus
3812   designation cannot be incorporated into a well-formed binomial, so in naming this species, we
3813   have used the current validly published name for the genus. The GC content of the type genome
3814   is 45.56% and the genome length is 1.9 Mbp.
3815
3816
3817   **Description of *Candidatus* Eubacterium faecigallinarum sp. nov.**
3818   *Candidatus* Eubacterium faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;
3819   L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
3820
3821   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3822   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3823   assigned the MAG ID 8396 and which is available via NCBI BioSample SAMN15816904.
3824   Although GTDB has assigned this species to the genus it calls Eubacterium_R , this genus
3825   designation cannot be incorporated into a well-formed binomial, so in naming this species, we
3826   have used the current validly published name for the genus. The GC content of the type genome
3827   is 43.37% and the genome length is 1.6 Mbp.
3828
3829
3830   **Description of *Candidatus* Eubacterium faecipullorum sp. nov.**
3831   *Candidatus* Eubacterium faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
3832   masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
3833
3834   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3835   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3836   assigned the MAG ID 421 and which is available via NCBI BioSample SAMN15816928. This is
3837   a new name for the alphanumeric GTDB species sp900546785. Although GTDB has assigned
3838   this species to the genus it calls Eubacterium_R , this genus designation cannot be incorporated
3839   into a well-formed binomial, so in naming this species, we have used the current validly
3840   published name for the genus. The GC content of the type genome is 47.26% and the genome
3841   length is 1.9 Mbp.
3842
3843
3844   **Description of *Candidatus* Eubacterium pullicola sp. nov.**

3845 *Candidatus* Eubacterium pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
3846 inhabitant of; N.L. n. *pullicola* inhabitant of young chicken)
3847
3848 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3849 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3850 assigned the MAG ID ChiHjej12B11-11929 and which is available via NCBI BioSample
3851 SAMN15816916. This is a new name for the alphanumeric GTDB species sp900540015.
3852 Although GTDB has assigned this species to the genus it calls Eubacterium_M , this genus
3853 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
3854 have used the current validly published name for the genus. The GC content of the type genome
3855 is 41.55% and the genome length is 1.2 Mbp.
3856
3857
3858 **Description of *Candidatus* Evtepia excrementipullorum sp. nov.**
3859 *Candidatus* Evtepia excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
3860 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
3861 chicken excrement)
3862
3863 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3864 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3865 assigned the MAG ID ChiSjej3B21-3892 and which is available via NCBI BioSample
3866 SAMN15816827. This is a new name for the alphanumeric GTDB species sp900546255. The
3867 GC content of the type genome is 63.06% and the genome length is 2.0 Mbp.
3868
3869
3870 **Description of *Candidatus* Evtepia faecavium sp. nov.**
3871 *Candidatus* Evtepia faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n. *avis*
3872 bird; N.L. gen. n. *faecavium* of bird faeces)
3873
3874 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3875 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3876 assigned the MAG ID ChiHecec3B27-8621 and which is available via NCBI BioSample
3877 SAMN15816713. The GC content of the type genome is 65.40% and the genome length is 2.0
3878 Mbp.
3879
3880
3881 **Description of *Candidatus* Evtepia faecigallinarum sp. nov.**
3882 *Candidatus* Evtepia faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
3883 fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
3884
3885 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3886 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3887 assigned the MAG ID ChiHcec3-601 and which is available via NCBI BioSample
3888 SAMN15816724. The GC content of the type genome is 63.50% and the genome length is 2.4
3889 Mbp.
3890

3891
3892 **Description of *Candidatus* Excrementavichristensenella gen. nov.**
3893 *Candidatus* Excrementavichristensenella (Ex.cre.ment.a.vi.chris.ten.sen.el'la. L. neut. n.
3894 *excrementum* excrement; L. fem. n. *avis* bird; N.L. fem. n. *Christensenella a* genus name*;* N.L.
3895 fem n. *Excrementavichristensenella* a genus related to the genus *Christensenella* but distinct
3896 from it and found in poultry faeces)
3897
3898 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
3899 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
3900 species *Excrementavichristensenella intestinipullorum.* This genus has been assigned by GTDB-
3901 Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the
3902 order *Christensenellales* and to the family *CAG-74.*
3903
3904
3905 **Description of *Candidatus* Excrementavichristensenella intestinipullorum sp. nov.**
3906 *Candidatus* Excrementavichristensenella intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n.
3907 *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of
3908 young chickens)
3909
3910 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3911 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3912 assigned the MAG ID ChiGjej2B2-1688 and which is available via NCBI BioSample
3913 SAMN15816955. The GC content of the type genome is 62.99% and the genome length is 2.8
3914 Mbp.
3915
3916
3917 **Description of *Candidatus* Faecalibacterium avium sp. nov.**
3918 *Candidatus* Faecalibacterium avium (a'vi.um. L. fem. pl. n. *avium* of birds)
3919
3920 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3921 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3922 assigned the MAG ID CHK182-10647 and which is available via NCBI BioSample
3923 SAMN15816876. This is a new name for the alphanumeric GTDB species sp002160915. The
3924 GC content of the type genome is 62.96% and the genome length is 2.2 Mbp.
3925
3926
3927 **Description of *Candidatus* Faecalibacterium faecigallinarum sp. nov.**
3928 *Candidatus* Faecalibacterium faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis*
3929 excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
3930
3931 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3932 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3933 assigned the MAG ID ChiSjej5B23-2810 and which is available via NCBI BioSample
3934 SAMN15816583. The GC content of the type genome is 63.38% and the genome length is 2.1
3935 Mbp.
3936

3937

3938 **Description of *Candidatus* Faecalibacterium faecipullorum sp. nov.**

3939 *Candidatus* Faecalibacterium faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement;

3940 L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

3941

3942 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

3943 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

3944 assigned the MAG ID ChiHjej9B8-13557 and which is available via NCBI BioSample

3945 SAMN15816651. The GC content of the type genome is 65.75% and the genome length is 2.1

3946 Mbp.

3947

3948

3949 **Description of *Candidatus* Faecalibacterium gallistercoris sp. nov.**

3950 *Candidatus* Faecalibacterium gallistercoris (gal.li.ster'co.ris. L. masc. n. *gallus* chicken; L. neut.

3951 n. *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)

3952

3953 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

3954 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

3955 assigned the MAG ID ChiBcec16-3735 and which is available via NCBI BioSample

3956 SAMN15816605. The GC content of the type genome is 64.68% and the genome length is 2.1

3957 Mbp.

3958

3959

3960 **Description of *Candidatus* Faecalibacterium intestinavium sp. nov.**

3961 *Candidatus* Faecalibacterium intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem.

3962 n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)

3963

3964 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

3965 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

3966 assigned the MAG ID 742 and which is available via NCBI BioSample SAMN15816744. The

3967 GC content of the type genome is 61.60% and the genome length is 1.8 Mbp.

3968

3969

3970 **Description of *Candidatus* Faecalibacterium intestinigallinarum sp. nov.**

3971 *Candidatus* Faecalibacterium intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum*

3972 gut; L.fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)

3973

3974 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

3975 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

3976 assigned the MAG ID ChiHcolR34-3080 and which is available via NCBI BioSample

3977 SAMN15816770. The GC content of the type genome is 64.34% and the genome length is 2.1

3978 Mbp.

3979

3980

3981 **Description of *Candidatus* Faecalibacterium intestinipullorum sp. nov.**

3982   *Candidatus* Faecalibacterium intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut;
3983   L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
3984
3985   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3986   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3987   assigned the MAG ID ChiHcolR21-11242 and which is available via NCBI BioSample
3988   SAMN15816785. The GC content of the type genome is 61.39% and the genome length is 2.1
3989   Mbp.
3990
3991
3992   **Description of *Candidatus* Faecalicoccus intestinipullorum sp. nov.**
3993   *Candidatus* Faecalicoccus intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
3994   masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
3995
3996   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
3997   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
3998   assigned the MAG ID ChiHjej8B7-5959 and which is available via NCBI BioSample
3999   SAMN15816766. The GC content of the type genome is 40.89% and the genome length is 1.4
4000   Mbp.
4001
4002
4003   **Description of *Candidatus* Faecaligallichristensenella gen. nov.**
4004   *Candidatus* Faecaligallichristensenella (Fae.ca.li.gal.li.chris.ten.sen.el'la. N.L. masc. adj. *faecalis*
4005   pertaining to faeces; L. masc. n. *gallus* chicken; N.L. fem. n. *Christensenella* a genus name; N.L.
4006   fem. n. *Faecaligallichristensenella* a genus related to the genus *Christensenella* but distinct from
4007   it and found in poultry faeces)
4008
4009   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4010   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4011   species *Faecaligallichristensenella faecipullorum.* This genus was identified but not named by
4012   Glendinning et al. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release
4013   05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the
4014   family *CAG-74.*
4015
4016
4017   **Description of *Candidatus* Faecaligallichristensenella faecipullorum sp. nov.**
4018   *Candidatus* Faecaligallichristensenella faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis*
4019   excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken
4020   faeces)
4021
4022   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4023   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4024   assigned the MAG ID ChiSjej6B24-5839 and which is available via NCBI BioSample
4025   SAMN15816940. The GC content of the type genome is 58.49% and the genome length is 2.6
4026   Mbp.
4027

4028
Description of *Candidatus* Faecenecus gen. nov.
Candidatus Faecenecus (Faecen.e'cus. L. fem. n. *faex* dregs; Gr. masc. *enoikos* inhabitant; N.L.
masc. n. *Faecenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
species *Faecenecus gallistercoris*. This is a name for the alphanumeric GTDB genus CAG-988.
This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
(Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-611*.

Description of *Candidatus* Faecenecus gallistercoris sp. nov.
Candidatus Faecenecus gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
stercus dung; N.L. gen. n. *gallistercoris* of chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with
genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
assigned the MAG ID CHK165-10780 and which is available via NCBI BioSample
SAMN15817166. This is a new name for the alphanumeric GTDB species sp003149915. The
GC content of the type genome is 34.49% and the genome length is 1.2 Mbp.

Description of *Candidatus* Faecicola gen. nov.
Candidatus Faecicola (Faec.i.co'la. L. fem. n. *faex* dregs; L. suff. -*cola* inhabitant of; N.L. fem.
n. *Faecicola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
species *Faecicola pullistercoris*. This is a name for the alphanumeric GTDB genus CAG-1138.
This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
(Chaumeil et al., 2019; Parks et al., 2020) to the order *4C28d-15* and to the family *CAG-917*.

Description of *Candidatus* Faecicola pullistercoris sp. nov.
Candidatus Faecicola pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L. fem.
n. *avis* bird; N.L. gen. n. *pullistercoris* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with
genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
assigned the MAG ID 5944 and which is available via NCBI BioSample SAMN15817151. The
GC content of the type genome is 48.54% and the genome length is 1.6 Mbp.

Description of *Candidatus* Faecimonas gen. nov.

4073 *Candidatus* Faecimonas (Faec.i.mo'nas. L. fem. n. *faex* dregs; L. fem. n. *monas* a monad; N.L.
4074 fem. n. *Faecimonas* a microbe associated with faeces)

4075

4076 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4077 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4078 species *Faecimonas intestinavium*. This is a name for the alphanumeric GTDB genus CAG-877.
4079 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
4080 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-611*.

4081

4082

4083 **Description of *Candidatus* Faecimonas gallistercoris sp. nov.**
4084 *Candidatus* Faecimonas gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
4085 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)

4086

4087 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4088 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4089 assigned the MAG ID CHK189-3136 and which is available via NCBI BioSample
4090 SAMN15817016. The GC content of the type genome is 28.18% and the genome length is 1.4
4091 Mbp.

4092

4093

4094 **Description of *Candidatus* Faecimonas intestinavium sp. nov.**
4095 *Candidatus* Faecimonas intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
4096 *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)

4097

4098 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4099 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4100 assigned the MAG ID USAMLcec2-12447 and which is available via NCBI BioSample
4101 SAMN15817225. This is a new name for the alphanumeric GTDB species sp900554305. The
4102 GC content of the type genome is 29.22% and the genome length is 1.8 Mbp.

4103

4104

4105 **Description of *Candidatus* Faecimorpha gen. nov.**
4106 *Candidatus* Faecimorpha (Faec.i.mor'pha. L. fem. n. *faex* dregs; Gr. fem. n. *morphe* a form,
4107 shape; N.L. fem. n. *Faecimorpha* a microbe associated with faeces)

4108

4109 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4110 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4111 species *Faecimorpha stercoravium*. This is a name for the alphanumeric GTDB genus
4112 UBA1390. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
4113 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
4114 *UBA1390*.

4115

4116

4117 **Description of *Candidatus* Faecimorpha stercoravium sp. nov.**

4118 *Candidatus* Faecimorpha stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
4119 bird; N.L. gen. n. *stercoravium* of bird faeces)

4120

4121 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4122 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4123 assigned the MAG ID CHK195-9767 and which is available via NCBI BioSample
4124 SAMN15817172. This is a new name for the alphanumeric GTDB species sp002305315. The
4125 GC content of the type genome is 49.81% and the genome length is 2.4 Mbp.

4126

4127

4128 **Description of *Candidatus* Faeciplasma gen. nov.**
4129 *Candidatus* Faeciplasma (Faec.i.plas'ma. L. fem. n. *faex* dregs; Gr. neut. n. *plasma* a form; N.L.
4130 neut. n. *Faeciplasma* a microbe associated with faeces)

4131

4132 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4133 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4134 species *Faeciplasma avium*. This is a name for the alphanumeric GTDB genus UBA1409. This
4135 genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
4136 al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family *Ruminococcaceae.*

4137

4138

4139 **Description of *Candidatus* Faeciplasma avium sp. nov.**
4140 *Candidatus* Faeciplasma avium (a'vi.um. L. fem. pl. n. *avium* of birds)

4141

4142 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4143 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4144 assigned the MAG ID 1370 and which is available via NCBI BioSample SAMN15817208. This
4145 is a new name for the alphanumeric GTDB species sp002305045. The GC content of the type
4146 genome is 51.56% and the genome length is 1.6 Mbp.

4147

4148

4149 **Description of *Candidatus* Faeciplasma gallinarum sp. nov.**
4150 *Candidatus* Faeciplasma gallinarum (gal.li.na'rum. L. fem. n. *gallina* a hen; L. gen.fem. pl. n.
4151 *gallinarum* of hens)

4152

4153 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4154 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4155 assigned the MAG ID CHK157-1446 and which is available via NCBI BioSample
4156 SAMN15817182. This is a new name for the alphanumeric GTDB species sp002338885. The
4157 GC content of the type genome is 49.59% and the genome length is 1.6 Mbp.

4158

4159

4160 **Description of *Candidatus* Faeciplasma pullistercoris sp. nov.**
4161 *Candidatus* Faeciplasma pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
4162 neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)

4163

4164   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4165   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4166   assigned the MAG ID CHK33-4379 and which is available via NCBI BioSample
4167   SAMN15817120. The GC content of the type genome is 49.45% and the genome length is 1.5
4168   Mbp.
4169
4170
4171   **Description of *Candidatus* Faecisoma gen. nov.**
4172   *Candidatus* Faecisoma (Faec.i.so'ma. L. fem. n. *faex* dregs; Gr. neut. n. *soma* a body; N.L. neut.
4173   n. *Faecisoma* a microbe associated with faeces)
4174
4175   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4176   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4177   species *Faecisoma merdavium*. This is a name for the alphanumeric GTDB genus CAG-878.
4178   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
4179   (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-822*.
4180
4181
4182   **Description of *Candidatus* Faecisoma merdavium sp. nov.**
4183   *Candidatus* Faecisoma merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
4184   N.L. gen. n. *merdavium* of bird faeces)
4185
4186   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4187   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4188   assigned the MAG ID 6595 and which is available via NCBI BioSample SAMN15817101. The
4189   GC content of the type genome is 24.63% and the genome length is 1.3 Mbp.
4190
4191
4192   **Description of *Candidatus* Faecivicinus gen. nov.**
4193   *Candidatus* Faecivicinus (Faec.i.vic.in'us. L. fem. n. *faex* dregs; L. masc. n. *vicinus* a neighbour;
4194   N.L. masc. n. *Faecivicinus* a microbe associated with faeces)
4195
4196   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4197   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4198   species *Faecivicinus avistercoris*. This is a name for the alphanumeric GTDB genus
4199   UMGS1603. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
4200   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family
4201   *CAG-74*.
4202
4203
4204   **Description of *Candidatus* Faecivicinus avistercoris sp. nov.**
4205   *Candidatus* Faecivicinus avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
4206   dung; N.L. gen. n. *avistercoris* of bird faeces)
4207
4208   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4209   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

4210 assigned the MAG ID 905 and which is available via NCBI BioSample SAMN15817031. The
4211 GC content of the type genome is 63.46% and the genome length is 2.7 Mbp.
4212
4213

4214 **Description of *Candidatus* Faecivivens gen. nov.**
4215 *Candidatus* Faecivivens (Faec.i.viv'ens. L. fem. n. *faex* dregs; N.L. pres. part. *vivens* living; N.L.
4216 fem. n. *Faecivivens* a microbe associated with faeces)
4217
4218 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4219 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4220 species *Faecivivens stercorigallinarum*. This is a name for the alphanumeric GTDB genus
4221 UBA1448. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
4222 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
4223 *Ruminococcaceae*.
4224
4225

4226 **Description of *Candidatus* Faecivivens stercoravium sp. nov.**
4227 *Candidatus* Faecivivens stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
4228 bird; N.L. gen. n. *stercoravium* of bird faeces)
4229
4230 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4231 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4232 assigned the MAG ID CHK189-12415 and which is available via NCBI BioSample
4233 SAMN15817018. The GC content of the type genome is 59.75% and the genome length is 2.3
4234 Mbp.
4235
4236

4237 **Description of *Candidatus* Faecivivens stercorigallinarum sp. nov.**
4238 *Candidatus* Faecivivens stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
4239 fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
4240
4241 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4242 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4243 assigned the MAG ID 4960 and which is available via NCBI BioSample SAMN15817121. The
4244 GC content of the type genome is 52.99% and the genome length is 2.2 Mbp.
4245
4246

4247 **Description of *Candidatus* Faecivivens stercoripullorum sp. nov.**
4248 *Candidatus* Faecivivens stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc.
4249 n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
4250
4251 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4252 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4253 assigned the MAG ID ChiBcec7-5410 and which is available via NCBI BioSample
4254 SAMN15817124. The GC content of the type genome is 50.38% and the genome length is 2.0
4255 Mbp.

4256
4257
4258 **Description of *Candidatus* Faecousia gen. nov.**
4259 *Candidatus* Faecousia (Faec.ou'si.a. L. fem. n. *faex* dregs; Gr. fem. n. *ousia* an essence; N.L.
4260 fem. n. *Faecousia* a microbe associated with faeces)
4261
4262 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4263 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4264 species *Faecousia intestinigallinarum*. This is a name for the alphanumeric GTDB genus CAG-
4265 110. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
4266 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
4267 *Oscillospiraceae.*
4268
4269
4270 **Description of *Candidatus* Faecousia excrementigallinarum sp. nov.**
4271 *Candidatus* Faecousia excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
4272 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
4273 excrement)
4274
4275 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4276 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4277 assigned the MAG ID 13361 and which is available via NCBI BioSample SAMN15817055. The
4278 GC content of the type genome is 56.40% and the genome length is 1.9 Mbp.
4279
4280
4281 **Description of *Candidatus* Faecousia excrementipullorum sp. nov.**
4282 *Candidatus* Faecousia excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
4283 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
4284 chicken excrement)
4285
4286 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4287 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4288 assigned the MAG ID ChiSxjej6B18-3616 and which is available via NCBI BioSample
4289 SAMN15817060. The GC content of the type genome is 56.19% and the genome length is 1.7
4290 Mbp.
4291
4292
4293 **Description of *Candidatus* Faecousia faecavium sp. nov.**
4294 *Candidatus* Faecousia faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n. *avis*
4295 bird; N.L. gen. n. *faecavium* of bird faeces)
4296
4297 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4298 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4299 assigned the MAG ID ChiBcec21-2751 and which is available via NCBI BioSample
4300 SAMN15817064. The GC content of the type genome is 53.76% and the genome length is 2.4
4301 Mbp.

4302
4303
4304   **Description of *Candidatus* Faecousia faecigallinarum sp. nov.**
4305   *Candidatus* Faecousia faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
4306   fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
4307
4308   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4309   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4310   assigned the MAG ID ChiHcolR29-948 and which is available via NCBI BioSample
4311   SAMN15817073. The GC content of the type genome is 58.86% and the genome length is 1.9
4312   Mbp.
4313
4314
4315   **Description of *Candidatus* Faecousia faecipullorum sp. nov.**
4316   *Candidatus* Faecousia faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
4317   masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
4318
4319   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4320   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4321   assigned the MAG ID ChiHecec2B26-1122 and which is available via NCBI BioSample
4322   SAMN15817098. The GC content of the type genome is 55.50% and the genome length is 1.9
4323   Mbp.
4324
4325
4326   **Description of *Candidatus* Faecousia gallistercoris sp. nov.**
4327   *Candidatus* Faecousia gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
4328   *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
4329
4330   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4331   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4332   assigned the MAG ID 7739 and which is available via NCBI BioSample SAMN15817186. This
4333   is a new name for the alphanumeric GTDB species sp900546915. The GC content of the type
4334   genome is 58.30% and the genome length is 1.8 Mbp.
4335
4336
4337   **Description of *Candidatus* Faecousia intestinavium sp. nov.**
4338   *Candidatus* Faecousia intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n. *avis*
4339   bird; N.L. gen. n. *intestinavium* of the gut of birds)
4340
4341   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4342   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4343   assigned the MAG ID ChiHcec3-9842 and which is available via NCBI BioSample
4344   SAMN15817111. The GC content of the type genome is 57.16% and the genome length is 2.1
4345   Mbp.
4346
4347

4348 **Description of *Candidatus* Faecousia intestinigallinarum sp. nov.**
4349 *Candidatus* Faecousia intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut; L.
4350 fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
4351
4352 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4353 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4354 assigned the MAG ID ChiSxjej3B15-29383 and which is available via NCBI BioSample
4355 SAMN15817112. The GC content of the type genome is 55.74% and the genome length is 2.1
4356 Mbp.
4357
4358
4359 **Description of *Candidatus* Fimadaptatus gen. nov.**
4360 *Candidatus* Fimadaptatus (Fim.adaptatus. L. neut. n. *fimum* dung; L. past part. masc. *adaptatus*
4361 adapted to; N.L. masc. n. *Fimadaptatus* a microbe associated with faeces)
4362
4363 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4364 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4365 species *Fimadaptatus faecigallinarum*. This is a name for the alphanumeric GTDB genus
4366 UMGS1633. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
4367 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family
4368 *CAG-74*.
4369
4370
4371 **Description of *Candidatus* Fimadaptatus faecigallinarum sp. nov.**
4372 *Candidatus* Fimadaptatus faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;
4373 L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
4374
4375 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4376 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4377 assigned the MAG ID ChiSxjej2B14-8506 and which is available via NCBI BioSample
4378 SAMN15817140. The GC content of the type genome is 60.44% and the genome length is 2.8
4379 Mbp.
4380
4381
4382 **Description of *Candidatus* Fimenecus gen. nov.**
4383 *Candidatus* Fimenecus (Fim.en.e'cus. L. neut. n. *fimum* dung; Gr. masc. *enoikos* inhabitant; N.L.
4384 masc. n. *Fimenecus* a microbe associated with faeces)
4385
4386 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4387 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4388 species *Fimenecus excrementigallinarum*. This is a name for the alphanumeric GTDB genus
4389 CAG-180. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
4390 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
4391 *Acutalibacteraceae*.
4392
4393

4394 **Description of *Candidatus* Fimenecus excrementavium sp. nov.**
4395 *Candidatus* Fimenecus excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
4396 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
4397
4398 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4399 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4400 assigned the MAG ID ChiSjej1B19-6168 and which is available via NCBI BioSample
4401 SAMN15817011. The GC content of the type genome is 50.61% and the genome length is 1.8
4402 Mbp.
4403
4404
4405 **Description of *Candidatus* Fimenecus excrementigallinarum sp. nov.**
4406 *Candidatus* Fimenecus excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
4407 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
4408 excrement)
4409
4410 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4411 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4412 assigned the MAG ID ChiGjej1B1-19959 and which is available via NCBI BioSample
4413 SAMN15817134. The GC content of the type genome is 60.29% and the genome length is 1.8
4414 Mbp.
4415
4416
4417 **Description of *Candidatus* Fimenecus stercoravium sp. nov.**
4418 *Candidatus* Fimenecus stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
4419 bird; N.L. gen. n. *stercoravium* of bird faeces)
4420
4421 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4422 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4423 assigned the MAG ID ChiHcolR13-3023 and which is available via NCBI BioSample
4424 SAMN15817181. This is a new name for the alphanumeric GTDB species sp002314305. The
4425 GC content of the type genome is 55.43% and the genome length is 1.9 Mbp.
4426
4427
4428 **Description of *Candidatus* Fimicola gen. nov.**
4429 *Candidatus* Fimicola (Fim.i.co'la. L. neut. n. *fimum* dung; L. suff. *-cola* inhabitant of; N.L. fem.
4430 n. *Fimicola* a microbe associated with faeces)
4431
4432 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4433 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4434 species *Fimicola merdigallinarum*. This is a name for the alphanumeric GTDB genus An114.
4435 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
4436 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
4437 *Anaerotignaceae.*
4438
4439

4440 **Description of *Candidatus* Fimicola cottocaccae sp. nov.**

4441 *Candidatus* Fimicola cottocaccae (cot.to.cac'cae. Gr. masc. n. *kottos* chicken Gr. fem. n. *kakke*

4442 faeces; N.L. gen. n. *cottocaccae* of chicken faeces)

4443

4444 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

4445 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

4446 assigned the MAG ID ChiW9-1577 and which is available via NCBI BioSample

4447 SAMN15817191. This is a new name for the alphanumeric GTDB species sp002161055. The

4448 GC content of the type genome is 31.91% and the genome length is 1.8 Mbp.

4449

4450

4451 **Description of *Candidatus* Fimicola merdigallinarum sp. nov.**

4452 *Candidatus* Fimicola merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem. n.

4453 *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)

4454

4455 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

4456 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

4457 assigned the MAG ID F6-4510 and which is available via NCBI BioSample SAMN15817136.

4458 The GC content of the type genome is 32.46% and the genome length is 1.8 Mbp.

4459

4460

4461 **Description of *Candidatus* Fimihabitans gen. nov.**

4462 *Candidatus* Fimihabitans (Fim.i.hab.it'ans. L. neut. n. *fimum* dung; L. pres. part. *habitans* an

4463 inhabitant; N.L. fem. n. *Fimihabitans* a microbe associated with faeces)

4464

4465 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with

4466 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type

4467 species *Fimihabitans intestinipullorum*. This is a name for the alphanumeric GTDB genus

4468 UMGS1648. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-

4469 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-822*.

4470

4471

4472 **Description of *Candidatus* Fimihabitans intestinipullorum sp. nov.**

4473 *Candidatus* Fimihabitans intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.

4474 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

4475

4476 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

4477 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

4478 assigned the MAG ID CHK197-8231 and which is available via NCBI BioSample

4479 SAMN15817229. This is a new name for the alphanumeric GTDB species sp900553765. The

4480 GC content of the type genome is 33.44% and the genome length is 1.3 Mbp.

4481

4482

4483 **Description of *Candidatus* Fimimonas gen. nov.**

4484 *Candidatus* Fimimonas (Fim.i.mo'nas. L. neut. n. *fimum* dung; L. fem. n. *monas* a monad; N.L.

4485 fem. n. *Fimimonas* a microbe associated with faeces)

4486

4487 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4488 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4489 species *Fimimonas gallinarum*. This is a name for the alphanumeric GTDB genus CAG-1435.
4490 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
4491 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family *CAG-*
4492 *314.*

4493

4494

4495 **Description of *Candidatus* Fimimonas gallinarum sp. nov.**
4496 *Candidatus* Fimimonas gallinarum (gal.li.na'rum. L. fem. n. *gallina* a hen; L. gen.fem. pl. n.
4497 *gallinarum* of hens)

4498

4499 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4500 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4501 assigned the MAG ID CHK121-14286 and which is available via NCBI BioSample
4502 SAMN15817176. This is a new name for the alphanumeric GTDB species sp000433775. The
4503 GC content of the type genome is 45.96% and the genome length is 1.4 Mbp.

4504

4505

4506 **Description of *Candidatus* Fimimonas merdipullorum sp. nov.**
4507 *Candidatus* Fimimonas merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
4508 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)

4509

4510 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4511 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4512 assigned the MAG ID ChiHjej12B11-7776 and which is available via NCBI BioSample
4513 SAMN15817153. The GC content of the type genome is 53.17% and the genome length is 1.3
4514 Mbp.

4515

4516

4517 **Description of *Candidatus* Fimimorpha gen. nov.**
4518 *Candidatus* Fimimorpha (Fim.i.mor'pha. L. neut. n. *fimum* dung; Gr. fem. n. *morphe* a form,
4519 shape; N.L. fem. n. *Fimimorpha* a microbe associated with faeces)

4520

4521 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4522 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4523 species *Fimimorpha faecalis*. This is a name for the alphanumeric GTDB genus CHKCI001.
4524 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
4525 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
4526 *Lachnospiraceae.*

4527

4528

4529 **Description of *Candidatus* Fimimorpha excrementavium sp. nov.**
4530 *Candidatus* Fimimorpha excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
4531 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)

4532

4533 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4534 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4535 assigned the MAG ID CHK193-21555 and which is available via NCBI BioSample
4536 SAMN15817029. The GC content of the type genome is 48.70% and the genome length is 3.1
4537 Mbp.

4538

4539

4540 **Description of *Candidatus* Fimimorpha faecalis sp. nov.**
4541 *Candidatus* Fimimorpha faecalis (fae.ca'lis. L. fem. adj. *faecalis* of faeces)

4542

4543 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4544 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4545 assigned the MAG ID ChiW13-3771 and which is available via NCBI BioSample
4546 SAMN15817177. This is a new name for the alphanumeric GTDB species sp900045905. The
4547 GC content of the type genome is 36.24% and the genome length is 2.9 Mbp.

4548

4549

4550 **Description of *Candidatus* Fimiplasma gen. nov.**
4551 *Candidatus* Fimiplasma (Fim.i.plas'ma. L. neut. n. *fimum* dung; Gr. neut. n. *plasma* a form; N.L.
4552 neut. n. *Fimiplasma* a microbe associated with faeces)

4553

4554 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4555 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4556 species *Fimiplasma intestinipullorum*. This is a name for the alphanumeric GTDB genus
4557 CHKCI006. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
4558 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Erysipelotrichales* and to the family
4559 *Erysipelatoclostridiaceae.*

4560

4561

4562 **Description of *Candidatus* Fimiplasma intestinipullorum sp. nov.**
4563 *Candidatus* Fimiplasma intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
4564 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

4565

4566 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4567 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4568 assigned the MAG ID CHK195-11698 and which is available via NCBI BioSample
4569 SAMN15817196. This is a new name for the alphanumeric GTDB species sp900018345. The
4570 GC content of the type genome is 43.31% and the genome length is 2.5 Mbp.

