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

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## ABSTRACT

**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 this 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.

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## INTRODUCTION

The domestic chicken is the most abundant bird and most abundant food animal on Earth, accounting for a larger fraction of the planet's biomass than all species of wild birds combined (Bennett et al., 2018). Consumption of chicken meat is growing faster than any other type of meat and is seen as a cheaper, healthier, low-carbon alternative to meat from mammalian livestock (Eshel et al., 2014; Willett et al., 2019). Chicken eggs remain a nutritious, affordable food across the globe (Réhault-Godbert, Guyot & Nys, 2019).

The chicken gastrointestinal tract is home to a complex community of microbes and their genes—the chicken gut microbiome—that underpins links between diet, health and productivity in poultry, as evidenced by the ability of antibiotics to promote growth in chicks (Bedford, 2000). This microbial community also acts as a source of pathogens associated with disease in birds or in humans—including *Campylobacter*, *Salmonella*, and *Escherichia coli*—as well as providing a reservoir of antimicrobial resistance genes (Florez-Cuadrado et al., 2018; Jørgensen et al., 2019; Hermans et al., 2012).

Previous studies of this community have documented a rich variety of microorganisms (dominated by bacteria, but including viruses, archaea and microbial eukaryotes) and have shown that the taxonomic composition of this community varies with age, breed and disease status (Shang et al., 2018; Rychlik, 2020). However, these earlier efforts have largely relied on analyses of molecular barcodes (in particular short 16S rRNA gene sequences), which fail to provide species-level resolution, are unable to detect viruses and reveal nothing about the genome sequences, population structures or functional repertoires of microbial species (Hillmann et al., 2018).

Two strategies have proven productive for exploring taxonomic and functional diversity in complex microbial communities (Almeida et al., 2019; Forster et al., 2019). Culture-independent approaches rely on shotgun metagenomic sequencing of DNA extracted from relevant samples, followed by bioinformatics-based community profiling and analysis (Glendinning et al., 2020; Sergeant et al., 2014). Culture-dependent approaches combine large-scale isolation of microorganisms in pure culture with whole-genome sequencing and phylogenomic analysis (Medvecky et al., 2018). To explore taxonomic novelty in the chicken gut microbiome, we generated phylogenetic profiles to document known and unknown diversity and then exploited culture-dependent and culture-independent approaches to create an unprecedented high-quality reference collection of microbial genes and genomes from the chicken gut, revealing and naming hundreds of new candidate species from this commonplace but important ecological setting.

## MATERIALS AND METHODS

### Sample collection and storage

Faecal samples were collected in South-East England from adult Lohmann Brown laying hens and adult Silkie hens in 2018. Birds were housed in a large outdoor run with a

substrate of stone chippings and small turf enrichment beds during the day and kept in a coop overnight. They were fed a commercial layer feed, Farmgate Layer pellets and mash (ForFarmers UK Limited, Rougham, Bury St Edmunds), according to the manufacturer's instructions and no antibiotics were used. Faecal sampling was approved by the University of Surrey's NASPA ethics committee.

Sixty faecal samples were collected from the Lohmann Brown laying hens and thirty samples from the Silkie hens (six and three samples per day, respectively, for 10 days). Freshly evacuated faeces from individual birds were collected in sterile containers and immediately stored at  $-20^{\circ}\text{C}$ . Samples were then transferred to the laboratory for culture and/or DNA extraction. DNA was extracted using DNeasy PowerSoil kit (Qiagen, Hilden, Germany), following manufacturer's instructions and then stored at  $-20^{\circ}\text{C}$ .

### Sequencing and subsequent workflow

Workflow from this point forward is summarised in Fig. 1. The fifty samples yielding  $>20$  ng DNA were processed according to the Low Input, Transpose Enabled (LITE) library construction pipeline (Perez-Sepulveda *et al.*, 2020) before being subjected to paired-end ( $2 \times 150$  bp) metagenomic sequencing on the Illumina Novaseq 6000 platform. Bioinformatics analyses were performed on the Earlham Institute's High Performance Computing cluster and on the Cloud Infrastructure for Microbial Bioinformatics (Connor *et al.*, 2016). Sequences were assessed for quality using FastQC Version 0.11.8 and trimmed using Trimmomatic Version 0.36, configured to a minimum read length of 40, 'leading' and 'trailing' settings of 3 (SLIDINGWINDOW:4:20) (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc>; Bolger, Lohse & Usadel, 2014). Metagenomic sequences for all samples have been uploaded to the Sequence Read Archive under Bioproject ID PRJNA543206.

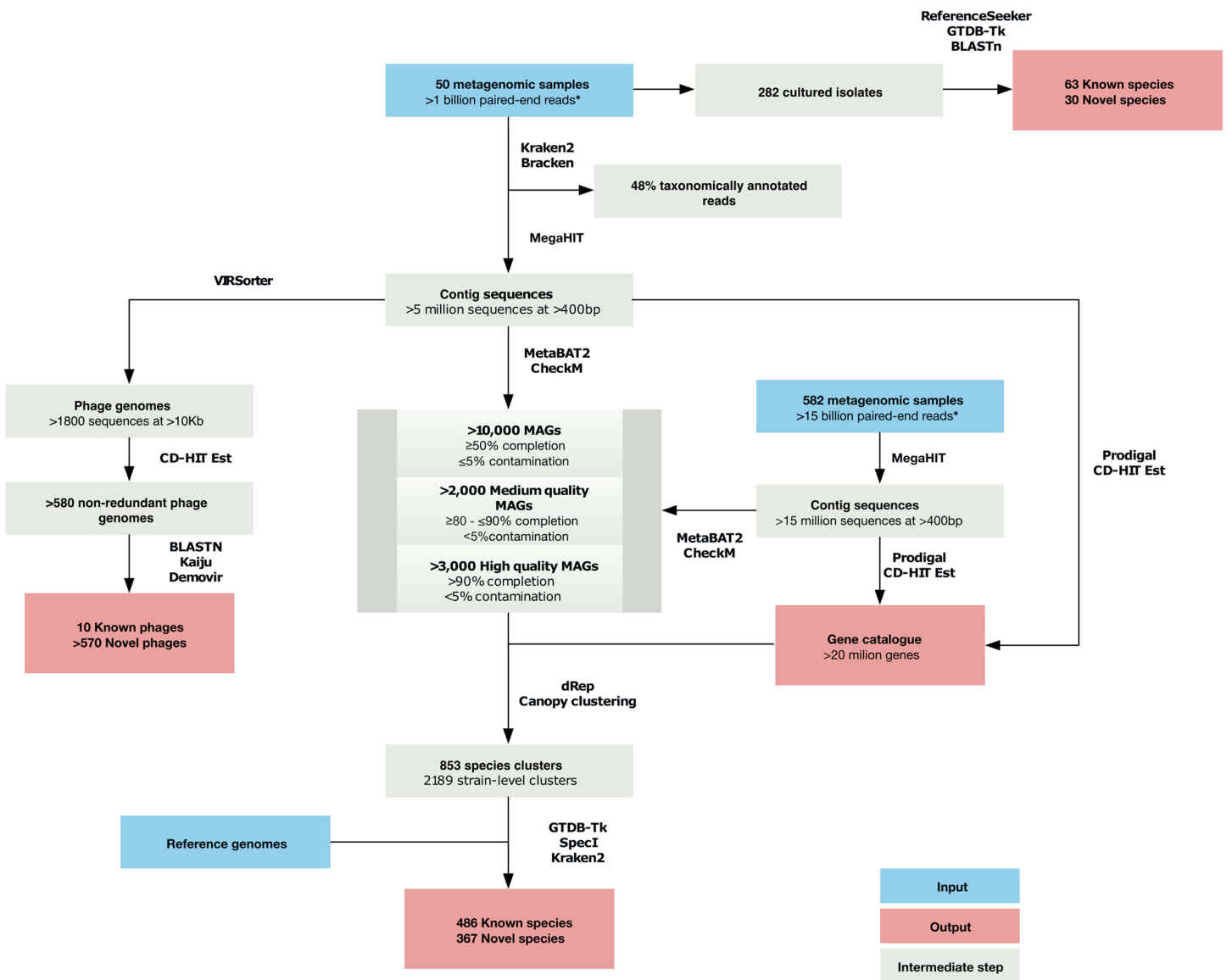
### Reference-based metagenomic analysis

An initial analysis of our chicken faecal sequences using the Kraken 2 taxonomic classifier (Wood, Lu & Langmead, 2019) was performed on custom databases representing the domestic chicken genome (GenBank assembly accession GCF\_000002315.6) and the food plants *Triticum aestivum* (wheat), *Aegilops tauschii* (diploid progenitor of the D genome of hexaploid wheat) and *Glycine max* (soy bean): GenBank assembly accessions GCF\_001957025.1, GCA\_900519105.1, GCF\_000004515.5. Kraken 2 revealed that 8% of reads originated from the chicken and at least 16% originated from the diet.

These sequences were filtered from our dataset and excluded from subsequent analyses by keeping only reads 'Unclassified' by Kraken 2 after comparison with each database in turn.

The remaining dataset underwent taxonomic profiling using Kraken 2 against a microbial database built from all complete/representative archaeal, bacterial, fungal, protozoan, viral and UniVec\_Core sequences in RefSeq (O'Leary *et al.*, 2016) in January 2020. Bracken (Lu *et al.*, 2017) was used to estimate taxon abundance from the Kraken 2 profiles, accepting only those taxa with  $\geq 1,000$  assigned reads. Bracken-database files were generated using 'bracken-build' on our microbial database and visualised using Pavian (Breitwieser & Salzberg, 2016).





**Figure 1 Analytical Workflow.** An asterisk (\*) indicates read numbers are detailed post-filtering of diet and host associated reads.

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## Metagenomic assembly

We searched the NCBI BioProjects database (<https://www.ncbi.nlm.nih.gov/bioproject/>) in November 2019 with the term ‘chicken gut microbiome’ and then selected nine publicly available projects that contained at least one metagenomic sequence dataset >1 GByte in size: PRJEB33338, PRJNA193217, PRJNA291299, PRJNA375762, PRJNA415593, PRJNA417359, PRJEB22062, PRJNA543206, PRJNA417359, PRJNA385038, PRJNA616250. Only four of these studies were linked to research publications at the time of publication (*Glendinning et al., 2020*; *Sergeant et al., 2014*; *Foster-Nyarko et al., 2020*; *Luiken et al., 2020*)

All shotgun metagenomic reads were quality-filtered by removing reads shorter than 70% of the maximum expected read length (100 bp, 250 bp for MiSeq data), an estimated accumulated error  $>2.5$  with a probability of  $\geq 0.01$  (Puente-Sánchez, Aguirre & Parro, 2016) or with an observed accumulated error  $>2$ , or  $>1$  ambiguous position to assist assembly. If base quality dropped below 20 in a window of 15 bases at the 3' end, or if the accumulated error exceeded 2, reads were trimmed. All these filter steps are integrated in sdm (Hildebrand et al., 2014). Reads mapping to the chicken genome and diet were removed from the metagenomic data as described previously, classifying reads with Kraken 2 against custom databases built on the aforementioned genomes.

Sequence datasets from our fifty samples—together with 582 samples from the selected BioProjects—were assembled using MegaHIT (Li et al., 2016) under the option '-k-list 25,43,67,87,101,127'. To avoid artefacts that sometimes result from co-assembly of sequences from different samples and different sources, we performed individual assemblies on each sample, with the exception of BioProject PRJNA417359. For that BioProject, as multiple metagenomic samples had been sourced from different tissues of the same individual bird, we co-assembled reads from the 120 BioSamples from that project.

### Bacteriophage identification and characterisation

Contig sequences from the MegaHIT assemblies of our 50 samples that were  $\geq 10$  kb were analysed with VirSorter v1.0.5 with the '-db 2' option to identify viral genomes (Roux et al., 2015). VirSorter Category 1 and 2 contig sequences were collapsed at 95% nucleotide identity over 70% of the sequence length using CD-Hit Est v4.6.1 (Fu et al., 2012). Classification of bacteriophage sequences relied on nucleotide searches using BLASTN against the NCBI NT database (Completed April 2020) and protein searches using Kaiju Version 1.7.3 against the RefSeq database (Completed April 2020) (Menzel, Ng & Krogh, 2016). Only bacteriophage genomes with BLASTN hit *E*-Value  $< 0.05$ , percentage identity  $>70\%$  and query covering  $>50\%$  were selected as reliable hits.

A taxonomic assignment was drawn from the highest scoring BLASTN (or in rare cases BLASTP) hit ranked by query cover and percentage ID. Synteny between predicted coliphages and their respective reference genomes were visualised using EasyFig (Sullivan, Petty & Beatson, 2011). *Escherichia* bacteriophage coverage per sample was determined using Anvi'o v6.1 (Eren et al., 2015) using default parameters and visualised in R using the Pheatmap package (<https://www.rdocumentation.org/packages/pheatmap>). Remaining viral genomes were filtered for completeness, retaining those that were circular and encoded a complete terminase gene (as predicted by VirSorter). Taxonomic assignments to the level of family were performed on viral genomes using Demovir (<https://github.com/feargalr/Demovir>).

### Gene catalogue

Complete genes identified by Prodigal v2.6.1 (Hyatt et al., 2010) were clustered at 95% nucleotide identity using CD-HIT-Est v4.6.1 (Fu et al., 2012). Incomplete genes were then mapped to this complete gene list using Bowtie2 v 2.3.4.1 (Langmead & Salzberg, 2012)

and any mapping at 95% nucleotide identity were incorporated into the relevant gene clusters. Finally, genes representing the 40 conserved marker genes defined by [Mende et al. \(2013\)](#) were clustered separately and then merged with the existing set of gene clusters. We thus obtained a gene catalogue of >20 million genes, defined as non-redundant at 95% average nucleotide identity (ANI). The final gene catalogue was uploaded to FigShare (<https://doi.org/10.6084/m9.figshare.13116809.v4>)

### Abundance estimates of contigs and genes

Prodigal ([Hyatt et al., 2010](#)) was applied in metagenome-mode to all contigs from the MegaHIT assemblies. Unfiltered reads from each sample were mapped against their respective assembly to provide an estimate of contig and gene abundance using Bowtie2 ([Langmead & Salzberg, 2012](#)) with the options ‘-no-unal-end-to-end -score-min L, -0.6, -0.6’. Samtools 1.3.1 was used to sort and index all resulting Bam files ([Li et al., 2009](#)). Only reads with mapping quality >20, >95% nucleotide identity and >75% overall alignment length were retained. BEDTools v2.21.0 ([Quinlan, 2014](#)) was used to create depth profiles from the Bam files. These depth profiles were then translated with rdCover (<https://github.com/hildebra/rdCover>) into average coverage (in a 50 bp window) per contig or per gene predicted from each contig. Bam files were translated to abundances using the ‘jgi\_summarize\_bam\_contig\_depths’ script from the MetaBAT 2 package ([Kang et al., 2019](#)).

Gene abundances were linked to their respective gene clusters and originating samples. Redundant genes representing the same orthologue were removed.

### Binning

We identified metagenomic species (MGSs) using the combinatorial approach described by [Hildebrand et al. \(2019\)](#), incorporating single-assembly binning in the creation of metagenome-assembled genomes (MAGs), gene catalogue binning in the creation of canopy clusters ([Nielsen et al., 2014](#)) and hierarchical clustering of candidate genes using the R function hclust, method = complete. To start with, we used MetaBAT 2 v2.15 ([Kang et al., 2019](#)) to bin contigs  $\geq 400$  bp. These were quality filtered using CheckM v1.0.11 ([Parks et al., 2015](#)) to obtain 5,595 bins at >80% completeness and <5% contamination.

Species-level clusters were formed using a combination of two distinct approaches. One approach removed redundancy between samples by pre-clustering bins if  $\geq 30\%$  of their genes overlapped with a higher-quality bin to create a set of pre-MGS bins. Lower-quality bins (>60% completeness and <10% contamination) were also included in the analysis but were not used to form new species clusters. To recover prokaryotic species usually obscured using single-sample assemblies and conventional binning techniques, we refined all species bins into ‘hcl-clusters’ using gene correlations and hierarchical clustering, as described by [Hildebrand et al. \(2019\)](#). We chose genes occurring in  $\geq 10\%$  of all associated MAGs as representatives for each pre-MGS bin and used these to fish for additional co-occurring genes from the gene catalogue, using a threshold of >0.75 Pearson correlation and >0.85 spearman rho to identify gene co-occurrences within this core gene set. We then merged MetaBAT 2 bins, canopy bins and co-occurring genes

into our species bins. We used the presence of 40 known single-copy marker genes, without duplicates, as a quality criterion in selection of sub-clusters, before extracting the final set of MGS gene representatives using MATAFILER (<https://github.com/hildebra/MATAFILER>). The final collection of MGS bins (canopy clusters + hcl-clusters) was re-assessed for contamination and completeness using CheckM (*Parks et al., 2015*), so that we could be confident that each bin represents a single species.

A second approach de-replicated all MAGs at 95% ANI (species-level) and 99% ANI (strain-level) using dRep Version 2.0 (*Olm et al., 2017*) and only species not identified in approach one were added to the resulting non-redundant species catalogue. The minimum aligned fraction used during ANI genome alignment was 60%. A single representative MAG for each novel species cluster was uploaded to NCBI SRA under BioProject PRJNA543206 and all MAGs generated were uploaded to FigShare (<https://doi.org/10.6084/m9.figshare.13116809.v4>). CompareM Version 0.1.1 (<https://github.com/dparks1134/CompareM>) was used to calculate average amino acid identity (AAI) when identifying novel genera, using a cut-off of 60% for the percentage identity and 70% for the minimum alignment length used to delineate genus boundaries.

### Taxonomy of metagenomic species

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

### Bacterial culture

To estimate species richness and diversity, the Phyloseq package of R (*R-Core-Team, 2018*) was applied to the output from Bracken (*Lu et al., 2017*) on all of our chicken faecal metagenomic datasets. The six faecal samples that showed highest species richness and taxonomic diversity were selected for culture-based studies. Frozen faecal samples were thawed, vortexed and two 0.5 g aliquots (once processed aerobically, the other anaerobically) from each sample were suspended in 5 ml PBS. Each aliquot was vortexed until homogenised, before performing serial dilutions in duplicate down to  $1 \times 10^{-5}$ .

Processing of samples for aerobic and anaerobic culture was identical, except that, for anaerobic culture, all culture media, diluent and consumables were pre-reduced to anaerobic conditions for at least 24 h before faecal samples were processed in a Whitley A95TG workstation.

For dilutions  $10^{-3}$ – $10^5$ , 200  $\mu$ l was plated directly on to a set of three agar plates for each culture medium (Brain Heart Infusion, Colombia Blood Agar, Yeast extract, casitone and fatty acid) with or without vancomycin supplementation at a concentration of 6  $\mu$ g/ml (Table S1). Cultures were incubated at 37 °C for 72 h in their respective conditions before assessment of colony growth. Well-isolated colonies were picked according to colonial morphotype distinctive in colour, shape and size, before being re-streaked on to the growth medium from which they were sourced to confirm purity. Individual colonies were subsequently used to inoculate 2 ml of broth based on the source culture medium, incubated at 37 °C for a further 24 h before bacterial DNA extraction. All isolates were archived at –80 °C in glycerol at 20% concentration.

### Genome sequencing and analysis

Genomic DNA was extracted using a DNeasy UltraClean DNA isolation kit according to the manufacturer's instructions (Qiagen, Hilden, Germany). DNA was quantified using a Qubit® fluorometer (Invitrogen, Carlsbad, CA, USA) high-sensitivity assay, before dilution to the required concentration in RNase-free water and purification on AMPure XP beads (Beckman Coulter, Brea, CA, USA). Sequencing libraries were prepared from 0.5 ng/ $\mu$ l of RNA free genomic DNA. A total of 282 isolates were included for genomic sequencing using the Nextera-Xt DNA sample preparation kit (Illumina, San Diego, CA, USA) and whole-genome sequencing performed using the Illumina NextSeq sequencing platform, generating paired-end reads (2 × 150 bp).

Paired-end reads were quality-assessed and trimmed using FastQC and Trimmomatic as described above. Trimmed reads were assembled into contigs using SPAdes version 3.13.1 (Bankevich *et al.*, 2012). Contigs shorter than 500 bp were discarded from analysis. Genome contamination and completeness was assessed using CheckM version 1.0.13. To confirm assembly quality, only genomes conforming to all the following criteria were included in further analysis: (i) contig N50 of >20 kbp (ii) 90% of assembled bases at >5× read coverage (iii) completeness of >95% (iv) contamination of <5% (v) complete 16S rRNA gene sequence.

### Genome sequence taxonomic assignment

Barrnap Version 0.9 (<https://github.com/tseemann/barrnap>) was applied to all genomes that passed the quality filters to extract full-length 16S rRNA gene sequences. These were then compared to NCBI 16S rRNA gene sequences from RefSeq genomes using the NCBI's web-based BLASTN facility (Altschul *et al.*, 1990). 16S rRNA gene sequences that showed an identity of <98.7% to known sequences were assigned to novel species, using the conservative approach in proposed minimal standards (Chun *et al.*, 2018). We used ReferenceSeeker Version 1.6.2 (Schwengers *et al.*, 2019) to determine ANI and conserved DNA values compared to RefSeq bacterial genomes (Completed March 2020)

(O'Leary *et al.*, 2016). Genomes that showed ANI  $\leq 95\%$  and conserved DNA  $\leq 69\%$  to the closest relative were designated novel species. The Genome Taxonomy Database Toolkit (GTDB-Tk Release 95) was used to perform taxonomic assignments on isolate genomes (Chaumeil *et al.*, 2019). Genomes were clustered at 95% and 99% ANI before selection of a single representative isolate per species using dRep (Olm *et al.*, 2017). Where a genome previously designated as novel clustered with a genome of assigned taxonomy, this taxonomy was then applied to the previously designated 'novel' genome. Final taxonomic assignments were based on genome-based ANI values derived from RefSeq and GTDB—with GTDB assignments taking precedence. A single representative genome for each novel or renamed species cluster was uploaded to NCBI SRA under BioProject PRJNA543206 and all genomes alongside respective 16S rRNA gene sequences generated were uploaded to FigShare (<https://doi.org/10.6084/m9.figshare.13234556>).

### Phylogenetic analysis

For phylogenetic analysis of all MGS and genome sequenced isolates we used PhyloPhlAn v3.0.58 (Asnicar *et al.*, 2020) with the 'diversity high' and a proteome input predicted from all genome sequences using Prodigal v2.6.1 (Hyatt *et al.*, 2010). Diamond v0.9.34 (Buchfink, Xie & Huson, 2015) was used to perform a search against 400 universal PhyloPhlAn markers. MAFFT v.7.271 (Katoh *et al.*, 2002) was used to perform multiple sequence alignment before refinement with trimAl v.1.4 (Capella-Gutiérrez, Silla-Martínez & Gabaldón, 2009) and reconstruction into trees using FastTree v2.1 and RAxML v. 8.2.12 (Price, Dehal & Arkin, 2010; Stamatakis, 2014). All trees were visualised and annotated manually using the online iTOLv5.7 platform (Letunic & Bork, 2016). Trees were scrutinised to confirm that species and genera were monophyletic. Phylogeny for all cultured genomes unassigned at species level was confirmed as previously described against all available reference proteomes of that respective genus downloaded from NCBI.

To investigate the phylogenetic placement of cultured isolates designated as *Escherichia marmotae* and *Escherichia* sp001660175 by GTDB, we constructed a core genome phylogenetic tree. The genomes from cultured isolates were compared to genomes representing the full diversity of the genus *Escherichia*. Three *Salmonella* genomes were included as an outgroup. The genome sequences were aligned using Mugsy (Angiuoli & Salzberg, 2011), and alignment blocks conserved across all genomes were concatenated to produce a core genome alignment. A phylogenetic tree was constructed by maximum likelihood with 100 rapid bootstrap replicates, using the general time reversible model of nucleotide substitution with gamma correction for rate heterogeneity, as implemented in RAxML version 8.2.12 (Stamatakis, 2014).

## RESULTS

### Reference-based profiling documents novel diversity

We collected faecal samples from 90 chickens reared in the UK belonging to two breeds: Lohman Browns ( $n = 60$ ) and Silkies ( $n = 30$ ). Short-read sequencing of 50 of these faecal samples generated a metagenomic dataset in excess of a billion paired-end reads or three hundred billion base pairs (Table S2).



We initially analysed the faecal samples using the k-mer-based programme Kraken 2, followed by refined phylogenetic analysis using the allied programme Bracken (Lu et al., 2017) (Table S3). Unsurprisingly, these programmes assigned sequence reads from the faecal samples to all three domains of life, as well as to viruses (Table S4), although relative abundance assignments show that bacteria predominate in this environment. Sequences were assigned to a wide range of bacterial phyla, including the three expected as predominant in the vertebrate gut (Bacteroidetes, Firmicutes, Proteobacteria), but also including over twenty additional phyla. Searches of the PubMed database with each phylum name and the term ‘chicken’ reveal that round half of these have been previously documented in the chicken gut. However, at least a dozen appear to be novel in this setting, including the *Aquificae*, *Balneolaeota*, *Calditrichaeota*, *Chlorobi*, *Dictyoglomi*, *Fibrobacteres*, *Gemmatimonadetes*, *Ignavibacteriae*, *Kiritimatiellaeota*, *Lentisphaerae*, *Nitrospirae*, and the *Thermodesulfobacteria*.

When we rank-ordered the species identified by Bracken according to maximum abundance in any one sample, we found, as expected, that species from the family *Lactobacillaceae* dominated among the top 20 most abundant organisms. However, we found that two species of *Escherichia*—*Escherichia coli* and *Escherichia marmotae*—accounted for  $\geq 5\%$  of reads in nearly half of the samples (22/50) and in two samples, accounted for more than 50%. Such monodominance of the gut microbiome by bacterial species has been described in diseased humans (Hildebrand et al., 2019; Ravi et al., 2019), but is surprising in the context of poultry reported as apparently healthy by their handlers. We also noted a high relative abundance of the recently described chicken pathogen *Gallibacterium anatis* (Narasinakuppe Krishnegowda et al., 2020) in most birds (with four birds showing  $>5\%$  reads assigned to this organism), despite their healthy status. Similarly, *Fusobacterium mortiferum*—an opportunistic pathogen of humans (Almohaya et al., 2020)—accounted for  $>10\%$  of sequences in 11 birds, corroborating a recent report of high abundance of 16S rRNA gene sequences from this organism obtained from the chicken caecum (Kollarcikova et al., 2019).

Bracken assigned sequences to over a hundred bacteriophage genomes, predominately phages infecting members of the *Enterobacteriaceae* assigned to the families *Myoviridae* and *Podoviridae*. Particularly noteworthy was the high abundance of reads in some samples from two distinct bacteriophages that prey on *E. coli*: phiEcoM-GJ1—a lytic bacteriophage isolated in Canada from pig sewage (Jamalludeen et al., 2008)—which accounted for 6.5% reads in a single sample and phAPEC8—a lytic bacteriophage with a large 147 kb genome, isolated from a Belgian poultry farm—which accounted for 10% of reads in a single sample and for  $>1\%$  of reads in three others (Tsonos et al., 2012).

Although these k-mer-based analyses can provide interesting insights into taxonomic diversity within the chicken gut, we quickly realised that they provide an incomplete and misleading picture of this important microbiome for several reasons: (1) they often report the presence of highly implausible organisms—for example, Kraken 2 reported the presence of human pathogens such as *Shigella flexneri* and *Plasmodium falciparum* that are simply not credible in this context on clinical grounds; (2) as with studies on 16S rRNA gene sequences, they fail to provide genomic data or insights into the functional

diversity or population structure of the microbial species that they identify and; (3) they rely on a reference database and so can only report previously known organisms and can never uncover ‘unknown unknowns’.

The scale of the problem of unknown diversity is clear from the observation that nearly three quarters (73%) of sequence reads from our chicken samples cannot be confidently classified by Kraken 2 to species level and more than half of the reads (52%) cannot be classified at all and are simply designated as ‘Unassigned’. We therefore sought to extend our understanding of this community through two powerful reference-free approaches: assembly-based metagenome analyses and high-throughput culture.

### Metagenomic assembly uncovers a wealth of viral diversity

Assembly of metagenomic sequences is a reference-free approach that involves aligning and merging short sequence reads into long contiguous sequences (contigs).

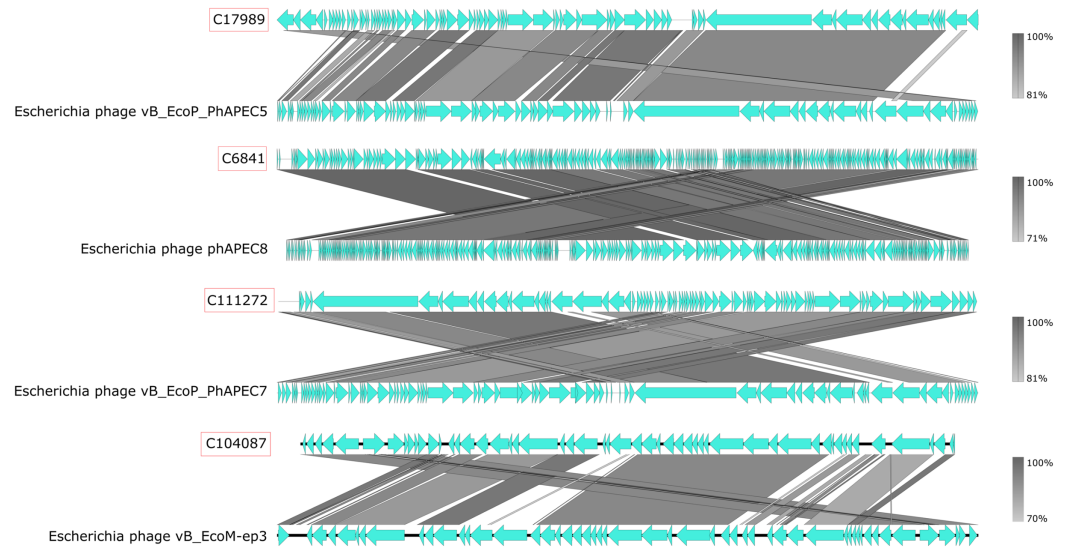
To confirm the presence of bacteriophages inferred through the reference-based analysis and to identify novel viral genomes, we assembled sequence reads from our fifty chicken faecal samples into contigs. Contigs  $\geq 10$  kb were analysed with VirSorter—a programme designed to detect viral signals in microbial sequence data to find novel viruses (Roux *et al.*, 2015).

VirSorter identified 184 of our chicken faecal contigs as Category 1 (‘most confident’) bacteriophage sequences and identified an additional 1,840 contigs as Category 2 (‘likely’) bacteriophage sequences. This was de-replicated to 1,455 genomes using similarity thresholds of 95% ANI over 70% of the genome (Table S5). BLASTN analysis revealed only 10 of these bacteriophage genomes showed high similarity (percentage identity  $> 70\%$ ; query covering  $> 50\%$ ) to known phages at the nucleotide level (Table S6). These included close relatives of the two phages (phiEcoM-GJ1 and phAPEC8) found highly abundant in the Bracken analyses (Fig. 2). Interestingly, more than one genus of coliphage (e.g. *Jilinvirus*, *Phapecoctavirus*, or *Gamaleyavirus*) was often detected in the same sample, along with an abundance of reads from their predicted prey (*Escherichia*) suggesting interesting dynamics in phage-host and phage-phage interactions (Fig. 3; Table S7).