4571

4572

4573 **Description of *Candidatus* Fimisoma gen. nov.**
4574 *Candidatus* Fimisoma (Fim.i.so'ma. L. neut. n. *fimum* dung; Gr. neut. n. *soma* a body; N.L. neut.
4575 n. *Fimisoma* a microbe associated with faeces)

4576

4577   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4578   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4579   species *Fimisoma avicola*. This is a name for the alphanumeric GTDB genus CAG-145. This
4580   genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
4581   al., 2019; Parks et al., 2020) to the order *Peptostreptococcales* and to the family
4582   *Anaerovoracaceae.*
4583
4584
4585   **Description of *Candidatus* Fimisoma avicola sp. nov.**
4586   *Candidatus* Fimisoma avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. -*cola* inhabitant of; N.L. n.
4587   *avicola* inhabitant of birds)
4588
4589   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4590   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4591   assigned the MAG ID 11300 and which is available via NCBI BioSample SAMN15817197. This
4592   is a new name for the alphanumeric GTDB species sp900542565. The GC content of the type
4593   genome is 47.90% and the genome length is 2.0 Mbp.
4594
4595
4596   **Description of *Candidatus* Fimivicinus gen. nov.**
4597   *Candidatus* Fimivicinus (Fim.i.vic.in'us. L. neut. n. *fimum* dung; L. masc. n. *vicinus* a neighbour;
4598   N.L. masc. n. *Fimivicinus* a microbe associated with faeces)
4599
4600   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4601   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4602   species *Fimivicinus intestinavium*. This is a name for the alphanumeric GTDB genus UBA1691.
4603   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
4604   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
4605   *Acutalibacteraceae.*
4606
4607
4608   **Description of *Candidatus* Fimivicinus intestinavium sp. nov.**
4609   *Candidatus* Fimivicinus intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
4610   *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
4611
4612   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4613   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4614   assigned the MAG ID 2526 and which is available via NCBI BioSample SAMN15817188. This
4615   is a new name for the alphanumeric GTDB species sp900552985. The GC content of the type
4616   genome is 55.20% and the genome length is 2.5 Mbp.
4617
4618
4619   **Description of *Candidatus* Fimivivens gen. nov.**
4620   *Candidatus* Fimivivens (Fim.i.viv'ens. L. neut. n. *fimum* dung; N.L. pres. part. *vivens* living; N.L.
4621   fem. n. *Fimivivens* a microbe associated with faeces)
4622

4623   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4624   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4625   species *Fimivivens faecavium*. This is a name for the alphanumeric GTDB genus D5. This genus
4626   has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al.,
4627   2019; Parks et al., 2020) to the order *Oscillospirales* and to the family *Ruminococcaceae*.
4628
4629
4630   **Description of *Candidatus* Fimivivens faecavium sp. nov.**
4631   *Candidatus* Fimivivens faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
4632   *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
4633
4634   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4635   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4636   assigned the MAG ID CHK195-35099 and which is available via NCBI BioSample
4637   SAMN15817038. The GC content of the type genome is 58.86% and the genome length is 2.0
4638   Mbp.
4639
4640
4641   **Description of *Candidatus* Fimousia gen. nov.**
4642   *Candidatus* Fimousia (Fim.ou'si.a. L. neut. n. *fimum* dung; Gr. fem. n. *ousia* an essence; N.L.
4643   fem. n. *Fimousia* a microbe associated with faeces)
4644
4645   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4646   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4647   species *Fimousia stercorigallinarum*. This is a name for the alphanumeric GTDB genus 992a.
4648   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
4649   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
4650   *Lachnospiraceae*.
4651
4652
4653   **Description of *Candidatus* Fimousia stercorigallinarum sp. nov.**
4654   *Candidatus* Fimousia stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L. fem.
4655   n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
4656
4657   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4658   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4659   assigned the MAG ID ChiSxjej3B15-1827 and which is available via NCBI BioSample
4660   SAMN15817114. The GC content of the type genome is 41.52% and the genome length is 2.3
4661   Mbp.
4662
4663
4664   **Description of *Candidatus* Flavonifractor avicola sp. nov.**
4665   *Candidatus* Flavonifractor avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of;
4666   N.L. n. *avicola* inhabitant of birds)
4667

4668 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4669 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4670 assigned the MAG ID CHK178-4001 and which is available via NCBI BioSample
4671 SAMN15816843. This is a new name for the alphanumeric GTDB species sp002161085. The
4672 GC content of the type genome is 60.44% and the genome length is 2.5 Mbp.
4673
4674
4675 **Description of *Candidatus* Flavonifractor avistercoris sp. nov.**
4676 *Candidatus* Flavonifractor avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
4677 dung; N.L. gen. n. *avistercoris* of bird faeces)
4678
4679 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4680 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4681 assigned the MAG ID 6084 and which is available via NCBI BioSample SAMN15816821. This
4682 is a new name for the alphanumeric GTDB species sp002161215. The GC content of the type
4683 genome is 65.16% and the genome length is 2.4 Mbp.
4684
4685
4686 **Description of *Candidatus* Flavonifractor intestinigallinarum sp. nov.**
4687 *Candidatus* Flavonifractor intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum*
4688 gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
4689
4690 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4691 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4692 assigned the MAG ID CHK192-8294 and which is available via NCBI BioSample
4693 SAMN15816592. The GC content of the type genome is 61.61% and the genome length is 2.5
4694 Mbp.
4695
4696
4697 **Description of *Candidatus* Flavonifractor intestinipullorum sp. nov.**
4698 *Candidatus* Flavonifractor intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
4699 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
4700
4701 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4702 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4703 assigned the MAG ID CHK189-11263 and which is available via NCBI BioSample
4704 SAMN15816594. The GC content of the type genome is 63.72% and the genome length is 2.2
4705 Mbp.
4706
4707
4708 **Description of *Candidatus* Flavonifractor merdavium sp. nov.**
4709 *Candidatus* Flavonifractor merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
4710 bird; N.L. gen. n. *merdavium* of bird faeces)
4711
4712 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4713 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

4714 assigned the MAG ID 3313 and which is available via NCBI BioSample SAMN15816644. The
4715 GC content of the type genome is 62.46% and the genome length is 2.7 Mbp.
4716
4717

4718 **Description of *Candidatus* Flavonifractor merdigallinarum sp. nov.**
4719 *Candidatus* Flavonifractor merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L.
4720 fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
4721
4722 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4723 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4724 assigned the MAG ID ChiBcec16-6824 and which is available via NCBI BioSample
4725 SAMN15816721. The GC content of the type genome is 61.09% and the genome length is 2.6
4726 Mbp.
4727
4728

4729 **Description of *Candidatus* Flavonifractor merdipullorum sp. nov.**
4730 *Candidatus* Flavonifractor merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc.
4731 n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
4732
4733 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4734 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4735 assigned the MAG ID ChiGjej6B6-1540 and which is available via NCBI BioSample
4736 SAMN15816748. The GC content of the type genome is 61.06% and the genome length is 2.1
4737 Mbp.
4738
4739

4740 **Description of *Candidatus* Fournierella excrementavium sp. nov.**
4741 *Candidatus* Fournierella excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
4742 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
4743
4744 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4745 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4746 assigned the MAG ID ChiHcec27-1717 and which is available via NCBI BioSample
4747 SAMN15816881. This is a new name for the alphanumeric GTDB species sp004558145. The
4748 GC content of the type genome is 63.90% and the genome length is 2.4 Mbp.
4749
4750

4751 **Description of *Candidatus* Fournierella excrementigallinarum sp. nov.**
4752 *Candidatus* Fournierella excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
4753 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
4754 excrement)
4755
4756 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4757 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4758 assigned the MAG ID 1136 and which is available via NCBI BioSample SAMN15816650. The
4759 GC content of the type genome is 64.27% and the genome length is 2.1 Mbp.

4760
4761
4762 **Description of *Candidatus* Fournierella merdavium sp. nov.**
4763 *Candidatus* Fournierella merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
4764 N.L. gen. n. *merdavium* of bird faeces)
4765
4766 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4767 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4768 assigned the MAG ID ChiBcec4-1730 and which is available via NCBI BioSample
4769 SAMN15816653. The GC content of the type genome is 64.33% and the genome length is 2.6
4770 Mbp.
4771
4772
4773 **Description of *Candidatus* Fournierella merdigallinarum sp. nov.**
4774 *Candidatus* Fournierella merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
4775 n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
4776
4777 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4778 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4779 assigned the MAG ID 6296 and which is available via NCBI BioSample SAMN15816675. The
4780 GC content of the type genome is 65.05% and the genome length is 2.4 Mbp.
4781
4782
4783 **Description of *Candidatus* Fournierella merdipullorum sp. nov.**
4784 *Candidatus* Fournierella merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
4785 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
4786
4787 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4788 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4789 assigned the MAG ID ChiGjej4B4-18154 and which is available via NCBI BioSample
4790 SAMN15816693. The GC content of the type genome is 62.57% and the genome length is 2.5
4791 Mbp.
4792
4793
4794 **Description of *Candidatus* Fournierella pullicola sp. nov.**
4795 *Candidatus* Fournierella pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
4796 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
4797
4798 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4799 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4800 assigned the MAG ID 2239 and which is available via NCBI BioSample SAMN15816745. The
4801 GC content of the type genome is 62.57% and the genome length is 2.4 Mbp.
4802
4803
4804 **Description of *Candidatus* Fournierella pullistercoris sp. nov.**

4805   *Candidatus* Fournierella pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
4806   neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
4807
4808   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4809   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4810   assigned the MAG ID B5-2728 and which is available via NCBI BioSample SAMN15816762.
4811   The GC content of the type genome is 52.45% and the genome length is 1.7 Mbp.
4812
4813
4814   **Description of *Candidatus* Fusicatenibacter intestinigallinarum sp. nov.**
4815   *Candidatus* Fusicatenibacter intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum*
4816   gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
4817
4818   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4819   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4820   assigned the MAG ID CHK185-5351 and which is available via NCBI BioSample
4821   SAMN15816585. The GC content of the type genome is 51.22% and the genome length is 2.9
4822   Mbp.
4823
4824
4825   **Description of *Candidatus* Fusicatenibacter intestinipullorum sp. nov.**
4826   *Candidatus* Fusicatenibacter intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut;
4827   L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
4828
4829   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4830   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4831   assigned the MAG ID ChiBcec11-5794 and which is available via NCBI BioSample
4832   SAMN15816833. This is a new name for the alphanumeric GTDB species sp900543115. The
4833   GC content of the type genome is 49.70% and the genome length is 2.6 Mbp.
4834
4835
4836   **Description of *Candidatus* Fusicatenibacter merdavium sp. nov.**
4837   *Candidatus* Fusicatenibacter merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
4838   bird; N.L. gen. n. *merdavium* of bird faeces)
4839
4840   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4841   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4842   assigned the MAG ID CHK183-1962 and which is available via NCBI BioSample
4843   SAMN15816614. The GC content of the type genome is 51.02% and the genome length is 2.7
4844   Mbp.
4845
4846
4847   **Description of *Candidatus* Fusobacterium pullicola sp. nov.**
4848   *Candidatus* Fusobacterium pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -
4849   *cola* inhabitant of; N.L. n. *pullicola* inhabitant of a young chicken)
4850

4851 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4852 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4853 assigned the MAG ID A6-441 and which is available via NCBI BioSample SAMN15816927.
4854 This is a new name for the alphanumeric GTDB species sp900549465. Although GTDB has
4855 assigned this species to the genus it calls Fusobacterium_A , this genus designation cannot be
4856 incorporated into a well-formed binomial, so in naming this species, we have used the current
4857 validly published name for the genus. The GC content of the type genome is 29.86% and the
4858 genome length is 1.8 Mbp.
4859
4860

4861 **Description of *Candidatus* Gallacutalibacter gen. nov.**
4862 *Candidatus* Gallacutalibacter (Gall.a.cu.ta.li.bac'ter. L. masc. n. *gallus* chicken; N.L. masc. n.
4863 *Acutalibacter* a genus name; N.L. masc. n. *Gallacutalibacter* a genus related to the genus
4864 *Acutalibacter* but distinct from it and found in poultry)
4865
4866 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4867 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4868 species *Gallacutalibacter pullicola.* This genus was identified but not named by Glendinning et
4869 al. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
4870 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
4871 *Acutalibacteraceae.*
4872
4873

4874 **Description of *Candidatus* Gallacutalibacter pullicola sp. nov.**
4875 *Candidatus* Gallacutalibacter pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -
4876 *cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
4877
4878 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4879 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4880 assigned the MAG ID ChiSjej1B19-7085 and which is available via NCBI BioSample
4881 SAMN15816935. The GC content of the type genome is 56.02% and the genome length is 2.5
4882 Mbp.
4883
4884

4885 **Description of *Candidatus* Gallacutalibacter pullistercoris sp. nov.**
4886 *Candidatus* Gallacutalibacter pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken;
4887 L. neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
4888
4889 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4890 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4891 assigned the MAG ID 13869 and which is available via NCBI BioSample SAMN15816961. The
4892 GC content of the type genome is 51.21% and the genome length is 2.4 Mbp.
4893
4894

4895 **Description of *Candidatus* Gallacutalibacter stercoravium sp. nov.**

4896 *Candidatus* Gallacutalibacter stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n.
4897 *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
4898
4899 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4900 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4901 assigned the MAG ID CHK176-13069 and which is available via NCBI BioSample
4902 SAMN15816939. The GC content of the type genome is 51.38% and the genome length is 2.7
4903 Mbp.
4904
4905
4906 **Description of *Candidatus* Gallibacteroides gen. nov.**
4907 *Candidatus* Gallibacteroides (Gal.li.bac.te.ro'i.des. L. masc. n. *gallus* chicken; N.L. masc. n.
4908 *Bacteroides* a genus name; N.L. masc. n. *Gallibacteroides* a genus related to the genus
4909 *Bacteroides* but distinct from it and found in poultry)
4910
4911 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4912 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4913 species *Gallibacteroides avistercoris*. This genus has been assigned by GTDB-Tk v1.3.0
4914 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
4915 *Bacteroidales* and to the family *Barnesiellaceae.*
4916
4917
4918 **Description of *Candidatus* Gallibacteroides avistercoris sp. nov.**
4919 *Candidatus* Gallibacteroides avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
4920 dung; N.L. gen. n. *avistercoris* of bird faeces)
4921
4922 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4923 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4924 assigned the MAG ID CHK158-818 and which is available via NCBI BioSample
4925 SAMN15816984. The GC content of the type genome is 46.12% and the genome length is 2.3
4926 Mbp.
4927
4928
4929 **Description of *Candidatus* Galligastranaerophilus gen. nov.**
4930 *Candidatus* Galligastranaerophilus (Gal.li.gastr.an.a.e.ro'phi.lus. L. masc. n. *gallus* chicken; N.L.
4931 masc. n. *Gastranaerophilus* a genus name; N.L. masc. n. *Galligastranaerophilus* a genus related
4932 to the genus *Gastranaerophilus* but distinct from it and found in poultry)
4933
4934 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4935 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4936 species *Galligastranaerophilus faecipullorum.* This genus has been assigned by GTDB-Tk
4937 v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the
4938 order *Gastranaerophilales* and to the family *Gastranaerophilaceae.*
4939
4940
4941 **Description of *Candidatus* Galligastranaerophilus faecipullorum sp. nov.**

4942 *Candidatus* Galligastranaerophilus faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis*
4943 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken
4944 faeces)
4945
4946 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4947 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4948 assigned the MAG ID ChiW23-1657 and which is available via NCBI BioSample
4949 SAMN15816949. The GC content of the type genome is 39.52% and the genome length is 1.7
4950 Mbp.
4951
4952
4953 **Description of *Candidatus* Galligastranaerophilus gallistercoris sp. nov.**
4954 *Candidatus* Galligastranaerophilus gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L.
4955 neut. n. *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
4956
4957 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4958 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4959 assigned the MAG ID CHK123-4750 and which is available via NCBI BioSample
4960 SAMN15816963. The GC content of the type genome is 35.45% and the genome length is 1.8
4961 Mbp.
4962
4963
4964 **Description of *Candidatus* Galligastranaerophilus intestinavium sp. nov.**
4965 *Candidatus* Galligastranaerophilus intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L.
4966 fem. n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
4967
4968 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4969 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4970 assigned the MAG ID CHK152-2871 and which is available via NCBI BioSample
4971 SAMN15816967. The GC content of the type genome is 35.80% and the genome length is 1.6
4972 Mbp.
4973
4974
4975 **Description of *Candidatus* Galligastranaerophilus intestinigallinarum sp. nov.**
4976 *Candidatus* Galligastranaerophilus intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n.
4977 *intestinum* gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
4978
4979 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
4980 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
4981 assigned the MAG ID CHK123-3438 and which is available via NCBI BioSample
4982 SAMN15816973. The GC content of the type genome is 32.50% and the genome length is 1.7
4983 Mbp.
4984
4985
4986 **Description of *Candidatus* Gallilactobacillus gen. nov.**

4987   *Candidatus* Gallilactobacillus (Gal.li.lac.to.ba.cil'lus. L. masc. n. *gallus* chicken; N.L. masc. n.
4988   *Lactobacillus* a genus name; N.L. masc. n. *Gallilactobacillus* a genus related to the genus
4989   *Lactobacillus* but distinct from it and found in poultry)
4990
4991   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
4992   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
4993   species *Gallilactobacillus intestinavium*. This genus has been assigned by GTDB-Tk v1.3.0
4994   working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
4995   *Lactobacillales* and to the family *Lactobacillaceae.*
4996
4997
4998   **Description of *Candidatus* Gallilactobacillus intestinavium sp. nov.**
4999   *Candidatus* Gallilactobacillus intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem.
5000   n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
5001
5002   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5003   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5004   assigned the MAG ID C6-149 and which is available via NCBI BioSample SAMN15816970.
5005   The GC content of the type genome is 29.69% and the genome length is 1.2 Mbp.
5006
5007
5008   **Description of *Candidatus* Gallimonas gallistercoris sp. nov.**
5009   *Candidatus* Gallimonas gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
5010   *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
5011
5012   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5013   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5014   assigned the MAG ID CHK156-179 and which is available via NCBI BioSample
5015   SAMN15816677. The GC content of the type genome is 58.55% and the genome length is 1.6
5016   Mbp.
5017
5018
5019   **Description of *Candidatus* Gallimonas intestinavium sp. nov.**
5020   *Candidatus* Gallimonas intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
5021   *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
5022
5023   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5024   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5025   assigned the MAG ID ChiW7-2402 and which is available via NCBI BioSample
5026   SAMN15816844. This is a new name for the alphanumeric GTDB species sp003343805. The
5027   GC content of the type genome is 58.63% and the genome length is 1.8 Mbp.
5028
5029
5030   **Description of *Candidatus* Gallimonas intestinigallinarum sp. nov.**
5031   *Candidatus* Gallimonas intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
5032   L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)

5033
5034   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5035   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5036   assigned the MAG ID CHK33-5263 and which is available via NCBI BioSample
5037   SAMN15816692. The GC content of the type genome is 57.82% and the genome length is 1.6
5038   Mbp.
5039
5040
5041   **Description of *Candidatus* Gallipaludibacter gen. nov.**
5042   *Candidatus* Gallipaludibacter (Gal.li.pa.lu.di.bac'ter. L. masc. n. *gallus* chicken; N.L. masc. n.
5043   *Paludibacter* a genus name; N.L. masc. n. *Gallipaludibacter* a genus related to the genus
5044   *Paludibacter* but distinct from it and found in poultry)
5045
5046   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5047   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5048   species *Gallipaludibacter merdavium.* This genus has been assigned by GTDB-Tk v1.3.0
5049   working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
5050   *Bacteroidales* and to the family *Paludibacteraceae.*
5051
5052
5053   **Description of *Candidatus* Gallipaludibacter merdavium sp. nov.**
5054   *Candidatus* Gallipaludibacter merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
5055   bird; N.L. gen. n. *merdavium* of bird faeces)
5056
5057   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5058   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5059   assigned the MAG ID G3-3990 and which is available via NCBI BioSample SAMN15816954.
5060   The GC content of the type genome is 41.91% and the genome length is 2.9 Mbp.
5061
5062
5063   **Description of *Candidatus* Gallitreponema gen. nov.**
5064   *Candidatus* Gallitreponema (Gal.li.tre.po.ne'ma. L. masc. n. *gallus* chicken; N.L. neut. n.
5065   *Treponema* a genus name; N.L. neut. n. *Gallitreponema* a genus related to the genus *Treponema*
5066   but distinct from it and found in poultry)
5067
5068   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5069   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5070   species *Gallitreponema excrementavium.* This genus has been assigned by GTDB-Tk v1.3.0
5071   working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
5072   *Treponematales* and to the family *Treponemataceae.*
5073
5074
5075   **Description of *Candidatus* Gallitreponema excrementavium sp. nov.**
5076   *Candidatus* Gallitreponema excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
5077   excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
5078

5079   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5080   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5081   assigned the MAG ID 10532 and which is available via NCBI BioSample SAMN15816962. The
5082   GC content of the type genome is 40.13% and the genome length is 2.4 Mbp.
5083
5084
5085   **Description of *Candidatus* Galloscillospira gen. nov.**
5086   *Candidatus* Galloscillospira (Gall.os.cil.lo.spi'ra. L. masc. n. *gallus* chicken; N.L. fem. n.
5087   *Oscillospira* a genus name; N.L. fem. n. *Galloscillospira.* a genus related to the genus
5088   *Oscillospira* but distinct from it and found in poultry)
5089
5090   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5091   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5092   species *Galloscillospira excrementipullorum.* This genus belongs to the new family *Candidatus*
5093   Galloscillospiraceae.
5094
5095
5096   **Description of *Candidatus* Galloscillospira excrementavium sp. nov.**
5097   *Candidatus* Galloscillospira excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
5098   excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
5099
5100   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5101   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5102   assigned the MAG ID ChiSjej1B19-13426 and which is available via NCBI BioSample
5103   SAMN15816937. The GC content of the type genome is 65.18% and the genome length is 2.1
5104   Mbp.
5105
5106
5107   **Description of *Candidatus* Galloscillospira excrementipullorum sp. nov.**
5108   *Candidatus* Galloscillospira excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
5109   *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
5110   young chicken excrement)
5111
5112   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5113   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5114   assigned the MAG ID ChiHjej8B7-10251 and which is available via NCBI BioSample
5115   SAMN15816946. The GC content of the type genome is 60.78% and the genome length is 1.6
5116   Mbp.
5117
5118
5119   **Description of *Candidatus* Galloscillospira stercoripullorum sp. nov.**
5120   *Candidatus* Galloscillospira stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
5121   masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
5122
5123   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5124   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

5125   assigned the MAG ID CHK33-6455 and which is available via NCBI BioSample
5126   SAMN15816975. The GC content of the type genome is 62.96% and the genome length is 1.9
5127   Mbp.
5128
5129
5130   **Description of *Candidatus* Galloscillospiraceae fam. nov.**
5131   *Candidatus* Galloscillospiraceae (Gall.os.cil.lo.spi.ra.ce'ae. N.L. fem. n. *Galloscillospira.* type
5132   genus of the family genus; N.L. suff. –*ceae* to denote a family; N.L. fem. pl. n.
5133   *Galloscillospiraceae*, the family of the genus *Galloscillospira*)
5134
5135   A bacterial family identified by metagenomic analyses. This family has been defined by the
5136   absence of a family assignment for the type species when GTDB-Tk v1.3.0 is applied to GTDB
5137   Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). GTDB assigns the type species and
5138   thus the family to the order *Oscillospirales*.
5139
5140
5141   **Description of *Candidatus* Gemmiger avicola sp. nov.**
5142   *Candidatus* Gemmiger avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. -*cola* inhabitant of; N.L.
5143   n. *avicola* inhabitant of birds)
5144
5145   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5146   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5147   assigned the MAG ID ChiBcec8-13705 and which is available via NCBI BioSample
5148   SAMN15816825. This is a new name for the alphanumeric GTDB species sp900548355. The
5149   GC content of the type genome is 61.69% and the genome length is 2.3 Mbp.
5150
5151
5152   **Description of *Candidatus* Gemmiger avistercoris sp. nov.**
5153   *Candidatus* Gemmiger avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung;
5154   N.L. gen. n. *avistercoris* of bird faeces)
5155
5156   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5157   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5158   assigned the MAG ID CHK188-11489 and which is available via NCBI BioSample
5159   SAMN15816604. The GC content of the type genome is 63.30% and the genome length is 2.2
5160   Mbp.
5161
5162
5163   **Description of *Candidatus* Gemmiger avium sp. nov.**
5164   *Candidatus* Gemmiger avium (a'vi.um. L. fem. pl. n. *avium* of birds)
5165
5166   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5167   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5168   assigned the MAG ID ChiGjej4B4-15321 and which is available via NCBI BioSample
5169   SAMN15816926. This is a new name for the alphanumeric GTDB species sp002160955.
5170   Although GTDB has assigned this species to the genus it calls Gemmiger_A , this genus

5171   designation cannot be incorporated into a well-formed binomial, so in naming this species, we
5172   have used the current validly published name for the genus. The GC content of the type genome
5173   is 62.71% and the genome length is 2.6 Mbp.
5174
5175
5176   **Description of *Candidatus* Gemmiger excrementavium sp. nov.**
5177   *Candidatus* Gemmiger excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
5178   excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
5179
5180   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5181   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5182   assigned the MAG ID 3436 and which is available via NCBI BioSample SAMN15816690. The
5183   GC content of the type genome is 60.89% and the genome length is 2.5 Mbp.
5184
5185
5186   **Description of *Candidatus* Gemmiger excrementigallinarum sp. nov.**
5187   *Candidatus* Gemmiger excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
5188   *excrementum* excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementigallinarum* of hen
5189   excrement)
5190
5191   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5192   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5193   assigned the MAG ID ChiSxjej1B13-11774 and which is available via NCBI BioSample
5194   SAMN15816691. The GC content of the type genome is 58.73% and the genome length is 2.4
5195   Mbp.
5196
5197
5198   **Description of *Candidatus* Gemmiger excrementipullorum sp. nov.**
5199   *Candidatus* Gemmiger excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
5200   excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
5201   chicken excrement)
5202
5203   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5204   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5205   assigned the MAG ID ChiHecec2B26-7398 and which is available via NCBI BioSample
5206   SAMN15816726. The GC content of the type genome is 64.11% and the genome length is 2.1
5207   Mbp.
5208
5209
5210   **Description of *Candidatus* Gemmiger faecavium sp. nov.**
5211   *Candidatus* Gemmiger faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n. *avis*
5212   bird; N.L. gen. n. *faecavium* of bird faeces)
5213
5214   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5215   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5216   assigned the MAG ID ChiSxjej1B13-1558 and which is available via NCBI BioSample

5217   SAMN15816740. The GC content of the type genome is 60.04% and the genome length is 2.5
5218   Mbp.
5219
5220
5221   **Description of *Candidatus* Gemmiger faecigallinarum sp. nov.**
5222   *Candidatus* Gemmiger faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
5223   fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
5224
5225   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5226   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5227   assigned the MAG ID 14795 and which is available via NCBI BioSample SAMN15816795. The
5228   GC content of the type genome is 63.90% and the genome length is 2.6 Mbp.
5229
5230
5231   **Description of *Candidatus* Gemmiger stercoravium sp. nov.**
5232   *Candidatus* Gemmiger stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
5233   bird; N.L. gen. n. *stercoravium* of bird faeces)
5234
5235   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5236   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5237   assigned the MAG ID ChiBcolR8-2160 and which is available via NCBI BioSample
5238   SAMN15816579. The GC content of the type genome is 65.46% and the genome length is 2.5
5239   Mbp.
5240
5241
5242   **Description of *Candidatus* Gemmiger stercorigallinarum sp. nov.**
5243   *Candidatus* Gemmiger stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
5244   fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
5245
5246   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5247   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5248   assigned the MAG ID CHK183-27628 and which is available via NCBI BioSample
5249   SAMN15816586. The GC content of the type genome is 64.08% and the genome length is 2.5
5250   Mbp.
5251
5252
5253   **Description of *Candidatus* Gemmiger stercoripullorum sp. nov.**
5254   *Candidatus* Gemmiger stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc.
5255   n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
5256
5257   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5258   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5259   assigned the MAG ID ChiSjej4B22-15101 and which is available via NCBI BioSample
5260   SAMN15816589. The GC content of the type genome is 64.37% and the genome length is 2.2
5261   Mbp.
5262

5263
5264 **Description of *Candidatus* Gordonibacter avicola sp. nov.**
5265 *Candidatus* Gordonibacter avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. -*cola* inhabitant of;
5266 N.L. n. *avicola* inhabitant of birds)
5267
5268 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5269 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5270 assigned the MAG ID ChiSxjej6B18-1472 and which is available via NCBI BioSample
5271 SAMN15816757. The GC content of the type genome is 59.91% and the genome length is 3.1
5272 Mbp.
5273
5274
5275 **Description of *Candidatus* Halomonas stercoripullorum sp. nov.**
5276 *Candidatus* Halomonas stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc.
5277 n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
5278
5279 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5280 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5281 assigned the MAG ID 1193 and which is available via NCBI BioSample SAMN15816734. The
5282 GC content of the type genome is 59.74% and the genome length is 2.1 Mbp.
5283
5284
5285 **Description of *Candidatus* Helicobacter avicola sp. nov.**
5286 *Candidatus* Helicobacter avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. -*cola* inhabitant of; N.L.
5287 n. *avicola* inhabitant of birds)
5288
5289 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5290 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5291 assigned the MAG ID 14449 and which is available via NCBI BioSample SAMN15816913.
5292 Although GTDB has assigned this species to the genus it calls Helicobacter_F , this genus
5293 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
5294 have used the current validly published name for the genus. The GC content of the type genome
5295 is 42.81% and the genome length is 1.7 Mbp.
5296
5297
5298 **Description of *Candidatus* Helicobacter avistercoris sp. nov.**
5299 *Candidatus* Helicobacter avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
5300 dung; N.L. gen. n. *avistercoris* of bird faeces)
5301
5302 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5303 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5304 assigned the MAG ID CHK158-8274 and which is available via NCBI BioSample
5305 SAMN15816903. Although GTDB has assigned this species to the genus it calls Helicobacter_G
5306 , this genus designation cannot be incorporated into a well-formed binomial, so in naming this
5307 species, we have used the current validly published name for the genus. The GC content of the
5308 type genome is 38.34% and the genome length is 1.4 Mbp.

5309

5310

Description of *Candidatus* Hungatella pullicola sp. nov.

Candidatus Hungatella pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with
genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
assigned the MAG ID CHK186-17716 and which is available via NCBI BioSample
SAMN15816620. The GC content of the type genome is 44.57% and the genome length is 2.9
Mbp.

Description of *Candidatus* Ignatzschineria merdigallinarum sp. nov.

Candidatus Ignatzschineria merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L.
fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with
genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
assigned the MAG ID CHK160-9182 and which is available via NCBI BioSample
SAMN15816769. The GC content of the type genome is 39.66% and the genome length is 2.3
Mbp.

Description of *Candidatus* Intestinimonas merdavium sp. nov.

Candidatus Intestinimonas merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
bird; N.L. gen. n. *merdavium* of bird faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with
genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
assigned the MAG ID CHK33-7979 and which is available via NCBI BioSample
SAMN15816706. The GC content of the type genome is 61.44% and the genome length is 2.4
Mbp.

Description of *Candidatus* Intestinimonas pullistercoris sp. nov.

Candidatus Intestinimonas pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with
genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
assigned the MAG ID CHK186-1790 and which is available via NCBI BioSample
SAMN15816581. The GC content of the type genome is 64.76% and the genome length is 2.4
Mbp.

5355 **Description of *Candidatus* Intestinimonas stercoravium sp. nov.**
5356 *Candidatus* Intestinimonas stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n.
5357 *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
5358
5359 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5360 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5361 assigned the MAG ID ChiBcolR2-622 and which is available via NCBI BioSample
5362 SAMN15816599. The GC content of the type genome is 65.33% and the genome length is 2.2
5363 Mbp.
5364
5365
5366 **Description of *Candidatus* Intestinimonas stercorigallinarum sp. nov.**
5367 *Candidatus* Intestinimonas stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
5368 fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
5369
5370 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5371 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5372 assigned the MAG ID ChiSxjej2B14-1745 and which is available via NCBI BioSample
5373 SAMN15816719. The GC content of the type genome is 65.69% and the genome length is 2.1
5374 Mbp.
5375
5376
5377 **Description of *Candidatus* Janibacter merdipullorum sp. nov.**
5378 *Candidatus* Janibacter merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
5379 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
5380
5381 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5382 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5383 assigned the MAG ID ChiHjej13B12-21492 and which is available via NCBI BioSample
5384 SAMN15816685. The GC content of the type genome is 71.49% and the genome length is 2.8
5385 Mbp.
5386
5387
5388 **Description of *Candidatus* Jeotgalibaca merdavium sp. nov.**
5389 *Candidatus* Jeotgalibaca merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
5390 N.L. gen. n. *merdavium* of bird faeces)
5391
5392 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5393 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5394 assigned the MAG ID CHK171-505 and which is available via NCBI BioSample
5395 SAMN15816828. This is a new name for the alphanumeric GTDB species sp001975685. The
5396 GC content of the type genome is 38.39% and the genome length is 2.0 Mbp.
5397
5398
5399 **Description of *Candidatus* Jeotgalibaca pullicola sp. nov.**

5400   *Candidatus* Jeotgalibaca pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
5401   inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
5402
5403   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5404   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5405   assigned the MAG ID CHK172-9797 and which is available via NCBI BioSample
5406   SAMN15816826. This is a new name for the alphanumeric GTDB species sp003955755. The
5407   GC content of the type genome is 36.93% and the genome length is 2.6 Mbp.
5408
5409
5410   **Description of *Candidatus* Jeotgalicoccus stercoravium sp. nov.**
5411   *Candidatus* Jeotgalicoccus stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n.
5412   *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
5413
5414   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5415   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5416   assigned the MAG ID CHK148-7025 and which is available via NCBI BioSample
5417   SAMN15816765. The GC content of the type genome is 36.17% and the genome length is 1.7
5418   Mbp.
5419
5420
5421   **Description of *Candidatus* Kurthia intestinigallinarum sp. nov.**
5422   *Candidatus* Kurthia intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut; L.
5423   fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
5424
5425   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5426   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5427   assigned the MAG ID CHK171-3164 and which is available via NCBI BioSample
5428   SAMN15816863. This is a new name for the alphanumeric GTDB species sp002418445. The
5429   GC content of the type genome is 39.62% and the genome length is 2.9 Mbp.
5430
5431
5432   **Description of *Candidatus* Lachnoclostridium avicola sp. nov.**
5433   *Candidatus* Lachnoclostridium avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant
5434   of; N.L. n. *avicola* inhabitant of birds)
5435
5436   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5437   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5438   assigned the MAG ID CHK190-19777 and which is available via NCBI BioSample
5439   SAMN15816889. Although GTDB has assigned this species to the genus it calls
5440   Lachnoclostridium_A , this genus designation cannot be incorporated into a well-formed
5441   binomial, so in naming this species, we have used the current validly published name for the
5442   genus. The GC content of the type genome is 54.75% and the genome length is 2.9 Mbp.
5443
5444
5445   **Description of *Candidatus* Lachnoclostridium pullistercoris sp. nov.**

5446 *Candidatus* Lachnoclostridium pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young
5447 chicken; L. neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
5448
5449 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5450 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5451 assigned the MAG ID CHK183-5548 and which is available via NCBI BioSample
5452 SAMN15816884. Although GTDB has assigned this species to the genus it calls
5453 Lachnoclostridium_A , this genus designation cannot be incorporated into a well-formed
5454 binomial, so in naming this species, we have used the current validly published name for the
5455 genus. The GC content of the type genome is 54.35% and the genome length is 2.8 Mbp.
5456
5457
5458 **Description of *Candidatus* Lachnoclostridium stercoravium sp. nov.**
5459 *Candidatus* Lachnoclostridium stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n.
5460 *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
5461
5462 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5463 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5464 assigned the MAG ID CHK178-16964 and which is available via NCBI BioSample
5465 SAMN15816887. Although GTDB has assigned this species to the genus it calls
5466 Lachnoclostridium_A , this genus designation cannot be incorporated into a well-formed
5467 binomial, so in naming this species, we have used the current validly published name for the
5468 genus. The GC content of the type genome is 49.55% and the genome length is 3.0 Mbp.
5469
5470
5471 **Description of *Candidatus* Lachnoclostridium stercorigallinarum sp. nov.**
5472 *Candidatus* Lachnoclostridium stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus*
5473 dung; L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
5474
5475 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5476 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5477 assigned the MAG ID ChiBcec1-1093 and which is available via NCBI BioSample
5478 SAMN15816897. Although GTDB has assigned this species to the genus it calls
5479 Lachnoclostridium_A , this genus designation cannot be incorporated into a well-formed
5480 binomial, so in naming this species, we have used the current validly published name for the
5481 genus. The GC content of the type genome is 54.29% and the genome length is 2.4 Mbp.
5482
5483
5484 **Description of *Candidatus* Lachnoclostridium stercoripullorum sp. nov.**
5485 *Candidatus* Lachnoclostridium stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung;
5486 L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young
5487 chickens)
5488
5489 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5490 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5491 assigned the MAG ID ChiGjej4B4-12881 and which is available via NCBI BioSample

5492   SAMN15816908. Although GTDB has assigned this species to the genus it calls
5493   Lachnoclostridium_A , this genus designation cannot be incorporated into a well-formed
5494   binomial, so in naming this species, we have used the current validly published name for the
5495   genus. The GC content of the type genome is 59.38% and the genome length is 2.3 Mbp.
5496
5497
5498   **Description of *Candidatus* Lactobacillus pullistercoris sp. nov.**
5499   *Candidatus* Lactobacillus pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
5500   neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
5501
5502   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5503   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5504   assigned the MAG ID F6-686 and which is available via NCBI BioSample SAMN15816686.
5505   The GC content of the type genome is 34.54% and the genome length is 1.7 Mbp.
5506
5507
5508   **Description of *Candidatus* Lawsonibacter pullicola sp. nov.**
5509   *Candidatus* Lawsonibacter pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -
5510   *cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
5511
5512   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5513   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5514   assigned the MAG ID CHK178-3907 and which is available via NCBI BioSample
5515   SAMN15816869. This is a new name for the alphanumeric GTDB species sp002160305. The
5516   GC content of the type genome is 62.98% and the genome length is 2.3 Mbp.
5517
5518
5519   **Description of *Candidatus* Levilactobacillus faecigallinarum sp. nov.**
5520   *Candidatus* Levilactobacillus faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis*
5521   excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
5522
5523   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5524   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5525   assigned the MAG ID CHK173-259 and which is available via NCBI BioSample
5526   SAMN15816755. The GC content of the type genome is 52.18% and the genome length is 1.8
5527   Mbp.
5528
5529
5530   **Description of *Candidatus* Ligilactobacillus avistercoris sp. nov.**
5531   *Candidatus* Ligilactobacillus avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
5532   dung; N.L. gen. n. *avistercoris* of bird faeces)
5533
5534   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5535   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5536   assigned the MAG ID ChiBile7-59 and which is available via NCBI BioSample