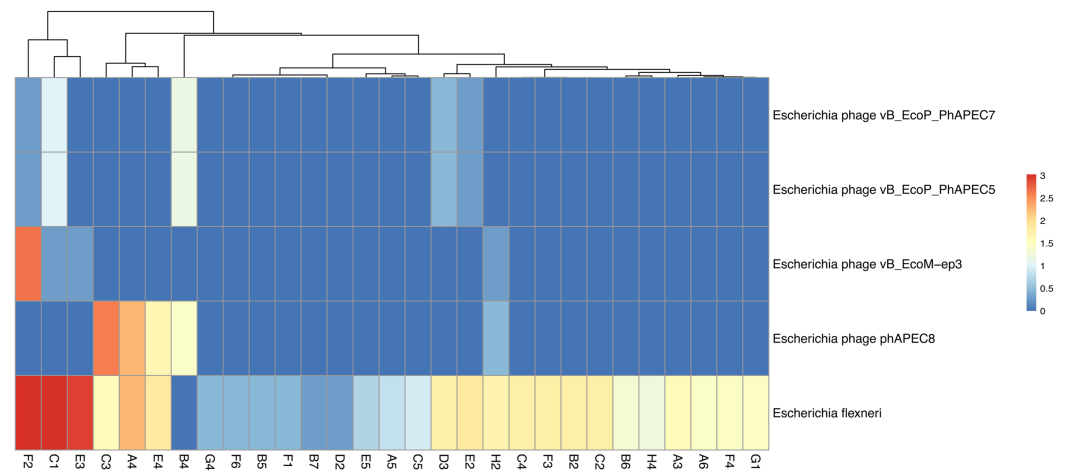
Of the remaining 1,445 unclassified bacteriophage genomes, nearly 600 encoded either an obvious terminase region or were circular and as such were suggested as being near-complete. Classification of these genomes revealed all genomes were predicted to belong to the order *Caudovirales* of tailed phages, with the majority belonging to the family *Siphoviridae* ( $n = 429$ ), but we also found representatives from the *Myoviridae* ( $n = 87$ ) and *Podoviridae* ( $n = 27$ ), plus some bacteriophages unclassified at family level ( $n = 28$ ) (Table S8).

### Remarkable microbial genome diversity in the chicken gut

Next, we subjected our samples to computational binning—a process of grouping contigs on the basis of sequence composition and depth of coverage into discrete population bins representing metagenome-assembled genomes (MAGs). However, to carry out a definitive survey of bacterial and archaeal diversity in the chicken gut microbiome—in addition to analysing the fifty faecal samples mentioned and before we started the



**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. [Full-size](#) DOI: 10.7717/peerj.10941/fig-2



**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  $\geq 1\times$  coverage are shown ( $n = 29$ ). All coverage values have been  $\text{Log}_{10}$  transformed with blue depicting low abundance and red high abundance. [Full-size](#) DOI: 10.7717/peerj.10941/fig-3

binning—we retrieved all publicly available chicken gut metagenomic datasets, to create an expansive dataset representing >630 samples, drawn from ten studies and twelve countries (Belgium, China, France, Germany, Italy, Malaysia, Netherlands, Poland, Spain, The Gambia, UK, USA) (Figs. S1A and S1B; Table S9).

Sequence assembly and binning on all these samples generated 5,595 MAGs that passed our quality threshold of  $\geq 80\%$  completion and  $\leq 5\%$  contamination (Fig. S1C). Of these 3,131 could be considered high-quality draft genomes, with  $>90\%$  completion and  $<5\%$  contamination, as judged by recently published criteria (Table S10) (Bowers *et al.*, 2017).

Genome sizes of the MAGs ranged from ~0.4 to 6.8 Mbp, while GC content ranged from 24% to 73%.

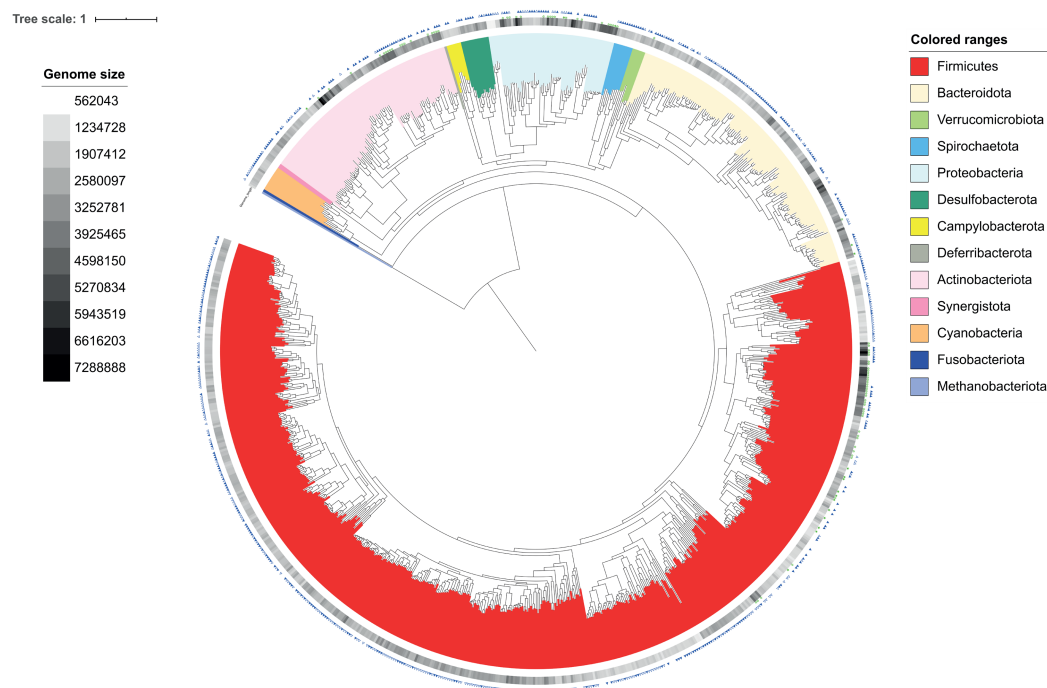
Then, we grouped the MAGs into metagenomic species (MGSs). Initially, this involved de-replicating MAGs at the widely accepted 95% average nucleotide identity (ANI) for defining bacterial and archaeal species and 99% ANI for defining bacterial and archaeal strains (Jain *et al.*, 2018; Luo, Rodriguez-R & Konstantinidis, 2014). De-replication of MAGs at 95% ANI resulted in 846 clusters representing bacterial and archaeal species, while de-replication at 99% ANI resulted in 2182 clusters, representing strains. However, to improve recovery of MAGs, MGSs and associated gene sets, we used gene correlations to identify species-representative genes and then applied hierarchical clustering to co-occurring genes across the samples. This allowed us to identify additional genes from the core genome of a species, even when they show divergent nucleotide compositions (such as genes from genomic islands and plasmids) (Hildebrand *et al.*, 2019). Similarly, using canopy clustering (Nielsen *et al.*, 2014), we could identify commonly occurring species of low abundance. Using these approaches, we were able to identify an additional seven MGSs (Table S11). These MGS were prevalent at >1× coverage in 53% of all analysed samples spanning at least 4 different BioProjects.

Analysis of bacterial metagenomic species, primarily using the Genome Taxonomy Database (GTDB) taxonomy (Parks *et al.*, 2020), confirmed and extended the taxonomic novelty uncovered by reference-based community profiling (Fig. 4), recovering species spanning nineteen of the bacterial phyla defined by GTDB (Table S12). These include *Cyanobacteria* (12 species; 32 strains); *Deferribacterota* (1 species; 1 strain) *Synergistota* (2 species; 5 strains) and the *Verrucomicrobiota* (7 species; 8 strains).

Of the 853 de-replicated bacterial metagenomic species, 321 represented previously delineated species catalogued in publicly available databases (Table S13). Following direct comparison, a further 165 metagenomic species had been previously identified by Glendinning *et al.* (2020), with these sequences not currently available in public archives. However, only 158 of our metagenomic species possess validly published names based on Latin binomials.

We performed a search of PubMed with the species name and 'chicken', leaving aside the 33 species named by Glendinning *et al.* (2020). This suggested that our study provides the first-evidence-in-chickens for the majority (81/125) of these species (Table S14). Examples include: *Jeotgalicoccus halophilus*, first isolated from the traditional fermented seafood, Jeotgal (Yoon *et al.*, 2003) and present in 197 chicken samples; *Aliicoccus persicus*, first isolated from a hypersaline lake (Amoozegar *et al.*, 2014) and present in 241 chicken samples; and *Bacteroides reticulotermitis*, first isolated from the gut of a termite (Sakamoto & Ohkuma, 2013) and present in 39 chicken samples.

We found that 309 of our metagenomic species could be assigned a taxonomy only at the level of genus and so represent novel candidate species. A further 56 species could be assigned a taxonomy only at the level of family and, after AAI clustering at 60%, were assigned to 36 novel candidate genera. One candidate bacterial species could be assigned a taxonomy only at the level of order (*Oscillospirales*) and so represent a new family.



**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 iTOLv5.7 tool including provision of a heat map according to individual genome length.

Full-size DOI: [10.7717/peerj.10941/fig-4](https://doi.org/10.7717/peerj.10941/fig-4)

Three MAGs were assigned to the domain Archaea. One represents the species *Methanobrevibacter woesei*—which is already known to inhabit the chicken gut (Saengkerdsub *et al.*, 2007)—while the other two represent novel species within the genera *Methanocorpusculum* and UBA71, which we have renamed *Candidatus* *Methanospyradousia*.

### Linnaean binomials for hundreds of new candidate species

Linnaeus first proposed the assignment of Latin binomials to provide a universal nomenclature for biological species (Linnaeus, 1759). The International Code of Nomenclature of Prokaryotes (ICNP) sets the rules for naming prokaryotic species (Parker, Tindall & Garrity, 2019), but currently precludes the valid publication of names of uncultivated organisms, represented by MAGs or other sequences. Furthermore, high-throughput generation of MAGs and of sequence-based taxonomies for bacteria,



such as the GTDB (Parks *et al.*, 2020) is often assumed to preclude the detailed attention usually given to one-by-one construction of Linnaean binomials. As a result, most uncultured taxa, as well as many taxa defined on sequence-based criteria, have been assigned unstable, confusing and hard to-remember alphanumeric identifiers.

To provide a stable, clear and memorable nomenclature for novel and/or previously unnamed bacterial and archaeal species from the chicken gut, we exploited the provision within the ICNP for naming uncultivated taxa via *Candidatus* assignments, which, although provisional, provide the scientific community with well-formed Latin binomials (Oren, 2017; Oren *et al.*, 2020). However, this prompted us into an unprecedented effort to create hundreds of new names for the purpose of this single research study—an effort that required us to devise a scalable combinatorial system for the creation of binomials. Here, we made extensive combinatorial use of several dozen Latin and Greek roots pertaining to poultry (*avi-*, *galli-*, *pulli-*, *alektryo*, *ptero*, *kotto-*, *ornitho-*), intestines (*intestini-* *entero-*), faeces (*faec-*, *kakke*, *merd-*, *kopro-*, *excrement-*) or microbial life (*-monas*, *-bacterium*, *-microbium*, *-coccus*, *-bacillus*, *-bium*, *-cola*)—twinned with addition of these roots (singly or in tandem) and/or prefixes (*allo*, *hetero*, *meta-*, *para-*, *crypto-*) to existing genus names—to create over 150 *Candidatus* genus names. For genera with alphanumeric designations in GTDB Release 05-RS95 (Parks *et al.*, 2020) known to occur also in gut microbiomes of other animals, we adopted a similar combinatorial approach, but avoided roots pertaining to poultry and stuck instead with combinations that simply meant ‘gut or faecal microbe’, for example *Fimicola*, *Caccocola*. An additional source of diversity stemmed from repetitive use of around forty *Candidatus* species epithets built from similar roots, which when combined with genus names gave us a total of over 650 distinctive binomials for new *Candidatus* species (Table 1; Table S15).

### Taxonomic diversity of cultured bacterial isolates

To extend our metagenomics analyses, we applied culture-based methods to six faecal samples that appeared species-rich in Kraken 2 analyses and in so doing obtained 282 isolates from aerobic culture (~80% of isolates) and anaerobic culture (~20% of isolates) (Table S16). All isolates underwent genome sequencing on the Illumina platform and phylogenetic analysis to enable taxonomic assignment. The resulting chicken gut culture collection was found to contain 56 genera, 93 species and 162 strains drawn from five phyla. These included thirty novel species, with all novel species confirmed to originate from a monophyletic group through phylogenetic analysis against all available reference genomes of their respective genus (Fig. S2). Curiously, there was no overlap between the species that we obtained and those reported by Medvecky *et al.* (2018), suggesting that we are far from exhausting the set of species that can be cultured from this habitat. As with the metagenomic species, all novel or previously unnamed genera and species from cultured isolates were assigned Linnaean binomials (Table 2; Table S17). Species-level ANI clustering of all MAGs and all cultured isolates according to phylum is provided in Fig. S3.

Interestingly, alongside ten cultured isolates of the well-characterised species *Escherichia coli*, we recovered three isolates from *Escherichia marmotae* (a species



**Table 1** Protologues for new *Candidatus* taxa identified from metagenomic analysis of chicken gut samples.**Description of *Candidatus Acetatifactor stercoripullorum* sp. nov.**

*Candidatus Acetatifactor stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-6426 and which is available via NCBI BioSample [SAMN15816622](#).

The GC content of the type genome is 48.46% and the genome length is 3.1 Mbp.

**Description of *Candidatus Acinetobacter avistercoris* sp. nov.**

*Candidatus Acinetobacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5402 and which is available via NCBI BioSample [SAMN15816735](#). The GC content of the type genome is 38.29% and the genome length is 3.9 Mbp.

**Description of *Candidatus Acutalibacter ornithocaccae* sp. nov.**

*Candidatus Acutalibacter ornithocaccae* (or.ni.tho.cac'cae. Gr. masc. or fem. n. *ornis*, *ornithos* bird; Gr. fem. n. *kakke* faeces; N.L. gen. n. *ornithocaccae* of bird faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcolR8-3208 and which is available via NCBI BioSample [SAMN15816822](#). This is a new name for the alphanumeric GTDB species sp000435395. The GC content of the type genome is 62.02% and the genome length is 2.1 Mbp.

**Description of *Candidatus Acutalibacter pullicola* sp. nov.**

*Candidatus Acutalibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK185-1770 and which is available via NCBI BioSample [SAMN15816590](#).

The GC content of the type genome is 58.43% and the genome length is 2.1 Mbp.

**Description of *Candidatus Acutalibacter pullistercoris* sp. nov.**

*Candidatus Acutalibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1282 and which is available via NCBI BioSample [SAMN15816718](#). The GC content of the type genome is 63.65% and the genome length is 2.0 Mbp.

**Description of *Candidatus Acutalibacter stercoravium* sp. nov.**

*Candidatus Acutalibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcolR1-495 and which is available via NCBI BioSample [SAMN15816868](#). This is a new name for the alphanumeric GTDB species sp900543555. The GC content of the type genome is 60.31% and the genome length is 2.0 Mbp.

**Description of *Candidatus Acutalibacter stercorigallinarum* sp. nov.**

*Candidatus Acutalibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-2649 and which is available via NCBI BioSample [SAMN15816629](#).

The GC content of the type genome is 63.77% and the genome length is 2.1 Mbp.

**Description of *Candidatus Agathobaculum intestinigallinarum* sp. nov.**

*Candidatus Agathobaculum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-20540 and which is available via NCBI BioSample [SAMN15816816](#).

This is a new name for the alphanumeric GTDB species sp900555465. The GC content of the type genome is 60.79% and the genome length is 2.0 Mbp.

Table 1 (continued)

**Description of *Candidatus Agathobaculum intestinipullorum* sp. nov.**

*Candidatus Agathobaculum intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec16-9926 and which is available via NCBI BioSample [SAMN15816670](#). The GC content of the type genome is 57.76% and the genome length is 1.9 Mbp.

**Description of *Candidatus Agathobaculum merdavium* sp. nov.**

*Candidatus Agathobaculum merdavium* (mer.da'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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec15-6302 and which is available via NCBI BioSample [SAMN15816712](#). The GC content of the type genome is 57.98% and the genome length is 2.0 Mbp.

**Description of *Candidatus Agathobaculum merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej1B19-3834 and which is available via NCBI BioSample [SAMN15816715](#). The GC content of the type genome is 57.98% and the genome length is 2.0 Mbp.

**Description of *Candidatus Agathobaculum merdipullorum* sp. nov.**

*Candidatus Agathobaculum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK149-1869 and which is available via NCBI BioSample [SAMN15816722](#). The GC content of the type genome is 56.28% and the genome length is 1.7 Mbp.

**Description of *Candidatus Agathobaculum pullicola* sp. nov.**

*Candidatus Agathobaculum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2940 and which is available via NCBI BioSample [SAMN15816725](#). The GC content of the type genome is 54.80% and the genome length is 2.0 Mbp.

**Description of *Candidatus Agathobaculum pullistercoris* sp. nov.**

*Candidatus Agathobaculum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK180-9785 and which is available via NCBI BioSample [SAMN15816619](#). The GC content of the type genome is 58.01% and the genome length is 2.3 Mbp.

**Description of *Candidatus Agathobaculum stercoravium* sp. nov.**

*Candidatus Agathobaculum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW21-6059 and which is available via NCBI BioSample [SAMN15816625](#). The GC content of the type genome is 59.83% and the genome length is 2.3 Mbp.

**Description of *Candidatus Agrococcus pullicola* sp. nov.**

*Candidatus Agrococcus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-98 and which is available via NCBI BioSample [SAMN15816710](#). The GC content of the type genome is 63.86% and the genome length is 3.0 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Akkermansia intestinavium* sp. nov.**

*Candidatus Akkermansia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-8097 and which is available via NCBI BioSample [SAMN15816856](#). This is a new name for the alphanumeric GTDB species sp900548895. The GC content of the type genome is 65.09% and the genome length is 2.2 Mbp.

**Description of *Candidatus Akkermansia intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 14975 and which is available via NCBI BioSample [SAMN15816742](#). The GC content of the type genome is 63.40% and the genome length is 2.1 Mbp.

**Description of *Candidatus Alectryobacillus* gen. nov.**

*Candidatus Alectryobacillus* (A.lec.try.o.ba.cil'lus. Gr. neut. n. *alektryon* chicken; L. masc. n. *bacillus* a rod; N.L. masc. n. *Alectryobacillus* a bacillus found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Alectryobacillus merdavium*. 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 *RFN20* and to the family *CAG-826*.

**Description of *Candidatus Alectryobacillus merdavium* sp. nov.**

*Candidatus Alectryobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 13038 and which is available via NCBI BioSample [SAMN15816966](#). The GC content of the type genome is 27.10% and the genome length is 1.2 Mbp.

**Description of *Candidatus Alectryococcobium* gen. nov.**

*Candidatus Alectryococcobium* (A.lec.try.o.cac.co'bi.um. Gr. neut. n. *alektryon* chicken; Gr. fem. n. *kakke* faeces; Gr. masc. n. *bios* life; N.L. neut. n. *Alectryococcobium* A life form found in chicken faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Alectryococcobium stercorigallarum*. 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 Alectryococcobium stercorigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-785 and which is available via NCBI BioSample [SAMN15816998](#). The GC content of the type genome is 46.32% and the genome length is 1.5 Mbp.

**Description of *Candidatus Alectryocaccomicrobium* gen. nov.**

*Candidatus Alectryocaccomicrobium* (A.lec.try.o.cac.co.mi.cro'bi.um. Gr. neut. n. *alektryon* chicken; Gr. fem. n. *kakke* faeces; N.L. neut. n. *microbium* a microbe; N.L. neut. n. *Alectryocaccomicrobium* A microbe found in chicken faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Alectryocaccomicrobium excrementavium*. 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 *Christensenellales* and to the family *CAG-74*.

**Description of *Candidatus Alectryocaccomicrobium excrementavium* sp. nov.**

*Candidatus Alectryocaccomicrobium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 13766 and which is available via NCBI BioSample [SAMN15816965](#). The GC content of the type genome is 59.90% and the genome length is 3.0 Mbp.

Table 1 (continued)

**Description of *Candidatus Alistipes avicola* sp. nov.**

*Candidatus Alistipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK169-11906 and which is available via NCBI BioSample [SAMN15816659](#).

The GC content of the type genome is 53.79% and the genome length is 1.6 Mbp.

**Description of *Candidatus Alistipes avistercoris* sp. nov.**

*Candidatus Alistipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 653 and which is available via NCBI BioSample [SAMN15816855](#). This is a new name for the alphanumeric GTDB species sp000434235. The GC content of the type genome is 62.33% and the genome length is 2.4 Mbp.

**Description of *Candidatus Alistipes cottocaccae* sp. nov.**

*Candidatus Alistipes cottocaccae* (cot.to.cac'cae. Gr. masc. n. *kottos* chicken Gr. fem. n. *kakke* faeces; N.L. gen. n. *cottocaccae* of chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec16-1783 and which is available via NCBI BioSample [SAMN15816853](#). This is a new name for the alphanumeric GTDB species sp002161445. The GC content of the type genome is 60.94% and the genome length is 2.4 Mbp.

**Description of *Candidatus Alistipes excrementavium* sp. nov.**

*Candidatus Alistipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK15-232 and which is available via NCBI BioSample [SAMN15816809](#). This is a new name for the alphanumeric GTDB species sp900021155. The GC content of the type genome is 61.18% and the genome length is 2.2 Mbp.

**Description of *Candidatus Alistipes excrementigallinarum* sp. nov.**

*Candidatus Alistipes excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK106-249 and which is available via NCBI BioSample [SAMN15816875](#). The GC content of the type genome is 63.33% and the genome length is 2.3 Mbp.

**Description of *Candidatus Alistipes excrementipullorum* sp. nov.**

*Candidatus Alistipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej8B7-9065 and which is available via NCBI BioSample [SAMN15816799](#). This is a new name for the alphanumeric GTDB species. The GC content of the type genome is 56.25% and the genome length is 1.7 Mbp.

**Description of *Candidatus Alistipes faecavium* sp. nov.**

*Candidatus Alistipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-19477 and which is available via NCBI BioSample [SAMN15816800](#). The GC content of the type genome is 62.24% and the genome length is 2.3 Mbp.

**Description of *Candidatus Alistipes faecigallinarum* sp. nov.**

*Candidatus Alistipes faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 6451 and which is available via NCBI BioSample [SAMN15816915](#). The GC content of the type genome is 61.37% and the genome length is 2.2 Mbp.

**Description of *Candidatus Alistipes intestinigallinarum* sp. nov.**

*Candidatus Alistipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5134 and which is available via NCBI BioSample [SAMN15816708](#). The GC content of the type genome is 59.58% and the genome length is 2.7 Mbp.

(Continued)



Table 1 (continued)

**Description of *Candidatus Alistipes intestinipullorum* sp. nov.**

*Candidatus Alistipes intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-5998 and which is available via NCBI BioSample [SAMN15816759](#). The GC content of the type genome is 59.58% and the genome length is 2.3 Mbp.

**Description of *Candidatus Alistipes merdavium* sp. nov.**

*Candidatus Alistipes merdavium* (mer.da'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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcolR5-1230 and which is available via NCBI BioSample [SAMN15816813](#). This is a new name for the alphanumeric GTDB species sp900544265. The GC content of the type genome is 63.44% and the genome length is 2.2 Mbp.

**Description of *Candidatus Alistipes merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2432 and which is available via NCBI BioSample [SAMN15816893](#). Although GTDB has assigned this species to the genus it calls *Alistipes\_A*, 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 49.96% and the genome length is 2.2 Mbp.

**Description of *Candidatus Alistipes merdipullorum* sp. nov.**

*Candidatus Alistipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej9B8-3741 and which is available via NCBI BioSample [SAMN15816807](#). This is a new name for the alphanumeric GTDB species sp900546065. The GC content of the type genome is 57.66% and the genome length is 2.3 Mbp.

**Description of *Candidatus Alistipes pullicola* sp. nov.**

*Candidatus Alistipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej10B9-11434 and which is available via NCBI BioSample [SAMN15816929](#). This is a new name for the alphanumeric GTDB species sp900546005. Although GTDB has assigned this species to the genus it calls *Alistipes\_A*, 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 52.02% and the genome length is 1.9 Mbp.

**Description of *Candidatus Alistipes pullistercoris* sp. nov.**

*Candidatus Alistipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3244 and which is available via NCBI BioSample [SAMN15816930](#). This is a new name for the alphanumeric GTDB species sp900240235. Although GTDB has assigned this species to the genus it calls *Alistipes\_A*, 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 56.88% and the genome length is 2.0 Mbp.

**Description of *Candidatus Alistipes stercoravium* sp. nov.**

*Candidatus Alistipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej8B7-9257 and which is available via NCBI BioSample [SAMN15816640](#). The GC content of the type genome is 61.39% and the genome length is 2.0 Mbp.

**Description of *Candidatus Alistipes stercorigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcolR4-13572 and which is available via NCBI BioSample [SAMN15816817](#). This is a new name for the alphanumeric GTDB species sp900542505. The GC content of the type genome is 62.42% and the genome length is 2.2 Mbp.

Table 1 (continued)

**Description of *Candidatus Alistipes stercoripullorum* sp. nov.**

*Candidatus Alistipes stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec8-6454 and which is available via NCBI BioSample [SAMN15816818](#). This is a new name for the alphanumeric GTDB species sp006542685. The GC content of the type genome is 62.87% and the genome length is 2.4 Mbp.

**Description of *Candidatus Anaerobiospirillum merdipullorum* sp. nov.**

*Candidatus Anaerobiospirillum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 687 and which is available via NCBI BioSample [SAMN15816911](#). Although GTDB has assigned this species to the genus it calls *Anaerobiospirillum\_A*, 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 49.84% and the genome length is 2.0 Mbp.

**Description of *Candidatus Anaerobiospirillum pullicola* sp. nov.**

*Candidatus Anaerobiospirillum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 378 and which is available via NCBI BioSample [SAMN15816727](#). The GC content of the type genome is 52.37% and the genome length is 3.9 Mbp.

**Description of *Candidatus Anaerobiospirillum pullistercoris* sp. nov.**

*Candidatus Anaerobiospirillum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID USASDec5-558 and which is available via NCBI BioSample [SAMN15816730](#). The GC content of the type genome is 49.01% and the genome length is 3.3 Mbp.

**Description of *Candidatus Anaerobiospirillum stercoravium* sp. nov.**

*Candidatus Anaerobiospirillum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID USASDcec2-551 and which is available via NCBI BioSample [SAMN15816778](#). The GC content of the type genome is 56.27% and the genome length is 2.9 Mbp.

**Description of *Candidatus Anaerobutyricum avicola* sp. nov.**

*Candidatus Anaerobutyricum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej6B18-9268 and which is available via NCBI BioSample [SAMN15816760](#). The GC content of the type genome is 50.20% and the genome length is 2.5 Mbp.

**Description of *Candidatus Anaerobutyricum faecale* sp. nov.**

*Candidatus Anaerobutyricum faecale* (fae.ca'le. L. neut. adj. *faecale* of faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK182-24705 and which is available via NCBI BioSample [SAMN15816814](#). This is a new name for the alphanumeric GTDB species sp002161065. The GC content of the type genome is 48.07% and the genome length is 2.8 Mbp.

**Description of *Candidatus Anaerobutyricum stercoripullorum* sp. nov.**

*Candidatus Anaerobutyricum stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej3B15-1167 and which is available via NCBI BioSample [SAMN15816729](#). The GC content of the type genome is 52.36% and the genome length is 2.3 Mbp.

**Description of *Candidatus Anaerobutyricum stercoris* sp. nov.**

*Candidatus Anaerobutyricum stercoris* (ster'co.ris. L. gen. n. *stercoris* of dung, excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK179-28034 and which is available via NCBI BioSample [SAMN15816848](#). This is a new name for the alphanumeric GTDB species sp900016875. The GC content of the type genome is 47.36% and the genome length is 3.0 Mbp.

(Continued)



Table 1 (continued)

**Description of *Candidatus Anaerofilum excrementigallinarum* sp. nov.**

*Candidatus Anaerofilum excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3951 and which is available via NCBI BioSample [SAMN15816720](#). The GC content of the type genome is 61.37% and the genome length is 2.5 Mbp.

**Description of *Candidatus Anaerofilum faecale* sp. nov.**

*Candidatus Anaerofilum faecale* (fae.ca'le. L. neut. adj. *faecale* of faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-374 and which is available via NCBI BioSample [SAMN15816865](#). This is a new name for the alphanumeric GTDB species sp002160015. The GC content of the type genome is 63.11% and the genome length is 2.3 Mbp.

**Description of *Candidatus Anaeromassilibacillus stercoravium* sp. nov.**

*Candidatus Anaeromassilibacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej5B23-4625 and which is available via NCBI BioSample [SAMN15816824](#). This is a new name for the alphanumeric GTDB species sp002159845. The GC content of the type genome is 54.17% and the genome length is 2.2 Mbp.

**Description of *Candidatus Anaerostipes avicola* sp. nov.**

*Candidatus Anaerostipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK189-27985 and which is available via NCBI BioSample [SAMN15816576](#). The GC content of the type genome is 43.22% and the genome length is 2.5 Mbp.

**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  $\geq 95\%$  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.men.ta'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  $\geq 95\%$  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  $\geq 95\%$  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  $\geq 95\%$  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.

**Description of *Candidatus Aphodenecus* gen. nov.**

*Candidatus Aphodenecus* (Aph.od.en.e'cus. Gr. fem. n. *aphodos* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Aphodenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Aphodenecus pullistercoris*. This is a name for the alphanumeric GTDB genus Spiro-01. 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 *Sphaerochaetales* and to the family *Sphaerochaetaceae*.

Table 1 (continued)

**Description of *Candidatus Aphodenecus pullistercoris* sp. nov.**

*Candidatus Aphodenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 11167 and which is available via NCBI BioSample [SAMN15817123](#). The GC content of the type genome is 59.34% and the genome length is 2.0 Mbp.

**Description of *Candidatus Aphodocola* gen. nov.**

*Candidatus Aphodocola* (Aph.o.do'co.la. Gr. fem. n. *aphodos* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Aphodocola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Aphodocola excrementigallinarum*. This is a name for the alphanumeric GTDB genus CAG-594. 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-433*.

**Description of *Candidatus Aphodocola excrementigallinarum* sp. nov.**

*Candidatus Aphodocola excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK193-30670 and which is available via NCBI BioSample [SAMN15817049](#). The GC content of the type genome is 27.74% and the genome length is 1.2 Mbp.

**Description of *Candidatus Aphodomonas* gen. nov.**

*Candidatus Aphodomonas* (Aph.o.do.mo'nas. Gr. fem. n. *aphodos* dung; L. fem. n. *monas* a monad; N.L. fem. n. *Aphodomonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Aphodomonas merdaviium*. This is a name for the alphanumeric GTDB genus SFFS01. 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 *Christensenellales* and to the family *CAG-74*.

**Description of *Candidatus Aphodomonas merdaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-35035 and which is available via NCBI BioSample [SAMN15817117](#). The GC content of the type genome is 59.45% and the genome length is 2.1 Mbp.

**Description of *Candidatus Aphodomorpha* gen. nov.**

*Candidatus Aphodomorpha* (Aph.o.do.mor'pha. Gr. fem. n. *aphodos* dung; Gr. fem. n. *morphe* a form, shape; N.L. fem. n. *Aphodomorpha* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Aphodomorpha intestinaviium*. This is a name for the alphanumeric GTDB genus UMG51241. 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 *Christensenellales* and to the family *CAG-138*.

**Description of *Candidatus Aphodomorpha intestinaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-16831 and which is available via NCBI BioSample [SAMN15817204](#). This is a new name for the alphanumeric GTDB species sp900550525. The GC content of the type genome is 68.13% and the genome length is 1.6 Mbp.

**Description of *Candidatus Aphodoplasma* gen. nov.**

*Candidatus Aphodoplasma* (Aph.o.do.plas'ma. Gr. fem. n. *aphodos* dung; Gr. neut. n. *plasma* a form; N.L. neut. n. *Aphodoplasma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Aphodoplasma excrementigallinarum*. This is a name for the alphanumeric GTDB genus UMG51253. 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 *Monoglobales\_A* and to the family *UMGS1253*.

(Continued)

Table 1 (continued)

**Description of *Candidatus Aphodoplasma excrementigallinarum* sp. nov.**

*Candidatus Aphodoplasma excrementigallinarum* (ex.cre.men.ti.galli.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 4920 and which is available via NCBI BioSample [SAMN15817155](#). The GC content of the type genome is 54.59% and the genome length is 1.8 Mbp.

**Description of *Candidatus Aphodosoma* gen. nov.**

*Candidatus Aphodosoma* (Aph.o.do.so'ma. Gr. fem. n. *aphodos* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Aphodosoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Aphodosoma intestinipullorum*. This is a name for the alphanumeric GTDB genus SFVR01. 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 *Paludibacteraceae*.

**Description of *Candidatus Aphodosoma intestinipullorum* sp. nov.**

*Candidatus Aphodosoma intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3924 and which is available via NCBI BioSample [SAMN15817132](#). The GC content of the type genome is 52.56% and the genome length is 2.4 Mbp.