5537   SAMN15816642. The GC content of the type genome is 51.08% and the genome length is 1.2
5538   Mbp.
5539
5540

5541   **Description of *Candidatus* Ligilactobacillus excrementavium sp. nov.**
5542   *Candidatus* Ligilactobacillus excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
5543   excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
5544
5545   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5546   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5547   assigned the MAG ID 2259 and which is available via NCBI BioSample SAMN15816683. The
5548   GC content of the type genome is 38.00% and the genome length is 1.9 Mbp.
5549
5550

5551   **Description of *Candidatus* Ligilactobacillus excrementigallinarum sp. nov.**
5552   *Candidatus* Ligilactobacillus excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
5553   *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
5554   excrement)
5555
5556   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5557   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5558   assigned the MAG ID 6627 and which is available via NCBI BioSample SAMN15816741. The
5559   GC content of the type genome is 34.16% and the genome length is 1.2 Mbp.
5560
5561

5562   **Description of *Candidatus* Ligilactobacillus excrementipullorum sp. nov.**
5563   *Candidatus* Ligilactobacillus excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
5564   *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
5565   young chicken excrement)
5566
5567   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5568   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5569   assigned the MAG ID CHK171-2193 and which is available via NCBI BioSample
5570   SAMN15816749. The GC content of the type genome is 42.06% and the genome length is 2.0
5571   Mbp.
5572
5573

5574   **Description of *Candidatus* Ligilactobacillus faecavium sp. nov.**
5575   *Candidatus* Ligilactobacillus faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem.
5576   n. *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
5577
5578   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5579   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5580   assigned the MAG ID 3439 and which is available via NCBI BioSample SAMN15816798. The
5581   GC content of the type genome is 40.05% and the genome length is 1.3 Mbp.
5582

5583
5584 **Description of *Candidatus* Limadaptatus gen. nov.**
5585 *Candidatus* Limadaptatus (Lim.adaptatus. L. masc. n. *limus* dung; L. past part. masc. *adaptatus*
5586 adapted to; N.L. masc. n. *Limadaptatus* a microbe associated with faeces)
5587
5588 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5589 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5590 species *Limadaptatus stercoripullorum*. This is a name for the alphanumeric GTDB genus
5591 UMGS1688. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
5592 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family
5593 *CAG-917*.
5594
5595
5596 **Description of *Candidatus* Limadaptatus stercoravium sp. nov.**
5597 *Candidatus* Limadaptatus stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
5598 bird; N.L. gen. n. *stercoravium* of bird faeces)
5599
5600 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5601 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5602 assigned the MAG ID CHK154-227 and which is available via NCBI BioSample
5603 SAMN15817097. The GC content of the type genome is 58.03% and the genome length is 1.4
5604 Mbp.
5605
5606
5607 **Description of *Candidatus* Limadaptatus stercorigallinarum sp. nov.**
5608 *Candidatus* Limadaptatus stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
5609 fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
5610
5611 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5612 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5613 assigned the MAG ID 1063 and which is available via NCBI BioSample SAMN15817231. This
5614 is a new name for the alphanumeric GTDB species sp900544575. The GC content of the type
5615 genome is 56.41% and the genome length is 1.5 Mbp.
5616
5617
5618 **Description of *Candidatus* Limadaptatus stercoripullorum sp. nov.**
5619 *Candidatus* Limadaptatus stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
5620 masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
5621
5622 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5623 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5624 assigned the MAG ID 10406 and which is available via NCBI BioSample SAMN15817154. The
5625 GC content of the type genome is 61.19% and the genome length is 1.4 Mbp.
5626
5627
5628 **Description of *Candidatus* Limenecus gen. nov.**

5629 *Candidatus* Limenecus (Lim.en.e'cus. L. masc. n. *limus* dung; Gr. masc. *enoikos* inhabitant; N.L.
5630 masc. n. *Limenecus* a microbe associated with faeces)
5631
5632 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5633 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5634 species *Limenecus avicola*. This is a name for the alphanumeric GTDB genus CAG-306. This
5635 genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
5636 al., 2019; Parks et al., 2020) to the order *Gastranaerophilales* and to the family
5637 *Gastranaerophilaceae.*
5638
5639
5640 **Description of *Candidatus* Limenecus avicola sp. nov.**
5641 *Candidatus* Limenecus avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L.
5642 n. *avicola* inhabitant of birds)
5643
5644 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5645 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5646 assigned the MAG ID CHK154-7741 and which is available via NCBI BioSample
5647 SAMN15817206. This is a new name for the alphanumeric GTDB species sp000980375. The
5648 GC content of the type genome is 36.63% and the genome length is 2.1 Mbp.
5649
5650
5651 **Description of *Candidatus* Limicola gen. nov.**
5652 *Candidatus* Limicola (Lim.i.co'la. L. masc. n. *limus* dung; L. suff. *-cola* inhabitant of; N.L. fem.
5653 n. *Limicola* a microbe associated with faeces)
5654
5655 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5656 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5657 species *Limicola stercorigallinarum*. This is a name for the alphanumeric GTDB genus An2-A.
5658 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
5659 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Coriobacteriales* and to the family
5660 *Coriobacteriaceae.*
5661
5662
5663 **Description of *Candidatus* Limicola stercorigallinarum sp. nov.**
5664 *Candidatus* Limicola stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L. fem.
5665 n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
5666
5667 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5668 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5669 assigned the MAG ID ChiGjej1B1-16188 and which is available via NCBI BioSample
5670 SAMN15817082. The GC content of the type genome is 60.48% and the genome length is 2.0
5671 Mbp.
5672
5673
5674 **Description of *Candidatus* Limihabitans gen. nov.**

5675 *Candidatus* Limihabitans (Lim.i.hab.it'ans. L. masc. n. *limus* dung; L. pres. part. *habitans* an
5676 inhabitant; N.L. fem. n. *Limihabitans* a microbe associated with faeces)
5677
5678 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5679 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5680 species *Limihabitans stercoravium*. This is a name for the alphanumeric GTDB genus
5681 UMGS1707. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
5682 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *4C28d-15* and to the family *CAG-
5683 314.*
5684
5685
5686 **Description of *Candidatus* Limihabitans stercoravium sp. nov.**
5687 *Candidatus* Limihabitans stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
5688 bird; N.L. gen. n. *stercoravium* of bird faeces)
5689
5690 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5691 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5692 assigned the MAG ID 3394 and which is available via NCBI BioSample SAMN15817227. This
5693 is a new name for the alphanumeric GTDB species sp900547645. The GC content of the type
5694 genome is 43.23% and the genome length is 1.6 Mbp.
5695
5696
5697 **Description of *Candidatus* Limimorpha gen. nov.**
5698 *Candidatus* Limimorpha (Lim.i.mor'pha. L. masc. n. *limus* dung; Gr. fem. n. *morphe* a form,
5699 shape; N.L. fem. n. *Limimorpha* a microbe associated with faeces)
5700
5701 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5702 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5703 species *Limimorpha avicola*. This is a name for the alphanumeric GTDB genus F082. This genus
5704 has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al.,
5705 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family *F082*.
5706
5707
5708 **Description of *Candidatus* Limimorpha avicola sp. nov.**
5709 *Candidatus* Limimorpha avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L.
5710 n. *avicola* inhabitant of birds)
5711
5712 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5713 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5714 assigned the MAG ID Gambia15-481 and which is available via NCBI BioSample
5715 SAMN15817194. This is a new name for the alphanumeric GTDB species sp002633315. The
5716 GC content of the type genome is 38.09% and the genome length is 2.5 Mbp.
5717
5718
5719 **Description of *Candidatus* Limiplasma gen. nov.**

5720   *Candidatus* Limiplasma (Lim.i.plas'ma. L. masc. n. *limus* dung; Gr. neut. n. *plasma* a form; N.L.
5721   neut. n. *Limiplasma* a microbe associated with faeces)

5722
5723   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5724   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5725   species *Limiplasma pullicola*. This is a name for the alphanumeric GTDB genus Firm-11. This
5726   genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
5727   al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family *CAG-74*.

5728
5729
5730   **Description of *Candidatus* Limiplasma merdipullorum sp. nov.**
5731   *Candidatus* Limiplasma merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
5732   *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)

5733
5734   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5735   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5736   assigned the MAG ID ChiBcec16-3123 and which is available via NCBI BioSample
5737   SAMN15817217. This is a new name for the alphanumeric GTDB species sp900540045. The
5738   GC content of the type genome is 61.78% and the genome length is 2.6 Mbp.

5739
5740
5741   **Description of *Candidatus* Limiplasma pullicola sp. nov.**
5742   *Candidatus* Limiplasma pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
5743   inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)

5744
5745   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5746   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5747   assigned the MAG ID 2223 and which is available via NCBI BioSample SAMN15817092. The
5748   GC content of the type genome is 62.99% and the genome length is 2.7 Mbp.

5749
5750
5751   **Description of *Candidatus* Limiplasma pullistercoris sp. nov.**
5752   *Candidatus* Limiplasma pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
5753   neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)

5754
5755   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5756   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5757   assigned the MAG ID ChiBcec15-2748 and which is available via NCBI BioSample
5758   SAMN15817228. This is a new name for the alphanumeric GTDB species sp900553905. The
5759   GC content of the type genome is 62.75% and the genome length is 2.8 Mbp.

5760
5761
5762   **Description of *Candidatus* Limiplasma stercoravium sp. nov.**
5763   *Candidatus* Limiplasma stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
5764   bird; N.L. gen. n. *stercoravium* of bird faeces)

5765

5766 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5767 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5768 assigned the MAG ID CHK169-20388 and which is available via NCBI BioSample
5769 SAMN15817129. The GC content of the type genome is 62.11% and the genome length is 2.4
5770 Mbp.

5771
5772
5773 **Description of *Candidatus* Limisoma gen. nov.**
5774 *Candidatus* Limisoma (Lim.i.so'ma. L. masc. n. *limus* dung; Gr. neut. n. *soma* a body; N.L. neut.
5775 n. *Limisoma* a microbe associated with faeces)

5776
5777 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5778 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5779 species *Limisoma faecipullorum*. This is a name for the alphanumeric GTDB genus CAG-279.
5780 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
5781 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family
5782 *Muribaculaceae*.

5783
5784
5785 **Description of *Candidatus* Limisoma faecipullorum sp. nov.**
5786 *Candidatus* Limisoma faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
5787 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

5788
5789 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5790 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5791 assigned the MAG ID 6919 and which is available via NCBI BioSample SAMN15817069. The
5792 GC content of the type genome is 45.95% and the genome length is 2.2 Mbp.

5793
5794
5795 **Description of *Candidatus* Limisoma gallistercoris sp. nov.**
5796 *Candidatus* Limisoma gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
5797 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)

5798
5799 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5800 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5801 assigned the MAG ID CHK136-1475 and which is available via NCBI BioSample
5802 SAMN15817174. This is a new name for the alphanumeric GTDB species sp900550025. The
5803 GC content of the type genome is 48.31% and the genome length is 2.2 Mbp.

5804
5805
5806 **Description of *Candidatus* Limisoma intestinavium sp. nov.**
5807 *Candidatus* Limisoma intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n. *avis*
5808 bird; N.L. gen. n. *intestinavium* of the gut of birds)

5809
5810 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5811 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

5812   assigned the MAG ID 17073 and which is available via NCBI BioSample SAMN15817199. This
5813   is a new name for the alphanumeric GTDB species sp900541555. The GC content of the type
5814   genome is 48.25% and the genome length is 1.8 Mbp.
5815
5816
5817   **Description of *Candidatus* Limivicinus gen. nov.**
5818   *Candidatus* Limivicinus (Lim.i.vic.in'us. L. masc. n. *limus* dung; L. masc. n. *vicinus* a neighbour;
5819   N.L. masc. n. *Limivicinus* a microbe associated with faeces)
5820
5821   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5822   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5823   species *Limivicinus faecipullorum*. This is a name for the alphanumeric GTDB genus UBA1777.
5824   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
5825   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
5826   *Oscillospiraceae.*
5827
5828
5829   **Description of *Candidatus* Limivicinus faecipullorum sp. nov.**
5830   *Candidatus* Limivicinus faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
5831   masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
5832
5833   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5834   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5835   assigned the MAG ID ChiHcec3-8852 and which is available via NCBI BioSample
5836   SAMN15817081. The GC content of the type genome is 58.52% and the genome length is 1.9
5837   Mbp.
5838
5839
5840   **Description of *Candidatus* Limivivens gen. nov.**
5841   *Candidatus* Limivivens (Lim.i.viv'ens. L. masc. n. *limus* dung; N.L. pres. part. *vivens* living;
5842   N.L. fem. n. *Limivivens* a microbe associated with faeces)
5843
5844   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5845   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5846   species *Limivivens intestinipullorum*. This is a name for the alphanumeric GTDB genus GCA-
5847   900066135. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
5848   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
5849   *Lachnospiraceae.*
5850
5851
5852   **Description of *Candidatus* Limivivens intestinipullorum sp. nov.**
5853   *Candidatus* Limivivens intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
5854   masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
5855
5856   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5857   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

5858 assigned the MAG ID CHK190-19873 and which is available via NCBI BioSample
5859 SAMN15817025. The GC content of the type genome is 52.58% and the genome length is 3.4
5860 Mbp.
5861
5862
5863 **Description of *Candidatus* Limivivens merdigallinarum sp. nov.**
5864 *Candidatus* Limivivens merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
5865 n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
5866
5867 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5868 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5869 assigned the MAG ID ChiSjej3B21-11622 and which is available via NCBI BioSample
5870 SAMN15817007. The GC content of the type genome is 50.09% and the genome length is 3.3
5871 Mbp.
5872
5873
5874 **Description of *Candidatus* Limosilactobacillus excrementigallinarum sp. nov.**
5875 *Candidatus* Limosilactobacillus excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
5876 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
5877 excrement)
5878
5879 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5880 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5881 assigned the MAG ID 2685 and which is available via NCBI BioSample SAMN15816672. The
5882 GC content of the type genome is 41.67% and the genome length is 1.4 Mbp.
5883
5884
5885 **Description of *Candidatus* Limosilactobacillus faecipullorum sp. nov.**
5886 *Candidatus* Limosilactobacillus faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis*
5887 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken
5888 faeces)
5889
5890 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5891 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5892 assigned the MAG ID 7774 and which is available via NCBI BioSample SAMN15816663. The
5893 GC content of the type genome is 43.03% and the genome length is 1.5 Mbp.
5894
5895
5896 **Description of *Candidatus* Limosilactobacillus gallistercoris sp. nov.**
5897 *Candidatus* Limosilactobacillus gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L.
5898 neut. n. *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
5899
5900 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5901 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5902 assigned the MAG ID CHK158-2993 and which is available via NCBI BioSample

5903 SAMN15816598. The GC content of the type genome is 52.74% and the genome length is 1.2
5904 Mbp.
5905
5906
5907 **Description of *Candidatus* Limosilactobacillus intestinavium sp. nov.**
5908 *Candidatus* Limosilactobacillus intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L.
5909 fem. n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
5910
5911 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5912 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5913 assigned the MAG ID 2331 and which is available via NCBI BioSample SAMN15816838. This
5914 is a new name for the alphanumeric GTDB species sp900557215. The GC content of the type
5915 genome is 38.77% and the genome length is 1.5 Mbp.
5916
5917
5918 **Description of *Candidatus* Limosilactobacillus intestinigallinarum sp. nov.**
5919 *Candidatus* Limosilactobacillus intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n.
5920 *intestinum* gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
5921
5922 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5923 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5924 assigned the MAG ID CHK176-5070 and which is available via NCBI BioSample
5925 SAMN15816600. The GC content of the type genome is 54.91% and the genome length is 1.5
5926 Mbp.
5927
5928
5929 **Description of *Candidatus* Limosilactobacillus intestinipullorum sp. nov.**
5930 *Candidatus* Limosilactobacillus intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum*
5931 gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young
5932 chickens)
5933
5934 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5935 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5936 assigned the MAG ID ChiHecolR2B26-165 and which is available via NCBI BioSample
5937 SAMN15816601. The GC content of the type genome is 49.12% and the genome length is 1.6
5938 Mbp.
5939
5940
5941 **Description of *Candidatus* Limosilactobacillus merdavium sp. nov.**
5942 *Candidatus* Limosilactobacillus merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n.
5943 *avis* bird; N.L. gen. n. *merdavium* of bird faeces)
5944
5945 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5946 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5947 assigned the MAG ID 876 and which is available via NCBI BioSample SAMN15816723. The
5948 GC content of the type genome is 39.60% and the genome length is 1.4 Mbp.

5949
5950
5951 **Description of *Candidatus* Limosilactobacillus merdigallinarum sp. nov.**
5952 *Candidatus* Limosilactobacillus merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces;
5953 L. fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
5954
5955 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5956 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5957 assigned the MAG ID ChiSxjej3B15-572 and which is available via NCBI BioSample
5958 SAMN15816736. The GC content of the type genome is 44.36% and the genome length is 1.4
5959 Mbp.
5960
5961
5962 **Description of *Candidatus* Limosilactobacillus merdipullorum sp. nov.**
5963 *Candidatus* Limosilactobacillus merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L.
5964 masc. n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
5965
5966 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5967 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5968 assigned the MAG ID ChiHejej3B27-2180 and which is available via NCBI BioSample
5969 SAMN15816756. The GC content of the type genome is 49.90% and the genome length is 1.3
5970 Mbp.
5971
5972
5973 **Description of *Candidatus* Limousia gen. nov.**
5974 *Candidatus* Limousia (Lim.ou'si.a. L. masc. n. *limus* dung; Gr. fem. n. *ousia* an essence; N.L.
5975 fem. n. *Limousia* a microbe associated with faeces)
5976
5977 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
5978 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
5979 species *Limousia pullorum*. This is a name for the alphanumeric GTDB genus An172. This
5980 genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
5981 al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family *Acutalibacteraceae.*
5982
5983
5984 **Description of *Candidatus* Limousia pullorum sp. nov.**
5985 *Candidatus* Limousia pullorum (pul.lo'rum. L. gen.pl. n. *pullorum* of young chickens)
5986
5987 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
5988 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
5989 assigned the MAG ID ChiGjej1B1-1684 and which is available via NCBI BioSample
5990 SAMN15817202. This is a new name for the alphanumeric GTDB species sp002160515. The
5991 GC content of the type genome is 40.91% and the genome length is 1.7 Mbp.
5992
5993
5994 **Description of *Candidatus* Luteimonas excrementigallinarum sp. nov.**

...

5995 *Candidatus* Luteimonas excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
5996 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
5997 excrement)
5998
5999 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6000 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6001 assigned the MAG ID CHK165-14161 and which is available via NCBI BioSample
6002 SAMN15816707. The GC content of the type genome is 68.39% and the genome length is 2.5
6003 Mbp.
6004
6005
6006 **Description of *Candidatus* Luteococcus avicola sp. nov.**
6007 *Candidatus* Luteococcus avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. -*cola* inhabitant of; N.L.
6008 n. *avicola* inhabitant of birds)
6009
6010 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6011 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6012 assigned the MAG ID 4979 and which is available via NCBI BioSample SAMN15816867. This
6013 is a new name for the alphanumeric GTDB species sp002387005. The GC content of the type
6014 genome is 68.14% and the genome length is 2.9 Mbp.
6015
6016
6017 **Description of *Candidatus* Mailhella excrementigallinarum sp. nov.**
6018 *Candidatus* Mailhella excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum*
6019 excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)
6020
6021 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6022 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6023 assigned the MAG ID 708 and which is available via NCBI BioSample SAMN15816871. This is
6024 a new name for the alphanumeric GTDB species sp003150275. The GC content of the type
6025 genome is 60.07% and the genome length is 3.0 Mbp.
6026
6027
6028 **Description of *Candidatus* Mailhella merdavium sp. nov.**
6029 *Candidatus* Mailhella merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
6030 N.L. gen. n. *merdavium* of bird faeces)
6031
6032 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6033 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6034 assigned the MAG ID ChiBcec6-11642 and which is available via NCBI BioSample
6035 SAMN15816648. The GC content of the type genome is 56.49% and the genome length is 2.7
6036 Mbp.
6037
6038
6039 **Description of *Candidatus* Mailhella merdigallinarum sp. nov.**

6040 *Candidatus* Mailhella merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem. n.
6041 *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
6042
6043 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6044 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6045 assigned the MAG ID CHK186-16707 and which is available via NCBI BioSample
6046 SAMN15816842. This is a new name for the alphanumeric GTDB species sp900541395. The
6047 GC content of the type genome is 61.96% and the genome length is 2.4 Mbp.
6048
6049
6050 **Description of *Candidatus* Massiliomicrobiota merdigallinarum sp. nov.**
6051 *Candidatus* Massiliomicrobiota merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces;
6052 L. fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
6053
6054 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6055 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6056 assigned the MAG ID CHK183-8118 and which is available via NCBI BioSample
6057 SAMN15816832. This is a new name for the alphanumeric GTDB species sp002160815. The
6058 GC content of the type genome is 31.33% and the genome length is 2.4 Mbp.
6059
6060
6061 **Description of *Candidatus* Mediterraneibacter avicola sp. nov.**
6062 *Candidatus* Mediterraneibacter avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant
6063 of; N.L. n. *avicola* inhabitant of birds)
6064
6065 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6066 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6067 assigned the MAG ID ChiGjej3B3-8055 and which is available via NCBI BioSample
6068 SAMN15816612. The GC content of the type genome is 48.65% and the genome length is 2.4
6069 Mbp.
6070
6071
6072 **Description of *Candidatus* Mediterraneibacter caccavium sp. nov.**
6073 *Candidatus* Mediterraneibacter caccavium (cacc.a'vi.um. Gr. fem. n. *kakke* faeces; L. fem. n. *avis*
6074 bird; N.L. gen. n. *caccavium* of bird faeces)
6075
6076 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6077 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6078 assigned the MAG ID ChiSjej5B23-15282 and which is available via NCBI BioSample
6079 SAMN15816861. This is a new name for the alphanumeric GTDB species sp002161355. The
6080 GC content of the type genome is 51.40% and the genome length is 2.6 Mbp.
6081
6082
6083 **Description of *Candidatus* Mediterraneibacter caccogallinarum sp. nov.**
6084 *Candidatus* Mediterraneibacter caccogallinarum (cac.co.gal.li.na'rum. Gr. fem. n. *kakke* faeces;
6085 L. fem. n. *gallina* hen; N.L. gen. n. *caccogallinarum* of hen faeces)

6086
6087 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6088 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6089 assigned the MAG ID ChiHcolR18-251 and which is available via NCBI BioSample
6090 SAMN15816801. This is a new name for the alphanumeric GTDB species sp002314255. The
6091 GC content of the type genome is 50.75% and the genome length is 2.6 Mbp.

6092
6093
6094 **Description of *Candidatus* Mediterraneibacter colneyensis sp. nov.**
6095 *Candidatus* Mediterraneibacter colneyensis (col.ney.en'sis. N.L. fem. adj. *colneyensis* pertaining
6096 to Colney, the Norfolk village which is home to the Quadram Institute where the species was
6097 first described)

6098
6099 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6100 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6101 assigned the MAG ID ChiGjej5B5-19924 and which is available via NCBI BioSample
6102 SAMN15816732. The GC content of the type genome is 50.96% and the genome length is 1.9
6103 Mbp.

6104
6105
6106 **Description of *Candidatus* Mediterraneibacter cottocaccae sp. nov.**
6107 *Candidatus* Mediterraneibacter cottocaccae (cot.to.cac'cae. Gr. masc. n. *kottos* chicken Gr. fem.
6108 n. *kakke* faeces; N.L. gen. n. *cottocaccae* of chicken faeces)

6109
6110 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6111 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6112 assigned the MAG ID CHK192-87 and which is available via NCBI BioSample
6113 SAMN15816835. This is a new name for the alphanumeric GTDB species sp002160525. The
6114 GC content of the type genome is 50.07% and the genome length is 4.0 Mbp.

6115
6116
6117 **Description of *Candidatus* Mediterraneibacter excrementavium sp. nov.**
6118 *Candidatus* Mediterraneibacter excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
6119 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)

6120
6121 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6122 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6123 assigned the MAG ID ChiGjej2B2-38138 and which is available via NCBI BioSample
6124 SAMN15816630. The GC content of the type genome is 51.42% and the genome length is 2.1
6125 Mbp.

6126
6127
6128 **Description of *Candidatus* Mediterraneibacter excrementigallinarum sp. nov.**
6129 *Candidatus* Mediterraneibacter excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
6130 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
6131 excrement)

6132
6133 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6134 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6135 assigned the MAG ID CHK143-6153 and which is available via NCBI BioSample
6136 SAMN15816575. The GC content of the type genome is 48.97% and the genome length is 3.1
6137 Mbp.
6138
6139
6140 **Description of *Candidatus* Mediterraneibacter excrementipullorum sp. nov.**
6141 *Candidatus* Mediterraneibacter excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
6142 *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
6143 young chicken excrement)
6144
6145 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6146 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6147 assigned the MAG ID ChiSjej6B24-3024 and which is available via NCBI BioSample
6148 SAMN15816810. This is a new name for the alphanumeric GTDB species sp9005552. The GC
6149 content of the type genome is 48.88% and the genome length is 2.4 Mbp.
6150
6151
6152 **Description of *Candidatus* Mediterraneibacter faecavium sp. nov.**
6153 *Candidatus* Mediterraneibacter faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L.
6154 fem. n. *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
6155
6156 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6157 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6158 assigned the MAG ID CHK196-7946 and which is available via NCBI BioSample
6159 SAMN15816577. The GC content of the type genome is 49.45% and the genome length is 2.8
6160 Mbp.
6161
6162
6163 **Description of *Candidatus* Mediterraneibacter faecigallinarum sp. nov.**
6164 *Candidatus* Mediterraneibacter faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis*
6165 excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
6166
6167 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6168 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6169 assigned the MAG ID ChiGjej1B1-1692 and which is available via NCBI BioSample
6170 SAMN15816637. The GC content of the type genome is 51.63% and the genome length is 2.6
6171 Mbp.
6172
6173
6174 **Description of *Candidatus* Mediterraneibacter faecipullorum sp. nov.**
6175 *Candidatus* Mediterraneibacter faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis*
6176 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken
6177 faeces)

6178
6179 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6180 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6181 assigned the MAG ID ChiW19-954 and which is available via NCBI BioSample
6182 SAMN15816638. The GC content of the type genome is 47.71% and the genome length is 2.7
6183 Mbp.
6184
6185
6186 **Description of *Candidatus* Mediterraneibacter gallistercoris sp. nov.**
6187 *Candidatus* Mediterraneibacter gallistercoris (gal.li.ster'co.ris. L. masc. n. *gallus* chicken; L.
6188 neut. n. *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
6189
6190 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6191 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6192 assigned the MAG ID CHK165-2605 and which is available via NCBI BioSample
6193 SAMN15816636. The GC content of the type genome is 47.20% and the genome length is 2.5
6194 Mbp.
6195
6196
6197 **Description of *Candidatus* Mediterraneibacter guildfordensis sp. nov.**
6198 *Candidatus* Mediterraneibacter guildfordensis (guild.ford.en'sis. N.L. fem. adj. *guildfordensis*
6199 pertaining to Guildford, English town that is home to the University of Surrey)
6200
6201 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6202 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6203 assigned the MAG ID ChiHcec3-18395 and which is available via NCBI BioSample
6204 SAMN15816784. The GC content of the type genome is 52.47% and the genome length is 2.2
6205 Mbp.
6206
6207
6208 **Description of *Candidatus* Mediterraneibacter intestinavium sp. nov.**
6209 *Candidatus* Mediterraneibacter intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L.
6210 fem. n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
6211
6212 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6213 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6214 assigned the MAG ID ChiBcec12-2655 and which is available via NCBI BioSample
6215 SAMN15816591. The GC content of the type genome is 50.53% and the genome length is 2.9
6216 Mbp.
6217
6218
6219 **Description of *Candidatus* Mediterraneibacter intestinigallinarum sp. nov.**
6220 *Candidatus* Mediterraneibacter intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n.
6221 *intestinum* gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
6222

6223 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6224 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6225 assigned the MAG ID ChiBcec15-2237 and which is available via NCBI BioSample
6226 SAMN15816645. The GC content of the type genome is 46.81% and the genome length is 3.1
6227 Mbp.

6228

6229

6230 **Description of *Candidatus* Mediterraneibacter intestinipullorum sp. nov.**
6231 *Candidatus* Mediterraneibacter intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum*
6232 gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young
6233 chickens)

6234

6235 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6236 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6237 assigned the MAG ID CHK161-4361 and which is available via NCBI BioSample
6238 SAMN15816656. The GC content of the type genome is 49.75% and the genome length is 2.5
6239 Mbp.

6240

6241

6242 **Description of *Candidatus* Mediterraneibacter merdavium sp. nov.**
6243 *Candidatus* Mediterraneibacter merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n.
6244 *avis* bird; N.L. gen. n. *merdavium* of bird faeces)

6245

6246 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6247 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6248 assigned the MAG ID ChiBcolR7-8672 and which is available via NCBI BioSample
6249 SAMN15816660. The GC content of the type genome is 49.88% and the genome length is 2.6
6250 Mbp.

6251

6252

6253 **Description of *Candidatus* Mediterraneibacter merdigallinarum sp. nov.**
6254 *Candidatus* Mediterraneibacter merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces;
6255 L. fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)

6256

6257 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6258 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6259 assigned the MAG ID ChiW16-1363 and which is available via NCBI BioSample
6260 SAMN15816674. The GC content of the type genome is 46.95% and the genome length is 2.4
6261 Mbp.

6262

6263

6264 **Description of *Candidatus* Mediterraneibacter merdipullorum sp. nov.**
6265 *Candidatus* Mediterraneibacter merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L.
6266 masc. n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
6267

6268 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6269 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6270 assigned the MAG ID ChiSxjej4B16-6421 and which is available via NCBI BioSample
6271 SAMN15816679. The GC content of the type genome is 54.17% and the genome length is 2.2
6272 Mbp.

6273
6274

6275 **Description of *Candidatus* Mediterraneibacter norfolkensis sp. nov.**
6276 *Candidatus* Mediterraneibacter norfolkensis (nor.folk.en'sis. N.L. fem. adj. *norfolkensis*
6277 pertaining to the English county of Norfolk)

6278
6279 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6280 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6281 assigned the MAG ID ChiW9-3490 and which is available via NCBI BioSample
6282 SAMN15816789. The GC content of the type genome is 48.85% and the genome length is 3.5
6283 Mbp.

6284
6285

6286 **Description of *Candidatus* Mediterraneibacter norwichensis sp. nov.**
6287 *Candidatus* Mediterraneibacter norwichensis (nor.wich.en'sis. N.L. fem. adj. *norwichensis*
6288 pertaining to English city of Norwich)

6289
6290 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6291 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6292 assigned the MAG ID CHK180-4461 and which is available via NCBI BioSample
6293 SAMN15816628. The GC content of the type genome is 47.61% and the genome length is 2.6
6294 Mbp.

6295
6296

6297 **Description of *Candidatus* Mediterraneibacter ornithocaccae sp. nov.**
6298 *Candidatus* Mediterraneibacter ornithocaccae (or.ni.tho.cac'cae. Gr. masc. or fem. n. *ornis,*
6299 *ornithos* bird Gr. fem. n. *kakke* faeces; N.L. gen. n. *ornithocaccae* of bird faeces)

6300
6301 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6302 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6303 assigned the MAG ID ChiGjej1B1-20579 and which is available via NCBI BioSample
6304 SAMN15816839. This is a new name for the alphanumeric GTDB species sp002159505. The
6305 GC content of the type genome is 47.31% and the genome length is 2.6 Mbp.

6306
6307

6308 **Description of *Candidatus* Mediterraneibacter pullicola sp. nov.**
6309 *Candidatus* Mediterraneibacter pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff.
6310 *-cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)

6311
6312 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6313 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

6314   assigned the MAG ID ChiSjej2B20-11307 and which is available via NCBI BioSample
6315   SAMN15816678. The GC content of the type genome is 47.35% and the genome length is 2.1
6316   Mbp.
6317
6318
6319   **Description of *Candidatus* Mediterraneibacter pullistercoris sp. nov.**
6320   *Candidatus* Mediterraneibacter pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young
6321   chicken; L. neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
6322
6323   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6324   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6325   assigned the MAG ID ChiHjej8B7-7219 and which is available via NCBI BioSample
6326   SAMN15816602. The GC content of the type genome is 48.73% and the genome length is 2.3
6327   Mbp.
6328
6329
6330   **Description of *Candidatus* Mediterraneibacter quadrami sp. nov.**
6331   *Candidatus* Mediterraneibacter quadrami (quad.ra'mi. N.L. gen. n. *quadrami* of the Quadram
6332   Institute)
6333
6334   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6335   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6336   assigned the MAG ID ChiBcec15-3976 and which is available via NCBI BioSample
6337   SAMN15816790. The GC content of the type genome is 52.68% and the genome length is 2.0
6338   Mbp.
6339
6340
6341   **Description of *Candidatus* Mediterraneibacter stercoravium sp. nov.**
6342   *Candidatus* Mediterraneibacter stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem.
6343   n. *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
6344
6345   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6346   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6347   assigned the MAG ID CHK196-3914 and which is available via NCBI BioSample
6348   SAMN15816603. The GC content of the type genome is 48.72% and the genome length is 2.5
6349   Mbp.
6350
6351
6352   **Description of *Candidatus* Mediterraneibacter stercorigallinarum sp. nov.**
6353   *Candidatus* Mediterraneibacter stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus*
6354   dung; L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
6355
6356   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6357   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6358   assigned the MAG ID ChiGjej1B1-13045 and which is available via NCBI BioSample

6359   SAMN15816697. The GC content of the type genome is 50.04% and the genome length is 2.3
6360   Mbp.
6361
6362
6363   **Description of *Candidatus* Mediterraneibacter stercoripullorum sp. nov.**
6364   *Candidatus* Mediterraneibacter stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung;
6365   L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young
6366   chickens)
6367
6368   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6369   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6370   assigned the MAG ID CHK195-1396 and which is available via NCBI BioSample
6371   SAMN15816610. The GC content of the type genome is 48.12% and the genome length is 3.2
6372   Mbp.
6373
6374
6375   **Description of *Candidatus* Mediterraneibacter surreyensis sp. nov.**
6376   *Candidatus* Mediterraneibacter surreyensis (sur.rey.en'sis. N.L. fem. adj. *surreyensis* pertaining
6377   to the English county of Surrey where the samples in the study were collected)
6378
6379   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6380   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6381   assigned the MAG ID CHK177-12742 and which is available via NCBI BioSample
6382   SAMN15816593. The GC content of the type genome is 46.80% and the genome length is 2.9
6383   Mbp.
6384
6385
6386   **Description of *Candidatus* Mediterraneibacter tabaqchaliae sp. nov.**
6387   *Candidatus* Mediterraneibacter tabaqchaliae (ta.baq.cha'li.ae. N.L. fem. gen. n. *tabaqchaliae*
6388   named in honour of British microbiologist Soad Tabaqchali)
6389
6390   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6391   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6392   assigned the MAG ID ChiGjej3B3-11674 and which is available via NCBI BioSample
6393   SAMN15816791. The GC content of the type genome is 51.91% and the genome length is 2.7
6394   Mbp.
6395
6396
6397   **Description of *Candidatus* Mediterraneibacter vanvlietii sp. nov.**
6398   *Candidatus* Mediterraneibacter vanvlietii (van.vliet'i.i. N.L. gen. n. *vanvlietii* named in honour of
6399   Dutch microbiologist Arnoud van Vliet)
6400
6401   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6402   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6403   assigned the MAG ID ChiBcec1-362 and which is available via NCBI BioSample

6404   SAMN15816623. The GC content of the type genome is 48.47% and the genome length is 3.0
6405   Mbp.
6406
6407

6408   **Description of *Candidatus* Megamonas gallistercoris sp. nov.**
6409   *Candidatus* Megamonas gallistercoris (gal.li.ster'co.ris. L. masc. n. *gallus* chicken; L. neut. n.
6410   *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
6411
6412   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6413   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6414   assigned the MAG ID ChiGjej6B6-7947 and which is available via NCBI BioSample
6415   SAMN15816859. This is a new name for the alphanumeric GTDB species sp900554895. The
6416   GC content of the type genome is 40.34% and the genome length is 2.2 Mbp.
6417
6418

6419   **Description of *Candidatus* Merdenecus gen. nov.**
6420   *Candidatus* Merdenecus (Merd.en.e'cus. L. fem. n. *merda* dung; Gr. masc. *enoikos* inhabitant;
6421   N.L. masc. n. *Merdenecus* a microbe associated with faeces)
6422
6423   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
6424   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
6425   species *Merdenecus merdavium*. This is a name for the alphanumeric GTDB genus MCWD5.
6426   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
6427   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
6428   *Lachnospiraceae.*
6429
6430

6431   **Description of *Candidatus* Merdenecus merdavium sp. nov.**
6432   *Candidatus* Merdenecus merdavium (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -
6433   *cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
6434
6435   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6436   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6437   assigned the MAG ID CHK160-2840 and which is available via NCBI BioSample
6438   SAMN15817122. The GC content of the type genome is 35.46% and the genome length is 2.6
6439   Mbp.
6440
6441

6442   **Description of *Candidatus* Merdibacter merdavium sp. nov.**
6443   *Candidatus* Merdibacter merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
6444   N.L. gen. n. *merdavium* of bird faeces)
6445
6446   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6447   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6448   assigned the MAG ID CHK187-11901 and which is available via NCBI BioSample

6449   SAMN15816582. The GC content of the type genome is 53.13% and the genome length is 2.1
6450   Mbp.
6451
6452

6453   **Description of *Candidatus* Merdibacter merdigallinarum sp. nov.**
6454   *Candidatus* Merdibacter merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
6455   n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
6456

6457   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6458   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6459   assigned the MAG ID ChiGjej6B6-453 and which is available via NCBI BioSample
6460   SAMN15816595. The GC content of the type genome is 53.92% and the genome length is 1.8
6461   Mbp.
6462
6463

6464   **Description of *Candidatus* Merdibacter merdipullorum sp. nov.**
6465   *Candidatus* Merdibacter merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
6466   *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
6467

6468   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6469   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6470   assigned the MAG ID ChiGjej1B1-19782 and which is available via NCBI BioSample
6471   SAMN15816850. This is a new name for the alphanumeric GTDB species sp900543035. The
6472   GC content of the type genome is 55.41% and the genome length is 1.9 Mbp.
6473
6474

6475   **Description of *Candidatus* Merdicola gen. nov.**
6476   *Candidatus* Merdicola (Merd.i.co'la. L. fem. n. *merda* dung; L. suff. *-cola* inhabitant of; N.L.
6477   fem. n. *Merdicola* a microbe associated with faeces)
6478

6479   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
6480   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
6481   species *Merdicola faecigallinarum*. This is a name for the alphanumeric GTDB genus CAG-354.
6482   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
6483   (Chaumeil et al., 2019; Parks et al., 2020) to the order *TANB77* and to the family *CAG-508*.
6484
6485

6486   **Description of *Candidatus* Merdicola faecigallinarum sp. nov.**
6487   *Candidatus* Merdicola faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
6488   fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
6489

6490   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6491   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6492   assigned the MAG ID CHK195-15760 and which is available via NCBI BioSample
6493   SAMN15817051. The GC content of the type genome is 28.83% and the genome length is 1.5
6494   Mbp.

6495
6496
6497 **Description of *Candidatus* Merdimorpha gen. nov.**
6498 *Candidatus* Merdimorpha (Merd.i.mor'pha. L. fem. n. *merda* dung; Gr. fem. n. *morphe* a form,
6499 shape; N.L. fem. n. *Merdimorpha* a microbe associated with faeces)
6500
6501 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
6502 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
6503 species *Merdimorpha intestinavium*. This is a name for the alphanumeric GTDB genus
6504 UBA1820. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
6505 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Flavobacteriales* and to the family
6506 *UBA1820.*
6507
6508
6509 **Description of *Candidatus* Merdimorpha intestinavium sp. nov.**
6510 *Candidatus* Merdimorpha intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
6511 *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
6512
6513 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6514 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6515 assigned the MAG ID CHK1-7158 and which is available via NCBI BioSample
6516 SAMN15817210. This is a new name for the alphanumeric GTDB species sp002314265. The
6517 GC content of the type genome is 56.50% and the genome length is 1.8 Mbp.
6518
6519
6520 **Description of *Candidatus* Merdimorpha stercoravium sp. nov.**
6521 *Candidatus* Merdimorpha stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
6522 bird; N.L. gen. n. *stercoravium* of bird faeces)
6523
6524 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6525 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6526 assigned the MAG ID 1383 and which is available via NCBI BioSample SAMN15817125. The
6527 GC content of the type genome is 57.82% and the genome length is 1.7 Mbp.
6528
6529
6530 **Description of *Candidatus* Merdiplasma gen. nov.**
6531 *Candidatus* Merdiplasma (Merd.i.plas'ma. L. fem. n. *merda* dung; Gr. neut. n. *plasma* a form;
6532 N.L. neut. n. *Merdiplasma* a microbe associated with faeces)
6533
6534 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
6535 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
6536 species *Merdiplasma excrementigallinarum*. This is a name for the alphanumeric GTDB genus
6537 UBA2856. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
6538 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
6539 *Lachnospiraceae.*
6540

6541
6542 **Description of *Candidatus* Merdiplasma excrementigallinarum sp. nov.**
6543 *Candidatus* Merdiplasma excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
6544 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
6545 excrement)
6546
6547 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6548 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6549 assigned the MAG ID ChiBcec6-7307 and which is available via NCBI BioSample
6550 SAMN15817161. The GC content of the type genome is 52.97% and the genome length is 2.4
6551 Mbp.
6552
6553
6554 **Description of *Candidatus* Merdisoma gen. nov.**
6555 *Candidatus* Merdisoma (Merd.i.so'ma. L. fem. n. *merda* dung; Gr. neut. n. *soma* a body; N.L.
6556 neut. n. *Merdisoma* a microbe associated with faeces)
6557
6558 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
6559 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
6560 species *Merdisoma merdipullorum*. This is a name for the alphanumeric GTDB genus GCA-
6561 900066575. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
6562 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
6563 *Lachnospiraceae.*
6564
6565
6566 **Description of *Candidatus* Merdisoma faecalis sp. nov.**
6567 *Candidatus* Merdisoma faecalis (fae.ca'lis. L. fem. adj. *faecalis* of faeces)
6568
6569 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6570 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6571 assigned the MAG ID ChiBcolR2-1241 and which is available via NCBI BioSample
6572 SAMN15817219. This is a new name for the alphanumeric GTDB species sp002160765. The
6573 GC content of the type genome is 51.56% and the genome length is 2.7 Mbp.
6574
6575
6576 **Description of *Candidatus* Merdisoma merdipullorum sp. nov.**
6577 *Candidatus* Merdisoma merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
6578 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
6579
6580 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6581 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6582 assigned the MAG ID CHK197-19677 and which is available via NCBI BioSample
6583 SAMN15817042. The GC content of the type genome is 50.06% and the genome length is 2.9
6584 Mbp.
6585
6586

6587 **Description of *Candidatus* Merdivicinus gen. nov.**
6588 *Candidatus* Merdivicinus (Merd.ivic.in'us. L. fem. n. *merda* dung; L. masc. n. *vicinus* a
6589 neighbour; N.L. masc. n. *Merdivicinus* a microbe associated with faeces)
6590
6591 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
6592 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
6593 species *Merdivicinus faecavium*. This is a name for the alphanumeric GTDB genus UMGS1826.
6594 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
6595 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
6596 *Ruminococcaceae.*
6597
6598
6599 **Description of *Candidatus* Merdivicinus excrementipullorum sp. nov.**
6600 *Candidatus* Merdivicinus excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
6601 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
6602 chicken excrement)
6603
6604 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6605 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6606 assigned the MAG ID CHK199-13235 and which is available via NCBI BioSample
6607 SAMN15817032. The GC content of the type genome is 54.67% and the genome length is 2.5
6608 Mbp.
6609
6610
6611 **Description of *Candidatus* Merdivicinus faecavium sp. nov.**
6612 *Candidatus* Merdivicinus faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
6613 *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
6614
6615 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6616 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6617 assigned the MAG ID CHK186-19003 and which is available via NCBI BioSample
6618 SAMN15817036. The GC content of the type genome is 61.26% and the genome length is 2.5
6619 Mbp.
6620
6621
6622 **Description of *Candidatus* Merdivicinus intestinavium sp. nov.**
6623 *Candidatus* Merdivicinus intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
6624 *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
6625
6626 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6627 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6628 assigned the MAG ID CHK188-1901 and which is available via NCBI BioSample
6629 SAMN15817003. The GC content of the type genome is 59.41% and the genome length is 2.3
6630 Mbp.
6631
6632

6633 **Description of *Candidatus* Merdivicinus intestinigallinarum sp. nov.**
6634 *Candidatus* Merdivicinus intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
6635 L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
6636
6637 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6638 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6639 assigned the MAG ID ChiBcec18-2170 and which is available via NCBI BioSample
6640 SAMN15817163. The GC content of the type genome is 56.27% and the genome length is 2.5
6641 Mbp.
6642
6643
6644 **Description of *Candidatus* Merdivivens gen. nov.**
6645 *Candidatus* Merdivivens (Merd.i.viv'ens. L. fem. n. *merda* dung; N.L. pres. part. *vivens* living;
6646 N.L. fem. n. *Merdivivens* a microbe associated with faeces)
6647
6648 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
6649 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
6650 species *Merdivivens pullistercoris*. This is a name for the alphanumeric GTDB genus UBA3382.
6651 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
6652 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family *UBA932*.
6653
6654
6655 **Description of *Candidatus* Merdivivens faecigallinarum sp. nov.**
6656 *Candidatus* Merdivivens faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;
6657 L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
6658
6659 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6660 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6661 assigned the MAG ID B3-2255 and which is available via NCBI BioSample SAMN15817168.
6662 This is a new name for the alphanumeric GTDB species sp002159555. The GC content of the
6663 type genome is 49.87% and the genome length is 1.9 Mbp.
6664
6665
6666 **Description of *Candidatus* Merdivivens pullicola sp. nov.**
6667 *Candidatus* Merdivivens pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -*cola*
6668 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
6669
6670 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6671 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6672 assigned the MAG ID B1-8020 and which is available via NCBI BioSample SAMN15817062.
6673 The GC content of the type genome is 48.22% and the genome length is 2.0 Mbp.
6674
6675
6676 **Description of *Candidatus* Merdivivens pullistercoris sp. nov.**
6677 *Candidatus* Merdivivens pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
6678 neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)

6679
6680   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6681   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6682   assigned the MAG ID 10037 and which is available via NCBI BioSample SAMN15817074. The
6683   GC content of the type genome is 48.95% and the genome length is 2.1 Mbp.
6684
6685
6686   **Description of *Candidatus* Merdousia gen. nov.**
6687   *Candidatus* Merdousia (Merd.ou'si.a. L. fem. n. *merda* dung; Gr. fem. n. *ousia* an essence; N.L.
6688   fem. n. *Merdousia* a microbe associated with faeces)
6689
6690   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
6691   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
6692   species *Merdousia gallistercoris*. This is a name for the alphanumeric GTDB genus CAG-312.
6693   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
6694   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Opitutales* and to the family *CAG-312*.
6695
6696
6697   **Description of *Candidatus* Merdousia gallistercoris sp. nov.**
6698   *Candidatus* Merdousia gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
6699   *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
6700
6701   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6702   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6703   assigned the MAG ID CHK197-16368 and which is available via NCBI BioSample
6704   SAMN15817207. This is a new name for the alphanumeric GTDB species sp900545715. The
6705   GC content of the type genome is 49.37% and the genome length is 2.4 Mbp.
6706
6707
6708   **Description of *Candidatus* Methanocorpusculum faecipullorum sp. nov.**
6709   *Candidatus* Methanocorpusculum faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis*
6710   excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken
6711   faeces)
6712
6713   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6714   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6715   assigned the MAG ID E1-3281 and which is available via NCBI BioSample SAMN15816796.
6716   The GC content of the type genome is 50.72% and the genome length is 1.2 Mbp.
6717
6718
6719   **Description of *Candidatus* Microbacterium pullistercoris sp. nov.**
6720   *Candidatus* Microbacterium pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken;
6721   L. neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
6722
6723   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6724   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

6725   assigned the MAG ID ChiGjej1B1-5908 and which is available via NCBI BioSample
6726   SAMN15816649. The GC content of the type genome is 68.74% and the genome length is 2.5
6727   Mbp.
6728
6729
6730   **Description of *Candidatus* Microbacterium stercoravium sp. nov.**
6731   *Candidatus* Microbacterium stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n.
6732   *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
6733
6734   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6735   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6736   assigned the MAG ID ChiHjej8B7-3636 and which is available via NCBI BioSample
6737   SAMN15816680. The GC content of the type genome is 69.44% and the genome length is 2.5
6738   Mbp.
6739
6740
6741   **Description of *Candidatus* Monoglobus merdigallinarum sp. nov.**
6742   *Candidatus* Monoglobus merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
6743   n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
6744
6745   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6746   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6747   assigned the MAG ID 5790 and which is available via NCBI BioSample SAMN15816780. The
6748   GC content of the type genome is 48.24% and the genome length is 1.5 Mbp.
6749
6750
6751   **Description of *Candidatus* Mucispirillum faecigallinarum sp. nov.**
6752   *Candidatus* Mucispirillum faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis*
6753   excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
6754
6755   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6756   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6757   assigned the MAG ID ChiW4-1371 and which is available via NCBI BioSample
6758   SAMN15816684. The GC content of the type genome is 31.75% and the genome length is 2.2
6759   Mbp.
6760
6761
6762   **Description of *Candidatus* Negativibacillus faecipullorum sp. nov.**
6763   *Candidatus* Negativibacillus faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement;
6764   L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
6765
6766   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6767   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6768   assigned the MAG ID ChiBcec6-1156 and which is available via NCBI BioSample
6769   SAMN15816879. This is a new name for the alphanumeric GTDB species sp900547455. The
6770   GC content of the type genome is 57.54% and the genome length is 2.0 Mbp.

6771
6772
6773 **Description of *Candidatus* Nesterenkonia stercoripullorum sp. nov.**
6774 *Candidatus* Nesterenkonia stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
6775 masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
6776
6777 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6778 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6779 assigned the MAG ID ChiHejej3B27-3195 and which is available via NCBI BioSample
6780 SAMN15816751. The GC content of the type genome is 65.88% and the genome length is 2.6
6781 Mbp.
6782
6783
6784 **Description of *Candidatus* Niameybacter stercoravium sp. nov.**
6785 *Candidatus* Niameybacter stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
6786 bird; N.L. gen. n. *stercoravium* of bird faeces)
6787
6788 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6789 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6790 assigned the MAG ID 2467 and which is available via NCBI BioSample SAMN15816773. The
6791 GC content of the type genome is 35.14% and the genome length is 2.9 Mbp.
6792
6793
6794 **Description of *Candidatus* Nocardiopsis merdipullorum sp. nov.**
6795 *Candidatus* Nocardiopsis merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
6796 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
6797
6798 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6799 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6800 assigned the MAG ID ChiHjej10B9-18110 and which is available via NCBI BioSample
6801 SAMN15816716. The GC content of the type genome is 65.81% and the genome length is 4.2
6802 Mbp.
6803
6804
6805 **Description of *Candidatus* Nosocomiicoccus stercorigallinarum sp. nov.**
6806 *Candidatus* Nosocomiicoccus stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus*
6807 dung; L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
6808
6809 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6810 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6811 assigned the MAG ID CHK169-14505 and which is available via NCBI BioSample
6812 SAMN15816647. The GC content of the type genome is 34.64% and the genome length is 1.3
6813 Mbp.
6814
6815
6816 **Description of *Candidatus* Oceanisphaera merdipullorum sp. nov.**

6817 *Candidatus* Oceanisphaera merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc.
6818 n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
6819
6820 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6821 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6822 assigned the MAG ID 819 and which is available via NCBI BioSample SAMN15816797. The
6823 GC content of the type genome is 50.19% and the genome length is 2.9 Mbp.
6824
6825
6826 **Description of *Candidatus* Odoribacter faecigallinarum sp. nov.**
6827 *Candidatus* Odoribacter faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;
6828 L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
6829
6830 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6831 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6832 assigned the MAG ID 23274 and which is available via NCBI BioSample SAMN15816743. The
6833 GC content of the type genome is 48.17% and the genome length is 2.2 Mbp.
6834
6835
6836 **Description of *Candidatus* Olsenella avicola sp. nov.**
6837 *Candidatus* Olsenella avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L. n.
6838 *avicola* inhabitant of birds)
6839
6840 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6841 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6842 assigned the MAG ID CHK1-7693 and which is available via NCBI BioSample
6843 SAMN15816923. This is a new name for the alphanumeric GTDB species sp002159625.
6844 Although GTDB has assigned this species to the genus it calls Olsenella_E , this genus
6845 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
6846 have used the current validly published name for the genus. The GC content of the type genome
6847 is 67.59% and the genome length is 2.2 Mbp.
6848
6849
6850 **Description of *Candidatus* Olsenella avistercoris sp. nov.**
6851 *Candidatus* Olsenella avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung;
6852 N.L. gen. n. *avistercoris* of bird faeces)
6853
6854 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6855 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6856 assigned the MAG ID CHK136-6238 and which is available via NCBI BioSample
6857 SAMN15816919. This is a new name for the alphanumeric GTDB species sp002160255.
6858 Although GTDB has assigned this species to the genus it calls Olsenella_E , this genus
6859 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
6860 have used the current validly published name for the genus. The GC content of the type genome
6861 is 69.05% and the genome length is 2.0 Mbp.
6862

6863
6864 **Description of *Candidatus* Olsenella excrementavium sp. nov.**
6865 *Candidatus* Olsenella excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum* excrement;
6866 L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
6867
6868 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6869 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6870 assigned the MAG ID ChiHjej10B9-743 and which is available via NCBI BioSample
6871 SAMN15816922. This is a new name for the alphanumeric GTDB species sp002305805.
6872 Although GTDB has assigned this species to the genus it calls Olsenella_E , this genus
6873 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
6874 have used the current validly published name for the genus. The GC content of the type genome
6875 is 66.50% and the genome length is 1.8 Mbp.
6876
6877
6878 **Description of *Candidatus* Olsenella excrementigallinarum sp. nov.**
6879 *Candidatus* Olsenella excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum*
6880 excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)
6881
6882 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6883 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6884 assigned the MAG ID ChiHjej12B11-23512 and which is available via NCBI BioSample
6885 SAMN15816920. This is a new name for the alphanumeric GTDB species sp900119915.
6886 Although GTDB has assigned this species to the genus it calls Olsenella_E , this genus
6887 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
6888 have used the current validly published name for the genus. The GC content of the type genome
6889 is 68.67% and the genome length is 1.8 Mbp.
6890
6891
6892 **Description of *Candidatus* Olsenella pullicola sp. nov.**
6893 *Candidatus* Olsenella pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -*cola*
6894 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
6895
6896 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6897 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6898 assigned the MAG ID ChiHecec1B25-7792 and which is available via NCBI BioSample
6899 SAMN15816895. Although GTDB has assigned this species to the genus it calls Olsenella_E ,
6900 this genus designation cannot be incorporated into a well-formed binomial, so in naming this
6901 species, we have used the current validly published name for the genus. The GC content of the
6902 type genome is 65.74% and the genome length is 2.3 Mbp.
6903
6904
6905 **Description of *Candidatus* Olsenella pullistercoris sp. nov.**
6906 *Candidatus* Olsenella pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L. neut.
6907 n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
6908

6909   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6910   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6911   assigned the MAG ID ChiHjej12B11-14209 and which is available via NCBI BioSample
6912   SAMN15816899. Although GTDB has assigned this species to the genus it calls Olsenella_E ,
6913   this genus designation cannot be incorporated into a well-formed binomial, so in naming this
6914   species, we have used the current validly published name for the genus. The GC content of the
6915   type genome is 67.21% and the genome length is 1.9 Mbp.
6916
6917
6918   **Description of *Candidatus* Olsenella stercoravium sp. nov.**
6919   *Candidatus* Olsenella stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
6920   bird; N.L. gen. n. *stercoravium* of bird faeces)
6921
6922   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6923   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6924   assigned the MAG ID ChiHecolR3B27-1887 and which is available via NCBI BioSample
6925   SAMN15816902. Although GTDB has assigned this species to the genus it calls Olsenella_E ,
6926   this genus designation cannot be incorporated into a well-formed binomial, so in naming this
6927   species, we have used the current validly published name for the genus. The GC content of the
6928   type genome is 67.26% and the genome length is 1.8 Mbp.
6929
6930
6931   **Description of *Candidatus* Onthenecus gen. nov.**
6932   *Candidatus* Onthenecus (Onthen.e'cus. Gr. masc. n. *onthos* dung; Gr. masc. *enoikos* inhabitant;
6933   N.L. masc. n. *Onthenecus* a microbe associated with faeces)
6934
6935   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
6936   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
6937   species *Onthenecus intestinigallinarum*. This is a name for the alphanumeric GTDB genus
6938   OEMS01. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
6939   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family
6940   *CAG-74*.
6941
6942
6943   **Description of *Candidatus* Onthenecus intestinigallinarum sp. nov.**
6944   *Candidatus* Onthenecus intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
6945   L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
6946
6947   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6948   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6949   assigned the MAG ID ChiSxjej2B14-6234 and which is available via NCBI BioSample
6950   SAMN15817054. The GC content of the type genome is 66.20% and the genome length is 2.4
6951   Mbp.
6952
6953
6954   **Description of *Candidatus* Onthocola gen. nov.**

6955   *Candidatus* Onthocola (On.tho.co'la. Gr. masc. n. *onthos* dung; L. suff. *-cola* inhabitant of; N.L.
6956   fem. n. *Onthocola* a microbe associated with faeces)
6957
6958   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
6959   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
6960   species *Onthocola gallistercoris*. This is a name for the alphanumeric GTDB genus. This genus
6961   has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al.,
6962   2019; Parks et al., 2020) to the order *Lachnospirales* and to the family *Lachnospiraceae.*
6963
6964
6965   **Description of *Candidatus* Onthocola gallistercoris sp. nov.**
6966   *Candidatus* Onthocola gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
6967   *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
6968
6969   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6970   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6971   assigned the MAG ID CHK187-14744 and which is available via NCBI BioSample
6972   SAMN15817044. The GC content of the type genome is 48.32% and the genome length is 2.4
6973   Mbp.
6974
6975
6976   **Description of *Candidatus* Onthocola stercoravium sp. nov.**
6977   *Candidatus* Onthocola stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
6978   bird; N.L. gen. n. *stercoravium* of bird faeces)
6979
6980   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6981   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6982   assigned the MAG ID ChiW5-5982 and which is available via NCBI BioSample
6983   SAMN15817021. The GC content of the type genome is 28.08% and the genome length is 1.4
6984   Mbp.
6985
6986
6987   **Description of *Candidatus* Onthocola stercorigallinarum sp. nov.**
6988   *Candidatus* Onthocola stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
6989   fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
6990
6991   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
6992   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
6993   assigned the MAG ID CHK195-3072 and which is available via NCBI BioSample
6994   SAMN15817046. The GC content of the type genome is 27.21% and the genome length is 1.3
6995   Mbp.
6996
6997
6998   **Description of *Candidatus* Onthomonas gen. nov.**
6999   *Candidatus* Onthomonas (On.tho.mo'nas. Gr. masc. n. *onthos* dung; L. fem. n. *monas* a monad;
7000   N.L. fem. n. *Onthomonas* a microbe associated with faeces)

7001
7002   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7003   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7004   species *Onthomonas avicola*. This is a name for the alphanumeric GTDB genus NK3B98. This
7005   genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
7006   al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family *Oscillospiraceae.*
7007
7008
7009   **Description of *Candidatus* Onthomonas avicola sp. nov.**
7010   *Candidatus* Onthomonas avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L.
7011   n. *avicola* inhabitant of birds)
7012
7013   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7014   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7015   assigned the MAG ID ChiGjej6B6-14002 and which is available via NCBI BioSample
7016   SAMN15817096. The GC content of the type genome is 63.01% and the genome length is 2.4
7017   Mbp.
7018
7019
7020   **Description of *Candidatus* Onthomorpha gen. nov.**
7021   *Candidatus* Onthomorpha (On.tho.mor'pha. Gr. masc. n. *onthos* dung; Gr. fem. n. *morphe* a
7022   form, shape; N.L. fem. n. *Onthomorpha* a microbe associated with faeces)
7023
7024   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7025   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7026   species *Onthomorpha intestinigallinarum*. This is a name for the alphanumeric GTDB genus
7027   UBA3388. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
7028   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Bacteroidales* and to the family *P3.*
7029
7030
7031   **Description of *Candidatus* Onthomorpha intestinigallinarum sp. nov.**
7032   *Candidatus* Onthomorpha intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
7033   L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
7034
7035   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7036   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7037   assigned the MAG ID Gambia16-930 and which is available via NCBI BioSample
7038   SAMN15817128. The GC content of the type genome is 42.76% and the genome length is 1.7
7039   Mbp.
7040
7041
7042   **Description of *Candidatus* Onthoplasma gen. nov.**
7043   *Candidatus* Onthoplasma (On.tho.plas'ma. Gr. masc. n. *onthos* dung; Gr. neut. n. *plasma* a form;
7044   N.L. neut. n. *Onthoplasma* a microbe associated with faeces)
7045

7046 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7047 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7048 species *Onthoplasma faecipullorum*. This is a name for the alphanumeric GTDB genus
7049 UBA4626. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
7050 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *4C28d-15* and to the family
7051 *UBA1242*.

7052
7053

7054 **Description of *Candidatus* Onthoplasma faecigallinarum sp. nov.**
7055 *Candidatus* Onthoplasma faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;
7056 L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

7057

7058 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7059 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7060 assigned the MAG ID 5992 and which is available via NCBI BioSample SAMN15817127. The
7061 GC content of the type genome is 34.71% and the genome length is 1.0 Mbp.

7062
7063

7064 **Description of *Candidatus* Onthoplasma faecipullorum sp. nov.**
7065 *Candidatus* Onthoplasma faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
7066 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

7067

7068 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7069 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7070 assigned the MAG ID CHK191-42317 and which is available via NCBI BioSample
7071 SAMN15817053. The GC content of the type genome is 31.88% and the genome length is 1.1
7072 Mbp.

7073
7074

7075 **Description of *Candidatus* Onthosoma gen. nov.**
7076 *Candidatus* Onthosoma (On.tho.so'ma. Gr. masc. n. *onthos* dung; Gr. neut. n. *soma* a body; N.L.
7077 neut. n. *Onthosoma* a microbe associated with faeces)

7078

7079 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7080 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7081 species *Onthosoma merdavium*. This is a name for the alphanumeric GTDB genus OEMR01.
7082 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
7083 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Erysipelotrichales* and to the family
7084 *Erysipelotrichaceae*.

7085
7086

7087 **Description of *Candidatus* Onthosoma merdavium sp. nov.**
7088 *Candidatus* Onthosoma merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
7089 N.L. gen. n. *merdavium* of bird faeces)
7090

7091   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7092   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7093   assigned the MAG ID ChiBcec15-4520 and which is available via NCBI BioSample
7094   SAMN15817169. This is a new name for the alphanumeric GTDB species sp900199515. The
7095   GC content of the type genome is 45.30% and the genome length is 1.6 Mbp.
7096
7097
7098   **Description of *Candidatus* Onthousia gen. nov.**
7099   *Candidatus* Onthousia (Onth.ou'si.a. Gr. masc. n. *onthos* dung; Gr. fem. n. *ousia* an essence;
7100   N.L. fem. n. *Onthousia* a microbe associated with faeces)
7101
7102   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7103   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7104   species *Onthousia faecavium*. This is a name for the alphanumeric GTDB genus CAG-451. This
7105   genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
7106   al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-611*.
7107
7108
7109   **Description of *Candidatus* Onthousia excrementipullorum sp. nov.**
7110   *Candidatus* Onthousia excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
7111   excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
7112   chicken excrement)
7113
7114   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7115   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7116   assigned the MAG ID CHK184-20233 and which is available via NCBI BioSample
7117   SAMN15817019. The GC content of the type genome is 27.72% and the genome length is 1.3
7118   Mbp.
7119
7120
7121   **Description of *Candidatus* Onthousia faecavium sp. nov.**
7122   *Candidatus* Onthousia faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n. *avis*
7123   bird; N.L. gen. n. *faecavium* of bird faeces)
7124
7125   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7126   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7127   assigned the MAG ID CHK195-6217 and which is available via NCBI BioSample
7128   SAMN15817026. The GC content of the type genome is 28.40% and the genome length is 1.3
7129   Mbp.
7130
7131
7132   **Description of *Candidatus* Onthousia faecigallinarum sp. nov.**
7133   *Candidatus* Onthousia faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
7134   fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
7135

7136 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7137 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7138 assigned the MAG ID CHK135-1819 and which is available via NCBI BioSample
7139 SAMN15817105. The GC content of the type genome is 32.62% and the genome length is 1.1
7140 Mbp.
7141
7142
7143 **Description of *Candidatus* Onthousia faecipullorum sp. nov.**
7144 *Candidatus* Onthousia faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
7145 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
7146
7147 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7148 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7149 assigned the MAG ID CHK195-26880 and which is available via NCBI BioSample
7150 SAMN15817040. The GC content of the type genome is 27.41% and the genome length is 1.4
7151 Mbp.
7152
7153
7154 **Description of *Candidatus* Onthovicinus gen. nov.**
7155 *Candidatus* Onthovicinus (On.tho.vic.in'us. Gr. masc. n. *onthos* dung; L. masc. n. *vicinus* a
7156 neighbour; N.L. masc. n. *Onthovicinus* a microbe associated with faeces)
7157
7158 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7159 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7160 species *Onthovicinus excrementipullorum*. This is a name for the alphanumeric GTDB genus
7161 UMGS1839. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
7162 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
7163 *Acutalibacteraceae.*
7164
7165
7166 **Description of *Candidatus* Onthovicinus excrementipullorum sp. nov.**
7167 *Candidatus* Onthovicinus excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
7168 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
7169 chicken excrement)
7170
7171 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7172 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7173 assigned the MAG ID CHK185-12131 and which is available via NCBI BioSample
7174 SAMN15817020. The GC content of the type genome is 55.55% and the genome length is 2.4
7175 Mbp.
7176
7177
7178 **Description of *Candidatus* Onthovivens gen. nov.**
7179 *Candidatus* Onthovivens (On.tho.viv'ens. Gr. masc. n. *onthos* dung; N.L. pres. part. *vivens*
7180 living; N.L. fem. n. *Onthovivens* a microbe associated with faeces)
7181

7182   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7183   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7184   species *Onthovivens merdipullorum*. This is a name for the alphanumeric GTDB genus
7185   UBA4855. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
7186   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RFN20* and to the family *CAG-826*.
7187
7188
7189   **Description of *Candidatus* Onthovivens merdipullorum sp. nov.**
7190   *Candidatus* Onthovivens merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
7191   *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
7192
7193   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7194   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7195   assigned the MAG ID 11159 and which is available via NCBI BioSample SAMN15817139. The
7196   GC content of the type genome is 27.05% and the genome length is 1.5 Mbp.
7197
7198
7199   **Description of *Candidatus* Ornithocaccomicrobium gen. nov.**
7200   *Candidatus* Ornithocaccomicrobium (Or.ni.tho.cac.co.mi.cro'bi.um. Gr. masc. or fem. n. *ornis,*
7201   *ornithos* bird; Gr. fem. n. *kakke* faeces; N.L. neut. n. *microbium* a microbe; N.L. neut. n.
7202   *Ornithocaccomicrobium* A microbe found in chicken faceces)
7203
7204   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7205   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7206   species *Ornithocaccomicrobium faecavium*. This genus was identified but not named by
7207   Glendinning et al. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release
7208   05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the
7209   family *CAG-74*.
7210
7211
7212   **Description of *Candidatus* Ornithocaccomicrobium faecavium sp. nov.**
7213   *Candidatus* Ornithocaccomicrobium faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement;
7214   L. fem. n. *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
7215
7216   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7217   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7218   assigned the MAG ID CHK183-6373 and which is available via NCBI BioSample
7219   SAMN15816945. The GC content of the type genome is 59.48% and the genome length is 2.9
7220   Mbp.
7221
7222
7223   **Description of *Candidatus* Ornithoclostridium gen. nov.**
7224   *Candidatus* Ornithoclostridium (Or.ni.tho.clos.tri'di.um. Gr. masc. or fem. n. *ornis, ornithos* bird;
7225   N.L. neut. n. *Clostridium* a genus name; N.L. neut. n. *Ornithoclostridium* a genus related to the
7226   genus *Clostridium* but distinct from it and found in poultry)
7227

7228 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7229 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7230 species *Ornithoclostridium excrementipullorum.* This genus has been assigned by GTDB-Tk
7231 v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the
7232 order *Christensenellales* and to the family *UBA3700.*

7233
7234

7235 **Description of *Candidatus* Ornithoclostridium excrementipullorum sp. nov.**
7236 *Candidatus* Ornithoclostridium excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
7237 *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
7238 young chicken excrement)

7239

7240 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7241 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7242 assigned the MAG ID ChiW5-1639 and which is available via NCBI BioSample
7243 SAMN15816971. The GC content of the type genome is 54.62% and the genome length is 1.6
7244 Mbp.