**Description of *Candidatus Aphodousia* gen. nov.**

*Candidatus Aphodousia* (Aph.od.ou'si.a. Gr. fem. n. *aphodos* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Aphodousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Aphodousia faecavium*. This is a name for the alphanumeric GTDB genus CAG-521. 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 *Burkholderiales* and to the family *Burkholderiaceae*.

**Description of *Candidatus Aphodousia faecalis* sp. nov.**

*Candidatus Aphodousia faecalis* (fae.ca'lis. L. fem. adj. *faecalis* of faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW13-1064 and which is available via NCBI BioSample [SAMN15817170](#). This is a new name for the alphanumeric GTDB species sp000437635. The GC content of the type genome is 47.35% and the genome length is 1.7 Mbp.

**Description of *Candidatus Aphodousia faecavium* sp. nov.**

*Candidatus Aphodousia faecavium* (fae.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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 10345 and which is available via NCBI BioSample [SAMN15817126](#). The GC content of the type genome is 48.23% and the genome length is 1.7 Mbp.

**Description of *Candidatus Aphodousia faecigallinarum* sp. nov.**

*Candidatus Aphodousia faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 7463 and which is available via NCBI BioSample [SAMN15817137](#). The GC content of the type genome is 48.37% and the genome length is 1.5 Mbp.

**Description of *Candidatus Aphodousia faecipullorum* sp. nov.**

*Candidatus Aphodousia faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK135-12538 and which is available via NCBI BioSample [SAMN15817146](#). The GC content of the type genome is 48.08% and the genome length is 1.8 Mbp.

Table 1 (continued)

**Description of *Candidatus Aphodousia gallistercoris* sp. nov.**

*Candidatus Aphodousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK121-301 and which is available via NCBI BioSample [SAMN15817147](#). The GC content of the type genome is 52.58% and the genome length is 1.8 Mbp.

**Description of *Candidatus Aphodovivens* gen. nov.**

*Candidatus Aphodovivens* (Aph.o.do.vi'vens. Gr. fem. n. *aphodos* dung; N.L. pres. part. *vivens* living; N.L. fem. n. *Aphodovivens* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Aphodovivens avicola*. This is a name for the alphanumeric GTDB genus UMG51293. 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 *Coriobacteriales* and to the family *Eggerthellaceae*.

**Description of *Candidatus Aphodovivens avicola* sp. nov.**

*Candidatus Aphodovivens 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-21069 and which is available via NCBI BioSample [SAMN15817067](#). The GC content of the type genome is 65.54% and the genome length is 2.2 Mbp.

**Description of *Candidatus Aphodovivens avistercoris* sp. nov.**

*Candidatus Aphodovivens 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej5B5-3278 and which is available via NCBI BioSample [SAMN15817093](#). The GC content of the type genome is 66.86% and the genome length is 2.4 Mbp.

**Description of *Candidatus Aphodovivens excrementavium* sp. nov.**

*Candidatus Aphodovivens excrementavium* (ex.cre.men.ta'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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-30709 and which is available via NCBI BioSample [SAMN15817109](#). The GC content of the type genome is 58.74% and the genome length is 2.1 Mbp.

**Description of *Candidatus Aquabacterium excrementipullorum* sp. nov.**

*Candidatus Aquabacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHile3-4534 and which is available via NCBI BioSample [SAMN15816783](#). The GC content of the type genome is 67.11% and the genome length is 4.7 Mbp.

**Description of *Candidatus Atopostipes pullistercoris* sp. nov.**

*Candidatus Atopostipes 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK169-4300 and which is available via NCBI BioSample [SAMN15816688](#). The GC content of the type genome is 34.84% and the genome length is 1.9 Mbp.

**Description of *Candidatus Avacholeplasma* gen. nov.**

*Candidatus Avacholeplasma* (Av.a.cho.le.plas'ma. L. fem. n. *avis* bird; N.L. neut. n. *Acholeplasma* a genus name; N.L. neut. n. *Avacholeplasma* a genus related to the genus *Acholeplasma* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avacholeplasma faecigallinarum*. 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 *Acholeplasmatales* and to the family *Anaeroplasmataceae*.

(Continued)



Table 1 (continued)

**Description of *Candidatus Avacholeplasma faecigallinarum* sp. nov.**

*Candidatus Avacholeplasma faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3263 and which is available via NCBI BioSample [SAMN15816972](#). The GC content of the type genome is 29.88% and the genome length is 1.3 Mbp.

**Description of *Candidatus Avacidaminococcus* gen. nov.**

*Candidatus Avacidaminococcus* (Av.a.cid.a.mi.no.coc'cus. L. fem. n. *avis* bird; N.L. masc. n. *Acidaminococcus* a genus name; N.L. masc. n. *Avacidaminococcus* a genus related to the genus *Acidaminococcus* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avacidaminococcus intestinavium*. 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 *Acidaminococcales* and to the family *Acidaminococcaceae*.

**Description of *Candidatus Avacidaminococcus intestinavium* sp. nov.**

*Candidatus Avacidaminococcus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK160-1198 and which is available via NCBI BioSample [SAMN15816987](#). The GC content of the type genome is 37.45% and the genome length is 1.6 Mbp.

**Description of *Candidatus Avamphibacillus* gen. nov.**

*Candidatus Avamphibacillus* (Av.am.phi.ba.cil'lus. L. fem. n. *avis* bird; N.L. masc. n. *Amphibacillus* a genus name; N.L. masc. n. *Avamphibacillus* a genus related to the genus *Amphibacillus* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avamphibacillus intestinigallinarum*. 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 *Bacillales* and to the family *Amphibacillaceae*.

**Description of *Candidatus Avamphibacillus intestinigallinarum* sp. nov.**

*Candidatus Avamphibacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK125-3527 and which is available via NCBI BioSample [SAMN15816959](#). The GC content of the type genome is 36.77% and the genome length is 2.0 Mbp.

**Description of *Candidatus Avanaerovorax* gen. nov.**

*Candidatus Avanaerovorax* (Av.an.a.e.ro.vo'rax. L. fem. n. *avis* bird; N.L. masc. n. *Anaerovorax* a genus name; N.L. masc. n. *Avanaerovorax* a genus related to the genus *Anaerovorax* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avanaerovorax faecigallinarum*. 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 *Peptostreptococcales* and to the family *Anaerovoracaceae*.

**Description of *Candidatus Avanaerovorax faecigallinarum* sp. nov.**

*Candidatus Avanaerovorax faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID Gambia13-1450 and which is available via NCBI BioSample [SAMN15816994](#). The GC content of the type genome is 48.68% and the genome length is 1.8 Mbp.

**Description of *Candidatus Aveggerthella* gen. nov.**

*Candidatus Aveggerthella* (Av.eg.ger.thel'la. L. fem. n. *avis* bird; N.L. fem. n. *Eggerthella* a genus name; N.L. fem. n. *Aveggerthella* a genus related to the genus *Eggerthella* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Aveggerthella excrementigallinarum*. 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 *Coriobacteriales* and to the family *Eggerthellaceae*.

Table 1 (continued)

**Description of *Candidatus Aveggerthella excrementigallinarum* sp. nov.**

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

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

**Description of *Candidatus Aveggerthella stercoripullorum* sp. nov.**

*Candidatus Aveggerthella stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-2707 and which is available via NCBI BioSample [SAMN15816950](#). The GC content of the type genome is 61.50% and the genome length is 2.1 Mbp.

**Description of *Candidatus Avelusimicrobium* gen. nov.**

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

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avelusimicrobium excrementipullorum*. 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 *Elusimicrobiales* and to the family *Elusimicrobiaceae*.

**Description of *Candidatus Avelusimicrobium excrementipullorum* sp. nov.**

*Candidatus Avelusimicrobium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK136-6324 and which is available via NCBI BioSample [SAMN15817002](#). The GC content of the type genome is 53.46% and the genome length is 1.3 Mbp.

**Description of *Candidatus Avibacteroides* gen. nov.**

*Candidatus Avibacteroides* (A.vi.bac.te.ro'i.des. L. fem. n. *avis* bird; N.L. masc. n. *Bacteroides* a genus name; N.L. masc. n. *Avibacteroides* a genus related to the genus *Bacteroides* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avibacteroides excrementipullorum*. 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 *Bacteroidaceae*.

**Description of *Candidatus Avibacteroides avistercoris* sp. nov.**

*Candidatus Avibacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID MalCec1-1739 and which is available via NCBI BioSample [SAMN15816974](#). The GC content of the type genome is 53.14% and the genome length is 2.2 Mbp.

**Description of *Candidatus Avibacteroides excrementipullorum* sp. nov.**

*Candidatus Avibacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-16860 and which is available via NCBI BioSample [SAMN15816958](#). The GC content of the type genome is 47.79% and the genome length is 2.2 Mbp.

**Description of *Candidatus Avibacteroides faecavium* sp. nov.**

*Candidatus Avibacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3702 and which is available via NCBI BioSample [SAMN15816980](#). The GC content of the type genome is 55.42% and the genome length is 2.1 Mbp.

(Continued)



Table 1 (continued)

**Description of *Candidatus Avichristensenella* gen. nov.**

*Candidatus Avichristensenella* (A.vi.chris.ten.sen.el'la. L. fem. n. *avis* bird; N.L. fem. n. *Christensenella* a genus name; N.L. fem. n. *Avichristensenella* a genus related to the genus *Christensenella* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avichristensenella intestinipullorum*. 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 *Christensenellales* and to the family *CAG-74*.

**Description of *Candidatus Avichristensenella intestinipullorum* sp. nov.**

*Candidatus Avichristensenella intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHile30-977 and which is available via NCBI BioSample SAMN15816947. The GC content of the type genome is 63.80% and the genome length is 2.3 Mbp.

**Description of *Candidatus Avidahalobacter* gen. nov.**

*Candidatus Avidahalobacter* (A.vi.de.ha.lo.bac'ter. L. fem. n. *avis* bird; N.L. masc. n. *Dehalobacter* a genus name; N.L. masc. n. *Avidahalobacter* a genus related to the genus *Dehalobacter* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avidahalobacter gallistercoris*. 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 *UBA4068* and to the family *UBA5755*.

**Description of *Candidatus Avidahalobacter gallistercoris* sp. nov.**

*Candidatus Avidahalobacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2830 and which is available via NCBI BioSample SAMN15816981. The GC content of the type genome is 52.20% and the genome length is 1.4 Mbp.

**Description of *Candidatus Avidesulfovibrio* gen. nov.**

*Candidatus Avidesulfovibrio* (A.vi.de.sul.fo.vi'bri.o. L. fem. n. *avis* bird; N.L. masc. n. *Desulfovibrio* a genus name; N.L. masc. n. *Avidesulfovibrio* a genus related to the genus *Desulfovibrio* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avidesulfovibrio excrementigallarinarum*. 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 *Desulfovibrionales* and to the family *Desulfovibrionaceae*.

**Description of *Candidatus Avidesulfovibrio excrementigallarinarum* sp. nov.**

*Candidatus Avidesulfovibrio excrementigallarinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallarinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHccc4-2777 and which is available via NCBI BioSample SAMN15816982. The GC content of the type genome is 60.70% and the genome length is 2.2 Mbp.

**Description of *Candidatus Avigastranaerophilus* gen. nov.**

*Candidatus Avigastranaerophilus* (A.vi.gastr.an.a.e.ro'phi.li.s. L. fem. n. *avis* bird; N.L. masc. n. *Gastranaerophilus* a genus name; N.L. masc. n. *Avigastranaerophilus* a genus related to the genus *Gastranaerophilus* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avigastranaerophilus faecigallarinarum*. 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 *Gastranaerophilales* and to the family *Gastranaerophilaceae*.

**Description of *Candidatus Avigastranaerophilus faecigallarinarum* sp. nov.**

*Candidatus Avigastranaerophilus faecigallarinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallarinarum* of hen faeces)

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

**Description of *Candidatus Avilachnospira* gen. nov.**

*Candidatus Avilachnospira* (A.vi.lach.no.spi'ra. L. fem. n. *avis* bird; N.L. fem. n. *Lachnospira* a genus name; N.L. fem. n. *Avilachnospira* a genus related to the genus *Lachnospira* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avilachnospira avistercoris*. 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*.

Table 1 (continued)

**Description of *Candidatus Avilachnospira avicola* sp. nov.**

*Candidatus Avilachnospira 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec3B27-5021 and which is available via NCBI BioSample [SAMN15816990](#). The GC content of the type genome is 49.15% and the genome length is 1.6 Mbp.

**Description of *Candidatus Avilachnospira avistercoris* sp. nov.**

*Candidatus Avilachnospira 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej5B5-15814 and which is available via NCBI BioSample [SAMN15816991](#). The GC content of the type genome is 50.02% and the genome length is 1.6 Mbp.

**Description of *Candidatus Avimonoglobus* gen. nov.**

*Candidatus Avimonoglobus* (A.vi.mo.no.glo'bus. L. fem. n. *avis* bird; N.L. masc. n. *Monoglobus* a genus name; N.L. masc. n. *Avimonoglobus* a genus related to the genus *Monoglobus* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avimonoglobus intestinipullorum*. 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 *Monoglobales\_A* and to the family *UBA1381*.

**Description of *Candidatus Avimonoglobus intestinipullorum* sp. nov.**

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

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

**Description of *Candidatus Avimuribaculum* gen. nov.**

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

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avimuribaculum pullicola*. 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 *Muribaculaceae*.

**Description of *Candidatus Avimuribaculum pullicola* sp. nov.**

*Candidatus Avimuribaculum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec3B27-9160 and which is available via NCBI BioSample [SAMN15816969](#). The GC content of the type genome is 47.58% and the genome length is 2.2 Mbp.

**Description of *Candidatus Aviproponibacterium* gen. nov.**

*Candidatus Aviproponibacterium* (A.vi.pro.pi.o.ni.bac.te'ri.um. L. fem. n. *avis* bird; N.L. neut. n. *Propionibacterium* a genus name; N.L. neut. n. *Aviproponibacterium* a genus related to the genus *Propionibacterium* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Aviproponibacterium avicola*. 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 *Propionibacteriales* and to the family *Propionibacteriaceae*.

**Description of *Candidatus Aviproponibacterium avicola* sp. nov.**

*Candidatus Aviproponibacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-24693 and which is available via NCBI BioSample [SAMN15816979](#). The GC content of the type genome is 69.14% and the genome length is 3.2 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Avirkenella* gen. nov.**

*Candidatus Avirkenella* (A.vi.ri.ke.nel'la. L. fem. n. *avis* bird; N.L. fem. n. *Rikenella* a genus name; N.L. fem. n. *Avirkenella* a genus related to the genus *Rikenella* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avirkenella pullistercoris*. 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 *Rikenellaceae*.

**Description of *Candidatus Avirkenella pullistercoris* sp. nov.**

*Candidatus Avirkenella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 9321 and which is available via NCBI BioSample SAMN15816960. The GC content of the type genome is 41.91% and the genome length is 1.9 Mbp.

**Description of *Candidatus Avisuccinivibrio* gen. nov.**

*Candidatus Avisuccinivibrio* (A.vi.suc.ci.ni.vi'bri.o. L. fem. n. *avis* bird; N.L. masc. n. *Succinivibrio* a genus name; N.L. masc. n. *Avisuccinivibrio* a genus related to the genus *Succinivibrio* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avisuccinivibrio stercorigallinarum*. 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 *Enterobacterales* and to the family *Succinivibrionaceae*.

**Description of *Candidatus Avisuccinivibrio pullicola* sp. nov.**

*Candidatus Avisuccinivibrio 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3820 and which is available via NCBI BioSample SAMN15816999. The GC content of the type genome is 55.94% and the genome length is 2.4 Mbp.

**Description of *Candidatus Avisuccinivibrio stercorigallinarum* sp. nov.**

*Candidatus Avisuccinivibrio 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 17213 and which is available via NCBI BioSample SAMN15817000. The GC content of the type genome is 54.49% and the genome length is 2.4 Mbp.

**Description of *Candidatus Avitreponema* gen. nov.**

*Candidatus Avitreponema* (A.vi.tre.po.ne'ma. L. fem. n. *avis* bird; N.L. neut. n. *Treponema* a genus name; N.L. neut. n. *Avitreponema* a genus related to the genus *Treponema* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avitreponema avistercoris*. 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 *Treponematales* and to the family *Treponemataceae*.

**Description of *Candidatus Avitreponema avistercoris* sp. nov.**

*Candidatus Avitreponema 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B3-4054 and which is available via NCBI BioSample SAMN15816977. The GC content of the type genome is 55.36% and the genome length is 1.9 Mbp.

**Description of *Candidatus Avoscollospira* gen. nov.**

*Candidatus Avoscollospira* (Av.os.cil.lo.spi'ra. L. fem. n. *avis* bird; N.L. fem. n. *Oscillospira* a genus name; N.L. fem. n. *Avoscollospira* a genus related to the genus *Oscillospira* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Avoscollospira stercorigallinarum*. 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*.

Table 1 (continued)

**Description of *Candidatus Avoscollospira avicola* sp. nov.**

*Candidatus Avoscollospira 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec15-4380 and which is available via NCBI BioSample [SAMN15816934](#). The GC content of the type genome is 61.76% and the genome length is 2.5 Mbp.

**Description of *Candidatus Avoscollospira avistercoris* sp. nov.**

*Candidatus Avoscollospira 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec16-1751 and which is available via NCBI BioSample [SAMN15816964](#). The GC content of the type genome is 58.00% and the genome length is 2.4 Mbp.

**Description of *Candidatus Avoscollospira stercorigallinarum* sp. nov.**

*Candidatus Avoscollospira 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej2B20-13462 and which is available via NCBI BioSample [SAMN15816948](#). The GC content of the type genome is 63.01% and the genome length is 2.2 Mbp.

**Description of *Candidatus Avoscollospira stercoripullorum* sp. nov.**

*Candidatus Avoscollospira stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej9B8-7071 and which is available via NCBI BioSample [SAMN15816951](#). The GC content of the type genome is 60.69% and the genome length is 1.9 Mbp.

**Description of *Candidatus Bacteroides avicola* sp. nov.**

*Candidatus Bacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-9795 and which is available via NCBI BioSample [SAMN15816830](#). This is a new name for the alphanumeric GTDB species sp002160055. The GC content of the type genome is 50.12% and the genome length is 3.0 Mbp.

**Description of *Candidatus Bacteroides intestinavium* sp. nov.**

*Candidatus Bacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec1B25-7008 and which is available via NCBI BioSample [SAMN15816665](#). The GC content of the type genome is 54.17% and the genome length is 2.6 Mbp.

**Description of *Candidatus Bacteroides intestinigallinarum* sp. nov.**

*Candidatus Bacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2926 and which is available via NCBI BioSample [SAMN15816831](#). This is a new name for the alphanumeric GTDB species sp003463205. The GC content of the type genome is 41.82% and the genome length is 5.8 Mbp.

**Description of *Candidatus Bacteroides intestinipullorum* sp. nov.**

*Candidatus Bacteroides intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B3-3758 and which is available via NCBI BioSample [SAMN15816671](#). The GC content of the type genome is 53.99% and the genome length is 2.7 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Bacteroides merdavium* sp. nov.**

*Candidatus Bacteroides merdavium* (mer.da.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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK118-2852 and which is available via NCBI BioSample [SAMN15816687](#). The GC content of the type genome is 49.76% and the genome length is 2.9 Mbp.

**Description of *Candidatus Bacteroides merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej9B8-1298 and which is available via NCBI BioSample [SAMN15816694](#). The GC content of the type genome is 54.52% and the genome length is 2.7 Mbp.

**Description of *Candidatus Bacteroides merdipullorum* sp. nov.**

*Candidatus Bacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-24981 and which is available via NCBI BioSample [SAMN15816699](#). The GC content of the type genome is 53.73% and the genome length is 2.5 Mbp.

**Description of *Candidatus Bacteroides pullicola* sp. nov.**

*Candidatus Bacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID Gambia2-208 and which is available via NCBI BioSample [SAMN15816704](#). The GC content of the type genome is 55.18% and the genome length is 2.7 Mbp.

**Description of *Candidatus Bariatricus faecipullorum* sp. nov.**

*Candidatus Bariatricus faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 9095 and which is available via NCBI BioSample [SAMN15816662](#). The GC content of the type genome is 51.54% and the genome length is 2.5 Mbp.

**Description of *Candidatus Barnesiella excrementavium* sp. nov.**

*Candidatus Barnesiella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 4398 and which is available via NCBI BioSample [SAMN15816714](#). The GC content of the type genome is 52.73% and the genome length is 2.7 Mbp.

**Description of *Candidatus Barnesiella excrementigallarum* sp. nov.**

*Candidatus Barnesiella excrementigallarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK169-14362 and which is available via NCBI BioSample [SAMN15816739](#). The GC content of the type genome is 47.04% and the genome length is 2.6 Mbp.

**Description of *Candidatus Barnesiella excrementipullorum* sp. nov.**

*Candidatus Barnesiella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-16260 and which is available via NCBI BioSample [SAMN15816862](#). This is a new name for the alphanumeric GTDB species sp900542255. The GC content of the type genome is 50.69% and the genome length is 2.1 Mbp.



**Table 1 (continued)****Description of *Candidatus Barnesiella merdigallarum* sp. nov.**

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

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

**Description of *Candidatus Barnesiella merdipullorum* sp. nov.**

*Candidatus Barnesiella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5648 and which is available via NCBI BioSample [SAMN15816849](#). This is a new name for the alphanumeric GTDB species sp002161555. The GC content of the type genome is 52.62% and the genome length is 2.6 Mbp.

**Description of *Candidatus Bilophila faecipullorum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxje5B17-1746 and which is available via NCBI BioSample [SAMN15816754](#). The GC content of the type genome is 63.22% and the genome length is 2.8 Mbp.

**Description of *Candidatus Blautia avicola* sp. nov.**

*Candidatus Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec6-4105 and which is available via NCBI BioSample [SAMN15816794](#). The GC content of the type genome is 46.40% and the genome length is 3.1 Mbp.

**Description of *Candidatus Blautia avistercoris* sp. nov.**

*Candidatus Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5548 and which is available via NCBI BioSample [SAMN15816924](#). This is a new name for the alphanumeric GTDB species sp002159835. Although GTDB has assigned this species to the genus it calls *Blautia\_A*, 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 45.38% and the genome length is 2.5 Mbp.

**Description of *Candidatus Blautia excrementigallarum* sp. nov.**

*Candidatus Blautia excrementigallarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSje6B24-370 and which is available via NCBI BioSample [SAMN15816894](#). Although GTDB has assigned this species to the genus it calls *Blautia\_A*, 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 49.44% and the genome length is 2.3 Mbp.

**Description of *Candidatus Blautia excrementipullorum* sp. nov.**

*Candidatus Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK197-7439 and which is available via NCBI BioSample [SAMN15816885](#). Although GTDB has assigned this species to the genus it calls *Blautia\_A*, 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 46.79% and the genome length is 3.3 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Blautia faecavium* sp. nov.**

*Candidatus* Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSje1B19-5720 and which is available via NCBI BioSample [SAMN15816886](#). Although GTDB has assigned this species to the genus it calls Blautia\_A, 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 45.35% and the genome length is 3.5 Mbp.

**Description of *Candidatus Blautia faecigallinarum* sp. nov.**

*Candidatus* Blautia faecigallinarum (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 14324 and which is available via NCBI BioSample [SAMN15816901](#). Although GTDB has assigned this species to the genus it calls Blautia\_A, 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 48.52% and the genome length is 2.9 Mbp.

**Description of *Candidatus Blautia faecipullorum* sp. nov.**

*Candidatus* Blautia faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxje6B18-2004 and which is available via NCBI BioSample [SAMN15816906](#). Although GTDB has assigned this species to the genus it calls Blautia\_A, 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 48.18% and the genome length is 3.5 Mbp.

**Description of *Candidatus Blautia gallistercoris* sp. nov.**

*Candidatus* Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSje1B19-8411 and which is available via NCBI BioSample [SAMN15816925](#). This is a new name for the alphanumeric GTDB species sp900542045. Although GTDB has assigned this species to the genus it calls Blautia\_A, 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 48.96% and the genome length is 2.8 Mbp.

**Description of *Candidatus Blautia intestinavium* sp. nov.**

*Candidatus* Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK186-553 and which is available via NCBI BioSample [SAMN15816890](#). Although GTDB has assigned this species to the genus it calls Blautia\_A, 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 47.27% and the genome length is 2.8 Mbp.

**Description of *Candidatus Blautia intestinigallinarum* sp. nov.**

*Candidatus* Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK186-9876 and which is available via NCBI BioSample [SAMN15816891](#). Although GTDB has assigned this species to the genus it calls Blautia\_A, 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 46.77% and the genome length is 2.7 Mbp.

**Description of *Candidatus Blautia intestinipullorum* sp. nov.**

*Candidatus* Blautia intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW16-4312 and which is available via NCBI BioSample [SAMN15816892](#). Although GTDB has assigned this species to the genus it calls Blautia\_A, 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 47.05% and the genome length is 2.4 Mbp.

Table 1 (continued)

**Description of *Candidatus Blautia merdavium* sp. nov.**

*Candidatus* Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec2-3848 and which is available via NCBI BioSample [SAMN15816633](#). The GC content of the type genome is 48.60% and the genome length is 3.3 Mbp.

**Description of *Candidatus Blautia merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej6B18-287 and which is available via NCBI BioSample [SAMN15816815](#). This is a new name for the alphanumeric GTDB species sp900543715. The GC content of the type genome is 45.18% and the genome length is 3.3 Mbp.

**Description of *Candidatus Blautia merdipullorum* sp. nov.**

*Candidatus* Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 17058 and which is available via NCBI BioSample [SAMN15816655](#). The GC content of the type genome is 45.05% and the genome length is 3.2 Mbp.

**Description of *Candidatus Blautia ornithocaccae* sp. nov.**

*Candidatus* Blautia ornithocaccae (or.ni.tho.cac'cae. Gr. masc. or fem. n. *ornis*, *ornithos* bird Gr. fem. n. *kakke* faeces; N.L. gen. n. *ornithocaccae* of bird faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec1-3711 and which is available via NCBI BioSample [SAMN15816880](#). This is a new name for the alphanumeric GTDB species sp002161285. The GC content of the type genome is 44.79% and the genome length is 3.1 Mbp.

**Description of *Candidatus Blautia pullicola* sp. nov.**

*Candidatus* Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1068 and which is available via NCBI BioSample [SAMN15816689](#). The GC content of the type genome is 45.62% and the genome length is 3.0 Mbp.

**Description of *Candidatus Blautia pullistercoris* sp. nov.**

*Candidatus* Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-1927 and which is available via NCBI BioSample [SAMN15816618](#). The GC content of the type genome is 45.73% and the genome length is 3.2 Mbp.

**Description of *Candidatus Blautia stercoravium* sp. nov.**

*Candidatus* Blautia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3268 and which is available via NCBI BioSample [SAMN15816738](#). The GC content of the type genome is 44.17% and the genome length is 2.7 Mbp.

**Description of *Candidatus Blautia stercorigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-9823 and which is available via NCBI BioSample [SAMN15816627](#). The GC content of the type genome is 45.83% and the genome length is 3.1 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Blautia stercoripullorum* sp. nov.**

*Candidatus* Blautia stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW19-6364 and which is available via NCBI BioSample [SAMN15816793](#). The GC content of the type genome is 44.78% and the genome length is 3.1 Mbp.

**Description of *Candidatus Borkfalkia avicola* sp. nov.**

*Candidatus* Borkfalkia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK192-19661 and which is available via NCBI BioSample [SAMN15816606](#). The GC content of the type genome is 58.92% and the genome length is 1.7 Mbp.

**Description of *Candidatus Borkfalkia avistercoris* sp. nov.**

*Candidatus* Borkfalkia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK187-5294 and which is available via NCBI BioSample [SAMN15816607](#). The GC content of the type genome is 53.99% and the genome length is 1.7 Mbp.

**Description of *Candidatus Borkfalkia excrementavium* sp. nov.**

*Candidatus* Borkfalkia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK199-9574 and which is available via NCBI BioSample [SAMN15816608](#). The GC content of the type genome is 52.76% and the genome length is 1.6 Mbp.

**Description of *Candidatus Borkfalkia excrementigallarum* sp. nov.**

*Candidatus* Borkfalkia excrementigallarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1345 and which is available via NCBI BioSample [SAMN15816609](#). The GC content of the type genome is 53.42% and the genome length is 1.9 Mbp.

**Description of *Candidatus Borkfalkia excrementipullorum* sp. nov.**

*Candidatus* Borkfalkia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK192-2667 and which is available via NCBI BioSample [SAMN15816611](#). The GC content of the type genome is 55.63% and the genome length is 1.6 Mbp.

**Description of *Candidatus Borkfalkia faecavium* sp. nov.**

*Candidatus* Borkfalkia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2189 and which is available via NCBI BioSample [SAMN15816731](#). The GC content of the type genome is 58.98% and the genome length is 1.7 Mbp.

**Description of *Candidatus Borkfalkia faecigallarum* sp. nov.**

*Candidatus* Borkfalkia faecigallarum (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 26628 and which is available via NCBI BioSample [SAMN15816617](#). The GC content of the type genome is 62.49% and the genome length is 1.6 Mbp.

Table 1 (continued)

**Description of *Candidatus Borkfalkia faecipullorum* sp. nov.**

*Candidatus Borkfalkia faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 811 and which is available via NCBI BioSample [SAMN15816621](#). The GC content of the type genome is 54.29% and the genome length is 1.9 Mbp.

**Description of *Candidatus Borkfalkia stercoripullorum* sp. nov.**

*Candidatus Borkfalkia stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK196-13738 and which is available via NCBI BioSample [SAMN15816588](#). The GC content of the type genome is 55.22% and the genome length is 1.8 Mbp.

**Description of *Candidatus Brachy bacterium intestinipullorum* sp. nov.**

*Candidatus Brachy bacterium intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK130-7132 and which is available via NCBI BioSample [SAMN15816812](#). This is a new name for the alphanumeric GTDB species sp003711805. The GC content of the type genome is 72.59% and the genome length is 3.5 Mbp.

**Description of *Candidatus Brachy bacterium merdaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej13B12-24818 and which is available via NCBI BioSample [SAMN15816666](#). The GC content of the type genome is 70.22% and the genome length is 3.7 Mbp.

**Description of *Candidatus Brachy bacterium merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej13B12-7362 and which is available via NCBI BioSample [SAMN15816717](#). The GC content of the type genome is 71.16% and the genome length is 3.1 Mbp.

**Description of *Candidatus Brevibacterium intestinaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5295 and which is available via NCBI BioSample [SAMN15816668](#). The GC content of the type genome is 66.76% and the genome length is 3.2 Mbp.

**Description of *Candidatus Brevibacterium intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK132-2174 and which is available via NCBI BioSample [SAMN15816673](#). The GC content of the type genome is 70.54% and the genome length is 2.7 Mbp.

**Description of *Candidatus Butyricococcus avicola* sp. nov.**

*Candidatus Butyricococcus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej6B24-14740 and which is available via NCBI BioSample [SAMN15816587](#). The GC content of the type genome is 59.67% and the genome length is 2.0 Mbp.

(Continued)



Table 1 (continued)

**Description of *Candidatus Butyricoccus avistercoris* sp. nov.**

*Candidatus* Butyricoccus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK193-4272 and which is available via NCBI BioSample [SAMN15816626](#). The GC content of the type genome is 35.60% and the genome length is 2.0 Mbp.

**Description of *Candidatus Butyricoccus stercorigallinarum* sp. nov.**

*Candidatus* Butyricoccus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHeccec2B26-12929 and which is available via NCBI BioSample [SAMN15816912](#). Although GTDB has assigned this species to the genus it calls *Butyricoccus\_A*, 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 62.06% and the genome length is 2.1 Mbp.

**Description of *Candidatus Butyricimonas faecavium* sp. nov.**

*Candidatus* Butyricimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK27-1272 and which is available via NCBI BioSample [SAMN15816676](#). The GC content of the type genome is 40.60% and the genome length is 3.6 Mbp.

**Description of *Candidatus Caccalectryoclostridium* gen. nov.**

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

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Caccalectryoclostridium excrementigallinarum. 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 *Christensenellales* and to the family *UBA3700*.

**Description of *Candidatus Caccalectryoclostridium excrementigallinarum* sp. nov.**

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

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

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

*Candidatus* Caccenecus (Cacc.en.e'cus. Gr. fem. n. *kakke* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Caccenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Caccenecus avistercoris. This is a name for the alphanumeric GTDB genus CAG-776. 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-1000*.

**Description of *Candidatus Caccenecus avistercoris* sp. nov.**

*Candidatus* Caccenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK193-13418 and which is available via NCBI BioSample [SAMN15817030](#). The GC content of the type genome is 28.47% and the genome length is 1.3 Mbp.

**Description of *Candidatus Caccocola* gen. nov.**

*Candidatus* Caccocola (Cac.co'co.la. Gr. fem. n. *kakke* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Caccocola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Caccocola faecigallinarum. This is a name for the alphanumeric GTDB genus An23. 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 *Synergistales* and to the family *Synergistaceae*.

Table 1 (continued)

**Description of *Candidatus Caccocola faecigallinarum* sp. nov.**

*Candidatus Caccocola faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej11B10-3130 and which is available via NCBI BioSample [SAMN15817215](#). This is a new name for the alphanumeric GTDB species sp900544635. The GC content of the type genome is 60.31% and the genome length is 2.3 Mbp.

**Description of *Candidatus Caccocola faecipullorum* sp. nov.**

*Candidatus Caccocola faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcec3-7374 and which is available via NCBI BioSample [SAMN15817103](#). The GC content of the type genome is 59.08% and the genome length is 2.2 Mbp.

**Description of *Candidatus Caccomonas* gen. nov.**

*Candidatus Caccomonas* (Cac.co.mo'nas. Gr. fem. n. *kakke* dung; L. fem. n. *monas* a monad; N.L. fem. n. *Caccomonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Caccomonas pullistercoris*. This is a name for the alphanumeric GTDB genus CAG-617. 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 *Bacteroidaceae*.

**Description of *Candidatus Caccomonas pullistercoris* sp. nov.**

*Candidatus Caccomonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5345 and which is available via NCBI BioSample [SAMN15817152](#). The GC content of the type genome is 59.45% and the genome length is 2.2 Mbp.

**Description of *Candidatus Caccomorpha* gen. nov.**

*Candidatus Caccomorpha* (Cac.co.mor'pha. Gr. fem. n. *kakke* dung; Gr. fem. n. *morphe* a form, shape; N.L. fem. n. *Caccomorpha* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Caccomorpha excrementavium*. This is a name for the alphanumeric GTDB genus SZUA-448. 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 Caccomorpha excrementavium* sp. nov.**

*Candidatus Caccomorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1999 and which is available via NCBI BioSample [SAMN15817145](#). The GC content of the type genome is 50.75% and the genome length is 2.7 Mbp.

**Description of *Candidatus Caccoplasma* gen. nov.**

*Candidatus Caccoplasma* (Cac.co.plas'ma. Gr. fem. n. *kakke* dung; Gr. neut. n. *plasma* a form; N.L. neut. n. *Caccoplasma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Caccoplasma merdaviium*. This is a name for the alphanumeric GTDB genus UBA11471. 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 UBA11471.

**Description of *Candidatus Caccoplasma intestinavium* sp. nov.**

*Candidatus Caccoplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 21143 and which is available via NCBI BioSample [SAMN15817187](#). This is a new name for the alphanumeric GTDB species sp000434215. The GC content of the type genome is 45.83% and the genome length is 2.4 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Caccoplasma merdavium* sp. nov.**

*Candidatus Caccoplasma merdavium* (mer.d.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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 6821 and which is available via NCBI BioSample [SAMN15817190](#). This is a new name for the alphanumeric GTDB species sp900542765. The GC content of the type genome is 52.79% and the genome length is 2.4 Mbp.

**Description of *Candidatus Caccoplasma merdipullorum* sp. nov.**

*Candidatus Caccoplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID G3-4614 and which is available via NCBI BioSample [SAMN15817135](#). The GC content of the type genome is 46.70% and the genome length is 2.0 Mbp.

**Description of *Candidatus Caccopulliclostridium* gen. nov.**

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

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Caccopulliclostridium gallistercoris*. This genus was identified but not named by [Glendinning et al. \(2020\)](#). 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 *UBA1242*.

**Description of *Candidatus Caccopulliclostridium gallistercoris* sp. nov.**

*Candidatus Caccopulliclostridium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK186-9395 and which is available via NCBI BioSample [SAMN15816943](#). The GC content of the type genome is 35.40% and the genome length is 1.0 Mbp.

**Description of *Candidatus Caccosoma* gen. nov.**

*Candidatus Caccosoma* (Cac.co.so'ma. Gr. fem. n. *kakke* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Caccosoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Caccosoma faecigallarum*. This is a name for the alphanumeric GTDB genus CAG-631. 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 *RFN20* and to the family *CAG-631*.

**Description of *Candidatus Caccosoma faecigallarum* sp. nov.**

*Candidatus Caccosoma faecigallarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 14508 and which is available via NCBI BioSample [SAMN15817185](#). This is a new name for the alphanumeric GTDB species sp000433015. The GC content of the type genome is 30.38% and the genome length is 1.3 Mbp.

**Description of *Candidatus Caccousia* gen. nov.**

*Candidatus Caccousia* (Cacc.ou'si.a. Gr. fem. n. *kakke* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Caccousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Caccousia avicola*. This is a name for the alphanumeric GTDB genus An200. 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 *Acutalibacteraceae*.

**Description of *Candidatus Caccousia avicola* sp. nov.**

*Candidatus Caccousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej1B13-7958 and which is available via NCBI BioSample [SAMN15817070](#). The GC content of the type genome is 58.28% and the genome length is 2.2 Mbp.

Table 1 (continued)

**Description of *Candidatus Caccousia avistercoris* sp. nov.**

*Candidatus Caccousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3024 and which is available via NCBI BioSample [SAMN15817047](#). The GC content of the type genome is 60.88% and the genome length is 2.6 Mbp.

**Description of *Candidatus Caccousia stercoris* sp. nov.**

*Candidatus Caccousia stercoris* (ster'co.ris. L. gen. n. *stercoris* of dung, excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 6086 and which is available via NCBI BioSample [SAMN15817184](#). This is a new name for the alphanumeric GTDB species sp002160025. The GC content of the type genome is 56.84% and the genome length is 2.3 Mbp.

**Description of *Candidatus Caccovicinus* gen. nov.**

*Candidatus Caccovicinus* (Cac.co.vi.ci'nus. Gr. fem. n. *kakke* dung; L. masc. n. *vicinus* a neighbour; N.L. masc. n. *Caccovicinus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Caccovicinus merdipullorum*. This is a name for the alphanumeric GTDB genus UMGs1370. 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 Caccovicinus merdipullorum* sp. nov.**

*Candidatus Caccovicinus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK198\_11255 and which is available via NCBI BioSample [SAMN15817041](#). The GC content of the type genome is 50.44% and the genome length is 3.0 Mbp.

**Description of *Candidatus Caccovivens* gen. nov.**

*Candidatus Caccovivens* (Cac.co.vi'vens. Gr. fem. n. *kakke* dung; N.L. pres. part. *vivens* living; N.L. fem. n. *Caccovivens* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Caccovivens faecavium*. This is a name for the alphanumeric GTDB genus UBA11517. 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 *Christensenellales* and to the family *UBA1242*.

**Description of *Candidatus Caccovivens faecavium* sp. nov.**

*Candidatus Caccovivens 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW6-1002 and which is available via NCBI BioSample [SAMN15817119](#). The GC content of the type genome is 34.22% and the genome length is 1.1 Mbp.

**Description of *Candidatus Cellulosilyticum pullistercoris* sp. nov.**

*Candidatus Cellulosilyticum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B5-657 and which is available via NCBI BioSample [SAMN15816752](#). The GC content of the type genome is 33.78% and the genome length is 2.3 Mbp.

**Description of *Candidatus Choladocola* gen. nov.**

*Candidatus Choladocola* (Cho.la.do'co.la. Gr. fem. n. *cholas* guts; L. suff. *-cola* inhabitant of; N.L. fem. n. *Choladocola* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Choladocola avistercoris*. This is a name for the alphanumeric GTDB genus UBA7182. 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*.

(Continued)



Table 1 (continued)

**Description of *Candidatus Chladocola avistercoris* sp. nov.**

*Candidatus Chladocola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec18-1958 and which is available via NCBI BioSample [SAMN15817180](#). This is a new name for the alphanumeric GTDB species sp002160135. The GC content of the type genome is 50.79% and the genome length is 2.4 Mbp.

**Description of *Candidatus Chladousia* gen. nov.**

*Candidatus Chladousia* (Cho.lad.ou'si.a. Gr. fem. n. *cholas* guts; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Chladousia* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Chladousia intestinavium*. This is a name for the alphanumeric GTDB genus UBA7160. 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 Chladousia intestinavium* sp. nov.**

*Candidatus Chladousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej4B22-8148 and which is available via NCBI BioSample [SAMN15817012](#). The GC content of the type genome is 49.57% and the genome length is 2.9 Mbp.

**Description of *Candidatus Chladousia intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec11-13528 and which is available via NCBI BioSample [SAMN15817065](#). The GC content of the type genome is 48.69% and the genome length is 3.1 Mbp.

**Description of *Candidatus Chladousia intestinipullorum* sp. nov.**

*Candidatus Chladousia intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej5B23-16397 and which is available via NCBI BioSample [SAMN15817078](#). The GC content of the type genome is 50.54% and the genome length is 2.2 Mbp.

**Description of *Candidatus Collinsella stercoripullorum* sp. nov.**

*Candidatus Collinsella stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-20822 and which is available via NCBI BioSample [SAMN15816681](#). The GC content of the type genome is 68.61% and the genome length is 2.3 Mbp.

**Description of *Candidatus Companilactobacillus pullicola* sp. nov.**

*Candidatus Companilactobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3204 and which is available via NCBI BioSample [SAMN15816700](#). The GC content of the type genome is 35.87% and the genome length is 2.9 Mbp.

**Description of *Candidatus Coprenecus* gen. nov.**

*Candidatus Coprenecus* (Copr.en.e'cus. Gr. fem. n. *kopros* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Coprenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Coprenecus pullicola*. This is a name for the alphanumeric GTDB genus CAG-831. 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*.



**Table 1 (continued)****Description of *Candidatus Coprenecus avistercoris* sp. nov.**

*Candidatus Coprenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej13B12-12457 and which is available via NCBI BioSample [SAMN15817175](#). This is a new name for the alphanumeric GTDB species sp000432775. The GC content of the type genome is 56.44% and the genome length is 2.0 Mbp.

**Description of *Candidatus Coprenecus merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecolR1B25-18470 and which is available via NCBI BioSample [SAMN15817066](#). The GC content of the type genome is 55.94% and the genome length is 2.2 Mbp.

**Description of *Candidatus Coprenecus merdipullorum* sp. nov.**

*Candidatus Coprenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID Gambia11-1358 and which is available via NCBI BioSample [SAMN15817068](#). The GC content of the type genome is 54.29% and the genome length is 2.1 Mbp.

**Description of *Candidatus Coprenecus pullicola* sp. nov.**

*Candidatus Coprenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej9B8-15444 and which is available via NCBI BioSample [SAMN15817077](#). The GC content of the type genome is 52.53% and the genome length is 2.1 Mbp.

**Description of *Candidatus Coprenecus pullistercoris* sp. nov.**

*Candidatus Coprenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID Gambia18-42 and which is available via NCBI BioSample [SAMN15817084](#). The GC content of the type genome is 52.64% and the genome length is 2.0 Mbp.

**Description of *Candidatus Coprenecus stercoravium* sp. nov.**

*Candidatus Coprenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID Gambia16-554 and which is available via NCBI BioSample [SAMN15817085](#). The GC content of the type genome is 51.84% and the genome length is 1.8 Mbp.

**Description of *Candidatus Coprenecus stercorigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3382 and which is available via NCBI BioSample [SAMN15817086](#). The GC content of the type genome is 53.66% and the genome length is 2.1 Mbp.

**Description of *Candidatus Coprenecus stercoripullorum* sp. nov.**

*Candidatus Coprenecus stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 7141 and which is available via NCBI BioSample [SAMN15817115](#). The GC content of the type genome is 50.92% and the genome length is 1.7 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Coprocola* gen. nov.**

*Candidatus Coprocola* (Co.pro'co.la. Gr. fem. n. *kopros* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Coprocola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Coprocola pullicola*. This is a name for the alphanumeric GTDB genus ASF356. 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 *Anaerotignaceae*.

**Description of *Candidatus Coprocola pullicola* sp. nov.**

*Candidatus Coprocola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK193-15662 and which is available via NCBI BioSample SAMN15817043. The GC content of the type genome is 33.91% and the genome length is 3.0 Mbp.

**Description of *Candidatus Copromonas* gen. nov.**

*Candidatus Copromonas* (Co.pro.mo'nas. Gr. fem. n. *kopros* dung; L. fem. n. *monas* a monad; N.L. fem. n. *Copromonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Copromonas avistercoris*. This is a name for the alphanumeric GTDB genus CAG-81. 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 Copromonas avistercoris* sp. nov.**

*Candidatus Copromonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSje3B21-5768 and which is available via NCBI BioSample SAMN15817005. The GC content of the type genome is 52.88% and the genome length is 2.2 Mbp.

**Description of *Candidatus Copromonas faecavium* sp. nov.**

*Candidatus Copromonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK180-2868 and which is available via NCBI BioSample SAMN15817009. The GC content of the type genome is 50.20% and the genome length is 2.7 Mbp.

**Description of *Candidatus Copromorpha* gen. nov.**

*Candidatus Copromorpha* (Co.pro.mor'pha. Gr. fem. n. *kopros* dung; Gr. fem. n. *morphe* a form, shape; N.L. fem. n. *Copromorpha* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Copromorpha excrementavium*. This is a name for the alphanumeric GTDB genus UBA1191. 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 *Peptostreptococcales* and to the family *Anaerovoracaceae*.

**Description of *Candidatus Copromorpha excrementavium* sp. nov.**

*Candidatus Copromorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK176-22527 and which is available via NCBI BioSample SAMN15817193. This is a new name for the alphanumeric GTDB species sp900542385. The GC content of the type genome is 42.88% and the genome length is 1.8 Mbp.

**Description of *Candidatus Copromorpha excrementigallinarum* sp. nov.**

*Candidatus Copromorpha excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcc3-6078 and which is available via NCBI BioSample SAMN15817131. The GC content of the type genome is 48.15% and the genome length is 2.0 Mbp.

Table 1 (continued)

**Description of *Candidatus Copromorpha excrementipullorum* sp. nov.**

*Candidatus Copromorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjeJ4B22-8349 and which is available via NCBI BioSample [SAMN15817205](#). This is a new name for the alphanumeric GTDB species sp900543485. The GC content of the type genome is 49.77% and the genome length is 1.9 Mbp.

**Description of *Candidatus Coproplasma* gen. nov.**

*Candidatus Coproplasma* (Co.pro.plas'ma. Gr. fem. n. *kopros* dung; Gr. neut. n. *plasma* a form; N.L. neut. n. *Coproplasma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Coproplasma stercoravium*. This is a name for the alphanumeric GTDB genus UBA11940. 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 *Christensenellales* and to the family *Borkfalkiaceae*.

**Description of *Candidatus Coproplasma avicola* sp. nov.**

*Candidatus Coproplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW16-3235 and which is available via NCBI BioSample [SAMN15817075](#). The GC content of the type genome is 51.11% and the genome length is 1.5 Mbp.

**Description of *Candidatus Coproplasma avistercoris* sp. nov.**

*Candidatus Coproplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW7-3743 and which is available via NCBI BioSample [SAMN15817023](#). The GC content of the type genome is 56.32% and the genome length is 1.4 Mbp.

**Description of *Candidatus Coproplasma excrementavium* sp. nov.**

*Candidatus Coproplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK179-18245 and which is available via NCBI BioSample [SAMN15817045](#). The GC content of the type genome is 50.26% and the genome length is 1.4 Mbp.

**Description of *Candidatus Coproplasma excrementigallarum* sp. nov.**

*Candidatus Coproplasma excrementigallarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-12923 and which is available via NCBI BioSample [SAMN15817050](#). The GC content of the type genome is 50.00% and the genome length is 1.4 Mbp.

**Description of *Candidatus Coproplasma excrementipullorum* sp. nov.**

*Candidatus Coproplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 10570 and which is available via NCBI BioSample [SAMN15817148](#). The GC content of the type genome is 51.24% and the genome length is 1.7 Mbp.

**Description of *Candidatus Coproplasma stercoravium* sp. nov.**

*Candidatus Coproplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK180-19203 and which is available via NCBI BioSample [SAMN15817006](#). The GC content of the type genome is 51.86% and the genome length is 1.6 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Coproplasma stercorigallinarum* sp. nov.**

*Candidatus Coproplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK191-24566 and which is available via NCBI BioSample [SAMN15817171](#). This is a new name for the alphanumeric GTDB species sp900549005. The GC content of the type genome is 51.83% and the genome length is 1.6 Mbp.

**Description of *Candidatus Coproplasma stercoripullorum* sp. nov.**

*Candidatus Coproplasma stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW25-3613 and which is available via NCBI BioSample [SAMN15817071](#). The GC content of the type genome is 51.17% and the genome length is 1.7 Mbp.

**Description of *Candidatus Coprosoma* gen. nov.**

*Candidatus Coprosoma* (Co.pro.so'ma. Gr. fem. n. *kopros* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Coprosoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Coprosoma intestinipullorum*. This is a name for the alphanumeric GTDB genus CAG-822. 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-822.

**Description of *Candidatus Coprosoma intestinipullorum* sp. nov.**

*Candidatus Coprosoma intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK147-3167 and which is available via NCBI BioSample [SAMN15817008](#). The GC content of the type genome is 31.20% and the genome length is 1.3 Mbp.

**Description of *Candidatus Coprousia* gen. nov.**

*Candidatus Coprousia* (Copr.ou'si.a. Gr. fem. n. *kopros* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Coprousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Coprousia avicola*. This is a name for the alphanumeric GTDB genus An7. 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 *Coriobacteriales* and to the family *Coriobacteriaceae*.

**Description of *Candidatus Coprousia avicola* sp. nov.**

*Candidatus Coprousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej11B10-5566 and which is available via NCBI BioSample [SAMN15817195](#). This is a new name for the alphanumeric GTDB species sp002159765. The GC content of the type genome is 65.47% and the genome length is 2.4 Mbp.

**Description of *Candidatus Coprovicinus* gen. nov.**

*Candidatus Coprovicinus* (Co.pro.vi.ci'nus. Gr. fem. n. *kopros* dung; L. masc. n. *vicinus* a neighbour; N.L. masc. n. *Coprovicinus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Coprovicinus avistercoris*. This is a name for the alphanumeric GTDB genus UMG51418. 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 *Coriobacteriales* and to the family *Atopobiaceae*.

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

*Candidatus Coprovicinus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-29160 and which is available via NCBI BioSample [SAMN15817198](#). This is a new name for the alphanumeric GTDB species sp900551595. The GC content of the type genome is 49.51% and the genome length is 1.7 Mbp.

Table 1 (continued)

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

*Candidatus Coprovivens* (Co.pro.vi'vens. Gr. fem. n. *kopros* dung; N.L. pres. part. *vivens* living; N.L. fem. n. *Coprovivens* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Coprovivens excrementavium*. This is a name for the alphanumeric GTDB genus UBA11963. 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-1000.

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

*Candidatus Coprovivens 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3297 and which is available via NCBI BioSample SAMN15817083. The GC content of the type genome is 28.25% and the genome length is 2.2 Mbp.

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

*Candidatus Corynebacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK32-1732 and which is available via NCBI BioSample SAMN15816750. The GC content of the type genome is 66.95% and the genome length is 3.1 Mbp.

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

*Candidatus Corynebacterium faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej13B12-4958 and which is available via NCBI BioSample SAMN15816631. The GC content of the type genome is 66.91% and the genome length is 2.8 Mbp.

**Description of *Candidatus Corynebacterium faecipullorum* sp. nov.**

*Candidatus Corynebacterium faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 913 and which is available via NCBI BioSample SAMN15816858. This is a new name for the alphanumeric GTDB species sp001836165. The GC content of the type genome is 61.16% and the genome length is 2.1 Mbp.

**Description of *Candidatus Corynebacterium gallistercoris* sp. nov.**

*Candidatus Corynebacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 4376 and which is available via NCBI BioSample SAMN15816747. The GC content of the type genome is 62.96% and the genome length is 2.0 Mbp.

**Description of *Candidatus Corynebacterium intestinavium* sp. nov.**

*Candidatus Corynebacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5925 and which is available via NCBI BioSample SAMN15816787. The GC content of the type genome is 65.59% and the genome length is 1.9 Mbp.

**Description of *Candidatus Cottocaccamicrobium* gen. nov.**

*Candidatus Cottocaccamicrobium* (Cot.to.cac.co.mi.cro'bi.um. Gr. masc. n. *kottos* chicken; Gr. fem. n. *kakke* faeces; N.L. neut. n. *microbium* a microbe; N.L. neut. n. *Cottocaccamicrobium* a microbe associated with chicken faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Cottocaccamicrobium excrementipullorum*. This genus was identified but not named by Glendinning et al. (2020). 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.

(Continued)



Table 1 (continued)

**Description of *Candidatus Cottocaccommicrobium excrementipullorum* sp. nov.**

*Candidatus Cottocaccommicrobium 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  $\geq 95\%$  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  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus 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  $\geq 95\%$  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)

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

**Description of *Candidatus Cryptobacteroides excrementavium* sp. nov.**

*Candidatus Cryptobacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B2-16538 and which is available via NCBI BioSample [SAMN15817059](#). The GC content of the type genome is 50.29% and the genome length is 2.1 Mbp.

**Description of *Candidatus Cryptobacteroides excrementigallinarum* sp. nov.**

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

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

**Description of *Candidatus Cryptobacteroides excrementipullorum* sp. nov.**

*Candidatus Cryptobacteroides excrementipullorum* (ex.cre.men.ti.pul.lo'rum. L. neut. n. *excrementum* excrement; L. masc. gen. pl. n. *pullorum* of young chickens; 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2478 and which is available via NCBI BioSample [SAMN15817061](#). The GC content of the type genome is 52.35% and the genome length is 2.5 Mbp.

**Description of *Candidatus Cryptobacteroides faecavium* sp. nov.**

*Candidatus Cryptobacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B2-22910 and which is available via NCBI BioSample [SAMN15817063](#). The GC content of the type genome is 52.41% and the genome length is 2.4 Mbp.

Table 1 (continued)

**Description of *Candidatus Cryptobacteroides faecigallinarum* sp. nov.**

*Candidatus Cryptobacteroides faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B1-13419 and which is available via NCBI BioSample [SAMN15817072](#). The GC content of the type genome is 49.87% and the genome length is 2.0 Mbp.

**Description of *Candidatus Cryptobacteroides faecipullorum* sp. nov.**

*Candidatus Cryptobacteroides faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B1-15692 and which is available via NCBI BioSample [SAMN15817080](#). The GC content of the type genome is 49.55% and the genome length is 2.3 Mbp.

**Description of *Candidatus Cryptobacteroides gallistercoris* sp. nov.**

*Candidatus Cryptobacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID F1-3629 and which is available via NCBI BioSample [SAMN15817088](#). The GC content of the type genome is 51.79% and the genome length is 2.0 Mbp.

**Description of *Candidatus Cryptobacteroides intestinavium* sp. nov.**

*Candidatus Cryptobacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B1-20833 and which is available via NCBI BioSample [SAMN15817087](#). The GC content of the type genome is 51.51% and the genome length is 2.4 Mbp.

**Description of *Candidatus Cryptobacteroides intestinigallinarum* sp. nov.**

*Candidatus Cryptobacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B1-3475 and which is available via NCBI BioSample [SAMN15817089](#). The GC content of the type genome is 49.55% and the genome length is 2.3 Mbp.

**Description of *Candidatus Cryptobacteroides intestinipullorum* sp. nov.**

*Candidatus Cryptobacteroides intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 33258 and which is available via NCBI BioSample [SAMN15817090](#). The GC content of the type genome is 50.60% and the genome length is 2.4 Mbp.

**Description of *Candidatus Cryptobacteroides merdavium* sp. nov.**

*Candidatus Cryptobacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID D5-748 and which is available via NCBI BioSample [SAMN15817104](#). The GC content of the type genome is 50.98% and the genome length is 2.5 Mbp.

**Description of *Candidatus Cryptobacteroides merdigallinarum* sp. nov.**

*Candidatus Cryptobacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 20514 and which is available via NCBI BioSample [SAMN15817110](#). The GC content of the type genome is 54.69% and the genome length is 2.3 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Cryptobacteroides merdipullorum* sp. nov.**

*Candidatus Cryptobacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec2B26-709 and which is available via NCBI BioSample [SAMN15817116](#). The GC content of the type genome is 57.16% and the genome length is 2.0 Mbp.

**Description of *Candidatus Cryptobacteroides pullicola* sp. nov.**

*Candidatus Cryptobacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec2B26-3624 and which is available via NCBI BioSample [SAMN15817179](#). This is a new name for the alphanumeric GTDB species sp001915575. The GC content of the type genome is 58.01% and the genome length is 1.7 Mbp.

**Description of *Candidatus Desulfovibrio faecigallinarum* sp. nov.**

*Candidatus Desulfovibrio faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 8923 and which is available via NCBI BioSample [SAMN15816873](#). This is a new name for the alphanumeric GTDB species sp002159665. The GC content of the type genome is 57.29% and the genome length is 2.0 Mbp.

**Description of *Candidatus Desulfovibrio gallistercoris* sp. nov.**

*Candidatus Desulfovibrio 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-32749 and which is available via NCBI BioSample [SAMN15816654](#). The GC content of the type genome is 64.54% and the genome length is 2.8 Mbp.

**Description of *Candidatus Desulfovibrio intestinavium* sp. nov.**

*Candidatus Desulfovibrio 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5032 and which is available via NCBI BioSample [SAMN15816664](#). The GC content of the type genome is 64.60% and the genome length is 2.5 Mbp.

**Description of *Candidatus Desulfovibrio intestinigallinarum* sp. nov.**

*Candidatus Desulfovibrio 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec3B27-2601 and which is available via NCBI BioSample [SAMN15816737](#). The GC content of the type genome is 61.03% and the genome length is 2.9 Mbp.

**Description of *Candidatus Desulfovibrio intestinipullorum* sp. nov.**

*Candidatus Desulfovibrio intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec2B26-446 and which is available via NCBI BioSample [SAMN15816774](#). The GC content of the type genome is 60.23% and the genome length is 2.8 Mbp.

**Description of *Candidatus Dietzia intestinigallinarum* sp. nov.**

*Candidatus Dietzia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-1528 and which is available via NCBI BioSample [SAMN15816635](#). The GC content of the type genome is 69.86% and the genome length is 3.9 Mbp.

Table 1 (continued)

**Description of *Candidatus Dietzia intestinipullorum* sp. nov.**

*Candidatus Dietzia intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej13B12-8321 and which is available via NCBI BioSample [SAMN15816639](#). The GC content of the type genome is 71.26% and the genome length is 3.0 Mbp.

**Description of *Candidatus Dietzia merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej8B7-16427 and which is available via NCBI BioSample [SAMN15816758](#). The GC content of the type genome is 68.76% and the genome length is 3.6 Mbp.

**Description of *Candidatus Dorea faecigallarum* sp. nov.**

*Candidatus Dorea faecigallarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-29902 and which is available via NCBI BioSample [SAMN15816646](#). The GC content of the type genome is 50.13% and the genome length is 2.0 Mbp.

**Description of *Candidatus Dorea faecipullorum* sp. nov.**

*Candidatus Dorea faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-10896 and which is available via NCBI BioSample [SAMN15816847](#). This is a new name for the alphanumeric GTDB species sp900543315. The GC content of the type genome is 45.40% and the genome length is 2.3 Mbp.

**Description of *Candidatus Dorea gallistercoris* sp. nov.**

*Candidatus Dorea 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej1B13-11762 and which is available via NCBI BioSample [SAMN15816753](#). The GC content of the type genome is 51.71% and the genome length is 2.2 Mbp.

**Description of *Candidatus Dorea intestinavium* sp. nov.**

*Candidatus Dorea 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK160-14747 and which is available via NCBI BioSample [SAMN15816767](#). The GC content of the type genome is 35.91% and the genome length is 1.9 Mbp.

**Description of *Candidatus Dorea intestinogallarum* sp. nov.**

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

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

**Description of *Candidatus Dorea merdavium* sp. nov.**

*Candidatus Dorea 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej1B13-1060 and which is available via NCBI BioSample [SAMN15816851](#). This is a new name for the alphanumeric GTDB species sp900312975. The GC content of the type genome is 53.23% and the genome length is 2.0 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Dorea stercoravium* sp. nov.**

*Candidatus Dorea 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej1B19-6982 and which is available via NCBI BioSample [SAMN15816837](#). This is a new name for the alphanumeric GTDB species sp002160985. The GC content of the type genome is 55.00% and the genome length is 2.5 Mbp.

**Description of *Candidatus Duodenibacillus intestinavium* sp. nov.**

*Candidatus Duodenibacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2430 and which is available via NCBI BioSample [SAMN15816841](#). This is a new name for the alphanumeric GTDB species sp900538905. The GC content of the type genome is 55.01% and the genome length is 1.8 Mbp.

**Description of *Candidatus Duodenibacillus intestinigallinarum* sp. nov.**

*Candidatus Duodenibacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK1-2119 and which is available via NCBI BioSample [SAMN15816840](#). This is a new name for the alphanumeric GTDB species sp003472385. The GC content of the type genome is 56.00% and the genome length is 2.0 Mbp.

**Description of *Candidatus Egerieenecus* gen. nov.**

*Candidatus Egerieenecus* (E.ge.ri.e.en.e'cus. L. fem. n. *egeries* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Egerieenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Egerieenecus merdigallinarum*. This is a name for the alphanumeric GTDB genus UMGs1600. 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 *Christensenellales* and to the family *CAG-74*.

**Description of *Candidatus Egerieenecus merdigallinarum* sp. nov.**

*Candidatus Egerieenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxje2B14-4419 and which is available via NCBI BioSample [SAMN15817218](#). This is a new name for the alphanumeric GTDB species sp900553295. The GC content of the type genome is 60.15% and the genome length is 2.5 Mbp.

**Description of *Candidatus Egerieicola* gen. nov.**

*Candidatus Egerieicola* (E.ge.ri.e.i'co.la. L. fem. n. *egeries* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Egerieicola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Egerieicola faecale*. This is a name for the alphanumeric GTDB genus UBA1375. 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 *Ruminococcaceae*.

**Description of *Candidatus Egerieicola faecalis* sp. nov.**

*Candidatus Egerieicola faecale* (fae.ca'lis. L. fem. adj. *faecalis* of faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 4509 and which is available via NCBI BioSample [SAMN15817200](#). This is a new name for the alphanumeric GTDB species sp002305795. The GC content of the type genome is 55.66% and the genome length is 1.8 Mbp.

**Description of *Candidatus Egerieicola pullicola* sp. nov.**

*Candidatus Egerieicola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK184-25365 and which is available via NCBI BioSample [SAMN15817017](#). The GC content of the type genome is 52.81% and the genome length is 1.9 Mbp.



Table 1 (continued)

**Description of *Candidatus Egerieimonas* gen. nov.**

*Candidatus Egerieimonas* (E.ge.ri.e.i.mo'nas. L. fem. n. *egeries* dung; L. fem. n. *monas* a monad; N.L. fem. n. *Egerieimonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Egerieimonas intestinavium*. This is a name for the alphanumeric GTDB genus UMG51472. 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 Egerieimonas faecigallinarum* sp. nov.**

*Candidatus Egerieimonas faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK180-10209 and which is available via NCBI BioSample SAMN15817015. The GC content of the type genome is 51.75% and the genome length is 2.9 Mbp.

**Description of *Candidatus Egerieimonas intestinavium* sp. nov.**

*Candidatus Egerieimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej1B13-7041 and which is available via NCBI BioSample SAMN15817079. The GC content of the type genome is 55.23% and the genome length is 2.6 Mbp.

**Description of *Candidatus Egerieisoma* gen. nov.**

*Candidatus Egerieisoma* (E.ge.ri.e.so'ma. L. fem. n. *egeries* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Egerieisoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Egerieisoma faecipullorum*. This is a name for the alphanumeric GTDB genus UMG51537. 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 *UBA1212* and to the family *UBA1255*.