7245
7246

7247 **Description of *Candidatus* Ornithoclostridium faecavium sp. nov.**
7248 *Candidatus* Ornithoclostridium faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L.
7249 fem. n. *avis* bird; N.L. gen. n. *faecavium* of bird faeces)

7250

7251 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7252 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7253 assigned the MAG ID 63 and which is available via NCBI BioSample SAMN15816992. The GC
7254 content of the type genome is 48.09% and the genome length is 1.8 Mbp.

7255
7256

7257 **Description of *Candidatus* Ornithoclostridium faecigallinarum sp. nov.**
7258 *Candidatus* Ornithoclostridium faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis*
7259 excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

7260

7261 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7262 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7263 assigned the MAG ID ChiHcolR4-3946 and which is available via NCBI BioSample
7264 SAMN15816996. The GC content of the type genome is 57.12% and the genome length is 1.6
7265 Mbp.

7266
7267

7268 **Description of *Candidatus* Ornithomonoglobus gen. nov.**
7269 *Candidatus* Ornithomonoglobus (Or.ni.tho.mo.no.glo'bus. Gr. masc. or fem. n. *ornis, ornithos*
7270 bird; N.L. masc. n. *Monoglobus* a genus name; N.L. masc. n. *Ornithomonoglobus* a genus related
7271 to the genus *Monoglobus* but distinct from it and found in poultry)
7272

7273 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7274 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7275 species *Ornithomonoglobus merdipullorum*. This genus was identified but not named by
7276 Glendinning et al. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release
7277 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Monoglobales* and to the family
7278 *UBA1381*.
7279
7280
7281 **Description of *Candidatus* Ornithomonoglobus intestinigallinarum sp. nov.**
7282 *Candidatus* Ornithomonoglobus intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n.
7283 *intestinum* gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
7284
7285 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7286 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7287 assigned the MAG ID CHK181-108 and which is available via NCBI BioSample
7288 SAMN15816941. The GC content of the type genome is 49.36% and the genome length is 2.2
7289 Mbp.
7290
7291
7292 **Description of *Candidatus* Ornithomonoglobus merdipullorum sp. nov.**
7293 *Candidatus* Ornithomonoglobus merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L.
7294 masc. n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
7295
7296 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7297 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7298 assigned the MAG ID USAMLcec3-3695 and which is available via NCBI BioSample
7299 SAMN15816942. The GC content of the type genome is 48.52% and the genome length is 2.7
7300 Mbp.
7301
7302
7303 **Description of *Candidatus* Ornithospirochaeta gen. nov.**
7304 *Candidatus* Ornithospirochaeta (Or.ni.tho.spi.ro.chae'ta. Gr. masc. or fem. n. *ornis, ornithos* bird;
7305 N.L. fem. n. *Spirochaeta* a genus name; N.L. fem. n. *Ornithospirochaeta* a genus related to the
7306 genus *Spirochaeta* but distinct from it and found in poultry)
7307
7308 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7309 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7310 species *Ornithospirochaeta stercoravium*. This genus has been assigned by GTDB-Tk v1.3.0
7311 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
7312 *Sphaerochaetales* and to the family *Sphaerochaetaceae*.
7313
7314
7315 **Description of *Candidatus* Ornithospirochaeta avicola sp. nov.**
7316 *Candidatus* Ornithospirochaeta avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant
7317 of; N.L. n. *avicola* inhabitant of birds)
7318

7319   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7320   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7321   assigned the MAG ID Gambia11-129 and which is available via NCBI BioSample
7322   SAMN15816993. The GC content of the type genome is 42.81% and the genome length is 1.5
7323   Mbp.
7324
7325
7326   **Description of *Candidatus* Ornithospirochaeta stercoravium sp. nov.**
7327   *Candidatus* Ornithospirochaeta stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem.
7328   n. *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
7329
7330   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7331   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7332   assigned the MAG ID 14700 and which is available via NCBI BioSample SAMN15816953. The
7333   GC content of the type genome is 46.26% and the genome length is 2.0 Mbp.
7334
7335
7336   **Description of *Candidatus* Ornithospirochaeta stercorigallinarum sp. nov.**
7337   *Candidatus* Ornithospirochaeta stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus*
7338   dung; L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
7339
7340   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7341   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7342   assigned the MAG ID ChiHecec3B27-9561 and which is available via NCBI BioSample
7343   SAMN15816957. The GC content of the type genome is 46.77% and the genome length is 1.9
7344   Mbp.
7345
7346
7347   **Description of *Candidatus* Ornithospirochaeta stercoripullorum sp. nov.**
7348   *Candidatus* Ornithospirochaeta stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung;
7349   L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young
7350   chickens)
7351
7352   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7353   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7354   assigned the MAG ID 7293 and which is available via NCBI BioSample SAMN15816978. The
7355   GC content of the type genome is 45.57% and the genome length is 2.0 Mbp.
7356
7357
7358   **Description of *Candidatus* Oscillibacter avistercoris sp. nov.**
7359   *Candidatus* Oscillibacter avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
7360   dung; N.L. gen. n. *avistercoris* of bird faeces)
7361
7362   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7363   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7364   assigned the MAG ID CHK176-14096 and which is available via NCBI BioSample

7365 SAMN15816820. This is a new name for the alphanumeric GTDB species sp900556925. The
7366 GC content of the type genome is 63.55% and the genome length is 2.3 Mbp.
7367
7368
7369 **Description of *Candidatus* Oscillibacter excrementavium sp. nov.**
7370 *Candidatus* Oscillibacter excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
7371 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
7372
7373 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7374 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7375 assigned the MAG ID 5302 and which is available via NCBI BioSample SAMN15816661. The
7376 GC content of the type genome is 63.73% and the genome length is 2.5 Mbp.
7377
7378
7379 **Description of *Candidatus* Oscillibacter excrementigallinarum sp. nov.**
7380 *Candidatus* Oscillibacter excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
7381 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
7382 excrement)
7383
7384 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7385 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7386 assigned the MAG ID ChiBcec18-1249 and which is available via NCBI BioSample
7387 SAMN15816667. The GC content of the type genome is 64.01% and the genome length is 2.4
7388 Mbp.
7389
7390
7391 **Description of *Candidatus* Oscillibacter pullicola sp. nov.**
7392 *Candidatus* Oscillibacter pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
7393 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
7394
7395 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7396 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7397 assigned the MAG ID ChiBcolR2-4535 and which is available via NCBI BioSample
7398 SAMN15816652. The GC content of the type genome is 63.62% and the genome length is 2.4
7399 Mbp.
7400
7401
7402 **Description of *Candidatus* Paenalcaligenes intestinipullorum sp. nov.**
7403 *Candidatus* Paenalcaligenes intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut;
7404 L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
7405
7406 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7407 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7408 assigned the MAG ID 9264 and which is available via NCBI BioSample SAMN15816786. The
7409 GC content of the type genome is 51.92% and the genome length is 1.8 Mbp.
7410

7411

Description of *Candidatus* Paenibacillus intestinavium sp. nov.
Candidatus Paenibacillus intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK172-12487 and which is available via NCBI BioSample SAMN15816909. Although GTDB has assigned this species to the genus it calls Paenibacillus_C , this genus designation cannot be incorporated into a well-formed binomial, so in naming this species, we have used the current validly published name for the genus. The GC content of the type genome is 39.31% and the genome length is 4.6 Mbp.

Description of *Candidatus* Parabacteroides faecavium sp. nov.
Candidatus Parabacteroides faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n. *avis* bird; N.L. gen. n. *faecavium* of bird faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK152-2511 and which is available via NCBI BioSample SAMN15816864. This is a new name for the alphanumeric GTDB species sp000436495. The GC content of the type genome is 42.40% and the genome length is 3.4 Mbp.

Description of *Candidatus* Parabacteroides intestinavium sp. nov.
Candidatus Parabacteroides intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n. *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej11B10-3189 and which is available via NCBI BioSample SAMN15816658. The GC content of the type genome is 44.93% and the genome length is 2.8 Mbp.

Description of *Candidatus* Parabacteroides intestinigallinarum sp. nov.
Candidatus Parabacteroides intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec2B26-12326 and which is available via NCBI BioSample SAMN15816728. The GC content of the type genome is 52.90% and the genome length is 2.9 Mbp.

7457
7458 **Description of *Candidatus* Parabacteroides intestinipullorum sp. nov.**
7459 *Candidatus* Parabacteroides intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut;
7460 L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
7461
7462 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7463 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7464 assigned the MAG ID ChiGjej6B6-14162 and which is available via NCBI BioSample
7465 SAMN15816857. This is a new name for the alphanumeric GTDB species sp900552415. The
7466 GC content of the type genome is 50.53% and the genome length is 3.2 Mbp.
7467
7468
7469 **Description of *Candidatus* Paralactobacillus gallistercoris sp. nov.**
7470 *Candidatus* Paralactobacillus gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut.
7471 n. *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
7472
7473 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7474 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7475 assigned the MAG ID F6-6636 and which is available via NCBI BioSample SAMN15816781.
7476 The GC content of the type genome is 35.69% and the genome length is 1.2 Mbp.
7477
7478
7479 **Description of *Candidatus* Paraprevotella stercoravium sp. nov.**
7480 *Candidatus* Paraprevotella stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n.
7481 *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
7482
7483 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7484 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7485 assigned the MAG ID G3-2149 and which is available via NCBI BioSample SAMN15816669.
7486 The GC content of the type genome is 45.06% and the genome length is 3.2 Mbp.
7487
7488
7489 **Description of *Candidatus* Paraprevotella stercorigallinarum sp. nov.**
7490 *Candidatus* Paraprevotella stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
7491 fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
7492
7493 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7494 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7495 assigned the MAG ID 11093 and which is available via NCBI BioSample SAMN15816852. This
7496 is a new name for the alphanumeric GTDB species sp900546665. The GC content of the type
7497 genome is 43.79% and the genome length is 2.9 Mbp.
7498
7499
7500 **Description of *Candidatus* Parasutterella gallistercoris sp. nov.**
7501 *Candidatus* Parasutterella gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
7502 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)

7503

7504 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7505 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7506 assigned the MAG ID 21611 and which is available via NCBI BioSample SAMN15816870. This
7507 is a new name for the alphanumeric GTDB species sp000980495. The GC content of the type
7508 genome is 49.58% and the genome length is 1.9 Mbp.

7509

7510

7511 **Description of *Candidatus* Pelethenecus gen. nov.**
7512 *Candidatus* Pelethenecus (Pel.eth.en.e'cus. Gr. masc. n. *pelethos* dung; Gr. masc. *enoikos*
7513 inhabitant; N.L. masc. n. *Pelethenecus* a microbe associated with faeces)

7514

7515 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7516 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7517 species *Pelethenecus faecipullorum*. This is a name for the alphanumeric GTDB genus
7518 UMGS268. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
7519 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Acholeplasmatales* and to the family
7520 *Anaeroplasmataceae.*

7521

7522

7523 **Description of *Candidatus* Pelethenecus faecipullorum sp. nov.**
7524 *Candidatus* Pelethenecus faecipullorum (ster.co.ri.gal.li.na'rum. L. fem. n. *faex, faecis*
7525 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken
7526 faeces)

7527

7528 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7529 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7530 assigned the MAG ID ChiW17-6978 and which is available via NCBI BioSample
7531 SAMN15817226. This is a new name for the alphanumeric GTDB species sp900540175. The
7532 GC content of the type genome is 39.85% and the genome length is 1.3 Mbp.

7533

7534

7535 **Description of *Candidatus* Pelethocola gen. nov.**
7536 *Candidatus* Pelethocola (Pel.eth.o.co'la. Gr. masc. n. *pelethos* dung; L. suff. -*cola* inhabitant of;
7537 N.L. fem. n. *Pelethocola* a microbe associated with faeces)

7538

7539 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7540 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7541 species *Pelethocola excrementipullorum*. This is a name for the alphanumeric GTDB genus
7542 UBA5416. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
7543 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
7544 *Lachnospiraceae.*

7545

7546

7547 **Description of *Candidatus* Pelethocola excrementipullorum sp. nov.**

7548 *Candidatus* Pelethocola excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
7549 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
7550 chicken excrement)
7551
7552 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7553 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7554 assigned the MAG ID CHK160-5124 and which is available via NCBI BioSample
7555 SAMN15817143. The GC content of the type genome is 43.72% and the genome length is 3.9
7556 Mbp.
7557
7558
7559 **Description of *Candidatus* Pelethomonas gen. nov.**
7560 *Candidatus* Pelethomonas (Pel.eth.omo'nas. Gr. masc. n. *pelethos* dung; L. fem. n. *monas* a
7561 monad; N.L. fem. n. *Pelethomonas* a microbe associated with faeces)
7562
7563 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7564 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7565 species *Pelethomonas intestinigallinarum*. This is a name for the alphanumeric GTDB genus
7566 UMGS1872. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
7567 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
7568 *Oscillospiraceae.*
7569
7570
7571 **Description of *Candidatus* Pelethomonas intestinigallinarum sp. nov.**
7572 *Candidatus* Pelethomonas intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
7573 L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
7574
7575 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7576 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7577 assigned the MAG ID ChiSjej2B20-3600 and which is available via NCBI BioSample
7578 SAMN15817014. The GC content of the type genome is 63.89% and the genome length is 2.2
7579 Mbp.
7580
7581
7582 **Description of *Candidatus* Pelethosoma gen. nov.**
7583 *Candidatus* Pelethosoma (Pel.eth.o.so'ma. Gr. masc. n. *pelethos* dung; Gr. neut. n. *soma* a body;
7584 N.L. neut. n. *Pelethosoma* a microbe associated with faeces)
7585
7586 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7587 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7588 species *Pelethosoma merdigallinarum*. This is a name for the alphanumeric GTDB genus
7589 UMGS2016. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
7590 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-822.*
7591
7592
7593 **Description of *Candidatus* Pelethosoma merdigallinarum sp. nov.**

7594   *Candidatus* Pelethosoma merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
7595   n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
7596
7597   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7598   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7599   assigned the MAG ID CHK195-5794 and which is available via NCBI BioSample
7600   SAMN15817039. The GC content of the type genome is 30.57% and the genome length is 1.3
7601   Mbp.
7602
7603
7604   **Description of *Candidatus* Pelethousia gen. nov.**
7605   *Candidatus* Pelethousia (Pel.eth.ou'si.a. Gr. masc. n. *pelethos* dung; Gr. fem. n. *ousia* an essence;
7606   N.L. fem. n. *Pelethousia* a microbe associated with faeces)
7607
7608   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7609   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7610   species *Pelethousia gallinarum*. This is a name for the alphanumeric GTDB genus UBA5394.
7611   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
7612   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family *CAG-*
7613   *138.*
7614
7615
7616   **Description of *Candidatus* Pelethousia gallinarum sp. nov.**
7617   *Candidatus* Pelethousia gallinarum (gal.li.na'rum. L. fem. n. *gallina* a hen; L. fem. gen.pl. n.
7618   *gallinarum* of hens)
7619
7620   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7621   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7622   assigned the MAG ID ChiHcec27-1353 and which is available via NCBI BioSample
7623   SAMN15817178. This is a new name for the alphanumeric GTDB species sp003150565. The
7624   GC content of the type genome is 59.40% and the genome length is 2.0 Mbp.
7625
7626
7627   **Description of *Candidatus* Phascolarctobacterium stercoravium sp. nov.**
7628   *Candidatus* Phascolarctobacterium stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L.
7629   fem. n. *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)
7630
7631   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7632   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7633   assigned the MAG ID ChiBcec14-732 and which is available via NCBI BioSample
7634   SAMN15816834. This is a new name for the alphanumeric GTDB species sp000436095. The
7635   GC content of the type genome is 46.50% and the genome length is 1.7 Mbp.
7636
7637
7638   **Description of *Candidatus* Phocaeicola caecigallinarum sp. nov.**

7639 *Candidatus* Phocaeicola caecigallinarum (cae.ci.gal.li.na'rum. L. neut. n. *caecum* the caecum; L.
7640 fem. n. *gallina* a hen; N.L. gen. n. *caecigallinarum* of the caecum of hens)
7641
7642 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7643 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7644 assigned the MAG ID ChiHjej11B10-3694 and which is available via NCBI BioSample
7645 SAMN15816802. This is a new name for the alphanumeric GTDB species sp002161565. The
7646 GC content of the type genome is 46.18% and the genome length is 3.2 Mbp.
7647
7648
7649 **Description of *Candidatus* Phocaeicola excrementigallinarum sp. nov.**
7650 *Candidatus* Phocaeicola excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
7651 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
7652 excrement)
7653
7654 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7655 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7656 assigned the MAG ID 12279 and which is available via NCBI BioSample SAMN15816632. The
7657 GC content of the type genome is 50.57% and the genome length is 2.5 Mbp.
7658
7659
7660 **Description of *Candidatus* Phocaeicola excrementipullorum sp. nov.**
7661 *Candidatus* Phocaeicola excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
7662 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
7663 chicken excrement)
7664
7665 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7666 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7667 assigned the MAG ID 8470 and which is available via NCBI BioSample SAMN15816808. This
7668 is a new name for the alphanumeric GTDB species sp900546095. The GC content of the type
7669 genome is 49.09% and the genome length is 3.1 Mbp.
7670
7671
7672 **Description of *Candidatus* Phocaeicola faecigallinarum sp. nov.**
7673 *Candidatus* Phocaeicola faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;
7674 L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
7675
7676 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7677 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7678 assigned the MAG ID G4-2901 and which is available via NCBI BioSample SAMN15816657.
7679 The GC content of the type genome is 40.33% and the genome length is 3.3 Mbp.
7680
7681
7682 **Description of *Candidatus* Phocaeicola faecipullorum sp. nov.**
7683 *Candidatus* Phocaeicola faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
7684 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

7685
7686 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7687 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7688 assigned the MAG ID 17637 and which is available via NCBI BioSample SAMN15816682. The
7689 GC content of the type genome is 39.94% and the genome length is 3.9 Mbp.
7690
7691
7692 **Description of *Candidatus* Phocaeicola gallinarum sp. nov.**
7693 *Candidatus* Phocaeicola gallinarum (gal.li.na'rum. L. fem. n. *gallina* a hen; L. fem. n. *avis* bird;
7694 N.L. gen. n. *faecavium* of bird faeces)
7695
7696 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7697 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7698 assigned the MAG ID ChiGjej6B6-595 and which is available via NCBI BioSample
7699 SAMN15816805. This is a new name for the alphanumeric GTDB species sp900540105. The
7700 GC content of the type genome is 45.79% and the genome length is 2.8 Mbp.
7701
7702
7703 **Description of *Candidatus* Phocaeicola gallistercoris sp. nov.**
7704 *Candidatus* Phocaeicola gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
7705 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
7706
7707 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7708 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7709 assigned the MAG ID Gambia9-593 and which is available via NCBI BioSample
7710 SAMN15816698. The GC content of the type genome is 38.34% and the genome length is 2.3
7711 Mbp.
7712
7713
7714 **Description of *Candidatus* Phocaeicola merdavium sp. nov.**
7715 *Candidatus* Phocaeicola merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
7716 N.L. gen. n. *merdavium* of bird faeces)
7717
7718 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7719 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7720 assigned the MAG ID CHK136-5299 and which is available via NCBI BioSample
7721 SAMN15816804. This is a new name for the alphanumeric GTDB species sp002161765. The
7722 GC content of the type genome is 44.54% and the genome length is 2.6 Mbp.
7723
7724
7725 **Description of *Candidatus* Phocaeicola merdigallinarum sp. nov.**
7726 *Candidatus* Phocaeicola merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
7727 n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
7728
7729 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7730 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

7731   assigned the MAG ID 17689 and which is available via NCBI BioSample SAMN15816829. This
7732   is a new name for the alphanumeric GTDB species sp900066455. The GC content of the type
7733   genome is 46.19% and the genome length is 3.3 Mbp.
7734
7735

7736   **Description of *Candidatus* Prevotella avicola sp. nov.**
7737   *Candidatus* Prevotella avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L. n.
7738   *avicola* inhabitant of birds)
7739
7740   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7741   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7742   assigned the MAG ID ChiHecec3B27-8219 and which is available via NCBI BioSample
7743   SAMN15816846. This is a new name for the alphanumeric GTDB species sp000435635. The
7744   GC content of the type genome is 51.22% and the genome length is 1.9 Mbp.
7745
7746

7747   **Description of *Candidatus* Prevotella intestinigallinarum sp. nov.**
7748   *Candidatus* Prevotella intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut; L.
7749   fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
7750
7751   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7752   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7753   assigned the MAG ID 146 and which is available via NCBI BioSample SAMN15816872. This is
7754   a new name for the alphanumeric GTDB species sp900540415. The GC content of the type
7755   genome is 56.37% and the genome length is 2.9 Mbp.
7756
7757

7758   **Description of *Candidatus* Prevotella stercoripullorum sp. nov.**
7759   *Candidatus* Prevotella stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc.
7760   n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
7761
7762   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7763   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7764   assigned the MAG ID USASDec6-549 and which is available via NCBI BioSample
7765   SAMN15816866. This is a new name for the alphanumeric GTDB species sp900554045. The
7766   GC content of the type genome is 53.35% and the genome length is 2.5 Mbp.
7767
7768

7769   **Description of *Candidatus* Protoclostridium stercorigallinarum sp. nov.**
7770   *Candidatus* Protoclostridium stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung;
7771   L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
7772
7773   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7774   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7775   assigned the MAG ID 12435 and which is available via NCBI BioSample SAMN15816772. The
7776   GC content of the type genome is 56.70% and the genome length is 1.7 Mbp.

7777
7778
7779 **Description of *Candidatus* Pseudogracilibacillus intestinigallinarum sp. nov.**
7780 *Candidatus* Pseudogracilibacillus intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n.
7781 *intestinum* gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
7782
7783 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7784 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7785 assigned the MAG ID CHK169-2315 and which is available via NCBI BioSample
7786 SAMN15816775. The GC content of the type genome is 35.03% and the genome length is 2.5
7787 Mbp.
7788
7789
7790 **Description of *Candidatus* Pseudomonas excrementavium sp. nov.**
7791 *Candidatus* Pseudomonas excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
7792 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
7793
7794 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7795 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7796 assigned the MAG ID CHK174-787 and which is available via NCBI BioSample
7797 SAMN15816898. Although GTDB has assigned this species to the genus it calls
7798 Pseudomonas_D , this genus designation cannot be incorporated into a well-formed binomial, so
7799 in naming this species, we have used the current validly published name for the genus. The GC
7800 content of the type genome is 61.84% and the genome length is 3.0 Mbp.
7801
7802
7803 **Description of *Candidatus* Pullibacteroides gen. nov.**
7804 *Candidatus* Pullibacteroides (Pul.li.bac.te.ro'i.des. L. masc. n. *pullus* a young chicken; N.L.
7805 masc. n. *Bacteroides* a genus name; N.L. masc. n. *Pullibacteroides* a genus related to the genus
7806 *Bacteroides* but distinct from it and found in poultry)
7807
7808 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7809 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7810 species *Pullibacteroides excrementavium.* This genus has been assigned by GTDB-Tk v1.3.0
7811 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
7812 *Bacteroidales* and to the family *P3.*
7813
7814
7815 **Description of *Candidatus* Pullibacteroides excrementavium sp. nov.**
7816 *Candidatus* Pullibacteroides excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
7817 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
7818
7819 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7820 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7821 assigned the MAG ID 2889 and which is available via NCBI BioSample SAMN15816989. The
7822 GC content of the type genome is 51.34% and the genome length is 2.4 Mbp.

7823
7824
7825 **Description of *Candidatus* Pullichristensenella gen. nov.**
7826 *Candidatus* Pullichristensenella (Pul.li.chris.ten.sen.el'la. L. masc. n. *pullus* a young chicken;
7827 N.L. fem. n. *Christensenella* a genus name; N.L. fem. n. *Pullichristensenella* a genus related to
7828 the genus *Christensenella* but distinct from it and found in poultry)
7829
7830 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
7831 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
7832 species *Pullichristensenella avicola.* This genus has been assigned by GTDB-Tk v1.3.0 working
7833 on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order
7834 *Christensenellales* and to the family *CAG-74.*
7835
7836
7837 **Description of *Candidatus* Pullichristensenella avicola sp. nov.**
7838 *Candidatus* Pullichristensenella avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant
7839 of; N.L. n. *avicola* inhabitant of birds)
7840
7841 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7842 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7843 assigned the MAG ID 10205 and which is available via NCBI BioSample SAMN15816956. The
7844 GC content of the type genome is 63.02% and the genome length is 2.3 Mbp.
7845
7846
7847 **Description of *Candidatus* Pullichristensenella excrementigallinarum sp. nov.**
7848 *Candidatus* Pullichristensenella excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
7849 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
7850 excrement)
7851
7852 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7853 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7854 assigned the MAG ID ChiHcec3-11533 and which is available via NCBI BioSample
7855 SAMN15816983. The GC content of the type genome is 57.19% and the genome length is 2.2
7856 Mbp.
7857
7858
7859 **Description of *Candidatus* Pullichristensenella excrementipullorum sp. nov.**
7860 *Candidatus* Pullichristensenella excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
7861 *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
7862 young chicken excrement)
7863
7864 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7865 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7866 assigned the MAG ID 1279 and which is available via NCBI BioSample SAMN15817001. The
7867 GC content of the type genome is 63.33% and the genome length is 2.7 Mbp.
7868

7869

7870 **Description of *Candidatus* Pullichristensenella stercorigallinarum sp. nov.**

7871 *Candidatus* Pullichristensenella stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus*

7872 dung; L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)

7873

7874 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

7875 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

7876 assigned the MAG ID ChiSjej6B24-2974 and which is available via NCBI BioSample

7877 SAMN15816933. The GC content of the type genome is 60.06% and the genome length is 2.7

7878 Mbp.

7879

7880

7881 **Description of *Candidatus* Pullichristensenella stercoripullorum sp. nov.**

7882 *Candidatus* Pullichristensenella stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung;

7883 L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young

7884 chickens)

7885

7886 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

7887 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

7888 assigned the MAG ID 5266 and which is available via NCBI BioSample SAMN15816952. The

7889 GC content of the type genome is 64.02% and the genome length is 2.3 Mbp.

7890

7891

7892 **Description of *Candidatus* Pullilachnospira gen. nov.**

7893 *Candidatus* Pullilachnospira (Pul.li.lach.no.spi'ra. L. masc. n. *pullus* a young chicken; N.L. fem.

7894 n. *Lachnospira* a genus name; N.L. fem. n. *Pullilachnospira* a genus related to the genus

7895 *Lachnospira* but distinct from it and found in poultry)

7896

7897 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with

7898 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type

7899 species *Pullilachnospira stercoravium.* This genus was identified but not named by Glendinning

7900 et al. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95

7901 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family

7902 *Lachnospiraceae.*

7903

7904

7905 **Description of *Candidatus* Pullilachnospira gallistercoris sp. nov.**

7906 *Candidatus* Pullilachnospira gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.

7907 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)

7908

7909 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

7910 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

7911 assigned the MAG ID ChiSjej5B23-6657 and which is available via NCBI BioSample

7912 SAMN15816936. The GC content of the type genome is 53.36% and the genome length is 2.5

7913 Mbp.

7914

7915

7916 **Description of *Candidatus* Pullilachnospira intestinigallinarum sp. nov.**

7917 *Candidatus* Pullilachnospira intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum*

7918 gut; L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)

7919

7920 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

7921 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

7922 assigned the MAG ID CHK192-16996 and which is available via NCBI BioSample

7923 SAMN15816938. The GC content of the type genome is 51.71% and the genome length is 2.8

7924 Mbp.

7925

7926

7927 **Description of *Candidatus* Pullilachnospira stercoravium sp. nov.**

7928 *Candidatus* Pullilachnospira stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n.

7929 *avis* bird; N.L. gen. n. *stercoravium* of bird faeces)

7930

7931 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

7932 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

7933 assigned the MAG ID ChiBcec2-4451 and which is available via NCBI BioSample

7934 SAMN15816944. The GC content of the type genome is 53.14% and the genome length is 2.8

7935 Mbp.

7936

7937

7938 **Description of *Candidatus* Pygmaiobacter gallistercoris sp. nov.**

7939 *Candidatus* Pygmaiobacter gallistercoris (gal.li.ster'co.ris. L. masc. n. *gallus* chicken; L. neut. n.

7940 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)

7941

7942 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

7943 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

7944 assigned the MAG ID ChiGjej6B6-17065 and which is available via NCBI BioSample

7945 SAMN15816776. The GC content of the type genome is 61.74% and the genome length is 1.6

7946 Mbp.

7947

7948

7949 **Description of *Candidatus* Rikenella faecigallinarum sp. nov.**

7950 *Candidatus* Rikenella faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.

7951 fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

7952

7953 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

7954 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

7955 assigned the MAG ID ChiBcec15-1070 and which is available via NCBI BioSample

7956 SAMN15816768. The GC content of the type genome is 56.15% and the genome length is 1.8

7957 Mbp.

7958

7959

7960 **Description of *Candidatus* Rothia avicola sp. nov.**

7961 *Candidatus* Rothia avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. -*cola* inhabitant of; N.L. n.
7962 *avicola* inhabitant of birds)
7963
7964 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7965 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7966 assigned the MAG ID ChiHjej12B11-9195 and which is available via NCBI BioSample
7967 SAMN15816701. The GC content of the type genome is 60.05% and the genome length is 2.1
7968 Mbp.
7969
7970
7971 **Description of *Candidatus* Rothia avistercoris sp. nov.**
7972 *Candidatus* Rothia avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung; N.L.
7973 gen. n. *avistercoris* of bird faeces)
7974
7975 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7976 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7977 assigned the MAG ID ChiHjej10B9-4811 and which is available via NCBI BioSample
7978 SAMN15816788. The GC content of the type genome is 59.79% and the genome length is 2.0
7979 Mbp.
7980
7981
7982 **Description of *Candidatus* Ruania gallistercoris sp. nov.**
7983 *Candidatus* Ruania gallistercoris (gal.li.ster'co.ris. L. masc. n. *gallus* chicken; L. neut. n. *stercus*
7984 dung; N.L. gen. n. *gallistercoris* of chicken faeces)
7985
7986 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7987 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7988 assigned the MAG ID ChiGjej4B4-7305 and which is available via NCBI BioSample
7989 SAMN15816695. The GC content of the type genome is 69.62% and the genome length is 4.4
7990 Mbp.
7991
7992
7993 **Description of *Candidatus* Rubneribacter avistercoris sp. nov.**
7994 *Candidatus* Rubneribacter avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
7995 dung; N.L. gen. n. *avistercoris* of bird faeces)
7996
7997 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
7998 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
7999 assigned the MAG ID ChiGjej6B6-20359 and which is available via NCBI BioSample
8000 SAMN15816703. The GC content of the type genome is 65.17% and the genome length is 3.2
8001 Mbp.
8002
8003
8004 **Description of *Candidatus* Ruminococcus avistercoris sp. nov.**
8005 *Candidatus* Ruminococcus avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus*
8006 dung; N.L. gen. n. *avistercoris* of bird faeces)

8007

8008 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8009 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8010 assigned the MAG ID CHK186-6582 and which is available via NCBI BioSample
8011 SAMN15816883. Although GTDB has assigned this species to the genus it calls
8012 Ruminococcus_G , this genus designation cannot be incorporated into a well-formed binomial,
8013 so in naming this species, we have used the current validly published name for the genus. The
8014 GC content of the type genome is 50.07% and the genome length is 2.3 Mbp.

8015

8016

8017 **Description of *Candidatus* Ruminococcus gallistercoris sp. nov.**
8018 *Candidatus* Ruminococcus gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
8019 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)

8020

8021 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8022 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8023 assigned the MAG ID ChiBcec12-341 and which is available via NCBI BioSample
8024 SAMN15816918. This is a new name for the alphanumeric GTDB species sp900552925.
8025 Although GTDB has assigned this species to the genus it calls Ruminococcus_H , this genus
8026 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
8027 have used the current validly published name for the genus. The GC content of the type genome
8028 is 62.03% and the genome length is 2.1 Mbp.

8029

8030

8031 **Description of *Candidatus* Ruminococcus intestinipullorum sp. nov.**
8032 *Candidatus* Ruminococcus intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
8033 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

8034

8035 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8036 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8037 assigned the MAG ID 1485 and which is available via NCBI BioSample SAMN15816905.
8038 Although GTDB has assigned this species to the genus it calls Ruminococcus_B , this genus
8039 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
8040 have used the current validly published name for the genus. The GC content of the type genome
8041 is 35.77% and the genome length is 2.1 Mbp.

8042

8043

8044 **Description of *Candidatus* Ruthenibacterium avium sp. nov.**
8045 *Candidatus* Ruthenibacterium avium (a'vi.um. L. fem. pl. n. *avium* of birds)

8046

8047 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8048 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8049 assigned the MAG ID ChiBcec8-14828 and which is available via NCBI BioSample
8050 SAMN15816823. This is a new name for the alphanumeric GTDB species sp002315015. The
8051 GC content of the type genome is 51.27% and the genome length is 2.2 Mbp.

8052

8053
8054 **Description of *Candidatus* Ruthenibacterium merdavium sp. nov.**
8055 *Candidatus* Ruthenibacterium merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
8056 bird; N.L. gen. n. *merdavium* of bird faeces)
8057
8058 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8059 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8060 assigned the MAG ID 5933 and which is available via NCBI BioSample SAMN15816578. The
8061 GC content of the type genome is 51.15% and the genome length is 2.0 Mbp.
8062
8063
8064 **Description of *Candidatus* Ruthenibacterium merdigallinarum sp. nov.**
8065 *Candidatus* Ruthenibacterium merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L.
8066 fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
8067
8068 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8069 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8070 assigned the MAG ID ChiSjej6B24-7098 and which is available via NCBI BioSample
8071 SAMN15816763. The GC content of the type genome is 65.28% and the genome length is 2.2
8072 Mbp.
8073
8074
8075 **Description of *Candidatus* Ruthenibacterium merdipullorum sp. nov.**
8076 *Candidatus* Ruthenibacterium merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L.
8077 masc. n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
8078
8079 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8080 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8081 assigned the MAG ID ChiSxjej5B17-15602 and which is available via NCBI BioSample
8082 SAMN15816878. This is a new name for the alphanumeric GTDB species sp900546885. The
8083 GC content of the type genome is 59.69% and the genome length is 2.1 Mbp.
8084
8085
8086 **Description of *Candidatus* Salinicoccus merdavium sp. nov.**
8087 *Candidatus* Salinicoccus merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
8088 N.L. gen. n. *merdavium* of bird faeces)
8089
8090 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8091 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8092 assigned the MAG ID ChiHjej12B11-20095 and which is available via NCBI BioSample
8093 SAMN15816874. This is a new name for the alphanumeric GTDB species sp002360325. The
8094 GC content of the type genome is 44.20% and the genome length is 1.8 Mbp.
8095
8096
8097 **Description of *Candidatus* Salinicoccus stercoripullorum sp. nov.**

8098   *Candidatus* Salinicoccus stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
8099   masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
8100
8101   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8102   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8103   assigned the MAG ID ChiHjej13B12-752 and which is available via NCBI BioSample
8104   SAMN15816771. The GC content of the type genome is 48.14% and the genome length is 2.3
8105   Mbp.
8106
8107
8108   **Description of *Candidatus* Savagella gallinarum sp. nov.**
8109   *Candidatus* Savagella gallinarum (gal.li.na'rum. L. fem. n. *gallina* a hen; L. fem. n. *gallina* hen;
8110   L. gen.pl. n. *gallinarum* of hens)
8111
8112   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8113   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8114   assigned the MAG ID CHK166-5537 and which is available via NCBI BioSample
8115   SAMN15816803. This is a new name for the alphanumeric GTDB species sp001655775. The
8116   GC content of the type genome is 26.42% and the genome length is 1.8 Mbp.
8117
8118
8119   **Description of *Candidatus* Scatarchaeum gen. nov.**
8120   *Candidatus* Scatarchaeum (Scat.archaeum. Gr. neut. n. *skor, skatos* dung; N.L. neut. n. *archaeum*
8121   an archaeon; N.L. neut. n. *Scatarchaeum* a microbe associated with faeces)
8122
8123   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8124   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8125   species *Scatarchaeum merdigallinarum*. This is a name for the alphanumeric GTDB genus
8126   UMGS403. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
8127   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
8128   *Acutalibacteraceae.*
8129
8130
8131   **Description of *Candidatus* Scatarchaeum merdigallinarum sp. nov.**
8132   *Candidatus* Scatarchaeum merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L.
8133   fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
8134
8135   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8136   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8137   assigned the MAG ID ChiSjej1B19-3389 and which is available via NCBI BioSample
8138   SAMN15817212. This is a new name for the alphanumeric GTDB species sp900541975. The
8139   GC content of the type genome is 46.67% and the genome length is 1.7 Mbp.
8140
8141
8142   **Description of *Candidatus* Scatenecus gen. nov.**

8143   *Candidatus* Scatenecus (Scat.en.e'cus. Gr. neut. n. *skor, skatos* dung; Gr. masc. *enoikos*
8144   inhabitant; N.L. masc. n. *Scatenecus* a microbe associated with the intestines)
8145
8146   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8147   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8148   species *Scatenecus faecavium*. This is a name for the alphanumeric GTDB genus QAMI01. This
8149   genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
8150   al., 2019; Parks et al., 2020) to the order *Gastranaerophilales* and to the family
8151   *Gastranaerophilaceae.*
8152
8153
8154   **Description of *Candidatus* Scatenecus faecavium sp. nov.**
8155   *Candidatus* Scatenecus faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
8156   *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
8157
8158   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8159   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8160   assigned the MAG ID CHK152-2994 and which is available via NCBI BioSample
8161   SAMN15817221. This is a new name for the alphanumeric GTDB species sp900551915. The
8162   GC content of the type genome is 37.15% and the genome length is 1.9 Mbp.
8163
8164
8165   **Description of *Candidatus* Scatocola gen. nov.**
8166   *Candidatus* Scatocola (Scat.o.co'la. Gr. neut. n. *skor, skatos* dung; L. suff. *-cola* inhabitant of;
8167   N.L. fem. n. *Scatocola* a microbe associated with faeces)
8168
8169   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8170   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8171   species *Scatocola faecipullorum*. This is a name for the alphanumeric GTDB genus CAG-495.
8172   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
8173   (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF32* and to the family *CAG-239*.
8174
8175
8176   **Description of *Candidatus* Scatocola faecigallinarum sp. nov.**
8177   *Candidatus* Scatocola faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L.
8178   fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
8179
8180   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8181   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8182   assigned the MAG ID 2846 and which is available via NCBI BioSample SAMN15817209. This
8183   is a new name for the alphanumeric GTDB species sp000436375. The GC content of the type
8184   genome is 49.31% and the genome length is 1.7 Mbp.
8185
8186
8187   **Description of *Candidatus* Scatocola faecipullorum sp. nov.**

8188   *Candidatus* Scatocola faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
8189   masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
8190
8191   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8192   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8193   assigned the MAG ID ChiW3-316 and which is available via NCBI BioSample
8194   SAMN15817201. This is a new name for the alphanumeric GTDB species sp001917125. The
8195   GC content of the type genome is 47.24% and the genome length is 1.7 Mbp.
8196
8197
8198   **Description of *Candidatus* Scatomonas gen. nov.**
8199   *Candidatus* Scatomonas (Scat.o.mo'nas. Gr. neut. n. *skor, skatos* dung; L. fem. n. *monas* a
8200   monad; N.L. fem. n. *Scatomonas* a microbe associated with the intestines)
8201
8202   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8203   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8204   species *Scatomonas merdigallinarum*. This is a name for the alphanumeric GTDB genus OF09-
8205   33XD. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
8206   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
8207   *Lachnospiraceae.*
8208
8209
8210   **Description of *Candidatus* Scatomonas merdavium sp. nov.**
8211   *Candidatus* Scatomonas merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
8212   N.L. gen. n. *merdavium* of bird faeces)
8213
8214   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8215   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8216   assigned the MAG ID ChiSjej5B23-9500 and which is available via NCBI BioSample
8217   SAMN15817033. The GC content of the type genome is 53.14% and the genome length is 2.3
8218   Mbp.
8219
8220
8221   **Description of *Candidatus* Scatomonas merdigallinarum sp. nov.**
8222   *Candidatus* Scatomonas merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
8223   n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
8224
8225   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8226   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8227   assigned the MAG ID CHK191-20366 and which is available via NCBI BioSample
8228   SAMN15817035. The GC content of the type genome is 53.29% and the genome length is 2.3
8229   Mbp.
8230
8231
8232   **Description of *Candidatus* Scatomonas pullistercoris sp. nov.**

8233 *Candidatus* Scatomonas pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
8234 neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
8235
8236 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8237 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8238 assigned the MAG ID CHK188-20938 and which is available via NCBI BioSample
8239 SAMN15817052. The GC content of the type genome is 53.16% and the genome length is 2.3
8240 Mbp.
8241
8242
8243 **Description of *Candidatus* Scatomorpha gen. nov.**
8244 *Candidatus* Scatomorpha (Scat.o.mor'pha. Gr. neut. n. *skor, skatos* dung; Gr. fem. n. *morphe* a
8245 form, shape; N.L. fem. n. *Scatomorpha* a microbe associated with faeces)
8246
8247 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8248 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8249 species *Scatomorpha merdavium*. This is a name for the alphanumeric GTDB genus UBA5446.
8250 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
8251 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
8252 *Oscillospiraceae.*
8253
8254
8255 **Description of *Candidatus* Scatomorpha gallistercoris sp. nov.**
8256 *Candidatus* Scatomorpha gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
8257 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
8258
8259 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8260 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8261 assigned the MAG ID ChiHjej12B11-5383 and which is available via NCBI BioSample
8262 SAMN15817213. This is a new name for the alphanumeric GTDB species sp900544765. The
8263 GC content of the type genome is 60.13% and the genome length is 2.4 Mbp.
8264
8265
8266 **Description of *Candidatus* Scatomorpha intestinavium sp. nov.**
8267 *Candidatus* Scatomorpha intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n.
8268 *avis* bird; N.L. gen. n. *intestinavium* of the gut of birds)
8269
8270 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8271 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8272 assigned the MAG ID ChiBcolR7-354 and which is available via NCBI BioSample
8273 SAMN15817058. The GC content of the type genome is 62.47% and the genome length is 2.0
8274 Mbp.
8275
8276
8277 **Description of *Candidatus* Scatomorpha intestinigallinarum sp. nov.**

8278 *Candidatus* Scatomorpha intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
8279 L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
8280
8281 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8282 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8283 assigned the MAG ID ChiGjej3B3-7149 and which is available via NCBI BioSample
8284 SAMN15817216. This is a new name for the alphanumeric GTDB species sp900544295. The
8285 GC content of the type genome is 63.01% and the genome length is 2.3 Mbp.
8286
8287
8288 **Description of *Candidatus* Scatomorpha intestinipullorum sp. nov.**
8289 *Candidatus* Scatomorpha intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.
8290 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)
8291
8292 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8293 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8294 assigned the MAG ID CHK1-1240 and which is available via NCBI BioSample
8295 SAMN15817022. The GC content of the type genome is 61.56% and the genome length is 2.5
8296 Mbp.
8297
8298
8299 **Description of *Candidatus* Scatomorpha merdavium sp. nov.**
8300 *Candidatus* Scatomorpha merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
8301 bird; N.L. gen. n. *merdavium* of bird faeces)
8302
8303 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8304 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8305 assigned the MAG ID ChiSxjej3B15-13231 and which is available via NCBI BioSample
8306 SAMN15817220. This is a new name for the alphanumeric GTDB species sp004553625. The
8307 GC content of the type genome is 61.38% and the genome length is 2.3 Mbp.
8308
8309
8310 **Description of *Candidatus* Scatomorpha merdigallinarum sp. nov.**
8311 *Candidatus* Scatomorpha merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L. fem.
8312 n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
8313
8314 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8315 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8316 assigned the MAG ID CHK187-5235 and which is available via NCBI BioSample
8317 SAMN15817028. The GC content of the type genome is 58.23% and the genome length is 2.3
8318 Mbp.
8319
8320
8321 **Description of *Candidatus* Scatomorpha merdipullorum sp. nov.**
8322 *Candidatus* Scatomorpha merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.
8323 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)

8324
8325 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8326 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8327 assigned the MAG ID ChiHjej10B9-9673 and which is available via NCBI BioSample
8328 SAMN15817099. The GC content of the type genome is 64.45% and the genome length is 1.8
8329 Mbp.
8330
8331
8332 **Description of *Candidatus* Scatomorpha pullicola sp. nov.**
8333 *Candidatus* Scatomorpha pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
8334 inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
8335
8336 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8337 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8338 assigned the MAG ID ChiSjej5B23-7677 and which is available via NCBI BioSample
8339 SAMN15817223. This is a new name for the alphanumeric GTDB species sp900543085. The
8340 GC content of the type genome is 62.30% and the genome length is 2.1 Mbp.
8341
8342
8343 **Description of *Candidatus* Scatomorpha pullistercoris sp. nov.**
8344 *Candidatus* Scatomorpha pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
8345 neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
8346
8347 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8348 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8349 assigned the MAG ID ChiHecec3B27-6122 and which is available via NCBI BioSample
8350 SAMN15817222. This is a new name for the alphanumeric GTDB species sp900546615. The
8351 GC content of the type genome is 61.20% and the genome length is 2.2 Mbp.
8352
8353
8354 **Description of *Candidatus* Scatomorpha stercoravium sp. nov.**
8355 *Candidatus* Scatomorpha stercoravium (ster.cor.a'vi.um. L. neut. n. *stercus* dung; L. fem. n. *avis*
8356 bird; N.L. gen. n. *stercoravium* of bird faeces)
8357
8358 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8359 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8360 assigned the MAG ID ChiHecec3B27-8609 and which is available via NCBI BioSample
8361 SAMN15817107. The GC content of the type genome is 64.50% and the genome length is 2.0
8362 Mbp.
8363
8364
8365 **Description of *Candidatus* Scatomorpha stercorigallinarum sp. nov.**
8366 *Candidatus* Scatomorpha stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* dung; L.
8367 fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
8368

[segment omitted]

8369   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8370   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8371   assigned the MAG ID ChiHjej9B8-2268 and which is available via NCBI BioSample
8372   SAMN15817162. The GC content of the type genome is 64.82% and the genome length is 2.0
8373   Mbp.
8374
8375
8376   **Description of *Candidatus* Scatoplasma gen. nov.**
8377   *Candidatus* Scatoplasma (Scat.o.plas'ma. Gr. neut. n. *skor, skatos* dung; Gr. neut. n. *plasma* a
8378   form; N.L. neut. n. *Scatoplasma* a microbe associated with faeces)
8379
8380   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8381   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8382   species *Scatoplasma merdavium*. This is a name for the alphanumeric GTDB genus UBA6879.
8383   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
8384   (Chaumeil et al., 2019; Parks et al., 2020) to the order *RFN20* and to the family *CAG-288*.
8385
8386
8387   **Description of *Candidatus* Scatoplasma merdavium sp. nov.**
8388   *Candidatus* Scatoplasma merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
8389   N.L. gen. n. *merdavium* of bird faeces)
8390
8391   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8392   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8393   assigned the MAG ID 1748 and which is available via NCBI BioSample SAMN15817159. The
8394   GC content of the type genome is 36.99% and the genome length is 1.0 Mbp.
8395
8396
8397   **Description of *Candidatus* Scatosoma gen. nov.**
8398   *Candidatus* Scatosoma (Scat.o.so'ma. Gr. neut. n. *skor, skatos* dung; Gr. neut. n. *soma* a body;
8399   N.L. neut. n. *Scatosoma* a microbe associated with the intestines)
8400
8401   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8402   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8403   species *Scatosoma pullicola*. This is a name for the alphanumeric GTDB genus QALS01. This
8404   genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
8405   al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family *Borkfalkiaceae*.
8406
8407
8408   **Description of *Candidatus* Scatosoma pullicola sp. nov.**
8409   *Candidatus* Scatosoma pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. *-cola*
8410   inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
8411
8412   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8413   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8414   assigned the MAG ID CHK183-20193 and which is available via NCBI BioSample

8415 SAMN15817013. The GC content of the type genome is 57.19% and the genome length is 2.0
8416 Mbp.
8417
8418
8419 **Description of *Candidatus* Scatosoma pullistercoris sp. nov.**
8420 *Candidatus* Scatosoma pullistercoris (pul.li.ster'co.ris. L. masc. n. *pullus* a young chicken; L.
8421 neut. n. *stercus* dung; N.L. gen. n. *pullistercoris* of young chicken faeces)
8422
8423 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8424 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8425 assigned the MAG ID 11687 and which is available via NCBI BioSample SAMN15817138. The
8426 GC content of the type genome is 55.35% and the genome length is 1.5 Mbp.
8427
8428
8429 **Description of *Candidatus* Scatousia gen. nov.**
8430 *Candidatus* Scatousia (Scat.ou'si.a. Gr. neut. n. *skor, skatos* dung; Gr. fem. n. *ousia* an essence;
8431 N.L. fem. n. *Scatousia* a microbe associated with faeces)
8432
8433 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8434 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8435 species *Scatousia excrementipullorum*. This is a name for the alphanumeric GTDB genus CAG-
8436 484. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
8437 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Gastranaerophilales* and to the family
8438 *Gastranaerophilaceae*.
8439
8440
8441 **Description of *Candidatus* Scatousia excrementigallinarum sp. nov.**
8442 *Candidatus* Scatousia excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum*
8443 excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)
8444
8445 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8446 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8447 assigned the MAG ID 6276 and which is available via NCBI BioSample SAMN15817091. The
8448 GC content of the type genome is 36.46% and the genome length is 2.8 Mbp.
8449
8450
8451 **Description of *Candidatus* Scatousia excrementipullorum sp. nov.**
8452 *Candidatus* Scatousia excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
8453 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
8454 chicken excrement)
8455
8456 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8457 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8458 assigned the MAG ID 10192 and which is available via NCBI BioSample SAMN15817157. The
8459 GC content of the type genome is 36.06% and the genome length is 1.8 Mbp.
8460

8461

8462 **Description of *Candidatus* Scatovicinus gen. nov.**

8463 *Candidatus* Scatovicinus (Scat.o.vic.in'us. Gr. neut. n. *skor, skatos* dung; L. masc. n. *vicinus* a

8464 neighbour; N.L. masc. n. *Scatovicinus* a microbe associated with faeces)

8465

8466 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with

8467 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type

8468 species *Scatovicinus merdipullorum*. This is a name for the alphanumeric GTDB genus

8469 UMGS403. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-

8470 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family

8471 *Acutalibacteraceae.*

8472

8473

8474 **Description of *Candidatus* Scatovicinus merdipullorum sp. nov.**

8475 *Candidatus* Scatovicinus merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces; L. masc. n.

8476 *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)

8477

8478 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

8479 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

8480 assigned the MAG ID CHK181-9830 and which is available via NCBI BioSample

8481 SAMN15817214. This is a new name for the alphanumeric GTDB species sp900541565. The

8482 GC content of the type genome is 46.80% and the genome length is 1.9 Mbp.

8483

8484

8485 **Description of *Candidatus* Scatovivens gen. nov.**

8486 *Candidatus* Scatovivens (Scat.o.viv'ens. Gr. neut. n. *skor, skatos* dung; N.L. pres. part. *vivens*

8487 living; N.L. fem. n. *Scatovivens* a microbe associated with faeces)

8488

8489 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with

8490 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type

8491 species *Scatovivens faecipullorum*. This is a name for the alphanumeric GTDB genus UBA7001.

8492 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95

8493 (Chaumeil et al., 2019; Parks et al., 2020) to the order *TANB77* and to the family *CAG-508.*

8494

8495

8496 **Description of *Candidatus* Scatovivens faecipullorum sp. nov.**

8497 *Candidatus* Scatovivens faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.

8498 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

8499

8500 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

8501 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

8502 assigned the MAG ID ChiSxjej5B17-16517 and which is available via NCBI BioSample

8503 SAMN15817189. This is a new name for the alphanumeric GTDB species sp900553685. The

8504 GC content of the type genome is 25.63% and the genome length is 1.9 Mbp.

8505

8506

8507 **Description of *Candidatus* Scubalenecus merdavium sp. nov.**
8508 *Candidatus* Scubalenecus merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
8509 bird; N.L. gen. n. *merdavium* of bird faeces)
8510
8511 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8512 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8513 assigned the MAG ID CHK176-6737 and which is available via NCBI BioSample
8514 SAMN15817203. This is a new name for the alphanumeric GTDB species sp900546735. The
8515 GC content of the type genome is 52.55% and the genome length is 1.8 Mbp.
8516
8517
8518 **Description of *Candidatus* Scubalocola faecavium sp. nov.**
8519 *Candidatus* Scubalocola faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
8520 *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
8521
8522 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8523 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8524 assigned the MAG ID CHK196-3395 and which is available via NCBI BioSample
8525 SAMN15817004. The GC content of the type genome is 45.55% and the genome length is 3.6
8526 Mbp.
8527
8528
8529 **Description of *Candidatus* Scubalocola faecigallinarum sp. nov.**
8530 *Candidatus* Scubalocola faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;
8531 L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)
8532
8533 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8534 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8535 assigned the MAG ID CHK178-757 and which is available via NCBI BioSample
8536 SAMN15817027. The GC content of the type genome is 46.78% and the genome length is 3.5
8537 Mbp.
8538
8539
8540 **Description of *Candidatus* Scubalocola faecipullorum sp. nov.**
8541 *Candidatus* Scubalocola faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
8542 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
8543
8544 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8545 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8546 assigned the MAG ID CHK194-7924 and which is available via NCBI BioSample
8547 SAMN15817034. The GC content of the type genome is 44.36% and the genome length is 2.5
8548 Mbp.
8549
8550
8551 **Description of *Candidatus* Scubalomonas excrementavium sp. nov.**

8552   *Candidatus* Scubalomonas excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
8553   excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
8554
8555   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8556   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8557   assigned the MAG ID E3-2379 and which is available via NCBI BioSample SAMN15817094.
8558   The GC content of the type genome is 32.78% and the genome length is 2.5 Mbp.
8559
8560
8561   **Description of *Candidatus* Scubalomonas excrementigallinarum sp. nov.**
8562   *Candidatus* Scubalomonas excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
8563   *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
8564   excrement)
8565
8566   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8567   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8568   assigned the MAG ID 3201 and which is available via NCBI BioSample SAMN15817095. The
8569   GC content of the type genome is 34.32% and the genome length is 3.2 Mbp.
8570
8571
8572   **Description of *Candidatus* Scubalosoma faecavium sp. nov.**
8573   *Candidatus* Scubalosoma faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
8574   *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
8575
8576   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8577   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8578   assigned the MAG ID ChiSxjej1B13-2233 and which is available via NCBI BioSample
8579   SAMN15817224. This is a new name for the alphanumeric GTDB species sp900545085. The
8580   GC content of the type genome is 47.85% and the genome length is 1.6 Mbp.
8581
8582
8583   **Description of *Candidatus* Scubalousia intestinigallinarum sp. nov.**
8584   *Candidatus* Scubalousia intestinigallinarum (in.tes.ti.ni.gal.li.na'rum. L. neut. n. *intestinum* gut;
8585   L. fem. n. *gallina* hen; N.L. gen. n. *intestinigallinarum* of the gut of the hens)
8586
8587   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8588   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8589   assigned the MAG ID CHK193-12526 and which is available via NCBI BioSample
8590   SAMN15817037. The GC content of the type genome is 31.54% and the genome length is 1.5
8591   Mbp.
8592
8593
8594   **Description of *Candidatus* Scybalenecus gen. nov.**
8595   *Candidatus* Scybalenecus (Scy.bal.en.e'cus. Gr. neut. n. *scybalon* dung; Gr. masc. *enoikos*
8596   inhabitant; N.L. masc. n. *Scybalenecus* a microbe associated with faeces)
8597

8598 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8599 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8600 species *Scybalenecus merdavium*. This is a name for the alphanumeric GTDB genus UMGS905.
8601 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
8602 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
8603 *Acutalibacteraceae.*

8604
8605

8606 **Description of *Candidatus* Scybalocola gen. nov.**
8607 *Candidatus* Scybalocola (Scy.bal.o.co'la. Gr. neut. n. *scybalon* dung; L. suff. *-cola* inhabitant of;
8608 N.L. fem. n. *Scybalocola* a microbe associated with the intestines)

8609

8610 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8611 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8612 species *Scybalocola faecigallinarum*. This is a name for the alphanumeric GTDB genus
8613 UBA7096. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
8614 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
8615 *Lachnospiraceae.*

8616
8617

8618 **Description of *Candidatus* Scybalomonas gen. nov.**
8619 *Candidatus* Scybalomonas (Scy.bal.omo'nas. Gr. neut. n. *scybalon* dung; L. fem. n. *monas* a
8620 monad; N.L. fem. n. *Scybalomonas* a microbe associated with faeces)

8621

8622 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8623 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8624 species *Scybalomonas excrementigallinarum*. This is a name for the alphanumeric GTDB genus
8625 UMGS680. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
8626 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
8627 *Lachnospiraceae.*

8628
8629

8630 **Description of *Candidatus* Scybalosoma gen. nov.**
8631 *Candidatus* Scybalosoma (Scy.bal.o.so'ma. Gr. neut. n. *scybalon* dung; Gr. neut. n. *soma* a body;
8632 N.L. neut. n. *Scybalosoma* a microbe associated with faeces)

8633

8634 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8635 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8636 species *Scybalosoma faecavium*. This is a name for the alphanumeric GTDB genus UMGS743.
8637 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
8638 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family
8639 *Christensenellaceae.*

8640
8641

8642 **Description of *Candidatus* Scybalousia gen. nov.**

8643 *Candidatus* Scybalousia (Scy.bal.ou'si.a. Gr. neut. n. *scybalon* dung; Gr. fem. n. *ousia* an
8644 essence; N.L. fem. n. *Scybalousia* a microbe associated with faeces)
8645
8646 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8647 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8648 species *Scybalousia intestinigallinarum*. This is a name for the alphanumeric GTDB genus
8649 UBA7057. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
8650 RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-611*.
8651
8652
8653 **Description of *Candidatus* Sellimonas avistercoris sp. nov.**
8654 *Candidatus* Sellimonas avistercoris (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung;
8655 N.L. gen. n. *avistercoris* of bird faeces)
8656
8657 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8658 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8659 assigned the MAG ID ChiBcec13-3606 and which is available via NCBI BioSample
8660 SAMN15816877. This is a new name for the alphanumeric GTDB species sp002161525. The
8661 GC content of the type genome is 46.79% and the genome length is 2.6 Mbp.
8662
8663
8664 **Description of *Candidatus* Sphingobacterium stercorigallinarum sp. nov.**
8665 *Candidatus* Sphingobacterium stercorigallinarum (ster.co.ri.gal.li.na'rum. L. neut. n. *stercus*
8666 dung; L. fem. n. *gallina* hen; N.L. gen. n. *stercorigallinarum* of hen faeces)
8667
8668 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8669 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8670 assigned the MAG ID CHK174-1108 and which is available via NCBI BioSample
8671 SAMN15816705. The GC content of the type genome is 44.57% and the genome length is 2.9
8672 Mbp.
8673
8674
8675 **Description of *Candidatus* Sphingobacterium stercoripullorum sp. nov.**
8676 *Candidatus* Sphingobacterium stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
8677 masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)
8678
8679 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8680 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8681 assigned the MAG ID 1719 and which is available via NCBI BioSample SAMN15816733. The
8682 GC content of the type genome is 39.36% and the genome length is 2.7 Mbp.
8683
8684
8685 **Description of *Candidatus* Sphingomonas excrementigallinarum sp. nov.**
8686 *Candidatus* Sphingomonas excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n.
8687 *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen
8688 excrement)

8689
8690   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8691   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8692   assigned the MAG ID 1562 and which is available via NCBI BioSample SAMN15816779. The
8693   GC content of the type genome is 66.49% and the genome length is 3.7 Mbp.
8694
8695
8696   **Description of *Candidatus* Spyradenecus gen. nov.**
8697   *Candidatus* Spyradenecus (Spy.rad.en.e'cus. Gr. fem. n. *spyras* ball of dung; Gr. masc. *enoikos*
8698   inhabitant; N.L. masc. n. *Spyradenecus* a microbe associated with the intestines)
8699
8700   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8701   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8702   species *Spyradenecus faecavium*. This is a name for the alphanumeric GTDB genus W1P29-020.
8703   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
8704   (Chaumeil et al., 2019; Parks et al., 2020) to the order *RFP12* and to the family *W1P29-020.*
8705
8706
8707   **Description of *Candidatus* Spyradenecus faecavium sp. nov.**
8708   *Candidatus* Spyradenecus faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
8709   *avis* bird; N.L. gen. n. *faecavium* of bird faeces)
8710
8711   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8712   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8713   assigned the MAG ID 35461 and which is available via NCBI BioSample SAMN15817160. The
8714   GC content of the type genome is 68.44% and the genome length is 1.8 Mbp.
8715
8716
8717   **Description of *Candidatus* Spyradocola gen. nov.**
8718   *Candidatus* Spyradocola (Spy.rad.o.co'la. Gr. fem. n. *spyras* ball of dung; L. suff. *-cola*
8719   inhabitant of; N.L. fem. n. *Spyradocola* a microbe associated with the intestines)
8720
8721   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8722   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8723   species *Spyradocola merdavium*. This is a name for the alphanumeric GTDB genus UBA7102.
8724   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
8725   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family
8726   *UBA1750.*
8727
8728
8729   **Description of *Candidatus* Spyradocola merdavium sp. nov.**
8730   *Candidatus* Spyradocola merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;
8731   N.L. gen. n. *merdavium* of bird faeces)
8732
8733   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8734   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

8735   assigned the MAG ID CHK191-18038 and which is available via NCBI BioSample
8736   SAMN15817024. The GC content of the type genome is 66.20% and the genome length is 2.6
8737   Mbp.
8738
8739
8740   **Description of *Candidatus* Spyradomonas gen. nov.**
8741   *Candidatus* Spyradomonas (Spy.rad.omo'nas. Gr. fem. n. *spyras* ball of dung; L. fem. n. *monas* a
8742   monad; N.L. fem. n. *Spyradomonas* a microbe associated with faeces)
8743
8744   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8745   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8746   species *Spyradomonas excrementavium*. This is a name for the alphanumeric GTDB genus
8747   UMGS951. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
8748   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Gastranaerophilales* and to the
8749   family *Gastranaerophilaceae.*
8750
8751
8752   **Description of *Candidatus* Spyradomonas excrementavium sp. nov.**
8753   *Candidatus* Spyradomonas excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
8754   excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
8755
8756   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8757   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8758   assigned the MAG ID CHK149-2741 and which is available via NCBI BioSample
8759   SAMN15817232. This is a new name for the alphanumeric GTDB species sp900547155. The
8760   GC content of the type genome is 41.54% and the genome length is 2.0 Mbp.
8761
8762
8763   **Description of *Candidatus* Spyradosoma gen. nov.**
8764   *Candidatus* Spyradosoma (Spy.rad.o.so'ma. Gr. fem. n. *spyras* ball of dung; Gr. neut. n. *soma* a
8765   body; N.L. neut. n. *Spyradosoma* a microbe associated with faeces)
8766
8767   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8768   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8769   species *Spyradosoma merdigallinarum*. This is a name for the alphanumeric GTDB genus
8770   W0P29-029. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-
8771   RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Opitutales* and to the family
8772   *UBA953.*
8773
8774
8775   **Description of *Candidatus* Spyradosoma merdigallinarum sp. nov.**
8776   *Candidatus* Spyradosoma merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda* faeces; L.
8777   fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
8778
8779   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8780   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

8781 assigned the MAG ID 10669 and which is available via NCBI BioSample SAMN15817156. The
8782 GC content of the type genome is 62.43% and the genome length is 1.6 Mbp.

8783

8784

8785 **Description of *Candidatus* Spyradousia gen. nov.**
8786 *Candidatus* Spyradousia (Spy.rad.ou'si.a. Gr. fem. n. *spyras* ball of dung; Gr. fem. n. *ousia* an
8787 essence; N.L. fem. n. *Spyradousia* a microbe associated with the intestines)

8788

8789 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8790 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8791 species *Spyradousia avicola*. This is a name for the alphanumeric GTDB genus UBA71. This
8792 genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
8793 al., 2019; Parks et al., 2020) to the order *Methanomassiliicoccales* and to the family
8794 *Methanomethylophilaceae.*

8795

8796

8797 **Description of *Candidatus* Spyradousia avicola sp. nov.**
8798 *Candidatus* Spyradousia avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L.
8799 n. *avicola* inhabitant of birds)

8800

8801 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8802 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8803 assigned the MAG ID 6227 and which is available via NCBI BioSample SAMN15817164. The
8804 GC content of the type genome is 60.22% and the genome length is 1.5 Mbp.

8805

8806

8807 **Description of *Candidatus* Stackebrandtia excrementipullorum sp. nov.**
8808 *Candidatus* Stackebrandtia excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n.
8809 *excrementum* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of
8810 young chicken excrement)

8811

8812 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8813 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8814 assigned the MAG ID ChiHjej8B7-33794 and which is available via NCBI BioSample
8815 SAMN15816761. The GC content of the type genome is 64.17% and the genome length is 4.1
8816 Mbp.

8817

8818

8819 **Description of *Candidatus* Stackebrandtia faecavium sp. nov.**
8820 *Candidatus* Stackebrandtia faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.
8821 *avis* bird; N.L. gen. n. *faecavium* of bird faeces)

8822

8823 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8824 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8825 assigned the MAG ID ChiGjej4B4-770 and which is available via NCBI BioSample

8826 SAMN15816782. The GC content of the type genome is 62.84% and the genome length is 3.4
8827 Mbp.
8828
8829

8830 **Description of *Candidatus* Stercoripulliclostridium gen. nov.**
8831 *Candidatus* Stercoripulliclostridium (Ster.co.ri.pul.li.clos.tri'di.um. L. neut. n. *stercus* dung; N.L.
8832 masc. n. *pullus* a young chicken; N.L. neut. n. *Clostridium* a genus name; N.L. neut. n.
8833 *Stercoripulliclostridium* a genus related to the genus *Clostridium* but distinct from it and found in
8834 poultry faeces)
8835

8836 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
8837 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
8838 species *Stercoripulliclostridium merdipullorum*. This genus has been assigned by GTDB-Tk
8839 v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020) to the
8840 order *Christensenellales* and to the family *DTU072*.
8841
8842

8843 **Description of *Candidatus* Stercoripulliclostridium merdigallinarum sp. nov.**
8844 *Candidatus* Stercoripulliclostridium merdigallinarum (mer.di.gal.li.na'rum. L. fem. n. *merda*
8845 faeces; L. fem. n. *gallina* hen; N.L. gen. n. *merdigallinarum* of hen faeces)
8846
8847 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8848 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8849 assigned the MAG ID 18911 and which is available via NCBI BioSample SAMN15816986. The
8850 GC content of the type genome is 48.67% and the genome length is 1.5 Mbp.
8851
8852

8853 **Description of *Candidatus* Stercoripulliclostridium merdipullorum sp. nov.**
8854 *Candidatus* Stercoripulliclostridium merdipullorum (mer.di.pul.lo'rum. L. fem. n. *merda* faeces;
8855 L. masc. n. *pullus* a young chicken; N.L. gen. n. *merdipullorum* of the faeces of young chickens)
8856
8857 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8858 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8859 assigned the MAG ID 23406 and which is available via NCBI BioSample SAMN15816995. The
8860 GC content of the type genome is 53.33% and the genome length is 1.7 Mbp.
8861
8862

8863 **Description of *Candidatus* Stercoripulliclostridium pullicola sp. nov.**
8864 *Candidatus* Stercoripulliclostridium pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L.
8865 suff. *-cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
8866
8867 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8868 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8869 assigned the MAG ID 517 and which is available via NCBI BioSample SAMN15816997. The
8870 GC content of the type genome is 52.41% and the genome length is 1.6 Mbp.
8871

8872

8873 **Description of *Candidatus* Stercorousia gen. nov.**

8874 *Candidatus* Stercorousia (Ster.cor.ou'si.a. L. neut. n. *stercus* dung; Gr. fem. n. *ousia* an essence;

8875 N.L. fem. n. *Stercorousia* a microbe associated with the intestines)

8876

8877 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with

8878 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type

8879 species *Stercorousia faecigallinarum*. This is a name for the alphanumeric GTDB genus Zag1.

8880 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95

8881 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Gastranaerophilales* and to the family

8882 *Gastranaerophilaceae*.