**Description of *Candidatus Egerieisoma faecipullorum* sp. nov.**

*Candidatus Egerieisoma faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-4489 and which is available via NCBI BioSample SAMN15817230. This is a new name for the alphanumeric GTDB species sp900543695. The GC content of the type genome is 50.69% and the genome length is 2.0 Mbp.

**Description of *Candidatus Egerieousia* gen. nov.**

*Candidatus Egerieousia* (E.ge.ri.e.ou'si.a. L. fem. n. *egeries* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Egerieousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Egerieousia excrementavium*. This is a name for the alphanumeric GTDB genus UBA1232. 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 Egerieousia excrementavium* sp. nov.**

*Candidatus Egerieousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 15467 and which is available via NCBI BioSample SAMN15817149. The GC content of the type genome is 46.96% and the genome length is 1.5 Mbp.

**Description of *Candidatus Eisenbergiella intestinogallinarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec1-1630 and which is available via NCBI BioSample SAMN15816806. This is a new name for the alphanumeric GTDB species sp900544445. The GC content of the type genome is 53.15% and the genome length is 3.4 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Eisenbergiella intestinipullorum* sp. nov.**

*Candidatus Eisenbergiella intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK177-9469 and which is available via NCBI BioSample [SAMN15816580](#). The GC content of the type genome is 54.63% and the genome length is 3.5 Mbp.

**Description of *Candidatus Eisenbergiella merdavium* sp. nov.**

*Candidatus Eisenbergiella merdavium* (mer.da'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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID USAMLcec2-132 and which is available via NCBI BioSample [SAMN15816641](#). The GC content of the type genome is 54.07% and the genome length is 4.2 Mbp.

**Description of *Candidatus Eisenbergiella merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  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  $\geq 95\%$  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  $\geq 95\%$  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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxje3B15-24422 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  $\geq 95\%$  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 stercorigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHje8B7-25341 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.

Table 1 (continued)

**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  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus 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  $\geq 95\%$  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)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiXje3B15-11837 and which is available via NCBI BioSample [SAMN15817165](#). The GC content of the type genome is 64.30% and the genome length is 1.5 Mbp.

**Description of *Candidatus Enterenecus faecium* sp. nov.**

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

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

**Description of *Candidatus Enterenecus merdae* sp. nov.**

*Candidatus Enterenecus merdae* (mer'dae. L. gen. n. *merdae* of faeces)

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

**Description of *Candidatus Enterenecus stercoripullorum* sp. nov.**

*Candidatus Enterenecus stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

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

**Description of *Candidatus Enterocloster excrementigallinarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK198-12963 and which is available via NCBI BioSample [SAMN15816811](#). This is a new name for the alphanumeric GTDB species sp900547035. The GC content of the type genome is 51.32% and the genome length is 3.1 Mbp.

**Description of *Candidatus Enterocloster excrementipullorum* sp. nov.**

*Candidatus Enterocloster 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK180-15479 and which is available via NCBI BioSample [SAMN15816584](#). The GC content of the type genome is 53.85% and the genome length is 2.9 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Enterocloster faecavium* sp. nov.**

*Candidatus* Enterocloster 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK188-4685 and which is available via NCBI BioSample [SAMN15816596](#). The GC content of the type genome is 52.23% and the genome length is 2.8 Mbp.

**Description of *Candidatus Enterococcus avicola* sp. nov.**

*Candidatus* Enterococcus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK172-16539 and which is available via NCBI BioSample [SAMN15816900](#). Although GTDB has assigned this species to the genus it calls Enterococcus\_I, 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 36.87% and the genome length is 2.2 Mbp.

**Description of *Candidatus Enterococcus stercoravium* sp. nov.**

*Candidatus* Enterococcus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK172-14336 and which is available via NCBI BioSample [SAMN15816907](#). Although GTDB has assigned this species to the genus it calls Enterococcus\_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 44.16% and the genome length is 2.3 Mbp.

**Description of *Candidatus Enterococcus stercoripullorum* sp. nov.**

*Candidatus* Enterococcus stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-924 and which is available via NCBI BioSample [SAMN15816914](#). Although GTDB has assigned this species to the genus it calls Enterococcus\_E, 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 36.20% and the genome length is 2.3 Mbp.

**Description of *Candidatus Enterocola* gen. nov.**

*Candidatus* Enterocola (En.te.ro'co.la. Gr. neut. n. *enteron* the gut; L. suff. *-cola* inhabitant of; N.L. fem. n. *Enterocola* a microbe associated with the gut)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Enterocola intestinipullorum. This is a name for the alphanumeric GTDB genus RUG163. 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 *Paludibacteraceae*.

**Description of *Candidatus Enterocola intestinipullorum* sp. nov.**

*Candidatus* Enterocola intestinipullorum (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID D3-1215 and which is available via NCBI BioSample [SAMN15817113](#). The GC content of the type genome is 47.46% and the genome length is 1.8 Mbp.

**Description of *Candidatus Enteromonas* gen. nov.**

*Candidatus* Enteromonas (En.te.ro.mo'nas. Gr. neut. n. *enteron* the gut; L. fem. n. *monas* a monad; N.L. fem. n. *Enteromonas* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Enteromonas pullistercoris. This is a name for the alphanumeric GTDB genus UBA733. 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 *RFN20* and to the family *CAG-826*.

Table 1 (continued)

**Description of *Candidatus Enteromonas pullicola* sp. nov.**

*Candidatus Enteromonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-22543 and which is available via NCBI BioSample [SAMN15817133](#). The GC content of the type genome is 57.43% and the genome length is 1.2 Mbp.

**Description of *Candidatus Enteromonas pullistercoris* sp. nov.**

*Candidatus Enteromonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 17113 and which is available via NCBI BioSample [SAMN15817142](#). The GC content of the type genome is 53.99% and the genome length is 1.4 Mbp.

**Description of *Candidatus Enterosoma* gen. nov.**

*Candidatus Enterosoma* (En.te.ro.so'ma. Gr. neut. n. *enteron* the gut; Gr. neut. n. *soma* a body; N.L. neut. n. *Enterosoma* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Enterosoma merdigallarum*. This is a name for the alphanumeric GTDB genus UBA7642. 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 *RFN20* and to the family *CAG-288*.

**Description of *Candidatus Enterosoma merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 33044 and which is available via NCBI BioSample [SAMN15817141](#). The GC content of the type genome is 51.22% and the genome length is 1.4 Mbp.

**Description of *Candidatus Enterousia* gen. nov.**

*Candidatus Enterousia* (En.ter.ou'si.a. Gr. neut. n. *enteron* the gut; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Enterousia* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Enterousia excrementavium*. This is a name for the alphanumeric GTDB genus Rs-D84. 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 *Rs-D84* and to the family *Rs-D84*.

**Description of *Candidatus Enterousia avicola* sp. nov.**

*Candidatus Enterousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK136-897 and which is available via NCBI BioSample [SAMN15817144](#). The GC content of the type genome is 39.01% and the genome length is 0.9 Mbp.

**Description of *Candidatus Enterousia avistercoris* sp. nov.**

*Candidatus Enterousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 8207 and which is available via NCBI BioSample [SAMN15817150](#). The GC content of the type genome is 43.79% and the genome length is 0.8 Mbp.

**Description of *Candidatus Enterousia excrementavium* sp. nov.**

*Candidatus Enterousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B1-16210 and which is available via NCBI BioSample [SAMN15817158](#). The GC content of the type genome is 44.26% and the genome length is 0.9 Mbp.

(Continued)



Table 1 (continued)

**Description of *Candidatus Enterousia intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej3B3-5194 and which is available via NCBI BioSample [SAMN15817183](#). This is a new name for the alphanumeric GTDB species sp900546185. The GC content of the type genome is 45.89% and the genome length is 0.9 Mbp.

**Description of *Candidatus Erysipelatoclostridium merdavium* sp. nov.**

*Candidatus* Erysipelatoclostridium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-14440 and which is available via NCBI BioSample [SAMN15816860](#). This is a new name for the alphanumeric GTDB species sp002160495. The GC content of the type genome is 29.32% and the genome length is 2.6 Mbp.

**Description of *Candidatus Eubacterium avistercoris* sp. nov.**

*Candidatus* Eubacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK192-9172 and which is available via NCBI BioSample [SAMN15816888](#). Although GTDB has assigned this species to the genus it calls Eubacterium\_I, 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 45.90% and the genome length is 2.6 Mbp.

**Description of *Candidatus Eubacterium faecale* sp. nov.**

*Candidatus* Eubacterium faecale (fae.ca'le. L. neut. adj. *faecale* of faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK188-16595 and which is available via NCBI BioSample [SAMN15816917](#). This is a new name for the alphanumeric GTDB species sp000431535. Although GTDB has assigned this species to the genus it calls Eubacterium\_R, 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 46.56% and the genome length is 1.8 Mbp.

**Description of *Candidatus Eubacterium faecavium* sp. nov.**

*Candidatus* Eubacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHec3B27-3607 and which is available via NCBI BioSample [SAMN15816921](#). This is a new name for the alphanumeric GTDB species sp900539845. Although GTDB has assigned this species to the genus it calls Eubacterium\_R, 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 45.56% and the genome length is 1.9 Mbp.

**Description of *Candidatus Eubacterium faecigallarum* sp. nov.**

*Candidatus* Eubacterium faecigallarum (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 8396 and which is available via NCBI BioSample [SAMN15816904](#). Although GTDB has assigned this species to the genus it calls Eubacterium\_R, 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 43.37% and the genome length is 1.6 Mbp.

**Description of *Candidatus Eubacterium faecipullorum* sp. nov.**

*Candidatus* Eubacterium faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 421 and which is available via NCBI BioSample [SAMN15816928](#). This is a new name for the alphanumeric GTDB species sp900546785. Although GTDB has assigned this species to the genus it calls Eubacterium\_R, 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 47.26% and the genome length is 1.9 Mbp.

Table 1 (continued)

**Description of *Candidatus Eubacterium pullicola* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-11929 and which is available via NCBI BioSample [SAMN15816916](#). This is a new name for the alphanumeric GTDB species sp900540015. Although GTDB has assigned this species to the genus it calls *Eubacterium\_M*, 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 41.55% and the genome length is 1.2 Mbp.

**Description of *Candidatus Eteptia excrementipullorum* sp. nov.**

*Candidatus Eteptia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej3B21-3892 and which is available via NCBI BioSample [SAMN15816827](#). This is a new name for the alphanumeric GTDB species sp900546255. The GC content of the type genome is 63.06% and the genome length is 2.0 Mbp.

**Description of *Candidatus Eteptia faecavium* sp. nov.**

*Candidatus Eteptia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcecc3B27-8621 and which is available via NCBI BioSample [SAMN15816713](#). The GC content of the type genome is 65.40% and the genome length is 2.0 Mbp.

**Description of *Candidatus Eteptia faecigallinarum* sp. nov.**

*Candidatus Eteptia faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcec3-601 and which is available via NCBI BioSample [SAMN15816724](#). The GC content of the type genome is 63.50% and the genome length is 2.4 Mbp.

**Description of *Candidatus Excrementavichristensenella* gen. nov.**

*Candidatus Excrementavichristensenella* (Ex.cre.ment.a.vi.chris.ten.sen.el'la. L. neut. n. *excrementum* excrement; L. fem. n. *avis* bird; N.L. fem. n. *Christensenella a* genus name; N.L. fem. n. *Excrementavichristensenella* a genus related to the genus *Christensenella* but distinct from it and found in poultry faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Excrementavichristensenella intestinipullorum*. 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 *Christensenellales* and to the family CAG-74.

**Description of *Candidatus Excrementavichristensenella intestinipullorum* sp. nov.**

*Candidatus Excrementavichristensenella intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-1688 and which is available via NCBI BioSample [SAMN15816955](#). The GC content of the type genome is 62.99% and the genome length is 2.8 Mbp.

**Description of *Candidatus Faecalibacterium avium* sp. nov.**

*Candidatus Faecalibacterium avium* (a'vi.um. L. fem. pl. n. *avium* of birds)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK182-10647 and which is available via NCBI BioSample [SAMN15816876](#). This is a new name for the alphanumeric GTDB species sp002160915. The GC content of the type genome is 62.96% and the genome length is 2.2 Mbp.

**Description of *Candidatus Faecalibacterium faecigallinarum* sp. nov.**

*Candidatus Faecalibacterium faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej5B23-2810 and which is available via NCBI BioSample [SAMN15816583](#). The GC content of the type genome is 63.38% and the genome length is 2.1 Mbp.

(Continued)

Table 1 (continued)

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

*Candidatus Faecalibacterium faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHje9B8-13557 and which is available via NCBI BioSample [SAMN15816651](#). The GC content of the type genome is 65.75% and the genome length is 2.1 Mbp.

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

*Candidatus Faecalibacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec16-3735 and which is available via NCBI BioSample [SAMN15816605](#). The GC content of the type genome is 64.68% and the genome length is 2.1 Mbp.

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

*Candidatus Faecalibacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 742 and which is available via NCBI BioSample [SAMN15816744](#). The GC content of the type genome is 61.60% and the genome length is 1.8 Mbp.

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

*Candidatus Faecalibacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcolR34-3080 and which is available via NCBI BioSample [SAMN15816770](#). The GC content of the type genome is 64.34% and the genome length is 2.1 Mbp.

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

*Candidatus Faecalibacterium intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcolR21-11242 and which is available via NCBI BioSample [SAMN15816785](#). The GC content of the type genome is 61.39% and the genome length is 2.1 Mbp.

**Description of *Candidatus Faecalicoccus intestinipullorum* sp. nov.**

*Candidatus Faecalicoccus intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHje8B7-5959 and which is available via NCBI BioSample [SAMN15816766](#). The GC content of the type genome is 40.89% and the genome length is 1.4 Mbp.

**Description of *Candidatus Faecaligallichristensenella* gen. nov.**

*Candidatus Faecaligallichristensenella* (Fae.ca.li.gal.li.chris.ten.sen.el'la. N.L. masc. adj. *faecalis* pertaining to faeces; L. masc. n. *gallus* chicken; N.L. fem. n. *Christensenella* a genus name; N.L. fem. n. *Faecaligallichristensenella* a genus related to the genus *Christensenella* but distinct from it and found in poultry faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Faecaligallichristensenella faecipullorum*. This genus was identified but not named by [Glendinning et al. \(2020\)](#). 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 *Christensenellales* and to the family *CAG-74*.

**Description of *Candidatus Faecaligallichristensenella faecipullorum* sp. nov.**

*Candidatus Faecaligallichristensenella faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSje6B24-5839 and which is available via NCBI BioSample [SAMN15816940](#). The GC content of the type genome is 58.49% and the genome length is 2.6 Mbp.

Table 1 (continued)

**Description of *Candidatus Faecenecus* gen. nov.**

*Candidatus Faecenecus* (Faec.en.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  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus 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  $\geq 95\%$  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* (Fae.ci'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  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus 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  $\geq 95\%$  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.**

*Candidatus Faecimonas* (Fae.ci.mo'nas. L. fem. n. *faex* dregs; L. fem. n. *monas* a monad; N.L. fem. n. *Faecimonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Faecimonas intestinavium*. This is a name for the alphanumeric GTDB genus CAG-877.

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 Faecimonas gallistercoris* sp. nov.**

*Candidatus Faecimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK189-3136 and which is available via NCBI BioSample SAMN15817016.

The GC content of the type genome is 28.18% and the genome length is 1.4 Mbp.

**Description of *Candidatus Faecimonas intestinavium* sp. nov.**

*Candidatus Faecimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID USAMLcec2-12447 and which is available via NCBI BioSample SAMN15817225.

This is a new name for the alphanumeric GTDB species sp900554305. The GC content of the type genome is 29.22% and the genome length is 1.8 Mbp.

**Description of *Candidatus Faecimorpha* gen. nov.**

*Candidatus Faecimorpha* (Fae.ci.mor'pha. L. fem. n. *faex* dregs; Gr. fem. n. *morphe* a form, shape; N.L. fem. n. *Faecimorpha* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Faecimorpha stercoravium*. This is a name for the alphanumeric GTDB genus UBA1390.

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 UBA1390.

(Continued)



Table 1 (continued)

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

*Candidatus Faecimorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-9767 and which is available via NCBI BioSample [SAMN15817172](#). This is a new name for the alphanumeric GTDB species sp002305315. The GC content of the type genome is 49.81% and the genome length is 2.4 Mbp.

**Description of *Candidatus Faecioplasma* gen. nov.**

*Candidatus Faecioplasma* (Fae.ci.plas'ma. L. fem. n. *faex* dregs; Gr. neut. n. *plasma* a form; N.L. neut. n. *Faecioplasma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Faecioplasma avium*. This is a name for the alphanumeric GTDB genus UBA1409. 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 *Ruminococcaceae*.

**Description of *Candidatus Faecioplasma avium* sp. nov.**

*Candidatus Faecioplasma avium* (a'vi.um. L. fem. pl. n. *avium* of birds)

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

**Description of *Candidatus Faecioplasma gallinarum* sp. nov.**

*Candidatus Faecioplasma gallinarum* (gal.li.na'rum. L. fem. n. *gallina* a hen; L. gen. fem. pl. n. *gallinarum* of hens)

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

**Description of *Candidatus Faecioplasma pullistercoris* sp. nov.**

*Candidatus Faecioplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK33-4379 and which is available via NCBI BioSample [SAMN15817120](#). The GC content of the type genome is 49.45% and the genome length is 1.5 Mbp.

**Description of *Candidatus Faecisoma* gen. nov.**

*Candidatus Faecisoma* (Fae.ci.so'ma. L. fem. n. *faex* dregs; Gr. neut. n. *soma* a body; N.L. neut. n. *Faecisoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Faecisoma merdaviium*. This is a name for the alphanumeric GTDB genus CAG-878. 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-822*.

**Description of *Candidatus Faecisoma merdaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 6595 and which is available via NCBI BioSample [SAMN15817101](#). The GC content of the type genome is 24.63% and the genome length is 1.3 Mbp.

**Description of *Candidatus Faecivicinus* gen. nov.**

*Candidatus Faecivicinus* (Fae.ci.vi.ci'nus. L. fem. n. *faex* dregs; L. masc. n. *vicinus* a neighbour; N.L. masc. n. *Faecivicinus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Faecivicinus avistercoris*. This is a name for the alphanumeric GTDB genus UMG51603. 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 *Christensenellales* and to the family *CAG-74*.



Table 1 (continued)

**Description of *Candidatus Faecivicinus avistercoris* sp. nov.**

*Candidatus Faecivicinus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 905 and which is available via NCBI BioSample [SAMN15817031](#). The GC content of the type genome is 63.46% and the genome length is 2.7 Mbp.

**Description of *Candidatus Faecivivens* gen. nov.**

*Candidatus Faecivivens* (Fae.ci.vi'vens. L. fem. n. *faex* dregs; N.L. pres. part. *vivens* living; N.L. fem. n. *Faecivivens* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Faecivivens stercorigallinarum*. This is a name for the alphanumeric GTDB genus UBA1448. 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 *Ruminococcaceae*.

**Description of *Candidatus Faecivivens stercoravium* sp. nov.**

*Candidatus Faecivivens 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK189-12415 and which is available via NCBI BioSample [SAMN15817018](#). The GC content of the type genome is 59.75% and the genome length is 2.3 Mbp.

**Description of *Candidatus Faecivivens stercorigallinarum* sp. nov.**

*Candidatus Faecivivens 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 4960 and which is available via NCBI BioSample [SAMN15817121](#). The GC content of the type genome is 52.99% and the genome length is 2.2 Mbp.

**Description of *Candidatus Faecivivens stercoripullorum* sp. nov.**

*Candidatus Faecivivens stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec7-5410 and which is available via NCBI BioSample [SAMN15817124](#). The GC content of the type genome is 50.38% and the genome length is 2.0 Mbp.

**Description of *Candidatus Faecousia* gen. nov.**

*Candidatus Faecousia* (Fae.ou'si.a. L. fem. n. *faex* dregs; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Faecousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Faecousia intestingallinarum*. This is a name for the alphanumeric GTDB genus CAG-110. 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 Faecousia excrementigallinarum* sp. nov.**

*Candidatus Faecousia excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 13361 and which is available via NCBI BioSample [SAMN15817055](#). The GC content of the type genome is 56.40% and the genome length is 1.9 Mbp.

**Description of *Candidatus Faecousia excrementipullorum* sp. nov.**

*Candidatus Faecousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej6B18-3616 and which is available via NCBI BioSample [SAMN15817060](#). The GC content of the type genome is 56.19% and the genome length is 1.7 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Faecousia faecavium* sp. nov.**

*Candidatus Faecousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec21-2751 and which is available via NCBI BioSample [SAMN15817064](#). The GC content of the type genome is 53.76% and the genome length is 2.4 Mbp.

**Description of *Candidatus Faecousia faecigallarum* sp. nov.**

*Candidatus Faecousia faecigallarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcolR29-948 and which is available via NCBI BioSample [SAMN15817073](#). The GC content of the type genome is 58.86% and the genome length is 1.9 Mbp.

**Description of *Candidatus Faecousia faecipullorum* sp. nov.**

*Candidatus Faecousia faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec2B26-1122 and which is available via NCBI BioSample [SAMN15817098](#). The GC content of the type genome is 55.50% and the genome length is 1.9 Mbp.

**Description of *Candidatus Faecousia gallistercoris* sp. nov.**

*Candidatus Faecousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 7739 and which is available via NCBI BioSample [SAMN15817186](#). This is a new name for the alphanumeric GTDB species sp900546915. The GC content of the type genome is 58.30% and the genome length is 1.8 Mbp.

**Description of *Candidatus Faecousia intestinavium* sp. nov.**

*Candidatus Faecousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcec3-9842 and which is available via NCBI BioSample [SAMN15817111](#). The GC content of the type genome is 57.16% and the genome length is 2.1 Mbp.

**Description of *Candidatus Faecousia intestinogallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej3B15-29383 and which is available via NCBI BioSample [SAMN15817112](#). The GC content of the type genome is 55.74% and the genome length is 2.1 Mbp.

**Description of *Candidatus Fimadaptatus* gen. nov.**

*Candidatus Fimadaptatus* (Fim.a.dap.ta'tus. L. neut. n. *fimum* dung; L. past part. masc. *adaptatus* adapted to; N.L. masc. n. *Fimadaptatus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimadaptatus faecigallarum*. This is a name for the alphanumeric GTDB genus UMG51633. 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 *Christensenellales* and to the family CAG-74.

**Description of *Candidatus Fimadaptatus faecigallarum* sp. nov.**

*Candidatus Fimadaptatus faecigallarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej2B14-8506 and which is available via NCBI BioSample [SAMN15817140](#). The GC content of the type genome is 60.44% and the genome length is 2.8 Mbp.

Table 1 (continued)

**Description of *Candidatus Fimenecus* gen. nov.**

*Candidatus Fimenecus* (Fim.en.e'cus. L. neut. n. *fimum* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Fimenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimenecus excrementigallinarum*. This is a name for the alphanumeric GTDB genus CAG-180. 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 *Acutalibacteraceae*.

**Description of *Candidatus Fimenecus excrementavium* sp. nov.**

*Candidatus Fimenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSje1B19-6168 and which is available via NCBI BioSample SAMN15817011. The GC content of the type genome is 50.61% and the genome length is 1.8 Mbp.

**Description of *Candidatus Fimenecus excrementigallinarum* sp. nov.**

*Candidatus Fimenecus excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-19959 and which is available via NCBI BioSample SAMN15817134. The GC content of the type genome is 60.29% and the genome length is 1.8 Mbp.

**Description of *Candidatus Fimenecus stercoravium* sp. nov.**

*Candidatus Fimenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcolR13-3023 and which is available via NCBI BioSample SAMN15817181. This is a new name for the alphanumeric GTDB species sp002314305. The GC content of the type genome is 55.43% and the genome length is 1.9 Mbp.

**Description of *Candidatus Fimicola* gen. nov.**

*Candidatus Fimicola* (Fi.mi'co.la. L. neut. n. *fimum* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Fimicola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimicola merdigallinarum*. This is a name for the alphanumeric GTDB genus An114. 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 *Anaerotignaceae*.

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

*Candidatus Fimicola cottocaccae* (cot.to.cac'cae. Gr. masc. n. *kottos* chicken Gr. fem. n. *kakke* faeces; N.L. gen. n. *cottocaccae* of chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW9-1577 and which is available via NCBI BioSample SAMN15817191. This is a new name for the alphanumeric GTDB species sp002161055. The GC content of the type genome is 31.91% and the genome length is 1.8 Mbp.

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

*Candidatus Fimicola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID F6-4510 and which is available via NCBI BioSample SAMN15817136. The GC content of the type genome is 32.46% and the genome length is 1.8 Mbp.

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

*Candidatus Fimihabitans* (Fi.mi.ha'bi.tans. L. neut. n. *fimum* dung; L. pres. part. *habitans* an inhabitant; N.L. fem. n. *Fimihabitans* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimihabitans intestinipullorum*. This is a name for the alphanumeric GTDB genus UMG51648. 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-822.

(Continued)

Table 1 (continued)

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

*Candidatus Fimihabitans intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK197-8231 and which is available via NCBI BioSample [SAMN15817229](#). This is a new name for the alphanumeric GTDB species sp900553765. The GC content of the type genome is 33.44% and the genome length is 1.3 Mbp.

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

*Candidatus Fimimonas* (Fi.mi.mo'nas. L. neut. n. *fimum* dung; L. fem. n. *monas* a monad; N.L. fem. n. *Fimimonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimimonas gallinarum*. This is a name for the alphanumeric GTDB genus CAG-1435. 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 *Christensenellales* and to the family CAG-314.

**Description of *Candidatus Fimimonas gallinarum* sp. nov.**

*Candidatus Fimimonas gallinarum* (gal.li.na'rum. L. fem. n. *gallina* a hen; L. gen. fem. pl. n. *gallarum* of hens)

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

**Description of *Candidatus Fimimonas merdipullorum* sp. nov.**

*Candidatus Fimimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-7776 and which is available via NCBI BioSample [SAMN15817153](#). The GC content of the type genome is 53.17% and the genome length is 1.3 Mbp.

**Description of *Candidatus Fimimorpha* gen. nov.**

*Candidatus Fimimorpha* (Fi.mi.mor'pha. L. neut. n. *fimum* dung; Gr. fem. n. *morphe* a form, shape; N.L. fem. n. *Fimimorpha* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimimorpha faecalis*. This is a name for the alphanumeric GTDB genus CHKCI001. 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 Fimimorpha excrementavium* sp. nov.**

*Candidatus Fimimorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK193-21555 and which is available via NCBI BioSample [SAMN15817029](#). The GC content of the type genome is 48.70% and the genome length is 3.1 Mbp.

**Description of *Candidatus Fimimorpha faecalis* sp. nov.**

*Candidatus Fimimorpha faecalis* (fae.ca'lis. L. fem. adj. *faecalis* of faeces)

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

**Description of *Candidatus Fimiplasma* gen. nov.**

*Candidatus Fimiplasma* (Fi.mi.plas'ma. L. neut. n. *fimum* dung; Gr. neut. n. *plasma* a form; N.L. neut. n. *Fimiplasma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimiplasma intestinipullorum*. This is a name for the alphanumeric GTDB genus CHKCI006. 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 *Erysipelotrichales* and to the family *Erysipelatoclostridiaceae*.

Table 1 (continued)

**Description of *Candidatus Fimiplasma intestinipullorum* sp. nov.**

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

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

**Description of *Candidatus Fimisoma* gen. nov.**

*Candidatus Fimisoma* (Fi.mi.so'ma. L. neut. n. *fimum* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Fimisoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimisoma avicola*. This is a name for the alphanumeric GTDB genus CAG-145. 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 *Peptostreptococcales* and to the family *Anaerovoracaceae*.

**Description of *Candidatus Fimisoma avicola* sp. nov.**

*Candidatus Fimisoma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 11300 and which is available via NCBI BioSample [SAMN15817197](#). This is a new name for the alphanumeric GTDB species sp900542565. The GC content of the type genome is 47.90% and the genome length is 2.0 Mbp.

**Description of *Candidatus Fimivicinus* gen. nov.**

*Candidatus Fimivicinus* (Fi.mi.vi.ci'nus. L. neut. n. *fimum* dung; L. masc. n. *vicinus* a neighbour; N.L. masc. n. *Fimivicinus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimivicinus intestinavium*. This is a name for the alphanumeric GTDB genus UBA1691. 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 *Acutalibacteraceae*.

**Description of *Candidatus Fimivicinus intestinavium* sp. nov.**

*Candidatus Fimivicinus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2526 and which is available via NCBI BioSample [SAMN15817188](#). This is a new name for the alphanumeric GTDB species sp900552985. The GC content of the type genome is 55.20% and the genome length is 2.5 Mbp.

**Description of *Candidatus Fimivivens* gen. nov.**

*Candidatus Fimivivens* (Fi.mi.vi'vens. L. neut. n. *fimum* dung; N.L. pres. part. *vivens* living; N.L. fem. n. *Fimivivens* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimivivens faecavium*. This is a name for the alphanumeric GTDB genus D5. 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 *Ruminococcaceae*.

**Description of *Candidatus Fimivivens faecavium* sp. nov.**

*Candidatus Fimivivens 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-35099 and which is available via NCBI BioSample [SAMN15817038](#). The GC content of the type genome is 58.86% and the genome length is 2.0 Mbp.

**Description of *Candidatus Fimousia* gen. nov.**

*Candidatus Fimousia* (Fim.ou'si.a. L. neut. n. *fimum* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Fimousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Fimousia stercorigallarum*. This is a name for the alphanumeric GTDB genus 992a. 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*.

(Continued)



**Table 1 (continued)****Description of *Candidatus Fimousia stercorigallinarum* sp. nov.**

*Candidatus Fimousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej3B15-1827 and which is available via NCBI BioSample [SAMN15817114](#). The GC content of the type genome is 41.52% and the genome length is 2.3 Mbp.

**Description of *Candidatus Flavonifractor avicola* sp. nov.**

*Candidatus Flavonifractor 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK178-4001 and which is available via NCBI BioSample [SAMN15816843](#). This is a new name for the alphanumeric GTDB species sp002161085. The GC content of the type genome is 60.44% and the genome length is 2.5 Mbp.

**Description of *Candidatus Flavonifractor avistercoris* sp. nov.**

*Candidatus Flavonifractor 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 6084 and which is available via NCBI BioSample [SAMN15816821](#). This is a new name for the alphanumeric GTDB species sp002161215. The GC content of the type genome is 65.16% and the genome length is 2.4 Mbp.

**Description of *Candidatus Flavonifractor intestinigallinarum* sp. nov.**

*Candidatus Flavonifractor 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK192-8294 and which is available via NCBI BioSample [SAMN15816592](#). The GC content of the type genome is 61.61% and the genome length is 2.5 Mbp.

**Description of *Candidatus Flavonifractor intestinipullorum* sp. nov.**

*Candidatus Flavonifractor intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK189-11263 and which is available via NCBI BioSample [SAMN15816594](#). The GC content of the type genome is 63.72% and the genome length is 2.2 Mbp.

**Description of *Candidatus Flavonifractor merdavium* sp. nov.**

*Candidatus Flavonifractor 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3313 and which is available via NCBI BioSample [SAMN15816644](#). The GC content of the type genome is 62.46% and the genome length is 2.7 Mbp.

**Description of *Candidatus Flavonifractor merdigallinarum* sp. nov.**

*Candidatus Flavonifractor 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec16-6824 and which is available via NCBI BioSample [SAMN15816721](#). The GC content of the type genome is 61.09% and the genome length is 2.6 Mbp.

**Description of *Candidatus Flavonifractor merdipullorum* sp. nov.**

*Candidatus Flavonifractor 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-1540 and which is available via NCBI BioSample [SAMN15816748](#). The GC content of the type genome is 61.06% and the genome length is 2.1 Mbp.

Table 1 (continued)

**Description of *Candidatus Fournierella excrementavium* sp. nov.**

*Candidatus Fournierella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcec27-1717 and which is available via NCBI BioSample [SAMN15816881](#). This is a new name for the alphanumeric GTDB species sp004558145. The GC content of the type genome is 63.90% and the genome length is 2.4 Mbp.