8883

8884

8885 **Description of *Candidatus* Stercorousia faecigallinarum sp. nov.**

8886 *Candidatus* Stercorousia faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement;

8887 L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

8888

8889 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

8890 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

8891 assigned the MAG ID CHK154-323 and which is available via NCBI BioSample

8892 SAMN15817192. This is a new name for the alphanumeric GTDB species sp000438175. The

8893 GC content of the type genome is 34.85% and the genome length is 2.1 Mbp.

8894

8895

8896 **Description of *Candidatus* Streptococcus faecavium sp. nov.**

8897 *Candidatus* Streptococcus faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.

8898 *avis* bird; N.L. gen. n. *faecavium* of bird faeces)

8899

8900 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

8901 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

8902 assigned the MAG ID ChiBcolR9-63 and which is available via NCBI BioSample

8903 SAMN15816845. This is a new name for the alphanumeric GTDB species sp002300045. The

8904 GC content of the type genome is 40.90% and the genome length is 1.4 Mbp.

8905

8906

8907 **Description of *Candidatus* Sutterella merdavium sp. nov.**

8908 *Candidatus* Sutterella merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird;

8909 N.L. gen. n. *merdavium* of bird faeces)

8910

8911 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

8912 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

8913 assigned the MAG ID ChiGjej6B6-11950 and which is available via NCBI BioSample

8914 SAMN15816882. This is a new name for the alphanumeric GTDB species sp900543805. The

8915 GC content of the type genome is 62.35% and the genome length is 2.1 Mbp.

8916

8917

8918 **Description of *Candidatus* Tetragenococcus pullicola sp. nov.**
8919 *Candidatus* Tetragenococcus pullicola (pul.li'co.la. L. masc. n. *pullus* a young chicken; L. suff. -
8920 *cola* inhabitant of; N.L. n. *pullicola* an inhabitant of young chickens)
8921
8922 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8923 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8924 assigned the MAG ID CHK175-10598 and which is available via NCBI BioSample
8925 SAMN15816709. The GC content of the type genome is 36.35% and the genome length is 2.6
8926 Mbp.
8927
8928
8929 **Description of *Candidatus* Tidjanibacter faecipullorum sp. nov.**
8930 *Candidatus* Tidjanibacter faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L.
8931 masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)
8932
8933 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8934 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8935 assigned the MAG ID ChiHjej11B10-19426 and which is available via NCBI BioSample
8936 SAMN15816696. The GC content of the type genome is 60.46% and the genome length is 1.8
8937 Mbp.
8938
8939
8940 **Description of *Candidatus* Tidjanibacter gallistercoris sp. nov.**
8941 *Candidatus* Tidjanibacter gallistercoris (gal.li.ster'co.ris. L. masc. n. *gallus* chicken; L. neut. n.
8942 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
8943
8944 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8945 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8946 assigned the MAG ID ChiSxjej4B16-7142 and which is available via NCBI BioSample
8947 SAMN15816746. The GC content of the type genome is 58.50% and the genome length is 2.0
8948 Mbp.
8949
8950
8951 **Description of *Candidatus* Treponema excrementipullorum sp. nov.**
8952 *Candidatus* Treponema excrementipullorum (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum*
8953 excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *excrementipullorum* of young
8954 chicken excrement)
8955
8956 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
8957 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
8958 assigned the MAG ID Gambia15-2214 and which is available via NCBI BioSample
8959 SAMN15816896. Although GTDB has assigned this species to the genus it calls Treponema_F ,
8960 this genus designation cannot be incorporated into a well-formed binomial, so in naming this
8961 species, we have used the current validly published name for the genus. The GC content of the
8962 type genome is 39.91% and the genome length is 2.3 Mbp.
8963

8964

8965 **Description of *Candidatus* Treponema faecavium sp. nov.**

8966 *Candidatus* Treponema faecavium (faec.a'vi.um. L. fem. n. *faex, faecis* excrement; L. fem. n.

8967 *avis* bird; N.L. gen. n. *faecavium* of bird faeces)

8968

8969 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

8970 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

8971 assigned the MAG ID USASDec8-330 and which is available via NCBI BioSample

8972 SAMN15816910. Although GTDB has assigned this species to the genus it calls Treponema_F ,

8973 this genus designation cannot be incorporated into a well-formed binomial, so in naming this

8974 species, we have used the current validly published name for the genus. The GC content of the

8975 type genome is 53.41% and the genome length is 2.2 Mbp.

8976

8977

8978 **Description of *Candidatus* Ureaplasma intestinipullorum sp. nov.**

8979 *Candidatus* Ureaplasma intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L.

8980 masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

8981

8982 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

8983 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

8984 assigned the MAG ID A5-1222 and which is available via NCBI BioSample SAMN15816777.

8985 The GC content of the type genome is 24.43% and the genome length is 0.6 Mbp.

8986

8987

8988 **Description of *Candidatus* Ventrenecus gen. nov.**

8989 *Candidatus* Ventrenecus (Ventren.e'cus. L. masc. n. *venter* the belly; Gr. masc. *enoikos*

8990 inhabitant; N.L. masc. n. *Ventrenecus* a microbe associated with faeces)

8991

8992 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with

8993 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type

8994 species *Ventrenecus avicola*. This is a name for the alphanumeric GTDB genus UMGS1217.

8995 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95

8996 (Chaumeil et al., 2019; Parks et al., 2020) to the order *RF39* and to the family *CAG-1000*.

8997

8998

8999 **Description of *Candidatus* Ventrenecus avicola sp. nov.**

9000 *Candidatus* Ventrenecus avicola (a.vi'co.la. L. fem. n. *avis* bird; L. suff. *-cola* inhabitant of; N.L.

9001 n. *avicola* inhabitant of birds)

9002

9003 A bacterial species identified by metagenomic analyses. This species includes all bacteria with

9004 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been

9005 assigned the MAG ID ChiW22-487 and which is available via NCBI BioSample

9006 SAMN15817076. The GC content of the type genome is 31.09% and the genome length is 1.3

9007 Mbp.

9008

9009

9010 **Description of *Candidatus* Ventrenecus stercoripullorum sp. nov.**
9011 *Candidatus* Ventrenecus stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L.
9012 masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faceces of young chickens)
9013
9014 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
9015 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
9016 assigned the MAG ID CHK197-17881 and which is available via NCBI BioSample
9017 SAMN15817010. The GC content of the type genome is 30.90% and the genome length is 1.4
9018 Mbp.
9019
9020
9021 **Description of *Candidatus* Ventricola gen. nov.**
9022 *Candidatus* Ventricola (Ven.tri.co'la. L. masc. n. *venter* the belly; L. suff. -*cola* inhabitant of;
9023 N.L. fem. n. *Ventricola* a microbe associated with faeces)
9024
9025 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
9026 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
9027 species *Ventricola intestinavium*. This is a name for the alphanumeric GTDB genus SFFH01.
9028 This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
9029 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Christensenellales* and to the family *CAG-*
9030 *74.*
9031
9032
9033 **Description of *Candidatus* Ventricola gallistercoris sp. nov.**
9034 *Candidatus* Ventricola gallistercoris (gal.li.ster'co.ris. L. masc. n *gallus* chicken; L. neut. n.
9035 *stercus* dung; N.L. gen. n. *gallistercoris* of chicken faeces)
9036
9037 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
9038 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
9039 assigned the MAG ID ChiHcec16-310 and which is available via NCBI BioSample
9040 SAMN15817100. The GC content of the type genome is 60.63% and the genome length is 2.4
9041 Mbp.
9042
9043
9044 **Description of *Candidatus* Ventricola intestinavium sp. nov.**
9045 *Candidatus* Ventricola intestinavium (in.tes.tin.a'vi.um. L. neut. n. *intestinum* gut; L. fem. n. *avis*
9046 bird; N.L. gen. n. *intestinavium* of the gut of birds)
9047
9048 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
9049 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
9050 assigned the MAG ID 8987 and which is available via NCBI BioSample SAMN15817130. The
9051 GC content of the type genome is 59.95% and the genome length is 2.2 Mbp.
9052
9053
9054 **Description of *Candidatus* Ventrimonas gen. nov.**

9055   *Candidatus* Ventrimonas (Ven.tri.mo'nas. L. masc. n. *venter* the belly; L. fem. n. *monas* a
9056   monad; N.L. fem. n. *Ventrimonas* a microbe associated with faeces)
9057
9058   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
9059   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
9060   species *Ventrimonas merdavium*. This is a name for the alphanumeric GTDB genus UBA9502.
9061   This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
9062   (Chaumeil et al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family
9063   *Lachnospiraceae.*
9064
9065
9066   **Description of *Candidatus* Ventrimonas merdavium sp. nov.**
9067   *Candidatus* Ventrimonas merdavium (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis*
9068   bird; N.L. gen. n. *merdavium* of bird faeces)
9069
9070   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
9071   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
9072   assigned the MAG ID USAMLcec2-739 and which is available via NCBI BioSample
9073   SAMN15817118. The GC content of the type genome is 57.43% and the genome length is 3.0
9074   Mbp.
9075
9076
9077   **Description of *Candidatus* Ventrisoma gen. nov.**
9078   *Candidatus* Ventrisoma (Ven.tri.so'ma. L. masc. n. *venter* the belly; Gr. neut. n. *soma* a body;
9079   N.L. neut. n. *Ventrisoma* a microbe associated with faeces)
9080
9081   A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
9082   genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
9083   species *Ventrisoma faecale*. This is a name for the alphanumeric GTDB genus UC5-1-2E3. This
9084   genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95 (Chaumeil et
9085   al., 2019; Parks et al., 2020) to the order *Lachnospirales* and to the family *Lachnospiraceae.*
9086
9087
9088   **Description of *Candidatus* Ventrisoma faecale sp. nov.**
9089   *Candidatus* Ventrisoma faecale (fae.ca'le. L. neut. adj. *faecale* of faeces)
9090
9091   A bacterial species identified by metagenomic analyses. This species includes all bacteria with
9092   genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
9093   assigned the MAG ID ChiHcolR19-5415 and which is available via NCBI BioSample
9094   SAMN15817173. This is a new name for the alphanumeric GTDB species sp001304875. The
9095   GC content of the type genome is 55.91% and the genome length is 2.8 Mbp.
9096
9097
9098   **Description of *Candidatus* Ventrousia gen. nov.**
9099   *Candidatus* Ventrousia (Ventr.ou'si.a. L. masc. n. *venter* the belly; Gr. fem. n. *ousia* an essence;
9100   N.L. fem. n. *Ventrousia* a microbe associated with faeces)

9101
9102 A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with
9103 genomes that show ≥60% average amino acid identity (AAI) to the type genome from the type
9104 species *Ventrousia excrementavium*. This is a name for the alphanumeric GTDB genus SCN-57-
9105 10. This genus has been assigned by GTDB-Tk v1.3.0 working on GTDB Release 05-RS95
9106 (Chaumeil et al., 2019; Parks et al., 2020) to the order *Oscillospirales* and to the family
9107 *Butyricicoccaceae.*
9108
9109
9110 **Description of *Candidatus* Ventrousia excrementavium sp. nov.**
9111 *Candidatus* Ventrousia excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum*
9112 excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
9113
9114 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
9115 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
9116 assigned the MAG ID CHK191-8634 and which is available via NCBI BioSample
9117 SAMN15817048. The GC content of the type genome is 57.61% and the genome length is 2.1
9118 Mbp.
9119
9120
9121 **Description of *Candidatus* Yaniella excrementavium sp. nov.**
9122 *Candidatus* Yaniella excrementavium (ex.cre.ment.a'vi.um. L. neut. n. *excrementum* excrement;
9123 L. fem. n. *avis* bird; N.L. gen. n. *excrementavium* of bird excrement)
9124
9125 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
9126 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
9127 assigned the MAG ID ChiHjej13B12-778 and which is available via NCBI BioSample
9128 SAMN15816702. The GC content of the type genome is 55.30% and the genome length is 2.5
9129 Mbp.
9130
9131
9132 **Description of *Candidatus* Yaniella excrementigallinarum sp. nov.**
9133 *Candidatus* Yaniella excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum*
9134 excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)
9135
9136 A bacterial species identified by metagenomic analyses. This species includes all bacteria with
9137 genomes that show ≥95% average nucleotide identity (ANI) to the type genome, which has been
9138 assigned the MAG ID 4905 and which is available via NCBI BioSample SAMN15816764. The
9139 GC content of the type genome is 53.17% and the genome length is 2.6 Mbp.
9140

Protologues for new taxa cultured from chicken faeces

1 **Description of *Acinetobacter pecorum* sp. nov.**
2 (pe.co'rum M.L. gen. pl. *pecorum* of flocks of sheep, birds etc., as this species has been isolated
3 from chickens and sheep)
4
5 The type strain for this bacterial species has been cultured from chicken faeces after overnight
6 incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
7 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
8 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
9 species within this genus has been confirmed by phylogenetic analysis of all available reference
10 genomes from the genus (Figure S3).
11
12 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
13 (ANI) to the genome of the type strain, which is available via GenBank accession
14 GCA_014837015.1. The GC content of the type strain is 42.9% and the genome size is 3.2 Mbp.
15 GTDB has given this species the alphanumerical designation sp001647535 and the two other
16 genomes assigned to this species are derived from sheep isolates (RefSeq assembly accessions
17 GCF_001647535.1, GCF_001647575.1) (Gupta et al., 2016). The type strain has been deposited
18 in NCTC and DSMZ, where it can be identified via the original strain reference Sa1BUA6.
19
20 **Description of *Arthrobacter gallicola* sp. nov.**
21 (gal.li'co.la. L. masc. n. *gallus* a cock; N.L. suff. -*cola* an inhabitant of; N.L. masc. or fem. n.
22 *gallicola* an inhabitant of the chicken)
23
24 The type strain for this bacterial species has been cultured from chicken faeces after overnight
25 incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been
26 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
27 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
28 species within this genus has been confirmed by phylogenetic analysis of all available reference
29 genomes from the genus (Figure S3).
30
31 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
32 (ANI) to the genome of the type strain, which is available via GenBank accession
33 GCA_014836775.1. The GC content of the type strain is 65.5% and the genome size is 3.7 Mbp.
34 Although GTDB has assigned this species to the genus it calls *Arthrobacter_B*, this genus
35 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
36 have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ,
37 where it can be identified via the original strain reference Sa2CUA1.
38
39 **Description of *Arthrobacter pullicola* sp. nov.**
40 (pul.li'co.la. L. masc. n. *pullus* a young chicken; N.L. suff. -*cola* an inhabitant of; N.L. masc. or
41 fem. n. *pullicola* an inhabitant of young chickens)
42
43 The type strain for this bacterial species has been cultured from chicken faeces after overnight
44 incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
45 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
46 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a

47 species within this genus has been confirmed by phylogenetic analysis of all available reference
48 genomes from the genus (Figure S3).
49
50 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
51 (ANI) to the genome of the type strain, which is available via GenBank accession
52 GCA_014836875.1. The GC content of the type strain is 65.7% and the genome size is 3.7 Mbp.
53 Although GTDB has assigned this species to the genus it calls *Arthrobacter_B*, this genus
54 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
55 have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ,
56 where it can be identified via the original strain reference Sa2BUA2.
57
58 **Description of *Bacillus norwichensis* sp. nov.**
59 (nor.wich.en'sis. N.L. masc. adj. *norwichensis* pertaining to English city of Norwich, where the
60 organism was isolated)
61
62 The type strain for this bacterial species has been cultured from chicken faeces after overnight
63 incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been
64 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
65 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
66 species within this genus has been confirmed by phylogenetic analysis of all available reference
67 genomes from the genus (Figure S3).
68
69 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
70 (ANI) to the genome of the type strain, which is available via GenBank accession
71 GCA_014836955.1. The GC content of the type strain is 40.2% and the genome size is 4.7 Mbp.
72 Although GTDB has assigned this species to the genus it calls *Bacillus_AM*, this genus
73 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
74 have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ,
75 where it can be identified via the original strain reference Sa1BUA2
76
77 **Description of *Brevibacterium gallinarum* sp. nov.**
78 (gal.li.na'rum. L. pl. gen. n. *gallinarum* of hens)
79
80 The type strain for this bacterial species has been cultured from chicken faeces after overnight
81 incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
82 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
83 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
84 species within this genus has been confirmed by phylogenetic analysis of all available reference
85 genomes from the genus (Figure S3).
86
87 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
88 (ANI) to the genome of the type strain, which is available via GenBank accession
89 GCA_014836885.1. The GC content of the type strain is 67.0% and the genome size is 3.2 Mbp.
90 The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
91 original strain reference Re57

Description of *Brevundimonas guildfordensis* sp. nov.

(guild.ford.en'sis. N.L. fem. adj. *guildfordensis* pertaining to English town Guildford, home to the University of Surrey, where the samples were processed)

The type strain for this bacterial species has been cultured from chicken faeces after overnight incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a species within this genus has been confirmed by phylogenetic analysis of all available reference genomes from the genus (Figure S3).

The species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession GCA_014836405.1. The GC content of the type strain is 67.3% and the genome size is 2.9 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa3CVA3

Description of *Cellulomonas avistercoris* sp. nov.

(a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung; N.L. gen. n. *avistercoris* of bird faeces)

The type strain for this bacterial species has been cultured from chicken faeces after overnight incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a species within this genus has been confirmed by phylogenetic analysis of all available reference genomes from the genus (Figure S3).

The species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession GCA_014836445.1. The GC content of the type strain is 74.5% and the genome size is 4.2 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa3CUA2

Description of *Clostridium cibarium* sp. nov.

(ci.ba'ri.um. L. neut. adj. *cibarium* pertaining to food, as this species has been isolated from chickens and zha-chili)

The type strain for this bacterial species has been cultured from chicken faeces after overnight incubation on Columbia blood agar at 37°C under anaerobic conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a species within this genus has been confirmed by phylogenetic analysis of all available reference genomes from the genus (Figure S3).

138 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
139 (ANI) to the genome of the type strain, which is available via GenBank accession
140 GCA_014836335.1. The GC content of the type strain is 29.8% and the genome size is 4.3 Mbp.
141 GTDB has given this species the alphanumerical designation sp007115085. One other isolate
142 from this species (RefSeq accession GCA_007115085.1) has been cultured from zha-chili, a
143 Chinese fermented food. The type strain has been deposited in NCTC and DSMZ, where it can
144 be identified via the original strain reference Sa3CVN1.
145
146 **Description of *Clostridium gallinarum* sp. nov.**
147 (gal.li.na'rum. L. pl. gen. n. *gallinarum* of hens)
148
149 The type strain for this bacterial species has been cultured from chicken faeces after overnight
150 incubation on Columbia blood agar at 37°C under anaerobic conditions. The species has been
151 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
152 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
153 species within this genus has been confirmed by phylogenetic analysis of all available reference
154 genomes from the genus (Figure S3).
155
156 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
157 (ANI) to the genome of the type strain, which is available via GenBank accession
158 GCA_014836325.1. The GC content of the type strain is 27.2% and the genome size is 3.4 Mbp.
159 The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
160 original strain reference Sa3CUN1.
161
162 **Description of *Clostridium faecium* sp. nov.**
163 (fae'ci.um N.L. gen. pl. n. *faecium*, of faeces, as this species has been isolated from chicken and
164 human faeces)
165
166 The type strain for this bacterial species has been cultured from chicken faeces after overnight
167 incubation on brain-heart infusion agar at 37°C under anaerobic conditions. The species has been
168 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
169 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
170 species within this genus has been confirmed by phylogenetic analysis of all available reference
171 genomes from the genus (Figure S3).
172
173 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
174 (ANI) to the genome of the type strain, which is available via GenBank accession
175 GCA_014836835.1. The GC content of the type strain is 28.7% and the genome size is 3.9 Mbp.
176 Although GTDB has assigned this species to the genus it calls *Clostridium_J*, this genus
177 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
178 have used the basonym for the genus. GTDB has given this species the alphanumerical
179 designation sp900547625, which includes a gut isolate from a preterm human infant (GenBank
180 accession GCA_900547625.1). The type strain has been deposited in NCTC and DSMZ, where it
181 can be identified via the original strain reference N37

Description of *Comamonas avium* sp. nov.

(a'vi.um. L. gen. pl. n. *avium* of birds)

The type strain for this bacterial species has been cultured from chicken faeces after overnight incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a species within this genus has been confirmed by phylogenetic analysis of all available reference genomes from the genus (Figure S3).

The species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession GCA_014836675.1. The GC content of the type strain is 57.5% and the genome size is 3.9 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2CVA6

Description of *Corynebacterium gallinarum* sp. nov.

(gal.li.na'rum. L. pl. gen. n. *gallinarum* of hens)

The type strain for this bacterial species has been cultured from chicken faeces after overnight incubation on YCFA (yeast extract, casitone and fatty acid) agar at 37°C under aerobic conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a species within this genus has been confirmed by phylogenetic analysis of all available reference genomes from the genus (Figure S3).

The species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession GCA_014837045.1. The GC content of the type strain is 63.1% and the genome size is 3.1 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1YVA5

Description of *Cytobacillus stercorigallinarum* sp. nov.

(ster.co.ri.gal.li.na'rum. L. neut. n. *stercus* faeces; L. fem. n. *gallina* a hen; N.L. gen. n. *stercorigallinarum* of hen faeces)

The type strain for this bacterial species has been cultured from chicken faeces after overnight incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a species within this genus has been confirmed by phylogenetic analysis of all available reference genomes from the genus (Figure S3).

The species includes all bacteria with genomes that show ≥95% average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession GCA_014836495.1. The GC content of the type strain is 36.8% and the genome size is 4.4 Mbp.

229 GTDB has assigned this species to the genus it calls *Bacillus_AA*, which cannot be incorporated
230 into a well-formed binomial. However, according to (Patel & Gupta, 2020), the newly named
231 genus *Cytobacillus* encompasses other species classified by GTDB within the genus designation
232 *Bacillus_AA* and therefore *Cytobacillus* is treated as a synonym of GTDB *Bacillus_AA*. The type
233 strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain
234 reference Sa5YUA1.

236 **Description of *Escherichia whittamii* sp. nov.**
237 (whitt.am'i.i. N.L. gen. n. *whittamii*, named in honour of American microbiologist Thomas S.
238 Whittam)

240 The type strain for this bacterial species has been cultured from chicken faeces after overnight
241 incubation on Columbia blood agar at 37°C under anaerobic conditions. The species has been
242 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
243 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
244 species within this genus has been confirmed by phylogenetic analysis of reference genomes
245 from the genus (Figure 4).

247 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
248 (ANI) to the genome of the type strain, which is available via GenBank accession
249 GCA_014836715.1. The GC content of the type strain is 50.6% and the genome size is 4.6 Mbp.
250 GTDB has given this species the alphanumerical designation sp001660175 and has assigned two
251 other cultured isolates to this species, both of which come from birds (RefSeq assembly
252 accessions GCF_001660175.1, GCF_002965485.1) (Clermont et al., 2011; Gangiredla et al.,
253 2018) The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
254 original strain reference Sa2BVA5.

255

256 **Description of *Fictibacillus norfolkensis* sp. nov.**
257 (nor.folk.en_sis. N.L. masc. adj. *norfolkensis* pertaining to the English county of Norfolk)

258

259 The type strain for this bacterial species has been cultured from chicken faeces after overnight
260 incubation on YCFA (yeast extract, casitone and fatty acid) agar at 37°C under aerobic
261 conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0
262 applied to the Genome Taxonomy Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019;
263 Parks et al., 2020). Its status as a species within this genus has been confirmed by phylogenetic
264 analysis of all available reference genomes from the genus (Figure S3).

265

266 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
267 (ANI) to the genome of the type strain, which is available via GenBank accession
268 GCA_014836645.1. The GC content of the type strain is 39.5% and the genome size is 4.0 Mbp.
269 Although GTDB has assigned this species to the genus it calls *Fictibacillus_B*, this genus
270 designation cannot be incorporated into a well-formed binomial, so in naming this species, we
271 have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ,
272 where it can be identified via the original strain reference Sa2CUA10

273

274   **Description of *Kaistella pullorum* sp. nov.**
275   (pul.lor_um. L. gen. pl. n. *pullorum* of chickens)
276
277   The type strain for this bacterial species has been cultured from chicken faeces after overnight
278   incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been
279   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
280   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
281   species within this genus has been confirmed by phylogenetic analysis of all available reference
282   genomes from the genus (Figure S3).
283
284   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
285   (ANI) to the genome of the type strain, which is available via GenBank accession
286   GCA_014837035.1. The GC content of the type strain is 42.9% and the genome size is 2.6 Mbp.
287   The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
288   original strain reference Sa1CVA4
289
290   **Description of *Limosilactobacillus avistercoris* sp. nov.**
291   (a.vi.ster'co.ris. L. fem. n. *avis* bird; L. neut. n. *stercus* dung; N.L. gen. n. *avistercoris* of bird
292   faeces)
293
294   The type strain for this bacterial species has been cultured from chicken faeces after overnight
295   incubation on brain-heart infusion agar at 37°C under anaerobic conditions. The species has been
296   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
297   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
298   species within this genus has been confirmed by phylogenetic analysis of all available reference
299   genomes from the genus (Figure S3).
300
301   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
302   (ANI) to the genome of the type strain, which is available via GenBank accession
303   GCA_014836425.1. The GC content of the type strain is 39.9% and the genome size is 1.8 Mbp.
304   GTDB has assigned this species to the genus it calls *Lactobacillus_H*, which cannot be
305   incorporated into a well-formed binomial. However, according to (Zheng et al., 2020)
306   *Limosilactobacillus* encompasses other species classified by GTDB within the genus designation
307   *Lactobacillus_H* and therefore *Limosilactobacillus* is treated as a synonym for GDTB
308   designation *Lactobacillus_H*. The type strain has been deposited in NCTC and DSMZ, where it
309   can be identified via the original strain reference Sa3CUN2
310
311   **Description of *Luteimonas colneyensis* sp. nov.**
312   (col.ney.en'sis. N.L. fem. adj. *colneyensis* pertaining to the English village of Colney, home to
313   the Quadram Institute, where the species was first described)
314
315   The type strain for this bacterial species has been cultured from chicken faeces after overnight
316   incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been
317   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
318   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a

319 species within this genus has been confirmed by phylogenetic analysis of all available reference
320 genomes from the genus (Figure S3).
321
322 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
323 (ANI) to the genome of the type strain, which is available via GenBank accession
324 GCA_014836665.1. The GC content of the type strain is 71.0% and the genome size is 3.0 Mbp.
325 The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
326 original strain reference Sa2BVA3
327
328 **Description of *Microbacterium commune* sp. nov.**
329 (com.mu_ne. L. neut. adj. *commune* common, referring to diverse habitats, as this species has
330 been isolated from mosquitos and chicken)
331
332 The type strain for this bacterial species has been cultured from chicken faeces after overnight
333 incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been
334 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
335 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
336 species within this genus has been confirmed by phylogenetic analysis of all available reference
337 genomes from the genus (Figure S3).
338
339 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
340 (ANI) to the genome of the type strain, which is available via GenBank accession
341 GCA_014836945.1. The GC content of the type strain is 70.3% and the genome size is 3.3 Mbp.
342 GTDB has given this species the alphanumerical designation sp001878835, which also contains
343 a mosquito isolate (RefSeq accession GCF_001878835.1). The type strain has been deposited in
344 NCTC and DSMZ, where it can be identified via the original strain reference Re1.
345
346 **Description of *Microbacterium gallinarum* sp. nov.**
347 (gal.li.na'rum. L. pl. gen. n. *gallinarum* of hens)
348
349 The type strain for this bacterial species has been cultured from chicken faeces after overnight
350 incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
351 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
352 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
353 species within this genus has been confirmed by phylogenetic analysis of all available reference
354 genomes from the genus (Figure S3).
355
356 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
357 (ANI) to the genome of the type strain, which is available via GenBank accession
358 GCA_014837165.1. The GC content of the type strain is 69.4% and the genome size is 2.8 Mbp.
359 The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
360 original strain reference Sa1CUA4
361
362 **Description of *Microbacterium pullorum* sp. nov.**
363 (pul.lor_um. L. gen. pl. n. *pullorum* of chickens)

364
365 The type strain for this bacterial species has been cultured from chicken faeces after overnight
366 incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been
367 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
368 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
369 species within this genus has been confirmed by phylogenetic analysis of all available reference
370 genomes from the genus (Figure S3).
371
372 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
373 (ANI) to the genome of the type strain, which is available via GenBank accession
374 GCA_014836535.1. The GC content of the type strain is 70.1% and the genome size is 3.1 Mbp.
375 The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
376 original strain reference Sa4CUA7
377

378 **Description of *Oceanitalea stevensii* sp. nov.**
379 (ste.ven'si.i. N.L. gen. n. *stevensii,* named in honour of British microbiologist Mark Stevens)
380
381 The type strain for this bacterial species has been cultured from chicken faeces after overnight
382 incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
383 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
384 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
385 species within this genus has been confirmed by phylogenetic analysis of all available reference
386 genomes from the genus (Figure S3).
387
388 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
389 (ANI) to the genome of the type strain, which is available via GenBank accession
390 GCA_014837105.1. The GC content of the type strain is 73.4% and the genome size is 3.5 Mbp.
391 The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
392 original strain reference Sa1BUA1.
393

394 **Description of *Ochrobactrum gallinarum* sp. nov.**
395 (gal.li.na'rum. L. pl. gen. n. *gallinarum* of hens)
396
397 The type strain for this bacterial species has been cultured from chicken faeces after overnight
398 incubation on brain-heart infusion at 37°C under aerobic conditions. The species has been
399 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
400 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
401 species within this genus has been confirmed by phylogenetic analysis of all available reference
402 genomes from the genus (Figure S3).
403
404 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
405 (ANI) to the genome of the type strain, which is available via GenBank accession
406 GCA_014836735.1. The GC content of the type strain is 53.5% and the genome size is 5.0 Mbp.
407 The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
408 original strain reference Sa2BUA5
409

410 **Description of *Oerskovia douganii* sp. nov.**
411 (dou.gan_i.i. N.L. gen. n. *douganii* named in honour of British microbiologist Gordon Dougan)
412
413 The type strain for this bacterial species has been cultured from chicken faeces after overnight
414 incubation on brain-heart infusion at 37°C under aerobic conditions. The species has been
415 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
416 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
417 species within this genus has been confirmed by phylogenetic analysis of all available reference
418 genomes from the genus (Figure S3).
419
420 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
421 (ANI) to the genome of the type strain, which is available via GenBank accession
422 GCA_015142735.1. The GC content of the type strain is 72.5% and the genome size is 4.3 Mbp.
423 The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
424 original strain reference Sa1BUA8
425
426 **Description of *Oerskovia gallyi* sp. nov.**
427 (gall.y'i. N.L. gen. n. *gallyi* named in honour of British microbiologist David Gally)
428
429 The type strain for this bacterial species has been cultured from chicken faeces after overnight
430 incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
431 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
432 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
433 species within this genus has been confirmed by phylogenetic analysis of all available reference
434 genomes from the genus (Figure S3).
435
436 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
437 (ANI) to the genome of the type strain, which is available via GenBank accession
438 GCA_014836745.1. The GC content of the type strain is 72.5% and the genome size is 4.3 Mbp.
439 The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
440 original strain reference Sa2CUA8
441
442 **Description of *Oerskovia merdavium* sp. nov.**
443 (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird; N.L. gen. n. *merdavium* of bird
444 faeces)
445
446 The type strain for this bacterial species has been cultured from chicken faeces after overnight
447 incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been
448 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
449 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
450 species within this genus has been confirmed by phylogenetic analysis of all available reference
451 genomes from the genus (Figure S3).
452
453 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
454 (ANI) to the genome of the type strain, which is available via GenBank accession
455 GCA_014836755.1. The GC content of the type strain is 72.1% and the genome size is 4.5 Mbp.

456   The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
457   original strain reference Sa2CUA9.
458

Description of *Oerskovia rustica* sp. nov.
460   (rus'tic.a L fem adj. *rustica* of the countryside, as isolates have been obtained from soil and
461   chickens)
462

463   The type strain for this bacterial species has been cultured from chicken faeces after overnight
464   incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been
465   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
466   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
467   species within this genus has been confirmed by phylogenetic analysis of all available reference
468   genomes from the genus (Figure S3).
469

470   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
471   (ANI) to the genome of the type strain, which is available via GenBank accession
472   GCA_014836555.1. The GC content of the type strain is 72.5% and the genome size is 4.4 Mbp.
473   GTDB has given this species the alphanumerical designation sp005937995, which includes a soil
474   isolate (RefSeq accession GCF_005937995.2). The type strain has been deposited in NCTC and
475   DSMZ, where it can be identified via the original strain reference Sa4CUA1.
476

Description of *Paenibacillus gallinarum* sp. nov.
478   (gal.li.na'rum. L. pl. gen. n. *gallinarum* of hens)
479

480   The type strain for this bacterial species has been cultured from chicken faeces after overnight
481   incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been
482   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
483   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
484   species within this genus has been confirmed by phylogenetic analysis of all available reference
485   genomes from the genus (Figure S3).
486

487   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
488   (ANI) to the genome of the type strain, which is available via GenBank accession
489   GCA_014836635.1. The GC content of the type strain is 41.2% and the genome size is 5.4 Mbp.
490   The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
491   original strain reference Sa2BVA9
492

Description of *Phocaeicola faecium* sp. nov.
494   (fae'ci.um N.L. gen. pl. n. *faecium*, of faeces)
495

496   The type strain for this bacterial species has been cultured from chicken faeces after overnight
497   incubation on YCFA (yeast extract, casitone and fatty acid) agar at 37°C under anaerobic
498   conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0
499   applied to the Genome Taxonomy Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019;

500   Parks et al., 2020). Its status as a species within this genus has been confirmed by phylogenetic
501   analysis of all available reference genomes from the genus (Figure S3).
502
503   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
504   (ANI) to the genome of the type strain, which is available via GenBank accession
505   GCA_014837055.1. The GC content of the type strain is 45.6% and the genome size is 3.5 Mbp.
506   GTDB has given this species the alphanumerical designation sp900540105, which includes a gut
507   isolate from an infant human (GenBank accession GCA_900540105.1). The type strain has been
508   deposited in NCTC and DSMZ, where it can be identified via the original strain reference
509   Sa1YUN3
510
511   **Description of *Phocaeicola intestinalis* sp. nov.**
512   (in.tes.ti.na'lis. N.L. masc./fem. adj. *intestinalis*, pertaining to the intestines)
513
514   The type strain for this bacterial species has been cultured from chicken faeces after overnight
515   incubation on Columbia blood agar at 37°C under anaerobic conditions. The species has been
516   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
517   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
518   species within this genus has been confirmed by phylogenetic analysis of all available reference
519   genomes from the genus (Figure S3).
520
521   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
522   (ANI) to the genome of the type strain, which is available via GenBank accession
523   GCA_014837065.1. The GC content of the type strain is 45.7% and the genome size is 4.1 Mbp.
524   GTDB has given this species the alphanumerical designation sp002161565, which includes
525   isolates from the human and chicken guts (GenBank accession numbers GCA_000432695.1,
526   GCA_900540165.1, GCF_002159615.1, GCF_002159755.1, GCF_002160215.1,
527   GCF_002161565.1). The type strain has been deposited in NCTC and DSMZ, where it can be
528   identified via the original strain reference Sa1CVN1.
529
530   **Description of *Planococcus wigleyi* sp. nov.**
531   (wig_ley.i. N.L. masc. gen. n. *wigleyi* named in honour of British microbiologist Paul Wigley)
532
533   The type strain for this bacterial species has been cultured from chicken faeces after overnight
534   incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
535   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
536   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
537   species within this genus has been confirmed by phylogenetic analysis of all available reference
538   genomes from the genus (Figure S3).
539
540   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
541   (ANI) to the genome of the type strain, which is available via GenBank accession
542   GCA_014836985.1. The GC content of the type strain is 45.0% and the genome size is 3.8 Mbp.
543   Although GTDB has assigned a genus name with an alphabetic suffix *Planococcus_A*, this genus
544   designation cannot be incorporated into a well-formed binomial, so in naming this species, we

545 have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ,
546 where it can be identified via the original strain reference Sa1BUA13
547

Description of *Psychrobacillus faecigallinarum* sp. nov.
549 (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* faeces; L. fem. n. *gallina* a hen; N.L. gen. n.
550 *faecigallinarum* of hen faeces)
551

552 The type strain for this bacterial species has been cultured from chicken faeces after overnight
553 incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
554 assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
555 Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
556 species within this genus has been confirmed by phylogenetic analysis of all available reference
557 genomes from the genus (Figure S3).
558

559 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
560 (ANI) to the genome of the type strain, which is available via GenBank accession
561 GCA_014836595.1. The GC content of the type strain is 36.5% and the genome size is 4.0 Mbp.
562 The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
563 original strain reference Sa2BUA9
564

Description of *Psychrobacter communis* sp. nov.
566 (com.mun_is L. masc. adj. *communis* common, referring to diverse habitats from which this
567 species has been isolated, including chickens and soil)
568

569 The type strain for this bacterial species has been cultured from chicken faeces after overnight
570 incubation on xyz medium at 37°C under aerobic conditions. The species has been assigned to
571 this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy Database
572 (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a species
573 within this genus has been confirmed by phylogenetic analysis of all available reference
574 genomes from the genus (Figure S3).
575

576 The species includes all bacteria with genomes that show ≥95% average nucleotide identity
577 (ANI) to the genome of the type strain, which is available via GenBank accession
578 GCA_014836505.1. The GC content of the type strain is 43.7% and the genome size is 3.0 Mbp.
579 GTDB has given this species the alphanumerical designation sp001652315, which contains six
580 environmental isolates from a variety of sources including soil (GCA_002332465.1,
581 GCA_002439405.1, GCA_003524605.1, GCA_007280595.1, GCF_001652315.1,
582 GCF_002836335.1.) The type strain has been deposited in NCTC and DSMZ, where it can be
583 identified via the original strain reference Sa4CVA2
584

Description of *Serpens gallinarum* sp. nov.
586 (gal.li.na'rum. L. pl. gen. n. *gallinarum* of hens)
587

588 The type strain for this bacterial species has been cultured from chicken faeces after overnight
589 incubation on Columbia blood agar at 37°C under aerobic conditions. The species has been

590   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
591   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
592   species within this genus has been confirmed by phylogenetic analysis of all available reference
593   genomes from the genus (Figure S3).
594
595   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
596   (ANI) to the genome of the type strain, which is available via GenBank accession
597   GCA_014836765.1. The GC content of the type strain is 61.0% and the genome size is 3.9 Mbp.
598   Although GTDB has assigned a genus name with an alphabetic suffix *Pseudomonas_H*, which
599   cannot be incorporated into a well-formed binomial. However, GDTB genus *Pseudomonas_H*
600   includes *Pseudomonas flexibilis*, where the basonym is *Serpens* (Hespell, 1977), so we have used
601   this genus name. The type strain has been deposited in NCTC and DSMZ, where it can be
602   identified via the original strain reference Sa2CUA2
603

Description of *Solibacillus faecavium* sp. nov.

605   (faec.a'vi.um. L. fem. n. *faex, faecis* faeces; L. fem. n. *avis* bird; N.L. gen. n. *faecavium* of bird
606   faeces)
607
608   The type strain for this bacterial species has been cultured from chicken faeces after overnight
609   incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
610   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
611   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
612   species within this genus has been confirmed by phylogenetic analysis of all available reference
613   genomes from the genus (Figure S3).
614
615   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
616   (ANI) to the genome of the type strain, which is available via GenBank accession
617   GCA_014836905.1. The GC content of the type strain is 37.1% and the genome size is 3.8 Mbp.
618   The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
619   original strain reference A46
620

Description of *Solibacillus merdavium* sp. nov.

622   (merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird; N.L. gen. n. *merdavium* of bird
623   faeces)
624
625   The type strain for this bacterial species has been cultured from chicken faeces after overnight
626   incubation on YCFA (yeast extract, casitone and fatty acid) agar at 37°C under aerobic
627   conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0
628   applied to the Genome Taxonomy Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019;
629   Parks et al., 2020). Its status as a species within this genus has been confirmed by phylogenetic
630   analysis of all available reference genomes from the genus (Figure S3).
631
632   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
633   (ANI) to the genome of the type strain, which is available via GenBank accession
634   GCA_014836935.1. The GC content of the type strain is 37.0% and the genome size is 3.8 Mbp.

635   The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
636   original strain reference Sa1YVA6
637
638   **Description of *Sporosarcina gallistercoris* sp. nov.**
639   (gal.li.ster'co.ris. L. masc. n. *gallus* a cock; L. neut. n. *stercus* dung; N.L. gen. n. *gallistercoris* of
640   faeces of a cock)
641
642   The type strain for this bacterial species has been cultured from chicken faeces after overnight
643   incubation on YCFA (yeast extract, casitone and fatty acid) agar at 37°C under aerobic
644   conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0
645   applied to the Genome Taxonomy Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019;
646   Parks et al., 2020). Its status as a species within this genus has been confirmed by phylogenetic
647   analysis of all available reference genomes from the genus (Figure S3).
648
649   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
650   (ANI) to the genome of the type strain, which is available via GenBank accession
651   GCA_014836415.1. The GC content of the type strain is 44.1% and the genome size is 3.1 Mbp.
652   Although GTDB has assigned a genus name with an alphabetic suffix *Sporosarcina_A*, this
653   genus designation cannot be incorporated into a well-formed binomial, so in naming this species,
654   we have used the basonym for the genus. The type strain has been deposited in NCTC and
655   DSMZ, where it can be identified via the original strain reference Sa3CUA8
656
657   **Description of *Sporosarcina quadrami* sp. nov.**
658   (qua.dra'mi. N.L. gen. n. *quadrami*, of the Quadram Institute, where the species was first
659   cultured.)
660
661   The type strain for this bacterial species has been cultured from chicken faeces after overnight
662   incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
663   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
664   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
665   species within this genus has been confirmed by phylogenetic analysis of all available reference
666   genomes from the genus (Figure S3).
667
668   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
669   (ANI) to the genome of the type strain, which is available via GenBank accession
670   GCA_014836615.1. The GC content of the type strain is 41.4% and the genome size is 3.6 Mbp.
671   Although GTDB has assigned a genus name with an alphabetic suffix *Sporosarcina_B*, this
672   genus designation cannot be incorporated into a well-formed binomial, so in naming this species,
673   we have used the basonym for the genus. The type strain has been deposited in NCTC and
674   DSMZ, where it can be identified via the original strain reference Sa2YVA2
675
676   **Description of *Stenotrophomonas pennii* sp. nov.**
677   (pen'ni.i. N.L. gen. n. *pennii*, named in honour of British microbiologist Charles W. Penn)
678

679   The type strain for this bacterial species has been cultured from chicken faeces after overnight
680   incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
681   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
682   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
683   species within this genus has been confirmed by phylogenetic analysis of all available reference
684   genomes from the genus (Figure S3).

685

686   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
687   (ANI) to the genome of the type strain, which is available via GenBank accession
688   GCA_014836545.1. The GC content of the type strain is 66.4% and the genome size is 3.9 Mbp.
689   GTDB has given this species the alphanumerical designation sp002836635, which includes four
690   environmental isolates (RefSeq accessions GCF_000834105.1, GCF_002836635.1,
691   GCF_002836645.1, GCF_002836675.1). The type strain has been deposited in NCTC and
692   DSMZ, where it can be identified via the original strain reference Sa5BUN4

693

694   ### Description of *Ureibacillus galli* sp. nov.
695   (gal_li. L. masc. gen. n. *galli* of a chicken)

696

697   The type strain for this bacterial species has been cultured from chicken faeces after overnight
698   incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
699   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
700   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
701   species within this genus has been confirmed by phylogenetic analysis of all available reference
702   genomes from the genus (Figure S3).

703

704   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
705   (ANI) to the genome of the type strain, which is available via GenBank accession
706   GCA_014836845.1. The GC content of the type strain is 35.2% and the genome size is 3.7 Mbp.
707   The type strain has been deposited in NCTC and DSMZ, where it can be identified via the
708   original strain reference Re31.

709

710   ### Description of *Xanthomonas surreyensis* sp. nov.
711   (sur.rey.en'sis. N.L. fem. adj. surreyensis pertaining to the English county of Surrey, where the
712   samples were obtained)

713

714   The type strain for this bacterial species has been cultured from chicken faeces after overnight
715   incubation on brain-heart infusion agar at 37°C under aerobic conditions. The species has been
716   assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy
717   Database (GTDB) Release 05-RS95 (Chaumeil et al., 2019; Parks et al., 2020). Its status as a
718   species within this genus has been confirmed by phylogenetic analysis of all available reference
719   genomes from the genus (Figure S3).

720

721   The species includes all bacteria with genomes that show ≥95% average nucleotide identity
722   (ANI) to the genome of the type strain, which is available via GenBank accession
723   GCA_014836395.1. The GC content of the type strain is 68.8% and the genome size is 5.4 Mbp.
724   Although GTDB has assigned a genus name with an alphabetic suffix *Xanthomonas_A*, this

725   genus designation cannot be incorporated into a well-formed binomial, so in naming this species,
726   we have used the basonym for the genus. The type strain has been deposited in NCTC and
727   DSMZ, where it can be identified via the original strain reference Sa3BUA13.
728

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762

Figure 1

Analytical Workflow

* indicates read numbers are detailed post-filtering of diet and host associated reads.

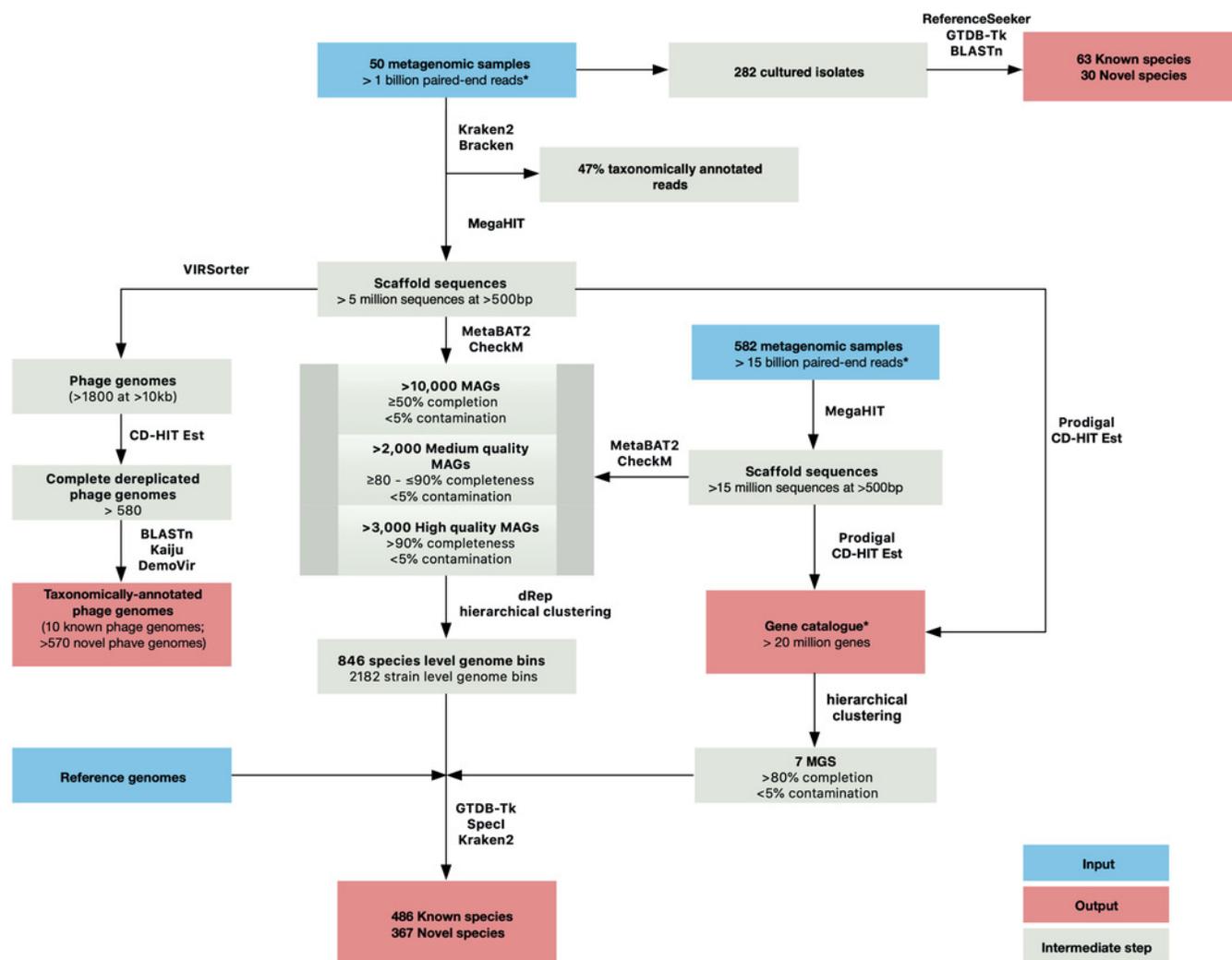



Figure 2

Genome synteny of recovered phage genomes

Synteny plots comparing four novel coliphage genomes recovered from chicken faecal metagenomes (in red) to closest reference genomes. The figure was generated using EasyFig.

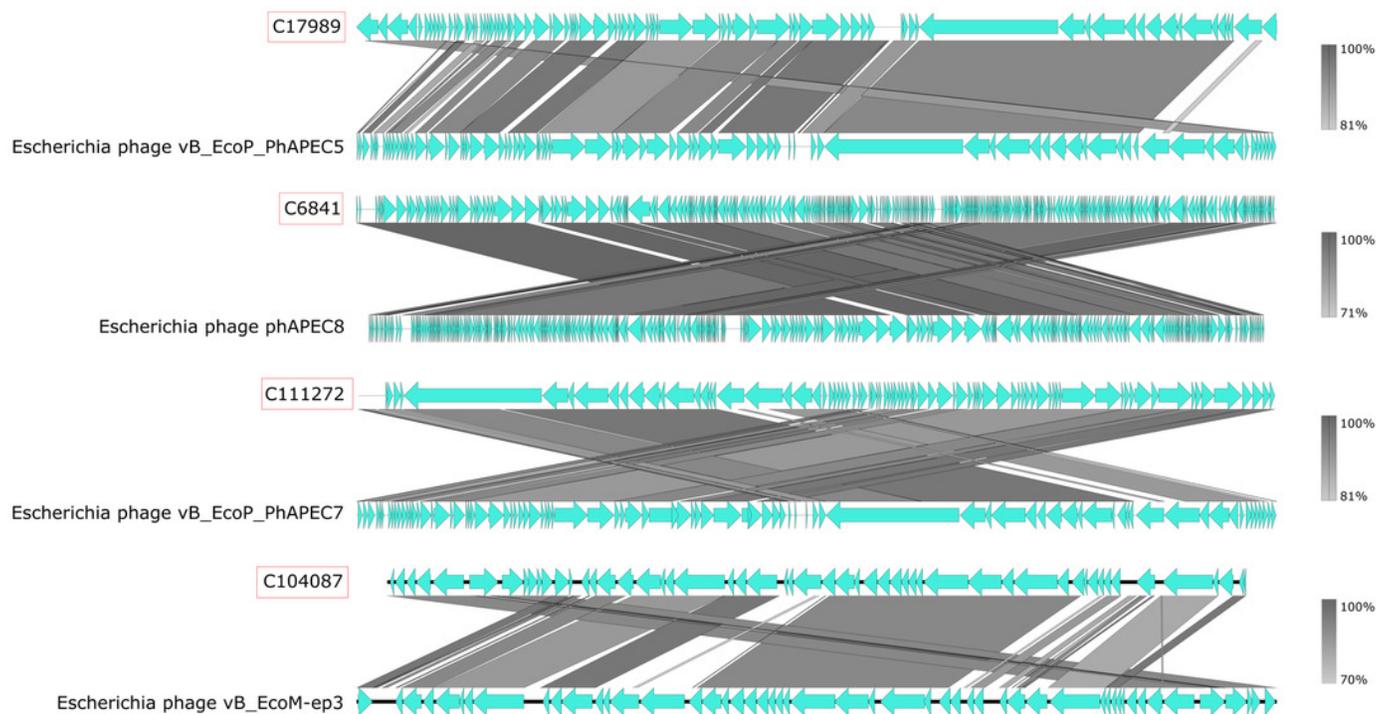



Figure 3

Coliphage abundance within chicken faecal samples

Coverage of four coliphages and of putative host bacterial species. Only samples in which at least one genome had ≥1x coverage are shown (n=29). All coverage values have been Log_{10} transformed with blue depicting low abundance and red high abundance.

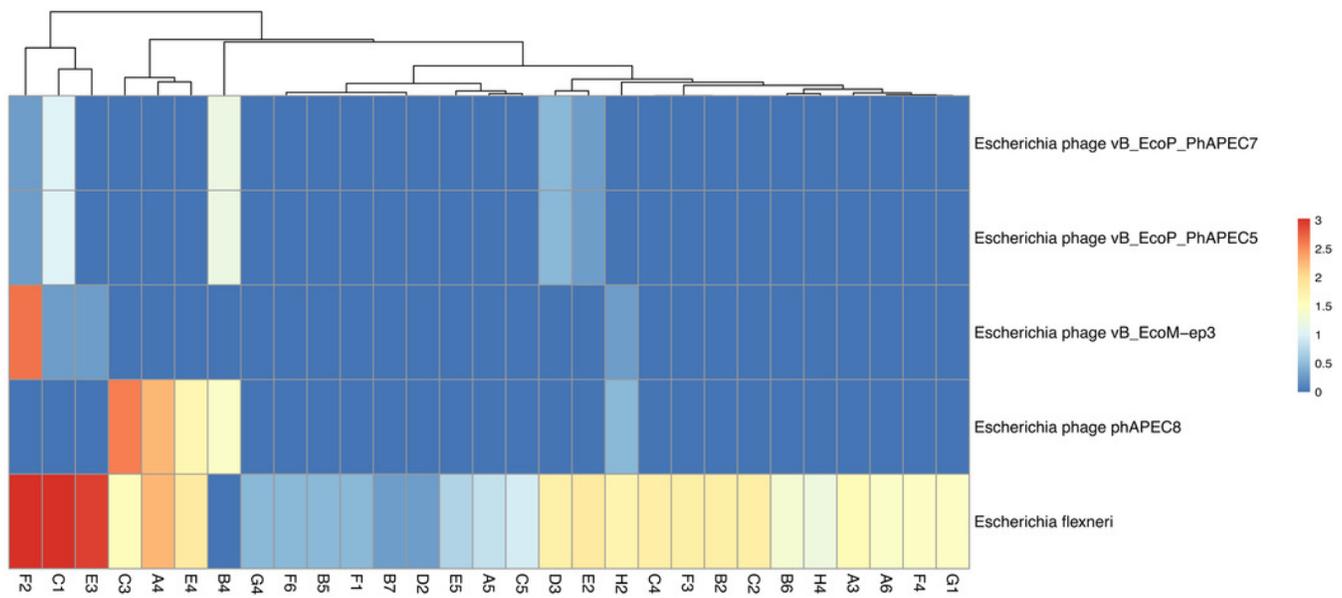



Figure 4

Phylogenetic tree of draft MGS genomes derived from 820 metagenomic samples of the chicken gut and draft genomes of 93 species cultured from chicken faecal samples

Phylum, generally as assigned by GTDB, is indicated by colour range. Data symbols in the outer layers have been used to describe further characteristics for each draft genomes. Triangles indicate sequence novelty and status of binomial designation within publicly available databases or published research with filled symbols indicating novel species assigned a binomial as part of this research, hollow symbol indicated a known species assigned a binomial as part of this research and no symbol indicated a known species with a well-formed binomial already assigned. Stars are used to indicate isolation source, with filled symbols indicating isolation of species in both culture and metagenomic assembly and hollow symbols indicating isolation in culture alone. Tree branches have been collapsed where duplicate species have been identified by different methodologies. The tree was reconstructed using PhyloPhlAn 3.0.58 against 400 marker genes before reconstruction using FastTree and RAxML of a MAFFT sequence alignment and visualised using the online iTOLv1.4 tool including provision of a heat map according to individual genome length.

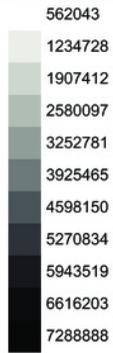
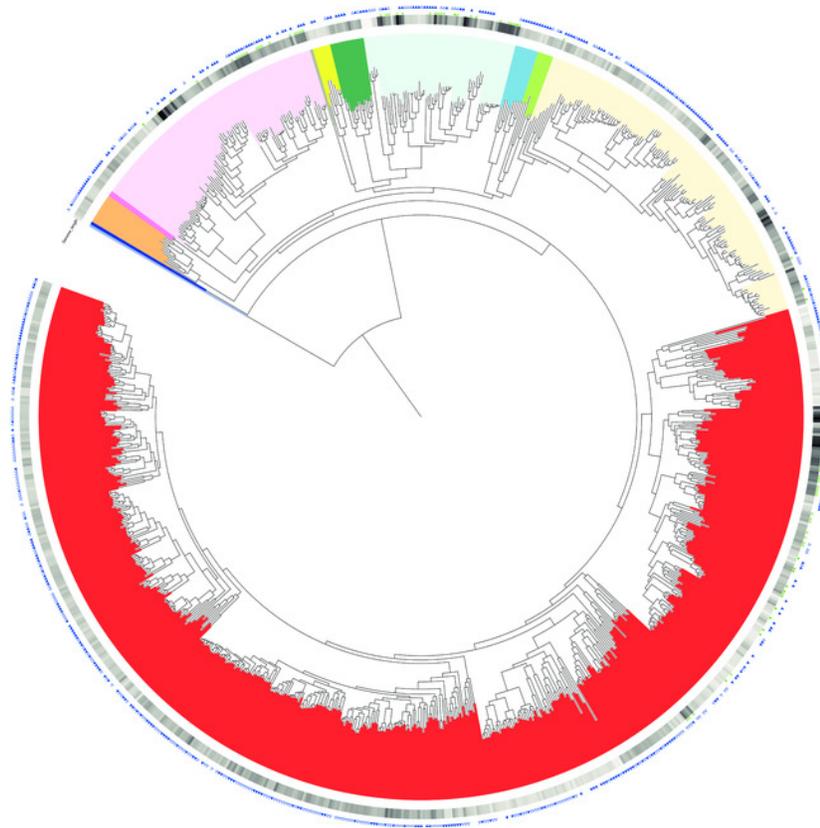
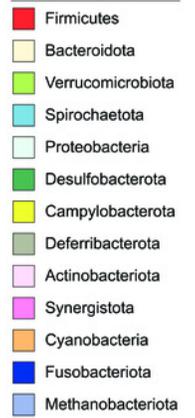



Figure 5

Phylogenetic tree showing the relationships between *Escherichia marmotae*, *Escherichia whittamii* and the other *Escherichia* species and cryptic clades

The tree was constructed by RAxML maximum likelihood analysis of a core genome alignment generated using Mugsy. The scale bar indicates the number of substitutions per site represented by the branch length shown. Numbers on branches indicate the percentage bootstrap support out of 100 replicates. Strains sequenced as part of this study are highlighted in red.

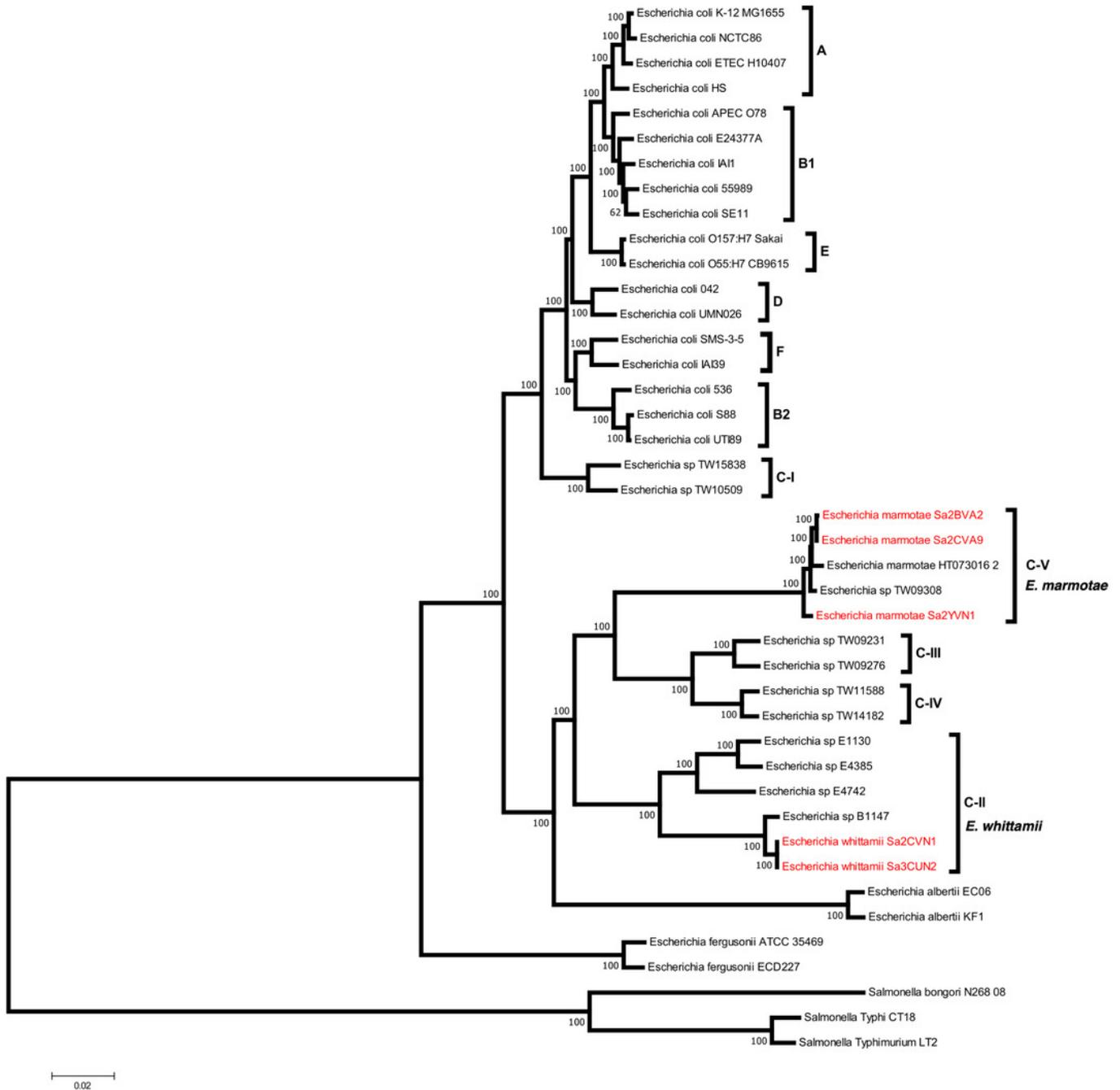



Figure 6

Sequence novelty

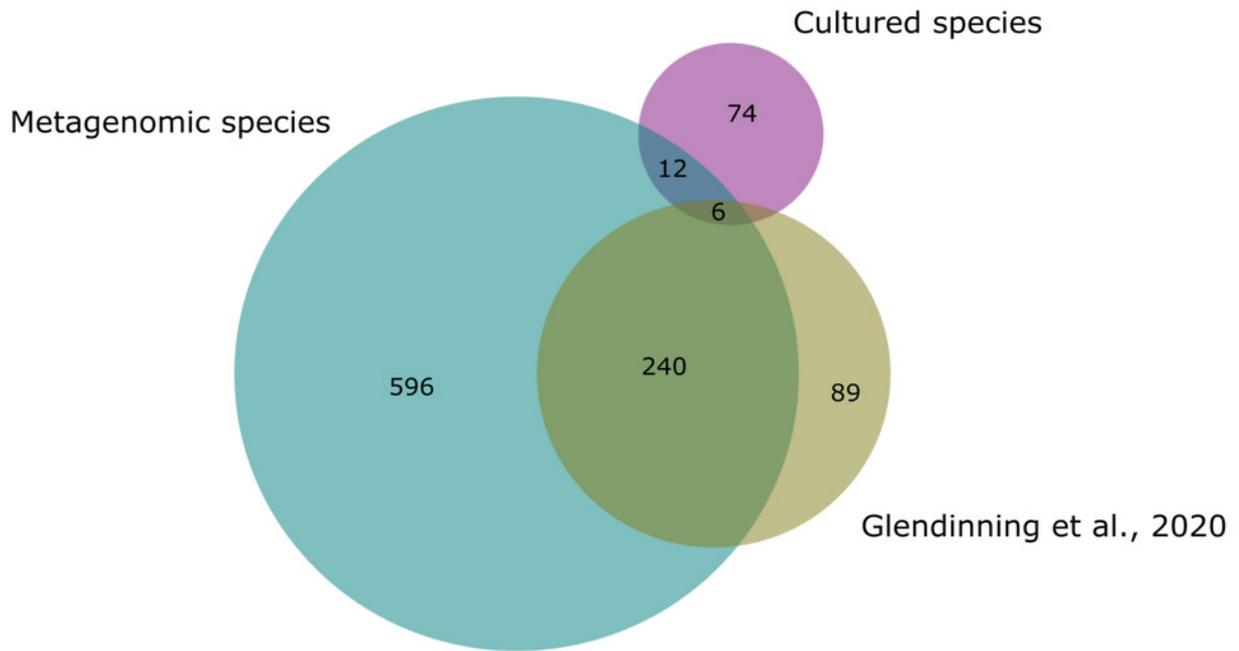
a. Venn diagram showing shared and unique taxonomic species among three data sources; cultured isolates derived from 6 chicken faecal samples (Cultured species), metagenomic species identified from a combined dataset of >630 chicken gastrointestinal metagenome samples (Metagenomic species); MAGs also found by Glendinning et al., 2020 (Glendinning et al., 2020)

b. Percentage of classified metagenomic reads derived from 50 chicken faecal samples according to a standard Kraken 2 database (Previously) and to a standard Kraken 2 database with the addition of the 2344 genomic and metagenomic sequences derived from this study (Now).

a.

Metagenomic species | Cultured species

596 | 240 | 89

Glendinning et al., 2020

b.

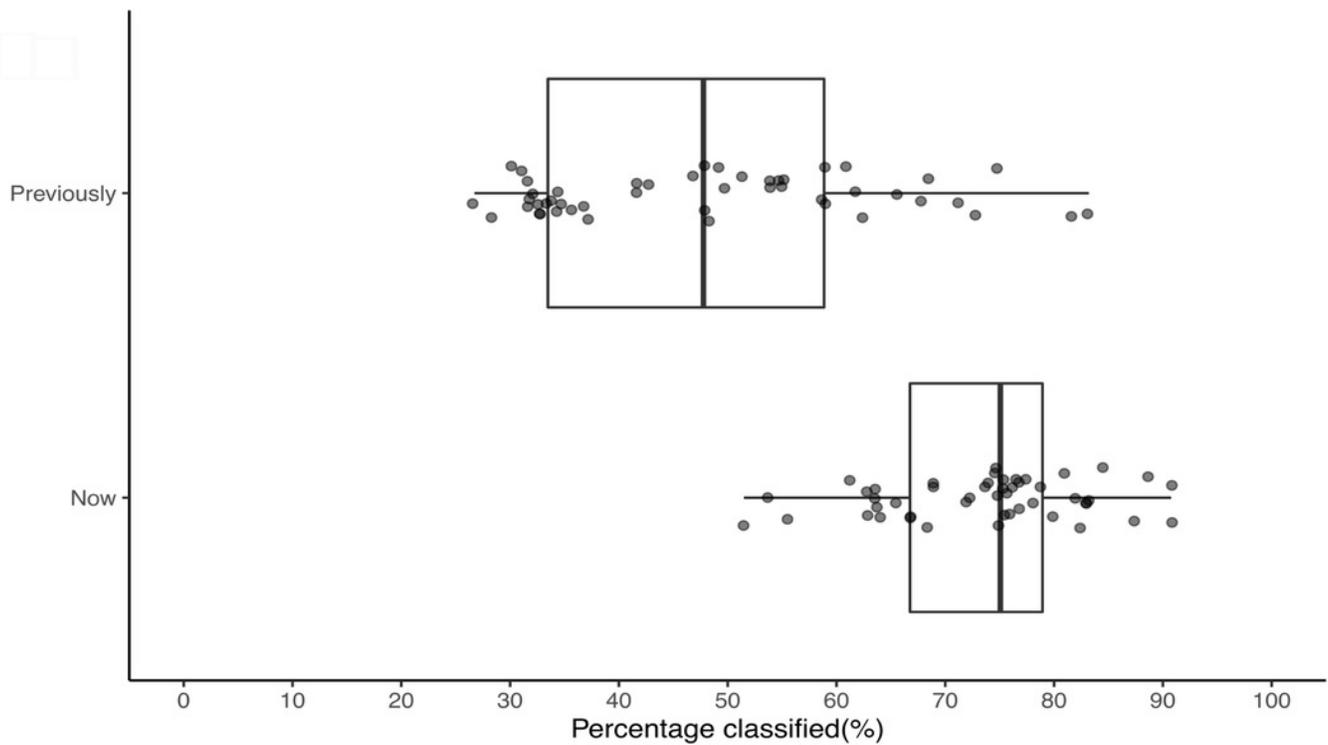



Figure 7

UpSet plots depicting presence of 820 metagenomic species across all BioProjects included within this study

a. 1x coverage

b. 10x coverage.

Bars are stacked according to taxonomic species novelty, with black-stacked bars depicting novel species and grey depicting species previously described in public databases or published studies. Only intersections with 5 or more species are shown.