**Description of *Candidatus Fournierella excrementigallarum* sp. nov.**

*Candidatus Fournierella excrementigallarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1136 and which is available via NCBI BioSample [SAMN15816650](#). The GC content of the type genome is 64.27% and the genome length is 2.1 Mbp.

**Description of *Candidatus Fournierella merdavium* sp. nov.**

*Candidatus Fournierella merdavium* (mer.da'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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec4-1730 and which is available via NCBI BioSample [SAMN15816653](#). The GC content of the type genome is 64.33% and the genome length is 2.6 Mbp.

**Description of *Candidatus Fournierella merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 6296 and which is available via NCBI BioSample [SAMN15816675](#). The GC content of the type genome is 65.05% and the genome length is 2.4 Mbp.

**Description of *Candidatus Fournierella merdipullorum* sp. nov.**

*Candidatus Fournierella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej4B4-18154 and which is available via NCBI BioSample [SAMN15816693](#). The GC content of the type genome is 62.57% and the genome length is 2.5 Mbp.

**Description of *Candidatus Fournierella pullicola* sp. nov.**

*Candidatus Fournierella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2239 and which is available via NCBI BioSample [SAMN15816745](#). The GC content of the type genome is 62.57% and the genome length is 2.4 Mbp.

**Description of *Candidatus Fournierella pullistercoris* sp. nov.**

*Candidatus Fournierella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B5-2728 and which is available via NCBI BioSample [SAMN15816762](#). The GC content of the type genome is 52.45% and the genome length is 1.7 Mbp.

**Description of *Candidatus Fusicatenibacter intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK185-5351 and which is available via NCBI BioSample [SAMN15816585](#). The GC content of the type genome is 51.22% and the genome length is 2.9 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Fusicatenibacter intestinipullorum* sp. nov.**

*Candidatus Fusicatenibacter intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec11-5794 and which is available via NCBI BioSample [SAMN15816833](#). This is a new name for the alphanumeric GTDB species sp900543115. The GC content of the type genome is 49.70% and the genome length is 2.6 Mbp.

**Description of *Candidatus Fusicatenibacter merdavium* sp. nov.**

*Candidatus Fusicatenibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK183-1962 and which is available via NCBI BioSample [SAMN15816614](#). The GC content of the type genome is 51.02% and the genome length is 2.7 Mbp.

**Description of *Candidatus Fusobacterium pullicola* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID A6-441 and which is available via NCBI BioSample [SAMN15816927](#). This is a new name for the alphanumeric GTDB species sp900549465. Although GTDB has assigned this species to the genus it calls *Fusobacterium\_A*, 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 29.86% and the genome length is 1.8 Mbp.

**Description of *Candidatus Gallacutalibacter* gen. nov.**

*Candidatus Gallacutalibacter* (Gall.a.cu.ta.li.bac'ter. L. masc. n. *gallus* chicken; N.L. masc. n. *Acutalibacter* a genus name; N.L. masc. n. *Gallacutalibacter* a genus related to the genus *Acutalibacter* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Gallacutalibacter pullicola*. This genus was identified but not named by [Glendinning et al. \(2020\)](#). 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 *Acutalibacteraceae*.

**Description of *Candidatus Gallacutalibacter pullicola* sp. nov.**

*Candidatus Gallacutalibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej1B19-7085 and which is available via NCBI BioSample [SAMN15816935](#). The GC content of the type genome is 56.02% and the genome length is 2.5 Mbp.

**Description of *Candidatus Gallacutalibacter pullistercoris* sp. nov.**

*Candidatus Gallacutalibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 13869 and which is available via NCBI BioSample [SAMN15816961](#). The GC content of the type genome is 51.21% and the genome length is 2.4 Mbp.

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

*Candidatus Gallacutalibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK176-13069 and which is available via NCBI BioSample [SAMN15816939](#). The GC content of the type genome is 51.38% and the genome length is 2.7 Mbp.

**Description of *Candidatus Gallibacteroides* gen. nov.**

*Candidatus Gallibacteroides* (Gal.li.bac.te.ro'i.des. L. masc. n. *gallus* chicken; N.L. masc. n. *Bacteroides* a genus name; N.L. masc. n. *Gallibacteroides* a genus related to the genus *Bacteroides* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Gallibacteroides avistercoris*. 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 *Barnesiellaceae*.

Table 1 (continued)

**Description of *Candidatus Gallibacteroides avistercoris* sp. nov.**

*Candidatus Gallibacteroides 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK158-818 and which is available via NCBI BioSample [SAMN15816984](#). The GC content of the type genome is 46.12% and the genome length is 2.3 Mbp.

**Description of *Candidatus Galligastranaerophilus* gen. nov.**

*Candidatus Galligastranaerophilus* (Gal.li.gastr.an.a.e.ro'phi.us. L. masc. n. *gallus* chicken; N.L. masc. n. *Gastranaerophilus* a genus name; N.L. masc. n. *Galligastranaerophilus* a genus related to the genus *Gastranaerophilus* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Galligastranaerophilus faecipullorum*. 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 *Gastranaerophilales* and to the family *Gastranaerophilaceae*.

**Description of *Candidatus Galligastranaerophilus faecipullorum* sp. nov.**

*Candidatus Galligastranaerophilus faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW23-1657 and which is available via NCBI BioSample [SAMN15816949](#). The GC content of the type genome is 39.52% and the genome length is 1.7 Mbp.

**Description of *Candidatus Galligastranaerophilus gallistercoris* sp. nov.**

*Candidatus Galligastranaerophilus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK123-4750 and which is available via NCBI BioSample [SAMN15816963](#). The GC content of the type genome is 35.45% and the genome length is 1.8 Mbp.

**Description of *Candidatus Galligastranaerophilus intestinavium* sp. nov.**

*Candidatus Galligastranaerophilus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK152-2871 and which is available via NCBI BioSample [SAMN15816967](#). The GC content of the type genome is 35.80% and the genome length is 1.6 Mbp.

**Description of *Candidatus Galligastranaerophilus intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK123-3438 and which is available via NCBI BioSample [SAMN15816973](#). The GC content of the type genome is 32.50% and the genome length is 1.7 Mbp.

**Description of *Candidatus Gallilactobacillus* gen. nov.**

*Candidatus Gallilactobacillus* (Gal.li.lac.to.ba.cil'lus. L. masc. n. *gallus* chicken; N.L. masc. n. *Lactobacillus* a genus name; N.L. masc. n. *Gallilactobacillus* a genus related to the genus *Lactobacillus* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Gallilactobacillus intestinavium*. 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 *Lactobacillales* and to the family *Lactobacillaceae*.

**Description of *Candidatus Gallilactobacillus intestinavium* sp. nov.**

*Candidatus Gallilactobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID C6-149 and which is available via NCBI BioSample [SAMN15816970](#). The GC content of the type genome is 29.69% and the genome length is 1.2 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Gallimonas gallistercoris* sp. nov.**

*Candidatus Gallimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK156-179 and which is available via NCBI BioSample [SAMN15816677](#). The GC content of the type genome is 58.55% and the genome length is 1.6 Mbp.

**Description of *Candidatus Gallimonas intestinavium* sp. nov.**

*Candidatus Gallimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW7-2402 and which is available via NCBI BioSample [SAMN15816844](#). This is a new name for the alphanumeric GTDB species sp003343805. The GC content of the type genome is 58.63% and the genome length is 1.8 Mbp.

**Description of *Candidatus Gallimonas intestinigallinarum* sp. nov.**

*Candidatus Gallimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK33-5263 and which is available via NCBI BioSample [SAMN15816692](#). The GC content of the type genome is 57.82% and the genome length is 1.6 Mbp.

**Description of *Candidatus Gallipaludibacter* gen. nov.**

*Candidatus Gallipaludibacter* (Gal.li.pa.lu.di.bac'ter. L. masc. n. *gallus* chicken; N.L. masc. n. *Paludibacter* a genus name; N.L. masc. n. *Gallipaludibacter* a genus related to the genus *Paludibacter* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Gallipaludibacter merdaviium*. 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 *Paludibacteraceae*.

**Description of *Candidatus Gallipaludibacter merdaviium* sp. nov.**

*Candidatus Gallipaludibacter merdaviium* (mer.da'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird; N.L. gen. n. *merdaviium* of bird faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID G3-3990 and which is available via NCBI BioSample [SAMN15816954](#). The GC content of the type genome is 41.91% and the genome length is 2.9 Mbp.

**Description of *Candidatus Gallitreponema* gen. nov.**

*Candidatus Gallitreponema* (Gal.li.tre.po.ne'ma. L. masc. n. *gallus* chicken; N.L. neut. n. *Treponema* a genus name; N.L. neut. n. *Gallitreponema* a genus related to the genus *Treponema* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Gallitreponema excrementavium*. 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 *Treponematales* and to the family *Treponemataceae*.

**Description of *Candidatus Gallitreponema excrementavium* sp. nov.**

*Candidatus Gallitreponema 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 10532 and which is available via NCBI BioSample [SAMN15816962](#). The GC content of the type genome is 40.13% and the genome length is 2.4 Mbp.

**Description of *Candidatus Galloscollospira* gen. nov.**

*Candidatus Galloscollospira* (Gall.os.cil.lo.spi'ra. L. masc. n. *gallus* chicken; N.L. fem. n. *Oscillospira* a genus name; N.L. fem. n. *Galloscollospira* a genus related to the genus *Oscillospira* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Galloscollospira excrementipullorum*. This genus belongs to the new family *Candidatus Galloscollospiraceae*.



Table 1 (continued)

**Description of *Candidatus Galloscollospira excrementavium* sp. nov.**

*Candidatus Galloscollospira 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej1B19-13426 and which is available via NCBI BioSample [SAMN15816937](#). The GC content of the type genome is 65.18% and the genome length is 2.1 Mbp.

**Description of *Candidatus Galloscollospira excrementipullorum* sp. nov.**

*Candidatus Galloscollospira 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej8B7-10251 and which is available via NCBI BioSample [SAMN15816946](#). The GC content of the type genome is 60.78% and the genome length is 1.6 Mbp.

**Description of *Candidatus Galloscollospira stercoripullorum* sp. nov.**

*Candidatus Galloscollospira stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK33-6455 and which is available via NCBI BioSample [SAMN15816975](#). The GC content of the type genome is 62.96% and the genome length is 1.9 Mbp.

**Description of *Candidatus Galloscollospiraceae* fam. nov.**

*Candidatus Galloscollospiraceae* (Gall.os.cil.lo.spi.ra.ce'ae. N.L. fem. n. *Galloscollospira*. type genus of the family genus; N.L. suff. *-ceae* to denote a family; N.L. fem. pl. n. *Galloscollospiraceae*, the family of the genus *Galloscollospira*)

A bacterial family identified by metagenomic analyses. This family has been defined by the absence of a family assignment for the type species when GTDB-Tk v1.3.0 is applied to GTDB Release 05-RS95 ([Chaumeil et al., 2019](#); [Parks et al., 2020](#)). GTDB assigns the type species and thus the family to the order *Oscillospirales*.

**Description of *Candidatus Gemmiger avicola* sp. nov.**

*Candidatus Gemmiger 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec8-13705 and which is available via NCBI BioSample [SAMN15816825](#). This is a new name for the alphanumeric GTDB species sp900548355. The GC content of the type genome is 61.69% and the genome length is 2.3 Mbp.

**Description of *Candidatus Gemmiger avistercoris* sp. nov.**

*Candidatus Gemmiger 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK188-11489 and which is available via NCBI BioSample [SAMN15816604](#). The GC content of the type genome is 63.30% and the genome length is 2.2 Mbp.

**Description of *Candidatus Gemmiger avium* sp. nov.**

*Candidatus Gemmiger avium* (a'vi.um. L. fem. pl. n. *avium* of birds)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej4B4-15321 and which is available via NCBI BioSample [SAMN15816926](#). This is a new name for the alphanumeric GTDB species sp002160955. Although GTDB has assigned this species to the genus it calls *Gemmiger\_A*, 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 62.71% and the genome length is 2.6 Mbp.

**Description of *Candidatus Gemmiger excrementavium* sp. nov.**

*Candidatus Gemmiger 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3436 and which is available via NCBI BioSample [SAMN15816690](#). The GC content of the type genome is 60.89% and the genome length is 2.5 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Gemmiger excrementigallinarum* sp. nov.**

*Candidatus Gemmiger excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *avis* bird; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej1B13-11774 and which is available via NCBI BioSample [SAMN15816691](#). The GC content of the type genome is 58.73% and the genome length is 2.4 Mbp.

**Description of *Candidatus Gemmiger excrementipullorum* sp. nov.**

*Candidatus Gemmiger 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec2B26-7398 and which is available via NCBI BioSample [SAMN15816726](#). The GC content of the type genome is 64.11% and the genome length is 2.1 Mbp.

**Description of *Candidatus Gemmiger faecavium* sp. nov.**

*Candidatus Gemmiger 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej1B13-1558 and which is available via NCBI BioSample [SAMN15816740](#). The GC content of the type genome is 60.04% and the genome length is 2.5 Mbp.

**Description of *Candidatus Gemmiger faecigallinarum* sp. nov.**

*Candidatus Gemmiger faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 14795 and which is available via NCBI BioSample [SAMN15816795](#). The GC content of the type genome is 63.90% and the genome length is 2.6 Mbp.

**Description of *Candidatus Gemmiger stercoravium* sp. nov.**

*Candidatus Gemmiger 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcolR8-2160 and which is available via NCBI BioSample [SAMN15816579](#). The GC content of the type genome is 65.46% and the genome length is 2.5 Mbp.

**Description of *Candidatus Gemmiger stercorigallinarum* sp. nov.**

*Candidatus Gemmiger 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK183-27628 and which is available via NCBI BioSample [SAMN15816586](#). The GC content of the type genome is 64.08% and the genome length is 2.5 Mbp.

**Description of *Candidatus Gemmiger stercoripullorum* sp. nov.**

*Candidatus Gemmiger stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej4B22-15101 and which is available via NCBI BioSample [SAMN15816589](#). The GC content of the type genome is 64.37% and the genome length is 2.2 Mbp.

**Description of *Candidatus Gordonibacter avicola* sp. nov.**

*Candidatus Gordonibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej6B18-1472 and which is available via NCBI BioSample [SAMN15816757](#). The GC content of the type genome is 59.91% and the genome length is 3.1 Mbp.

Table 1 (continued)

**Description of *Candidatus Halomonas stercoripullorum* sp. nov.**

*Candidatus Halomonas stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1193 and which is available via NCBI BioSample [SAMN15816734](#). The GC content of the type genome is 59.74% and the genome length is 2.1 Mbp.

**Description of *Candidatus Helicobacter avicola* sp. nov.**

*Candidatus Helicobacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 14449 and which is available via NCBI BioSample [SAMN15816913](#). Although GTDB has assigned this species to the genus it calls *Helicobacter\_F*, 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 42.81% and the genome length is 1.7 Mbp.

**Description of *Candidatus Helicobacter avistercoris* sp. nov.**

*Candidatus Helicobacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK158-8274 and which is available via NCBI BioSample [SAMN15816903](#). Although GTDB has assigned this species to the genus it calls *Helicobacter\_G*, 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 38.34% and the genome length is 1.4 Mbp.

**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  $\geq 95\%$  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 merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  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  $\geq 95\%$  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  $\geq 95\%$  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.

**Description of *Candidatus Intestinimonas stercoravium* sp. nov.**

*Candidatus Intestinimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcolR2-622 and which is available via NCBI BioSample [SAMN15816599](#). The GC content of the type genome is 65.33% and the genome length is 2.2 Mbp.

(Continued)

**Table 1 (continued)****Description of *Candidatus Intestinimonas stercorigallinarum* sp. nov.**

*Candidatus Intestinimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxje13B14-1745 and which is available via NCBI BioSample [SAMN15816719](#). The GC content of the type genome is 65.69% and the genome length is 2.1 Mbp.

**Description of *Candidatus Janibacter merdipullorum* sp. nov.**

*Candidatus Janibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHje13B12-21492 and which is available via NCBI BioSample [SAMN15816685](#). The GC content of the type genome is 71.49% and the genome length is 2.8 Mbp.

**Description of *Candidatus Jeotgalibaca merdavium* sp. nov.**

*Candidatus Jeotgalibaca merdavium* (mer.da'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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK171-505 and which is available via NCBI BioSample [SAMN15816828](#). This is a new name for the alphanumeric GTDB species sp001975685. The GC content of the type genome is 38.39% and the genome length is 2.0 Mbp.

**Description of *Candidatus Jeotgalibaca pullicola* sp. nov.**

*Candidatus Jeotgalibaca 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK172-9797 and which is available via NCBI BioSample [SAMN15816826](#). This is a new name for the alphanumeric GTDB species sp003955755. The GC content of the type genome is 36.93% and the genome length is 2.6 Mbp.

**Description of *Candidatus Jeotgalicoccus stercoravium* sp. nov.**

*Candidatus Jeotgalicoccus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK148-7025 and which is available via NCBI BioSample [SAMN15816765](#). The GC content of the type genome is 36.17% and the genome length is 1.7 Mbp.

**Description of *Candidatus Kurthia intestinigallinarum* sp. nov.**

*Candidatus Kurthia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK171-3164 and which is available via NCBI BioSample [SAMN15816863](#). This is a new name for the alphanumeric GTDB species sp002418445. The GC content of the type genome is 39.62% and the genome length is 2.9 Mbp.

**Description of *Candidatus Lachnospirillum avicola* sp. nov.**

*Candidatus Lachnospirillum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK190-19777 and which is available via NCBI BioSample [SAMN15816889](#). Although GTDB has assigned this species to the genus it calls *Lachnospirillum\_A*, 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 54.75% and the genome length is 2.9 Mbp.

**Description of *Candidatus Lachnospirillum pullistercoris* sp. nov.**

*Candidatus Lachnospirillum 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK183-5548 and which is available via NCBI BioSample [SAMN15816884](#). Although GTDB has assigned this species to the genus it calls *Lachnospirillum\_A*, 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 54.35% and the genome length is 2.8 Mbp.

Table 1 (continued)

**Description of *Candidatus Lachnoclostridium stercoravium* sp. nov.**

*Candidatus Lachnoclostridium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK178-16964 and which is available via NCBI BioSample [SAMN15816887](#).

Although GTDB has assigned this species to the genus it calls *Lachnoclostridium\_A*, 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 49.55% and the genome length is 3.0 Mbp.

**Description of *Candidatus Lachnoclostridium stercorigallinarum* sp. nov.**

*Candidatus Lachnoclostridium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec1-1093 and which is available via NCBI BioSample [SAMN15816897](#).

Although GTDB has assigned this species to the genus it calls *Lachnoclostridium\_A*, 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 54.29% and the genome length is 2.4 Mbp.

**Description of *Candidatus Lachnoclostridium stercoripullorum* sp. nov.**

*Candidatus Lachnoclostridium stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej4B4-12881 and which is available via NCBI BioSample [SAMN15816908](#).

Although GTDB has assigned this species to the genus it calls *Lachnoclostridium\_A*, 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 59.38% and the genome length is 2.3 Mbp.

**Description of *Candidatus Lactobacillus pullistercoris* sp. nov.**

*Candidatus Lactobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID F6-686 and which is available via NCBI BioSample [SAMN15816686](#). The GC content of the type genome is 34.54% and the genome length is 1.7 Mbp.

**Description of *Candidatus Lawsonibacter pullicola* sp. nov.**

*Candidatus Lawsonibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK178-3907 and which is available via NCBI BioSample [SAMN15816869](#). This is a new name for the alphanumeric GTDB species sp002160305. The GC content of the type genome is 62.98% and the genome length is 2.3 Mbp.

**Description of *Candidatus Levilactobacillus faecigallinarum* sp. nov.**

*Candidatus Levilactobacillus faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK173-259 and which is available via NCBI BioSample [SAMN15816755](#). The GC content of the type genome is 52.18% and the genome length is 1.8 Mbp.

**Description of *Candidatus Ligilactobacillus avistercoris* sp. nov.**

*Candidatus Ligilactobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBile7-59 and which is available via NCBI BioSample [SAMN15816642](#). The GC content of the type genome is 51.08% and the genome length is 1.2 Mbp.

(Continued)



**Table 1 (continued)****Description of *Candidatus Ligilactobacillus excrementavium* sp. nov.**

*Candidatus Ligilactobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2259 and which is available via NCBI BioSample [SAMN15816683](#). The GC content of the type genome is 38.00% and the genome length is 1.9 Mbp.

**Description of *Candidatus Ligilactobacillus excrementigallinarum* sp. nov.**

*Candidatus Ligilactobacillus excrementigallinarum* (ex.cre.men.ti.gal.li.na'r.um. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 6627 and which is available via NCBI BioSample [SAMN15816741](#). The GC content of the type genome is 34.16% and the genome length is 1.2 Mbp.

**Description of *Candidatus Ligilactobacillus excrementipullorum* sp. nov.**

*Candidatus Ligilactobacillus excrementipullorum* (ex.cre.men.ti.pul.lo'r.um. 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK171-2193 and which is available via NCBI BioSample [SAMN15816749](#). The GC content of the type genome is 42.06% and the genome length is 2.0 Mbp.

**Description of *Candidatus Ligilactobacillus faecavium* sp. nov.**

*Candidatus Ligilactobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3439 and which is available via NCBI BioSample [SAMN15816798](#). The GC content of the type genome is 40.05% and the genome length is 1.3 Mbp.

**Description of *Candidatus Limadaptatus* gen. nov.**

*Candidatus Limadaptatus* (Lim.a.dap.ta'tus. L. masc. n. *limus* dung; L. past part. masc. *adaptatus* adapted to; N.L. masc. n. *Limadaptatus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Limadaptatus stercoripullorum*. This is a name for the alphanumeric GTDB genus UMG51688. 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 *Christensenellales* and to the family *CAG-917*.

**Description of *Candidatus Limadaptatus stercoravium* sp. nov.**

*Candidatus Limadaptatus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK154-227 and which is available via NCBI BioSample [SAMN15817097](#). The GC content of the type genome is 58.03% and the genome length is 1.4 Mbp.

**Description of *Candidatus Limadaptatus stercorigallinarum* sp. nov.**

*Candidatus Limadaptatus stercorigallinarum* (ster.co.ri.gal.li.na'r.um. 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1063 and which is available via NCBI BioSample [SAMN15817231](#). This is a new name for the alphanumeric GTDB species sp900544575. The GC content of the type genome is 56.41% and the genome length is 1.5 Mbp.

**Description of *Candidatus Limadaptatus stercoripullorum* sp. nov.**

*Candidatus Limadaptatus stercoripullorum* (ster.co.ri.pul.lo'r.um. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 10406 and which is available via NCBI BioSample [SAMN15817154](#). The GC content of the type genome is 61.19% and the genome length is 1.4 Mbp.

Table 1 (continued)

**Description of *Candidatus Limenecus* gen. nov.**

*Candidatus Limenecus* (Lim.en.e'cus. L. masc. n. *limus* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Limenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Limenecus avicola*. This is a name for the alphanumeric GTDB genus CAG-306. 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 *Gastranaerophilales* and to the family *Gastranaerophilaceae*.

**Description of *Candidatus Limenecus avicola* sp. nov.**

*Candidatus Limenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK154-7741 and which is available via NCBI BioSample SAMN15817206. This is a new name for the alphanumeric GTDB species sp000980375. The GC content of the type genome is 36.63% and the genome length is 2.1 Mbp.

**Description of *Candidatus Limicola* gen. nov.**

*Candidatus Limicola* (Li.mi'co.la. L. masc. n. *limus* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Limicola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Limicola stercorigallinarum*. This is a name for the alphanumeric GTDB genus An2-A. 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 *Coriobacteriales* and to the family *Coriobacteriaceae*.

**Description of *Candidatus Limicola stercorigallinarum* sp. nov.**

*Candidatus Limicola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-16188 and which is available via NCBI BioSample SAMN15817082. The GC content of the type genome is 60.48% and the genome length is 2.0 Mbp.

**Description of *Candidatus Limihabitans* gen. nov.**

*Candidatus Limihabitans* (Li.mi.ha'bi.tans. L. masc. n. *limus* dung; L. pres. part. *habitans* an inhabitant; N.L. fem. n. *Limihabitans* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Limihabitans stercoravium*. This is a name for the alphanumeric GTDB genus UMGS1707. 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-314*.

**Description of *Candidatus Limihabitans stercoravium* sp. nov.**

*Candidatus Limihabitans 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3394 and which is available via NCBI BioSample SAMN15817227. This is a new name for the alphanumeric GTDB species sp900547645. The GC content of the type genome is 43.23% and the genome length is 1.6 Mbp.

**Description of *Candidatus Limimorpha* gen. nov.**

*Candidatus Limimorpha* (Li.mi.mor'pha. L. masc. n. *limus* dung; Gr. fem. n. *morphe* a form, shape; N.L. fem. n. *Limimorpha* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Limimorpha avicola*. This is a name for the alphanumeric GTDB genus F082. 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 *F082*.

**Description of *Candidatus Limimorpha avicola* sp. nov.**

*Candidatus Limimorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID Gambia15-481 and which is available via NCBI BioSample SAMN15817194. This is a new name for the alphanumeric GTDB species sp002633315. The GC content of the type genome is 38.09% and the genome length is 2.5 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Limiplasma* gen. nov.**

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

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Limiplasma pullicola. This is a name for the alphanumeric GTDB genus Firm-11. 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 Christensenellales and to the family CAG-74.

**Description of *Candidatus Limiplasma merdipullorum* sp. nov.**

*Candidatus* Limiplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec16-3123 and which is available via NCBI BioSample SAMN15817217. This is a new name for the alphanumeric GTDB species sp900540045. The GC content of the type genome is 61.78% and the genome length is 2.6 Mbp.

**Description of *Candidatus Limiplasma pullicola* sp. nov.**

*Candidatus* Limiplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2223 and which is available via NCBI BioSample SAMN15817092. The GC content of the type genome is 62.99% and the genome length is 2.7 Mbp.

**Description of *Candidatus Limiplasma pullistercoris* sp. nov.**

*Candidatus* Limiplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec15-2748 and which is available via NCBI BioSample SAMN15817228. This is a new name for the alphanumeric GTDB species sp900553905. The GC content of the type genome is 62.75% and the genome length is 2.8 Mbp.

**Description of *Candidatus Limiplasma stercoravium* sp. nov.**

*Candidatus* Limiplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK169-20388 and which is available via NCBI BioSample SAMN15817129. The GC content of the type genome is 62.11% and the genome length is 2.4 Mbp.

**Description of *Candidatus Limisoma* gen. nov.**

*Candidatus* Limisoma (Li.mi.so'ma. L. masc. n. *limus* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Limisoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Limisoma faecipullorum. This is a name for the alphanumeric GTDB genus CAG-279. 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 Muribaculaceae.

**Description of *Candidatus Limisoma faecipullorum* sp. nov.**

*Candidatus* Limisoma faecipullorum (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

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

**Description of *Candidatus Limisoma gallistercoris* sp. nov.**

*Candidatus* Limisoma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK136-1475 and which is available via NCBI BioSample SAMN15817174. This is a new name for the alphanumeric GTDB species sp900550025. The GC content of the type genome is 48.31% and the genome length is 2.2 Mbp.

Table 1 (continued)

**Description of *Candidatus Limisoma intestinavium* sp. nov.**

*Candidatus Limisoma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 17073 and which is available via NCBI BioSample [SAMN15817199](#). This is a new name for the alphanumeric GTDB species sp900541555. The GC content of the type genome is 48.25% and the genome length is 1.8 Mbp.

**Description of *Candidatus Limivicinus* gen. nov.**

*Candidatus Limivicinus* (Li.mi.vi.ci'nus. L. masc. n. *limus* dung; L. masc. n. *vicinus* a neighbour; N.L. masc. n. *Limivicinus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Limivicinus faecipullorum*. This is a name for the alphanumeric GTDB genus UBA1777. 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 Limivicinus faecipullorum* sp. nov.**

*Candidatus Limivicinus faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcec3-8852 and which is available via NCBI BioSample [SAMN15817081](#). The GC content of the type genome is 58.52% and the genome length is 1.9 Mbp.

**Description of *Candidatus Limivivens* gen. nov.**

*Candidatus Limivivens* (Li.mi.vi'vens. L. masc. n. *limus* dung; N.L. pres. part. *vivens* living; N.L. fem. n. *Limivivens* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Limivivens intestinipullorum*. This is a name for the alphanumeric GTDB genus GCA-900066135. 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 Limivivens intestinipullorum* sp. nov.**

*Candidatus Limivivens intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK190-19873 and which is available via NCBI BioSample [SAMN15817025](#). The GC content of the type genome is 52.58% and the genome length is 3.4 Mbp.

**Description of *Candidatus Limivivens merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej3B21-11622 and which is available via NCBI BioSample [SAMN15817007](#). The GC content of the type genome is 50.09% and the genome length is 3.3 Mbp.

**Description of *Candidatus Limosilactobacillus excrementigallarum* sp. nov.**

*Candidatus Limosilactobacillus excrementigallarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2685 and which is available via NCBI BioSample [SAMN15816672](#). The GC content of the type genome is 41.67% and the genome length is 1.4 Mbp.

**Description of *Candidatus Limosilactobacillus faecipullorum* sp. nov.**

*Candidatus Limosilactobacillus faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 7774 and which is available via NCBI BioSample [SAMN15816663](#). The GC content of the type genome is 43.03% and the genome length is 1.5 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Limosilactobacillus gallistercoris* sp. nov.**

*Candidatus Limosilactobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK158-2993 and which is available via NCBI BioSample [SAMN15816598](#). The GC content of the type genome is 52.74% and the genome length is 1.2 Mbp.

**Description of *Candidatus Limosilactobacillus intestinavium* sp. nov.**

*Candidatus Limosilactobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2331 and which is available via NCBI BioSample [SAMN15816838](#). This is a new name for the alphanumeric GTDB species sp900557215. The GC content of the type genome is 38.77% and the genome length is 1.5 Mbp.

**Description of *Candidatus Limosilactobacillus intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK176-5070 and which is available via NCBI BioSample [SAMN15816600](#). The GC content of the type genome is 54.91% and the genome length is 1.5 Mbp.

**Description of *Candidatus Limosilactobacillus intestinipullorum* sp. nov.**

*Candidatus Limosilactobacillus intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecolR2B26-165 and which is available via NCBI BioSample [SAMN15816601](#). The GC content of the type genome is 49.12% and the genome length is 1.6 Mbp.

**Description of *Candidatus Limosilactobacillus merdavium* sp. nov.**

*Candidatus Limosilactobacillus merdavium* (mer.da'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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 876 and which is available via NCBI BioSample [SAMN15816723](#). The GC content of the type genome is 39.60% and the genome length is 1.4 Mbp.

**Description of *Candidatus Limosilactobacillus merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej3B15-572 and which is available via NCBI BioSample [SAMN15816736](#). The GC content of the type genome is 44.36% and the genome length is 1.4 Mbp.

**Description of *Candidatus Limosilactobacillus merdipullorum* sp. nov.**

*Candidatus Limosilactobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHejej3B27-2180 and which is available via NCBI BioSample [SAMN15816756](#). The GC content of the type genome is 49.90% and the genome length is 1.3 Mbp.

**Description of *Candidatus Limousia* gen. nov.**

*Candidatus Limousia* (Lim.ou'si.a. L. masc. n. *limus* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Limousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Limousia pullorum*. This is a name for the alphanumeric GTDB genus An172. 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 *Acutalibacteraceae*.



Table 1 (continued)

**Description of *Candidatus Limousia pullorum* sp. nov.**

*Candidatus* Limousia pullorum (pul.lo'rum. L. gen. pl. n. *pullorum* of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-1684 and which is available via NCBI BioSample [SAMN15817202](#). This is a new name for the alphanumeric GTDB species sp002160515. The GC content of the type genome is 40.91% and the genome length is 1.7 Mbp.

**Description of *Candidatus Luteimonas excrementigallinarum* sp. nov.**

*Candidatus* Luteimonas excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK165-14161 and which is available via NCBI BioSample [SAMN15816707](#). The GC content of the type genome is 68.39% and the genome length is 2.5 Mbp.

**Description of *Candidatus Luteococcus avicola* sp. nov.**

*Candidatus* Luteococcus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 4979 and which is available via NCBI BioSample [SAMN15816867](#). This is a new name for the alphanumeric GTDB species sp002387005. The GC content of the type genome is 68.14% and the genome length is 2.9 Mbp.

**Description of *Candidatus Mailhella excrementigallinarum* sp. nov.**

*Candidatus* Mailhella excrementigallinarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 708 and which is available via NCBI BioSample [SAMN15816871](#). This is a new name for the alphanumeric GTDB species sp003150275. The GC content of the type genome is 60.07% and the genome length is 3.0 Mbp.

**Description of *Candidatus Mailhella merdavium* sp. nov.**

*Candidatus* Mailhella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec6-11642 and which is available via NCBI BioSample [SAMN15816648](#). The GC content of the type genome is 56.49% and the genome length is 2.7 Mbp.

**Description of *Candidatus Mailhella merdigallinarum* sp. nov.**

*Candidatus* Mailhella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK186-16707 and which is available via NCBI BioSample [SAMN15816842](#). This is a new name for the alphanumeric GTDB species sp900541395. The GC content of the type genome is 61.96% and the genome length is 2.4 Mbp.

**Description of *Candidatus Massiliomicrobiota merdigallinarum* sp. nov.**

*Candidatus* Massiliomicrobiota 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK183-8118 and which is available via NCBI BioSample [SAMN15816832](#). This is a new name for the alphanumeric GTDB species sp002160815. The GC content of the type genome is 31.33% and the genome length is 2.4 Mbp.

**Description of *Candidatus Mediterraneibacter avicola* sp. nov.**

*Candidatus* Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej3B3-8055 and which is available via NCBI BioSample [SAMN15816612](#). The GC content of the type genome is 48.65% and the genome length is 2.4 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Mediterraneibacter caccavium* sp. nov.**

*Candidatus Mediterraneibacter caccavium* (cacc.a'vi.um. Gr. fem. n. *kakke* faeces; L. fem. n. *avis* bird; N.L. gen. n. *caccavium* of bird faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej5B23-15282 and which is available via NCBI BioSample [SAMN15816861](#). This is a new name for the alphanumeric GTDB species sp002161355. The GC content of the type genome is 51.40% and the genome length is 2.6 Mbp.

**Description of *Candidatus Mediterraneibacter caccogallinarum* sp. nov.**

*Candidatus Mediterraneibacter caccogallinarum* (cac.co.gal.li.na'rum. Gr. fem. n. *kakke* faeces; L. fem. n. *gallina* hen; N.L. gen. n. *caccogallinarum* of hen faeces)

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

**Description of *Candidatus Mediterraneibacter colneyensis* sp. nov.**

*Candidatus Mediterraneibacter colneyensis* (col.ney.en'sis. N.L. fem. adj. *colneyensis* pertaining to Colney, the Norfolk village which is home to the Quadram Institute where the species was first described)

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

**Description of *Candidatus Mediterraneibacter cottocaccae* sp. nov.**

*Candidatus Mediterraneibacter cottocaccae* (cot.to.cac'cae. Gr. masc. n. *kottos* chicken Gr. fem. n. *kakke* faeces; N.L. gen. n. *cottocaccae* of chicken faeces)

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

**Description of *Candidatus Mediterraneibacter excrementavium* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej2B2-38138 and which is available via NCBI BioSample [SAMN15816630](#). The GC content of the type genome is 51.42% and the genome length is 2.1 Mbp.

**Description of *Candidatus Mediterraneibacter excrementigallinarum* sp. nov.**

*Candidatus Mediterraneibacter excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK143-6153 and which is available via NCBI BioSample [SAMN15816575](#). The GC content of the type genome is 48.97% and the genome length is 3.1 Mbp.

**Description of *Candidatus Mediterraneibacter excrementipullorum* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej6B24-3024 and which is available via NCBI BioSample [SAMN15816810](#). This is a new name for the alphanumeric GTDB species sp9005552. The GC content of the type genome is 48.88% and the genome length is 2.4 Mbp.

**Description of *Candidatus Mediterraneibacter faecavium* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK196-7946 and which is available via NCBI BioSample [SAMN15816577](#). The GC content of the type genome is 49.45% and the genome length is 2.8 Mbp.

Table 1 (continued)

**Description of *Candidatus Mediterraneibacter faecigallinarum* sp. nov.**

*Candidatus Mediterraneibacter faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-1692 and which is available via NCBI BioSample [SAMN15816637](#). The GC content of the type genome is 51.63% and the genome length is 2.6 Mbp.

**Description of *Candidatus Mediterraneibacter faecipullorum* sp. nov.**

*Candidatus Mediterraneibacter faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW19-954 and which is available via NCBI BioSample [SAMN15816638](#). The GC content of the type genome is 47.71% and the genome length is 2.7 Mbp.

**Description of *Candidatus Mediterraneibacter gallistercoris* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK165-2605 and which is available via NCBI BioSample [SAMN15816636](#). The GC content of the type genome is 47.20% and the genome length is 2.5 Mbp.

**Description of *Candidatus Mediterraneibacter guildfordensis* sp. nov.**

*Candidatus Mediterraneibacter guildfordensis* (guild.ford.en'sis. N.L. masc. adj. *guildfordensis* pertaining to Guildford, English town that is home to the University of Surrey)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcec3-18395 and which is available via NCBI BioSample [SAMN15816784](#). The GC content of the type genome is 52.47% and the genome length is 2.2 Mbp.

**Description of *Candidatus Mediterraneibacter intestinavium* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec12-2655 and which is available via NCBI BioSample [SAMN15816591](#). The GC content of the type genome is 50.53% and the genome length is 2.9 Mbp.

**Description of *Candidatus Mediterraneibacter intestinigallinarum* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec15-2237 and which is available via NCBI BioSample [SAMN15816645](#). The GC content of the type genome is 46.81% and the genome length is 3.1 Mbp.

**Description of *Candidatus Mediterraneibacter intestinipullorum* sp. nov.**

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

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

**Description of *Candidatus Mediterraneibacter merdavium* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcolR7-8672 and which is available via NCBI BioSample [SAMN15816660](#). The GC content of the type genome is 49.88% and the genome length is 2.6 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Mediterraneibacter merdigallinarum* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW16-1363 and which is available via NCBI BioSample [SAMN15816674](#). The GC content of the type genome is 46.95% and the genome length is 2.4 Mbp.

**Description of *Candidatus Mediterraneibacter merdipullorum* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej4B16-6421 and which is available via NCBI BioSample [SAMN15816679](#). The GC content of the type genome is 54.17% and the genome length is 2.2 Mbp.

**Description of *Candidatus Mediterraneibacter norfolkensis* sp. nov.**

*Candidatus Mediterraneibacter norfolkensis* (nor.folk.en'sis. N.L. masc. adj. *norfolkensis* pertaining to the English county of Norfolk)

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

**Description of *Candidatus Mediterraneibacter norwichensis* sp. nov.**

*Candidatus Mediterraneibacter norwichensis* (nor.wich.en'sis. N.L. masc. adj. *norwichensis* pertaining to English city of Norwich)

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

**Description of *Candidatus Mediterraneibacter ornithocaccae* sp. nov.**

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

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

**Description of *Candidatus Mediterraneibacter pullicola* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej2B20-11307 and which is available via NCBI BioSample [SAMN15816678](#). The GC content of the type genome is 47.35% and the genome length is 2.1 Mbp.

**Description of *Candidatus Mediterraneibacter pullistercoris* sp. nov.**

*Candidatus Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej8B7-7219 and which is available via NCBI BioSample [SAMN15816602](#). The GC content of the type genome is 48.73% and the genome length is 2.3 Mbp.

**Description of *Candidatus Mediterraneibacter quadrami* sp. nov.**

*Candidatus Mediterraneibacter quadrami* (quad.ra'mi. N.L. gen. n. *quadrami* of the Quadram Institute)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec15-3976 and which is available via NCBI BioSample [SAMN15816790](#). The GC content of the type genome is 52.68% and the genome length is 2.0 Mbp.

Table 1 (continued)

**Description of *Candidatus Mediterraneibacter stercoravium* sp. nov.**

*Candidatus* Mediterraneibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK196-3914 and which is available via NCBI BioSample [SAMN15816603](#).

The GC content of the type genome is 48.72% and the genome length is 2.5 Mbp.

**Description of *Candidatus Mediterraneibacter stercorigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-13045 and which is available via NCBI BioSample [SAMN15816697](#).

The GC content of the type genome is 50.04% and the genome length is 2.3 Mbp.

**Description of *Candidatus Mediterraneibacter stercoripullorum* sp. nov.**

*Candidatus* Mediterraneibacter stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-1396 and which is available via NCBI BioSample [SAMN15816610](#).

The GC content of the type genome is 48.12% and the genome length is 3.2 Mbp.

**Description of *Candidatus Mediterraneibacter surreyensis* sp. nov.**

*Candidatus* Mediterraneibacter surreyensis (sur.rey.en'sis. N.L. masc. adj. *surreyensis* pertaining to the English county of Surrey where the samples in the study were collected)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK177-12742 and which is available via NCBI BioSample [SAMN15816593](#).

The GC content of the type genome is 46.80% and the genome length is 2.9 Mbp.

**Description of *Candidatus Mediterraneibacter tabaqchaliae* sp. nov.**

*Candidatus* Mediterraneibacter tabaqchaliae (ta.baq.cha'li.ae. N.L. fem. gen. n. *taqaqchaliae* named in honour of British microbiologist Soad Tabaqchali)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej3B3-11674 and which is available via NCBI BioSample [SAMN15816791](#).

The GC content of the type genome is 51.91% and the genome length is 2.7 Mbp.

**Description of *Candidatus Mediterraneibacter vanvlietii* sp. nov.**

*Candidatus* Mediterraneibacter vanvlietii (van.vliet'i.i. N.L. gen. n. *vanvlietii* named in honour of Dutch microbiologist Arnoud van Vliet)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec1-362 and which is available via NCBI BioSample [SAMN15816623](#). The GC content of the type genome is 48.47% and the genome length is 3.0 Mbp.

**Description of *Candidatus Megamonas gallistercoris* sp. nov.**

*Candidatus* Megamonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-7947 and which is available via NCBI BioSample [SAMN15816859](#). This is a new name for the alphanumeric GTDB species sp900554895. The GC content of the type genome is 40.34% and the genome length is 2.2 Mbp.

**Description of *Candidatus Merdenecus* gen. nov.**

*Candidatus* Merdenecus (Merd.en'e'cus. L. fem. n. *merda* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Merdenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Merdenecus merdavium. This is a name for the alphanumeric GTDB genus MCWD5.

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*.

(Continued)



Table 1 (continued)

**Description of *Candidatus Merdenecus pullicola* sp. nov.**

*Candidatus Merdenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK160-2840 and which is available via NCBI BioSample [SAMN15817122](#). The GC content of the type genome is 35.46% and the genome length is 2.6 Mbp.

**Description of *Candidatus Merdibacter merdavium* sp. nov.**

*Candidatus Merdibacter merdavium* (mer.da'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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK187-11901 and which is available via NCBI BioSample [SAMN15816582](#). The GC content of the type genome is 53.13% and the genome length is 2.1 Mbp.

**Description of *Candidatus Merdibacter merdigallinarum* sp. nov.**

*Candidatus Merdibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-19782 and which is available via NCBI BioSample [SAMN15816595](#). The GC content of the type genome is 53.92% and the genome length is 1.8 Mbp.

**Description of *Candidatus Merdibacter merdipullorum* sp. nov.**

*Candidatus Merdibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-19782 and which is available via NCBI BioSample [SAMN15816850](#). This is a new name for the alphanumeric GTDB species sp900543035. The GC content of the type genome is 55.41% and the genome length is 1.9 Mbp.

**Description of *Candidatus Merdicola* gen. nov.**

*Candidatus Merdicola* (Mer.di'co.la. L. fem. n. *merda* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Merdicola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Merdicola faecigallinarum*. This is a name for the alphanumeric GTDB genus CAG-354. 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 TANB77 and to the family CAG-508.

**Description of *Candidatus Merdicola faecigallinarum* sp. nov.**

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

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

**Description of *Candidatus Merdimorpha* gen. nov.**

*Candidatus Merdimorpha* (Mer.di.mor'pha. L. fem. n. *merda* dung; Gr. fem. n. *morphe* a form, shape; N.L. fem. n. *Merdimorpha* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Merdimorpha intestinavium*. This is a name for the alphanumeric GTDB genus UBA1820. 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 *Flavobacteriales* and to the family UBA1820.

**Description of *Candidatus Merdimorpha intestinavium* sp. nov.**

*Candidatus Merdimorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK1-7158 and which is available via NCBI BioSample [SAMN15817210](#). This is a new name for the alphanumeric GTDB species sp002314265. The GC content of the type genome is 56.50% and the genome length is 1.8 Mbp.

Table 1 (continued)

**Description of *Candidatus Merdimorpha stercoravium* sp. nov.**

*Candidatus Merdimorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1383 and which is available via NCBI BioSample [SAMN15817125](#). The GC content of the type genome is 57.82% and the genome length is 1.7 Mbp.

**Description of *Candidatus Merdiplasma* gen. nov.**

*Candidatus Merdiplasma* (Mer.di.plas'ma. L. fem. n. *merda* dung; Gr. neut. n. *plasma* a form; N.L. neut. n. *Merdiplasma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Merdiplasma excrementigallinarum*. This is a name for the alphanumeric GTDB genus UBA2856. 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 Merdiplasma excrementigallinarum* sp. nov.**

*Candidatus Merdiplasma excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec6-7307 and which is available via NCBI BioSample [SAMN15817161](#). The GC content of the type genome is 52.97% and the genome length is 2.4 Mbp.

**Description of *Candidatus Merdisoma* gen. nov.**

*Candidatus Merdisoma* (Mer.di.so'ma. L. fem. n. *merda* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Merdisoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Merdisoma merdipullorum*. This is a name for the alphanumeric GTDB genus GCA-900066575. 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 Merdisoma faecale* sp. nov.**

*Candidatus Merdisoma faecalis* (fae.ca'le. L. neut. adj. *faecale* of faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcolR2-1241 and which is available via NCBI BioSample [SAMN15817219](#). This is a new name for the alphanumeric GTDB species sp002160765. The GC content of the type genome is 51.56% and the genome length is 2.7 Mbp.

**Description of *Candidatus Merdisoma merdipullorum* sp. nov.**

*Candidatus Merdisoma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK197-19677 and which is available via NCBI BioSample [SAMN15817042](#). The GC content of the type genome is 50.06% and the genome length is 2.9 Mbp.

**Description of *Candidatus Merdivicinus* gen. nov.**

*Candidatus Merdivicinus* (Mer.di.vi.ci'nus. L. fem. n. *merda* dung; L. masc. n. *vicinus* a neighbour; N.L. masc. n. *Merdivicinus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Merdivicinus faecavium*. This is a name for the alphanumeric GTDB genus UMG1826. 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 *Ruminococcaceae*.

**Description of *Candidatus Merdivicinus excrementipullorum* sp. nov.**

*Candidatus Merdivicinus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK199-13235 and which is available via NCBI BioSample [SAMN15817032](#). The GC content of the type genome is 54.67% and the genome length is 2.5 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Merdivicinus faecavium* sp. nov.**

*Candidatus Merdivicinus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK186-19003 and which is available via NCBI BioSample [SAMN15817036](#). The GC content of the type genome is 61.26% and the genome length is 2.5 Mbp.

**Description of *Candidatus Merdivicinus intestinavium* sp. nov.**

*Candidatus Merdivicinus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK188-1901 and which is available via NCBI BioSample [SAMN15817003](#). The GC content of the type genome is 59.41% and the genome length is 2.3 Mbp.

**Description of *Candidatus Merdivicinus intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec18-2170 and which is available via NCBI BioSample [SAMN15817163](#). The GC content of the type genome is 56.27% and the genome length is 2.5 Mbp.

**Description of *Candidatus Merdivivens* gen. nov.**

*Candidatus Merdivivens* (Mer.di.vi'vens. L. fem. n. *merda* dung; N.L. pres. part. *vivens* living; N.L. fem. n. *Merdivivens* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Merdivivens pullistercoris*. This is a name for the alphanumeric GTDB genus UBA3382. 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 Merdivivens faecigallarum* sp. nov.**

*Candidatus Merdivivens faecigallarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B3-2255 and which is available via NCBI BioSample [SAMN15817168](#). This is a new name for the alphanumeric GTDB species sp002159555. The GC content of the type genome is 49.87% and the genome length is 1.9 Mbp.

**Description of *Candidatus Merdivivens pullicola* sp. nov.**

*Candidatus Merdivivens 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID B1-8020 and which is available via NCBI BioSample [SAMN15817062](#). The GC content of the type genome is 48.22% and the genome length is 2.0 Mbp.

**Description of *Candidatus Merdivivens pullistercoris* sp. nov.**

*Candidatus Merdivivens 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 10037 and which is available via NCBI BioSample [SAMN15817074](#). The GC content of the type genome is 48.95% and the genome length is 2.1 Mbp.

**Description of *Candidatus Merdousia* gen. nov.**

*Candidatus Merdousia* (Mer.d.ou'si.a. L. fem. n. *merda* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Merdousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Merdousia gallistercoris*. This is a name for the alphanumeric GTDB genus CAG-312. 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 *Opitutales* and to the family *CAG-312*.

Table 1 (continued)

**Description of *Candidatus Merdousia gallistercoris* sp. nov.**

*Candidatus Merdousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK197-16368 and which is available via NCBI BioSample [SAMN15817207](#). This is a new name for the alphanumeric GTDB species sp900545715. The GC content of the type genome is 49.37% and the genome length is 2.4 Mbp.

**Description of *Candidatus Methanocorpusculum faecipullorum* sp. nov.**

*Candidatus Methanocorpusculum faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

An archaeal species identified by metagenomic analyses. This species includes all archaea with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID E1-3281 and which is available via NCBI BioSample [SAMN15816796](#). The GC content of the type genome is 50.72% and the genome length is 1.2 Mbp.

**Description of *Candidatus Methanospyradosia* gen. nov.**

*Candidatus Methanospyradosia* (Meth.an.o.spy.rad.ou'si.a. N.L. neut. n. *methanum*, methane; N.L. pref. *methano-*, pertaining to methane; Gr. fem. n. *spyras* ball of dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Methanospyradosia* a methanogenic microbe associated with the intestines)

An archaeal genus identified by metagenomic analyses. The genus includes all archaea with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Methanospyradosia avicola*. This is a name for the alphanumeric GTDB genus UBA71. 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 *Methanomassiliicoccales* and to the family *Methanomethylophilaceae*.

**Description of *Candidatus Methanospyradosia avicola* sp. nov.**

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

An archaeal species identified by metagenomic analyses. This species includes all archaea with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 6227 and which is available via NCBI BioSample [SAMN15817164](#). The GC content of the type genome is 60.22% and the genome length is 1.5 Mbp.

**Description of *Candidatus Microbacterium pullistercoris* sp. nov.**

*Candidatus Microbacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej1B1-5908 and which is available via NCBI BioSample [SAMN15816649](#). The GC content of the type genome is 68.74% and the genome length is 2.5 Mbp.

**Description of *Candidatus Microbacterium stercoravium* sp. nov.**

*Candidatus Microbacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej8B7-3636 and which is available via NCBI BioSample [SAMN15816680](#). The GC content of the type genome is 69.44% and the genome length is 2.5 Mbp.

**Description of *Candidatus Monoglobus merdigallinarum* sp. nov.**

*Candidatus Monoglobus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5790 and which is available via NCBI BioSample [SAMN15816780](#). The GC content of the type genome is 48.24% and the genome length is 1.5 Mbp.

**Description of *Candidatus Mucispirillum faecigallinarum* sp. nov.**

*Candidatus Mucispirillum faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW4-1371 and which is available via NCBI BioSample [SAMN15816684](#). The GC content of the type genome is 31.75% and the genome length is 2.2 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Negativibacillus faecipullorum* sp. nov.**

*Candidatus Negativibacillus faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec6-1156 and which is available via NCBI BioSample [SAMN15816879](#). This is a new name for the alphanumeric GTDB species sp900547455. The GC content of the type genome is 57.54% and the genome length is 2.0 Mbp.

**Description of *Candidatus Nesterenkonia stercoripullorum* sp. nov.**

*Candidatus Nesterenkonia stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHejej3B27-3195 and which is available via NCBI BioSample [SAMN15816751](#). The GC content of the type genome is 65.88% and the genome length is 2.6 Mbp.

**Description of *Candidatus Niameybacter stercoravium* sp. nov.**

*Candidatus Niameybacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2467 and which is available via NCBI BioSample [SAMN15816773](#). The GC content of the type genome is 35.14% and the genome length is 2.9 Mbp.

**Description of *Candidatus Nocardiosis merdipullorum* sp. nov.**

*Candidatus Nocardiosis 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej10B9-18110 and which is available via NCBI BioSample [SAMN15816716](#). The GC content of the type genome is 65.81% and the genome length is 4.2 Mbp.

**Description of *Candidatus Nosocomiicoccus stercorigallinarum* sp. nov.**

*Candidatus Nosocomiicoccus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK169-14505 and which is available via NCBI BioSample [SAMN15816647](#). The GC content of the type genome is 34.64% and the genome length is 1.3 Mbp.

**Description of *Candidatus Oceanisphaera merdipullorum* sp. nov.**

*Candidatus Oceanisphaera 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 819 and which is available via NCBI BioSample [SAMN15816797](#). The GC content of the type genome is 50.19% and the genome length is 2.9 Mbp.

**Description of *Candidatus Odoribacter faecigallinarum* sp. nov.**

*Candidatus Odoribacter faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 23274 and which is available via NCBI BioSample [SAMN15816743](#). The GC content of the type genome is 48.17% and the genome length is 2.2 Mbp.

**Description of *Candidatus Olsenella avicola* sp. nov.**

*Candidatus Olsenella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK1-7693 and which is available via NCBI BioSample [SAMN15816923](#). This is a new name for the alphanumeric GTDB species sp002159625. Although GTDB has assigned this species to the genus it calls *Olsenella\_E*, 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 67.59% and the genome length is 2.2 Mbp.



Table 1 (continued)

**Description of *Candidatus Olsenella avistercoris* sp. nov.**

*Candidatus* Olsenella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK136-6238 and which is available via NCBI BioSample [SAMN15816919](#). This is a new name for the alphanumeric GTDB species sp002160255. Although GTDB has assigned this species to the genus it calls Olsenella\_E, 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 69.05% and the genome length is 2.0 Mbp.

**Description of *Candidatus Olsenella excrementavium* sp. nov.**

*Candidatus* Olsenella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej10B9-743 and which is available via NCBI BioSample [SAMN15816922](#). This is a new name for the alphanumeric GTDB species sp002305805. Although GTDB has assigned this species to the genus it calls Olsenella\_E, 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 66.50% and the genome length is 1.8 Mbp.

**Description of *Candidatus Olsenella excrementigallarum* sp. nov.**

*Candidatus* Olsenella excrementigallarum (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-23512 and which is available via NCBI BioSample [SAMN15816920](#). This is a new name for the alphanumeric GTDB species sp900119915. Although GTDB has assigned this species to the genus it calls Olsenella\_E, 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 68.67% and the genome length is 1.8 Mbp.

**Description of *Candidatus Olsenella pullicola* sp. nov.**

*Candidatus* Olsenella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHhec1B25-7792 and which is available via NCBI BioSample [SAMN15816895](#). Although GTDB has assigned this species to the genus it calls Olsenella\_E, 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 65.74% and the genome length is 2.3 Mbp.

**Description of *Candidatus Olsenella pullistercoris* sp. nov.**

*Candidatus* Olsenella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-14209 and which is available via NCBI BioSample [SAMN15816899](#). Although GTDB has assigned this species to the genus it calls Olsenella\_E, 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 67.21% and the genome length is 1.9 Mbp.

**Description of *Candidatus Olsenella stercoravium* sp. nov.**

*Candidatus* Olsenella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecolR3B27-1887 and which is available via NCBI BioSample [SAMN15816902](#). Although GTDB has assigned this species to the genus it calls Olsenella\_E, 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 67.26% and the genome length is 1.8 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Onthenecus* gen. nov.**

*Candidatus* Onthenecus (Onth.en.e'cus. Gr. masc. n. *onthos* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Onthenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Onthenecus intestinigallinarum. This is a name for the alphanumeric GTDB genus OEMS01. 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 Christensenellales and to the family CAG-74.

**Description of *Candidatus Onthenecus intestinigallinarum* sp. nov.**

*Candidatus* Onthenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxje2B14-6234 and which is available via NCBI BioSample SAMN15817054. The GC content of the type genome is 66.20% and the genome length is 2.4 Mbp.

**Description of *Candidatus Onthocola* gen. nov.**

*Candidatus* Onthocola (On.tho'co.la. Gr. masc. n. *onthos* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Onthocola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Onthocola gallistercoris. This is a name for the alphanumeric GTDB genus. 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 Onthocola gallistercoris* sp. nov.**

*Candidatus* Onthocola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK187-14744 and which is available via NCBI BioSample SAMN15817044. The GC content of the type genome is 48.32% and the genome length is 2.4 Mbp.

**Description of *Candidatus Onthocola stercoravium* sp. nov.**

*Candidatus* Onthocola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW5-5982 and which is available via NCBI BioSample SAMN15817021. The GC content of the type genome is 28.08% and the genome length is 1.4 Mbp.

**Description of *Candidatus Onthocola stercorigallinarum* sp. nov.**

*Candidatus* Onthocola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-3072 and which is available via NCBI BioSample SAMN15817046. The GC content of the type genome is 27.21% and the genome length is 1.3 Mbp.

**Description of *Candidatus Onthomonas* gen. nov.**

*Candidatus* Onthomonas (On.tho.mo'nas. Gr. masc. n. *onthos* dung; L. fem. n. *monas* a monad; N.L. fem. n. *Onthomonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Onthomonas avicola. This is a name for the alphanumeric GTDB genus NK3B98. 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 Onthomonas avicola* sp. nov.**

*Candidatus* Onthomonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-14002 and which is available via NCBI BioSample SAMN15817096. The GC content of the type genome is 63.01% and the genome length is 2.4 Mbp.

Table 1 (continued)

**Description of *Candidatus Onthomorpha* gen. nov.**

*Candidatus Onthomorpha* (On.tho.mor'pha. Gr. masc. n. *onthos* dung; Gr. fem. n. *morphe* a form, shape; N.L. fem. n. *Onthomorpha* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Onthomorpha intestinigallinarum*. This is a name for the alphanumeric GTDB genus UBA3388. 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 *P3*.

**Description of *Candidatus Onthomorpha intestinigallinarum* sp. nov.**

*Candidatus Onthomorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID Gambia16-930 and which is available via NCBI BioSample SAMN15817128. The GC content of the type genome is 42.76% and the genome length is 1.7 Mbp.

**Description of *Candidatus Onthoplasma* gen. nov.**

*Candidatus Onthoplasma* (On.tho.plas'ma. Gr. masc. n. *onthos* dung; Gr. neut. n. *plasma* a form; N.L. neut. n. *Onthoplasma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Onthoplasma faecipullorum*. This is a name for the alphanumeric GTDB genus UBA4626. 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 *UBA1242*.

**Description of *Candidatus Onthoplasma faecigallinarum* sp. nov.**

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

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

**Description of *Candidatus Onthoplasma faecipullorum* sp. nov.**

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

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

**Description of *Candidatus Onthosoma* gen. nov.**

*Candidatus Onthosoma* (On.tho.so'ma. Gr. masc. n. *onthos* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Onthosoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Onthosoma merdaviium*. This is a name for the alphanumeric GTDB genus OEMR01. 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 *Erysipelotrichales* and to the family *Erysipelotrichaceae*.

**Description of *Candidatus Onthosoma merdaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec15-4520 and which is available via NCBI BioSample SAMN15817169. This is a new name for the alphanumeric GTDB species sp900199515. The GC content of the type genome is 45.30% and the genome length is 1.6 Mbp.

**Description of *Candidatus Onthousia* gen. nov.**

*Candidatus Onthousia* (Onth.ou'si.a. Gr. masc. n. *onthos* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Onthousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Onthousia faecaviium*. This is a name for the alphanumeric GTDB genus CAG-451. 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*.

(Continued)

Table 1 (continued)

**Description of *Candidatus Onthousia excrementipullorum* sp. nov.**

*Candidatus Onthousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK184-20233 and which is available via NCBI BioSample [SAMN15817019](#). The GC content of the type genome is 27.72% and the genome length is 1.3 Mbp.

**Description of *Candidatus Onthousia faecavium* sp. nov.**

*Candidatus Onthousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-6217 and which is available via NCBI BioSample [SAMN15817026](#). The GC content of the type genome is 28.40% and the genome length is 1.3 Mbp.

**Description of *Candidatus Onthousia faecigallinarum* sp. nov.**

*Candidatus Onthousia faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK135-1819 and which is available via NCBI BioSample [SAMN15817105](#). The GC content of the type genome is 32.62% and the genome length is 1.1 Mbp.

**Description of *Candidatus Onthousia faecipullorum* sp. nov.**

*Candidatus Onthousia faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-26880 and which is available via NCBI BioSample [SAMN15817040](#). The GC content of the type genome is 27.41% and the genome length is 1.4 Mbp.

**Description of *Candidatus Onthovicinus* gen. nov.**

*Candidatus Onthovicinus* (On.tho.vi.ci'nus. Gr. masc. n. *onthos* dung; L. masc. n. *vicinus* a neighbour; N.L. masc. n. *Onthovicinus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Onthovicinus excrementipullorum*. This is a name for the alphanumeric GTDB genus UMG51839. 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 *Acutalibacteraceae*.

**Description of *Candidatus Onthovicinus excrementipullorum* sp. nov.**

*Candidatus Onthovicinus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK185-12131 and which is available via NCBI BioSample [SAMN15817020](#). The GC content of the type genome is 55.55% and the genome length is 2.4 Mbp.

**Description of *Candidatus Onthovivens* gen. nov.**

*Candidatus Onthovivens* (On.tho.vi'vens. Gr. masc. n. *onthos* dung; N.L. pres. part. *vivens* living; N.L. fem. n. *Onthovivens* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Onthovivens merdipullorum*. This is a name for the alphanumeric GTDB genus UBA4855. 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 *RFN20* and to the family *CAG-826*.

**Description of *Candidatus Onthovivens merdipullorum* sp. nov.**

*Candidatus Onthovivens 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 11159 and which is available via NCBI BioSample [SAMN15817139](#). The GC content of the type genome is 27.05% and the genome length is 1.5 Mbp.

Table 1 (continued)

**Description of *Candidatus Ornithocaccomicrobium* gen. nov.**

*Candidatus* Ornithocaccomicrobium (Or.ni.tho.cac.co.mi.cro'bi.um. Gr. masc. or fem. n. *ornis*, *ornithos* bird; Gr. fem. n. *kakke* faeces; N.L. neut. n. *microbium* a microbe; N.L. neut. n. *Ornithocaccomicrobium* A microbe found in chicken faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Ornithocaccomicrobium faecavium. This genus was identified but not named by [Glendinning et al. \(2020\)](#). 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 *Christensenellales* and to the family CAG-74.

**Description of *Candidatus Ornithocaccomicrobium faecavium* sp. nov.**

*Candidatus* Ornithocaccomicrobium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK183-6373 and which is available via NCBI BioSample [SAMN15816945](#). The GC content of the type genome is 59.48% and the genome length is 2.9 Mbp.

**Description of *Candidatus Ornithoclostridium* gen. nov.**

*Candidatus* Ornithoclostridium (Or.ni.tho.clos.tri'di.um. Gr. masc. or fem. n. *ornis*, *ornithos* bird; N.L. neut. n. *Clostridium* a genus name; N.L. neut. n. *Ornithoclostridium* a genus related to the genus *Clostridium* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Ornithoclostridium excrementipullorum. 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 *Christensenellales* and to the family UBA3700.

**Description of *Candidatus Ornithoclostridium excrementipullorum* sp. nov.**

*Candidatus* Ornithoclostridium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW5-1639 and which is available via NCBI BioSample [SAMN15816971](#). The GC content of the type genome is 54.62% and the genome length is 1.6 Mbp.

**Description of *Candidatus Ornithoclostridium faecavium* sp. nov.**

*Candidatus* Ornithoclostridium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 63 and which is available via NCBI BioSample [SAMN15816992](#). The GC content of the type genome is 48.09% and the genome length is 1.8 Mbp.

**Description of *Candidatus Ornithoclostridium faecigallinarum* sp. nov.**

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

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

**Description of *Candidatus Ornithomonoglobus* gen. nov.**

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

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Ornithomonoglobus merdipullorum. This genus was identified but not named by [Glendinning et al. \(2020\)](#). 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 *Monoglobales* and to the family UBA1381.

**Description of *Candidatus Ornithomonoglobus intestinigallinarum* sp. nov.**

*Candidatus* Ornithomonoglobus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK181-108 and which is available via NCBI BioSample [SAMN15816941](#). The GC content of the type genome is 49.36% and the genome length is 2.2 Mbp.

(Continued)



Table 1 (continued)

**Description of *Candidatus Ornithomonoglobus merdipullorum* sp. nov.**

*Candidatus Ornithomonoglobus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID USAMLcec3-3695 and which is available via NCBI BioSample [SAMN15816942](#). The GC content of the type genome is 48.52% and the genome length is 2.7 Mbp.

**Description of *Candidatus Ornithospirochaeta* gen. nov.**

*Candidatus Ornithospirochaeta* (Or.ni.tho.spi.ro.chae'ta. Gr. masc. or fem. n. *ornis*, *ornithos* bird; N.L. fem. n. *Spirochaeta* a genus name; N.L. fem. n. *Ornithospirochaeta* a genus related to the genus *Spirochaeta* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Ornithospirochaeta stercorarium*. 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 *Sphaerochaetales* and to the family *Sphaerochaetaceae*.

**Description of *Candidatus Ornithospirochaeta avicola* sp. nov.**

*Candidatus Ornithospirochaeta 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID Gambia11-129 and which is available via NCBI BioSample [SAMN15816993](#). The GC content of the type genome is 42.81% and the genome length is 1.5 Mbp.

**Description of *Candidatus Ornithospirochaeta stercorarium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 14700 and which is available via NCBI BioSample [SAMN15816953](#). The GC content of the type genome is 46.26% and the genome length is 2.0 Mbp.

**Description of *Candidatus Ornithospirochaeta stercorigallinarum* sp. nov.**

*Candidatus Ornithospirochaeta 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec3B27-9561 and which is available via NCBI BioSample [SAMN15816957](#). The GC content of the type genome is 46.77% and the genome length is 1.9 Mbp.

**Description of *Candidatus Ornithospirochaeta stercoripullorum* sp. nov.**

*Candidatus Ornithospirochaeta stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 7293 and which is available via NCBI BioSample [SAMN15816978](#). The GC content of the type genome is 45.57% and the genome length is 2.0 Mbp.

**Description of *Candidatus Oscillibacter avistercoris* sp. nov.**

*Candidatus Oscillibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK176-14096 and which is available via NCBI BioSample [SAMN15816820](#). This is a new name for the alphanumeric GTDB species sp900556925. The GC content of the type genome is 63.55% and the genome length is 2.3 Mbp.

**Description of *Candidatus Oscillibacter excrementarium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5302 and which is available via NCBI BioSample [SAMN15816661](#). The GC content of the type genome is 63.73% and the genome length is 2.5 Mbp.

Table 1 (continued)

**Description of *Candidatus Oscillibacter excrementigallinarum* sp. nov.**

*Candidatus Oscillibacter excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec18-1249 and which is available via NCBI BioSample [SAMN15816667](#). The GC content of the type genome is 64.01% and the genome length is 2.4 Mbp.

**Description of *Candidatus Oscillibacter pullicola* sp. nov.**

*Candidatus Oscillibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcolR2-4535 and which is available via NCBI BioSample [SAMN15816652](#). The GC content of the type genome is 63.62% and the genome length is 2.4 Mbp.

**Description of *Candidatus Paenalcaligenes intestinipullorum* sp. nov.**

*Candidatus Paenalcaligenes intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 9264 and which is available via NCBI BioSample [SAMN15816786](#). The GC content of the type genome is 51.92% and the genome length is 1.8 Mbp.

**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  $\geq 95\%$  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  $\geq 95\%$  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  $\geq 95\%$  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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHeccec2B26-12326 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.

**Description of *Candidatus Parabacteroides intestinipullorum* sp. nov.**

*Candidatus Parabacteroides intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-14162 and which is available via NCBI BioSample [SAMN15816857](#). This is a new name for the alphanumeric GTDB species sp900552415. The GC content of the type genome is 50.53% and the genome length is 3.2 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Paralactobacillus gallistercoris* sp. nov.**

*Candidatus Paralactobacillus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID F6-6636 and which is available via NCBI BioSample [SAMN15816781](#). The GC content of the type genome is 35.69% and the genome length is 1.2 Mbp.

**Description of *Candidatus Paraprevotella stercoravium* sp. nov.**

*Candidatus Paraprevotella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID G3-2149 and which is available via NCBI BioSample [SAMN15816669](#). The GC content of the type genome is 45.06% and the genome length is 3.2 Mbp.

**Description of *Candidatus Paraprevotella stercorigallinarum* sp. nov.**

*Candidatus Paraprevotella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 11093 and which is available via NCBI BioSample [3SAMN15816852](#). This is a new name for the alphanumeric GTDB species sp900546665. The GC content of the type genome is 43.79% and the genome length is 2.9 Mbp.

**Description of *Candidatus Parasutterella gallistercoris* sp. nov.**

*Candidatus Parasutterella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 21611 and which is available via NCBI BioSample [SAMN15816870](#). This is a new name for the alphanumeric GTDB species sp000980495. The GC content of the type genome is 49.58% and the genome length is 1.9 Mbp.

**Description of *Candidatus Pelethenecus* gen. nov.**

*Candidatus Pelethenecus* (Pe.leth.en.e'cus. Gr. masc. n. *pelethos* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Pelethenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Pelethenecus faecipullorum*. This is a name for the alphanumeric GTDB genus UMG5268. 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 *Acholeplasmatales* and to the family *Anaeroplasmataceae*.

**Description of *Candidatus Pelethenecus faecipullorum* sp. nov.**

*Candidatus Pelethenecus faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

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

**Description of *Candidatus Pelethocola* gen. nov.**

*Candidatus Pelethocola* (Pe.le.tho'co.la. Gr. masc. n. *pelethos* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Pelethocola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Pelethocola excrementipullorum*. This is a name for the alphanumeric GTDB genus UBA5416. 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 Pelethocola excrementipullorum* sp. nov.**

*Candidatus Pelethocola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK160-5124 and which is available via NCBI BioSample [SAMN15817143](#). The GC content of the type genome is 43.72% and the genome length is 3.9 Mbp.

Table 1 (continued)

**Description of *Candidatus Pelethomonas* gen. nov.**

*Candidatus* Pelethomonas (Pe.le.tho.mo'nas. Gr. masc. n. *pelethos* dung; L. fem. n. *monas* a monad; N.L. fem. n. *Pelethomonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Pelethomonas intestinigallarum. This is a name for the alphanumeric GTDB genus UMG51872. 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 Pelethomonas intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSje2B20-3600 and which is available via NCBI BioSample SAMN15817014. The GC content of the type genome is 63.89% and the genome length is 2.2 Mbp.

**Description of *Candidatus Pelethosoma* gen. nov.**

*Candidatus* Pelethosoma (Pe.le.tho.so'ma. Gr. masc. n. *pelethos* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Pelethosoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Pelethosoma merdigallarum. This is a name for the alphanumeric GTDB genus UMG52016. 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-822*.

**Description of *Candidatus Pelethosoma merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK195-5794 and which is available via NCBI BioSample SAMN15817039. The GC content of the type genome is 30.57% and the genome length is 1.3 Mbp.

**Description of *Candidatus Pelethousia* gen. nov.**

*Candidatus* Pelethousia (Pe.leth.ou'si.a. Gr. masc. n. *pelethos* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Pelethousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Pelethousia gallinarum. This is a name for the alphanumeric GTDB genus UBA5394. 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 *Christensenellales* and to the family *CAG-138*.

**Description of *Candidatus Pelethousia gallinarum* sp. nov.**

*Candidatus* Pelethousia gallinarum (gal.li.na'rum. L. fem. n. *gallina* a hen; L. fem. gen. pl. n. *gallarum* of hens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcec27-1353 and which is available via NCBI BioSample SAMN15817178. This is a new name for the alphanumeric GTDB species sp003150565. The GC content of the type genome is 59.40% and the genome length is 2.0 Mbp.

**Description of *Candidatus Phascolarctobacterium stercoravium* sp. nov.**

*Candidatus* Phascolarctobacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec14-732 and which is available via NCBI BioSample SAMN15816834. This is a new name for the alphanumeric GTDB species sp000436095. The GC content of the type genome is 46.50% and the genome length is 1.7 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Phocaeicola caecigallinarum* sp. nov.**

*Candidatus Phocaeicola caecigallinarum* (cae.ci.gal.li.na'rum. L. neut. n. *caecum* the caecum; L. fem. n. *gallina* a hen; N.L. gen. n. *caecigallinarum* of the caecum of hens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej11B10-3694 and which is available via NCBI BioSample [SAMN15816802](#). This is a new name for the alphanumeric GTDB species sp002161565. The GC content of the type genome is 46.18% and the genome length is 3.2 Mbp.

**Description of *Candidatus Phocaeicola excrementigallinarum* sp. nov.**

*Candidatus Phocaeicola excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 12279 and which is available via NCBI BioSample [SAMN15816632](#). The GC content of the type genome is 50.57% and the genome length is 2.5 Mbp.

**Description of *Candidatus Phocaeicola excrementipullorum* sp. nov.**

*Candidatus Phocaeicola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 8470 and which is available via NCBI BioSample [SAMN15816808](#). This is a new name for the alphanumeric GTDB species sp900546095. The GC content of the type genome is 49.09% and the genome length is 3.1 Mbp.

**Description of *Candidatus Phocaeicola faecigallinarum* sp. nov.**

*Candidatus Phocaeicola faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex, faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID G4-2901 and which is available via NCBI BioSample [SAMN15816657](#). The GC content of the type genome is 40.33% and the genome length is 3.3 Mbp.

**Description of *Candidatus Phocaeicola faecipullorum* sp. nov.**

*Candidatus Phocaeicola faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex, faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 17637 and which is available via NCBI BioSample [SAMN15816682](#). The GC content of the type genome is 39.94% and the genome length is 3.9 Mbp.

**Description of *Candidatus Phocaeicola gallinarum* sp. nov.**

*Candidatus Phocaeicola gallinarum* (gal.li.na'rum. L. fem. n. *gallina* a hen; L. gen. pl. n. *gallinarum* of hens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-595 and which is available via NCBI BioSample [SAMN15816805](#). This is a new name for the alphanumeric GTDB species sp900540105. The GC content of the type genome is 45.79% and the genome length is 2.8 Mbp.

**Description of *Candidatus Phocaeicola gallistercoris* sp. nov.**

*Candidatus Phocaeicola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID Gambia9-593 and which is available via NCBI BioSample [SAMN15816698](#). The GC content of the type genome is 38.34% and the genome length is 2.3 Mbp.

**Description of *Candidatus Phocaeicola merdavium* sp. nov.**

*Candidatus Phocaeicola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK136-5299 and which is available via NCBI BioSample [SAMN15816804](#). This is a new name for the alphanumeric GTDB species sp002161765. The GC content of the type genome is 44.54% and the genome length is 2.6 Mbp.



Table 1 (continued)

**Description of *Candidatus Phocaecicola merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 17689 and which is available via NCBI BioSample [SAMN15816829](#). This is a new name for the alphanumeric GTDB species sp900066455. The GC content of the type genome is 46.19% and the genome length is 3.3 Mbp.

**Description of *Candidatus Prevotella avicola* sp. nov.**

*Candidatus Prevotella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHeccec3B27-8219 and which is available via NCBI BioSample [SAMN15816846](#). This is a new name for the alphanumeric GTDB species sp000435635. The GC content of the type genome is 51.22% and the genome length is 1.9 Mbp.

**Description of *Candidatus Prevotella intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 146 and which is available via NCBI BioSample [SAMN15816872](#). This is a new name for the alphanumeric GTDB species sp900540415. The GC content of the type genome is 56.37% and the genome length is 2.9 Mbp.

**Description of *Candidatus Prevotella stercoripullorum* sp. nov.**

*Candidatus Prevotella stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID USASDec6-549 and which is available via NCBI BioSample [SAMN15816866](#). This is a new name for the alphanumeric GTDB species sp900554045. The GC content of the type genome is 53.35% and the genome length is 2.5 Mbp.

**Description of *Candidatus Protochloridium stercorigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 12435 and which is available via NCBI BioSample [SAMN15816772](#). The GC content of the type genome is 56.70% and the genome length is 1.7 Mbp.

**Description of *Candidatus Pseudogracilibacillus intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK174-787 and which is available via NCBI BioSample [SAMN15816775](#). The GC content of the type genome is 35.03% and the genome length is 2.5 Mbp.

**Description of *Candidatus Pseudomonas excrementarium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK174-787 and which is available via NCBI BioSample [SAMN15816898](#). Although GTDB has assigned this species to the genus it calls *Pseudomonas\_D*, 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 61.84% and the genome length is 3.0 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Pullibacteroides* gen. nov.**

*Candidatus Pullibacteroides* (Pul.li.bac.te.ro'i.des. L. masc. n. *pullus* a young chicken; N.L. masc. n. *Bacteroides* a genus name; N.L. masc. n. *Pullibacteroides* a genus related to the genus *Bacteroides* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Pullibacteroides excrementarium*. 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 *P3*.

**Description of *Candidatus Pullibacteroides excrementarium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2889 and which is available via NCBI BioSample SAMN15816989. The GC content of the type genome is 51.34% and the genome length is 2.4 Mbp.

**Description of *Candidatus Pullichristensenella* gen. nov.**

*Candidatus Pullichristensenella* (Pul.li.chris.ten.sen.el'la. L. masc. n. *pullus* a young chicken; N.L. fem. n. *Christensenella* a genus name; N.L. fem. n. *Pullichristensenella* a genus related to the genus *Christensenella* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Pullichristensenella avicola*. 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 *Christensenellales* and to the family *CAG-74*.

**Description of *Candidatus Pullichristensenella avicola* sp. nov.**

*Candidatus Pullichristensenella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 10205 and which is available via NCBI BioSample SAMN15816956. The GC content of the type genome is 63.02% and the genome length is 2.3 Mbp.

**Description of *Candidatus Pullichristensenella excrementigallarum* sp. nov.**

*Candidatus Pullichristensenella excrementigallarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcec3-11533 and which is available via NCBI BioSample SAMN15816983. The GC content of the type genome is 57.19% and the genome length is 2.2 Mbp.

**Description of *Candidatus Pullichristensenella excrementipullorum* sp. nov.**

*Candidatus Pullichristensenella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1279 and which is available via NCBI BioSample SAMN15817001. The GC content of the type genome is 63.33% and the genome length is 2.7 Mbp.

**Description of *Candidatus Pullichristensenella stercorigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej6B24-2974 and which is available via NCBI BioSample SAMN15816933. The GC content of the type genome is 60.06% and the genome length is 2.7 Mbp.

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

*Candidatus Pullichristensenella stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5266 and which is available via NCBI BioSample SAMN15816952. The GC content of the type genome is 64.02% and the genome length is 2.3 Mbp.

Table 1 (continued)

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

*Candidatus Pullilachnospira* (Pul.li.lach.no.spi'ra. L. masc. n. *pullus* a young chicken; N.L. fem. n. *Lachnospira* a genus name; N.L. fem. n. *Pullilachnospira* a genus related to the genus *Lachnospira* but distinct from it and found in poultry)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Pullilachnospira stercorarium*. This genus was identified but not named by [Glendinning et al. \(2020\)](#). 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 Pullilachnospira gallistercoris* sp. nov.**

*Candidatus Pullilachnospira 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej5B23-6657 and which is available via NCBI BioSample [SAMN15816938](#). The GC content of the type genome is 53.36% and the genome length is 2.5 Mbp.

**Description of *Candidatus Pullilachnospira intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK192-16996 and which is available via NCBI BioSample [SAMN15816938](#). The GC content of the type genome is 51.71% and the genome length is 2.8 Mbp.

**Description of *Candidatus Pullilachnospira stercorarium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec2-4451 and which is available via NCBI BioSample [SAMN15816944](#). The GC content of the type genome is 53.14% and the genome length is 2.8 Mbp.

**Description of *Candidatus Pygmaibacter gallistercoris* sp. nov.**

*Candidatus Pygmaibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-17065 and which is available via NCBI BioSample [SAMN15816776](#). The GC content of the type genome is 61.74% and the genome length is 1.6 Mbp.

**Description of *Candidatus Rikenella faecigallarum* sp. nov.**

*Candidatus Rikenella faecigallarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjec15-1070 and which is available via NCBI BioSample [SAMN15816768](#). The GC content of the type genome is 56.15% and the genome length is 1.8 Mbp.

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

*Candidatus Rothia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-9195 and which is available via NCBI BioSample [SAMN15816701](#). The GC content of the type genome is 60.05% and the genome length is 2.1 Mbp.

**Description of *Candidatus Rothia avistercoris* sp. nov.**

*Candidatus Rothia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej10B9-4811 and which is available via NCBI BioSample [SAMN15816788](#). The GC content of the type genome is 59.79% and the genome length is 2.0 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Ruania gallistercoris* sp. nov.**

*Candidatus* Ruania 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej4B4-7305 and which is available via NCBI BioSample [SAMN15816695](#). The GC content of the type genome is 69.62% and the genome length is 4.4 Mbp.

**Description of *Candidatus Rubneribacter avistercoris* sp. nov.**

*Candidatus* Rubneribacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-20359 and which is available via NCBI BioSample [SAMN15816703](#). The GC content of the type genome is 65.17% and the genome length is 3.2 Mbp.

**Description of *Candidatus Ruminococcus avistercoris* sp. nov.**

*Candidatus* Ruminococcus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK186-6582 and which is available via NCBI BioSample [SAMN15816883](#). Although GTDB has assigned this species to the genus it calls Ruminococcus\_G, 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 50.07% and the genome length is 2.3 Mbp.

**Description of *Candidatus Ruminococcus gallistercoris* sp. nov.**

*Candidatus* Ruminococcus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcec12-341 and which is available via NCBI BioSample [SAMN15816918](#). This is a new name for the alphanumeric GTDB species sp900552925. Although GTDB has assigned this species to the genus it calls Ruminococcus\_H, 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 62.03% and the genome length is 2.1 Mbp.

**Description of *Candidatus Ruminococcus intestinipullorum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1485 and which is available via NCBI BioSample [SAMN15816905](#). Although GTDB has assigned this species to the genus it calls Ruminococcus\_B, 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 35.77% and the genome length is 2.1 Mbp.

**Description of *Candidatus Ruthenibacterium avium* sp. nov.**

*Candidatus* Ruthenibacterium avium (a'vi.um. L. fem. pl. n. *avium* of birds)

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

**Description of *Candidatus Ruthenibacterium merdaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 5933 and which is available via NCBI BioSample [SAMN15816578](#). The GC content of the type genome is 51.15% and the genome length is 2.0 Mbp.

**Description of *Candidatus Ruthenibacterium merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej6B24-7098 and which is available via NCBI BioSample [SAMN15816763](#). The GC content of the type genome is 65.28% and the genome length is 2.2 Mbp.

Table 1 (continued)

**Description of *Candidatus Ruthenibacterium merdipullorum* sp. nov.**

*Candidatus* Ruthenibacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxje5B17-15602 and which is available via NCBI BioSample [SAMN15816878](#). This is a new name for the alphanumeric GTDB species sp900546885. The GC content of the type genome is 59.69% and the genome length is 2.1 Mbp.

**Description of *Candidatus Salinicoccus merdavium* sp. nov.**

*Candidatus* Salinicoccus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHje12B11-20095 and which is available via NCBI BioSample [SAMN15816874](#). This is a new name for the alphanumeric GTDB species sp002360325. The GC content of the type genome is 44.20% and the genome length is 1.8 Mbp.

**Description of *Candidatus Salinicoccus stercoripullorum* sp. nov.**

*Candidatus* Salinicoccus stercoripullorum (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHje13B12-752 and which is available via NCBI BioSample [SAMN15816771](#). The GC content of the type genome is 48.14% and the genome length is 2.3 Mbp.

**Description of *Candidatus Savagella gallinarum* sp. nov.**

*Candidatus* Savagella gallinarum (gal.li.na'rum. L. fem. n. *gallina* a hen; L. gen. pl. n. *gallinarum* of hens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK166-5537 and which is available via NCBI BioSample [SAMN15816803](#). This is a new name for the alphanumeric GTDB species sp001655775. The GC content of the type genome is 26.42% and the genome length is 1.8 Mbp.

**Description of *Candidatus Scatavimonas* gen. nov.**

*Candidatus* Scatavimonas (Scat.a.vi.mon'as Gr. neut. n. *skor*, *skatos* dung; L. fem. n. *avis* bird; L. fem. n. *monas* a monad; N.L. fem. n. N.L. neut. n. *Scatavimonas* a microbe associated with bird faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Scatavimonas merdigallinarum. This is a name for the alphanumeric GTDB genus UMG5403. 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 *Acutalibacteraceae*.

**Description of *Candidatus Scatavimonas merdigallinarum* sp. nov.**

*Candidatus* Scatavimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSje1B19-3389 and which is available via NCBI BioSample [SAMN15817212](#). This is a new name for the alphanumeric GTDB species sp900541975. The GC content of the type genome is 46.67% and the genome length is 1.7 Mbp.

**Description of *Candidatus Scatenecus* gen. nov.**

*Candidatus* Scatenecus (Scat.en.e'cus. Gr. neut. n. *skor*, *skatos* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Scatenecus* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* Scatenecus faecavium. This is a name for the alphanumeric GTDB genus QAMI01. 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 *Gastranaerophilales* and to the family *Gastranaerophilaceae*.

(Continued)



Table 1 (continued)

**Description of *Candidatus Scatenecus faecavium* sp. nov.**

*Candidatus Scatenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK152-2994 and which is available via NCBI BioSample [SAMN15817221](#). This is a new name for the alphanumeric GTDB species sp900551915. The GC content of the type genome is 37.15% and the genome length is 1.9 Mbp.

**Description of *Candidatus Scatocola* gen. nov.**

*Candidatus Scatocola* (Sca.to'co.la. Gr. neut. n. *skor*, *skatos* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Scatocola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scatocola faecipullorum*. This is a name for the alphanumeric GTDB genus CAG-495.

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 RF32 and to the family CAG-239.

**Description of *Candidatus Scatocola faecigallinarum* sp. nov.**

*Candidatus Scatocola faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 2846 and which is available via NCBI BioSample [SAMN15817209](#). This is a new name for the alphanumeric GTDB species sp000436375. The GC content of the type genome is 49.31% and the genome length is 1.7 Mbp.

**Description of *Candidatus Scatocola faecipullorum* sp. nov.**

*Candidatus Scatocola faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW3-316 and which is available via NCBI BioSample [SAMN15817201](#). This is a new name for the alphanumeric GTDB species sp001917125. The GC content of the type genome is 47.24% and the genome length is 1.7 Mbp.

**Description of *Candidatus Scatomonas* gen. nov.**

*Candidatus Scatomonas* (Sca.to.mo'nas. Gr. neut. n. *skor*, *skatos* dung; L. fem. n. *monas* a monad; N.L. fem. n. *Scatomonas* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scatomonas merdigallinarum*. This is a name for the alphanumeric GTDB genus OF09-33XD.

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 Scatomonas merdavium* sp. nov.**

*Candidatus Scatomonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSje5B23-9500 and which is available via NCBI BioSample [SAMN15817033](#).

The GC content of the type genome is 53.14% and the genome length is 2.3 Mbp.

**Description of *Candidatus Scatomonas merdigallinarum* sp. nov.**

*Candidatus Scatomonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK191-20366 and which is available via NCBI BioSample [SAMN15817035](#).

The GC content of the type genome is 53.29% and the genome length is 2.3 Mbp.

**Description of *Candidatus Scatomonas pullistercoris* sp. nov.**

*Candidatus Scatomonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK188-20938 and which is available via NCBI BioSample [SAMN15817052](#).

The GC content of the type genome is 53.16% and the genome length is 2.3 Mbp.

Table 1 (continued)

**Description of *Candidatus Scatomorpha* gen. nov.**

*Candidatus Scatomorpha* (Sca.to.mor'pha. Gr. neut. n. *skor*, *skatos* dung; Gr. fem. n. *morphe* a form, shape; N.L. fem. n. *Scatomorpha* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scatomorpha merdaviium*. This is a name for the alphanumeric GTDB genus UBA5446. 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 Scatomorpha gallistercoris* sp. nov.**

*Candidatus Scatomorpha gallistercoris* (gal.li.ster'a'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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej12B11-5383 and which is available via NCBI BioSample SAMN15817213. This is a new name for the alphanumeric GTDB species sp900544765. The GC content of the type genome is 60.13% and the genome length is 2.4 Mbp.

**Description of *Candidatus Scatomorpha intestinavium* sp. nov.**

*Candidatus Scatomorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcolR7-354 and which is available via NCBI BioSample SAMN15817058. The GC content of the type genome is 62.47% and the genome length is 2.0 Mbp.

**Description of *Candidatus Scatomorpha intestinigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej3B3-7149 and which is available via NCBI BioSample SAMN15817216. This is a new name for the alphanumeric GTDB species sp900544295. The GC content of the type genome is 63.01% and the genome length is 2.3 Mbp.

**Description of *Candidatus Scatomorpha intestinipullorum* sp. nov.**

*Candidatus Scatomorpha intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK1-1240 and which is available via NCBI BioSample SAMN15817022. The GC content of the type genome is 61.56% and the genome length is 2.5 Mbp.

**Description of *Candidatus Scatomorpha merdaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej3B15-13231 and which is available via NCBI BioSample SAMN15817220. This is a new name for the alphanumeric GTDB species sp004553625. The GC content of the type genome is 61.38% and the genome length is 2.3 Mbp.

**Description of *Candidatus Scatomorpha merdigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK187-5235 and which is available via NCBI BioSample SAMN15817028. The GC content of the type genome is 58.23% and the genome length is 2.3 Mbp.

**Description of *Candidatus Scatomorpha merdipullorum* sp. nov.**

*Candidatus Scatomorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej10B9-9673 and which is available via NCBI BioSample SAMN15817099. The GC content of the type genome is 64.45% and the genome length is 1.8 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Scatomorpha pullicola* sp. nov.**

*Candidatus Scatomorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSjej5B23-7677 and which is available via NCBI BioSample [SAMN15817223](#). This is a new name for the alphanumeric GTDB species sp900543085. The GC content of the type genome is 62.30% and the genome length is 2.1 Mbp.

**Description of *Candidatus Scatomorpha pullistercoris* sp. nov.**

*Candidatus Scatomorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec3B27-6122 and which is available via NCBI BioSample [SAMN15817222](#). This is a new name for the alphanumeric GTDB species sp900546615. The GC content of the type genome is 61.20% and the genome length is 2.2 Mbp.

**Description of *Candidatus Scatomorpha stercoravium* sp. nov.**

*Candidatus Scatomorpha 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHecec3B27-8609 and which is available via NCBI BioSample [SAMN15817107](#). The GC content of the type genome is 64.50% and the genome length is 2.0 Mbp.

**Description of *Candidatus Scatomorpha stercorigallarum* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej9B8-2268 and which is available via NCBI BioSample [SAMN15817162](#). The GC content of the type genome is 64.82% and the genome length is 2.0 Mbp.

**Description of *Candidatus Scatoplasma* gen. nov.**

*Candidatus Scatoplasma* (Sca.to.plas'ma. Gr. neut. n. *skor*, *skatos* dung; Gr. neut. n. *plasma* a form; N.L. neut. n. *Scatoplasma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scatoplasma merdavium*. This is a name for the alphanumeric GTDB genus UBA6879. 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 *RFN20* and to the family *CAG-288*.

**Description of *Candidatus Scatoplasma merdavium* sp. nov.**

*Candidatus Scatoplasma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1748 and which is available via NCBI BioSample [SAMN15817159](#). The GC content of the type genome is 36.99% and the genome length is 1.0 Mbp.

**Description of *Candidatus Scatosoma* gen. nov.**

*Candidatus Scatosoma* (Sca.to.so'ma. Gr. neut. n. *skor*, *skatos* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Scatosoma* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scatosoma pullicola*. This is a name for the alphanumeric GTDB genus QALS01. 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 *Christensenellales* and to the family *Borkfalkiaceae*.

**Description of *Candidatus Scatosoma pullicola* sp. nov.**

*Candidatus Scatosoma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK183-20193 and which is available via NCBI BioSample [SAMN15817013](#). The GC content of the type genome is 57.19% and the genome length is 2.0 Mbp.

Table 1 (continued)

**Description of *Candidatus Scatosoma pullistercoris* sp. nov.**

*Candidatus Scatosoma 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 11687 and which is available via NCBI BioSample [SAMN15817138](#). The GC content of the type genome is 55.35% and the genome length is 1.5 Mbp.

**Description of *Candidatus Scatousia* gen. nov.**

*Candidatus Scatousia* (Scat.ou'si.a. Gr. neut. n. *skor*, *skatos* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Scatousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scatousia excrementipullorum*. This is a name for the alphanumeric GTDB genus CAG-484. 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 *Gastranaerophilales* and to the family *Gastranaerophilaceae*.

**Description of *Candidatus Scatousia excrementigallinarum* sp. nov.**

*Candidatus Scatousia excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 6276 and which is available via NCBI BioSample [SAMN15817091](#). The GC content of the type genome is 36.46% and the genome length is 2.8 Mbp.

**Description of *Candidatus Scatousia excrementipullorum* sp. nov.**

*Candidatus Scatousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 10192 and which is available via NCBI BioSample [SAMN15817157](#). The GC content of the type genome is 36.06% and the genome length is 1.8 Mbp.

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

*Candidatus Scatovicinus* (Sca.to.vi.ci'nus. Gr. neut. n. *skor*, *skatos* dung; L. masc. n. *vicinus* a neighbour; N.L. masc. n. *Scatovicinus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scatovicinus merdipullorum*. This is a name for the alphanumeric GTDB genus UMG5403. 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 *Acutalibacteraceae*.

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

*Candidatus Scatovicinus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK181-9830 and which is available via NCBI BioSample [SAMN15817214](#). This is a new name for the alphanumeric GTDB species sp900541565. The GC content of the type genome is 46.80% and the genome length is 1.9 Mbp.

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

*Candidatus Scatovivens* (Sca.to.vi'vens. Gr. neut. n. *skor*, *skatos* dung; N.L. pres. part. *vivens* living; N.L. fem. n. *Scatovivens* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scatovivens faecipullorum*. This is a name for the alphanumeric GTDB genus UBA7001. 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 *TANB77* and to the family *CAG-508*.

(Continued)

Table 1 (continued)

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

*Candidatus Scatovivens faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej5B17-16517 and which is available via NCBI BioSample [SAMN15817189](#). This is a new name for the alphanumeric GTDB species sp900553685. The GC content of the type genome is 25.63% and the genome length is 1.9 Mbp.

**Description of *Candidatus Scybalenecus merdaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK176-6737 and which is available via NCBI BioSample [SAMN15817203](#). This is a new name for the alphanumeric GTDB species sp900546735. The GC content of the type genome is 52.55% and the genome length is 1.8 Mbp.

**Description of *Candidatus Scybalocola faecaviium* sp. nov.**

*Candidatus Scybalocola faecaviium* (faec.a'vi.um. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *avis* bird; N.L. gen. n. *faecaviium* of bird faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK196-3395 and which is available via NCBI BioSample [SAMN15817004](#). The GC content of the type genome is 45.55% and the genome length is 3.6 Mbp.

**Description of *Candidatus Scybalocola faecigallinarum* sp. nov.**

*Candidatus Scybalocola faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK178-757 and which is available via NCBI BioSample [SAMN15817027](#). The GC content of the type genome is 46.78% and the genome length is 3.5 Mbp.

**Description of *Candidatus Scybalocola faecipullorum* sp. nov.**

*Candidatus Scybalocola faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK194-7924 and which is available via NCBI BioSample [SAMN15817034](#). The GC content of the type genome is 44.36% and the genome length is 2.5 Mbp.

**Description of *Candidatus Scybalomonas excrementaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID E3-2379 and which is available via NCBI BioSample [SAMN15817094](#). The GC content of the type genome is 32.78% and the genome length is 2.5 Mbp.

**Description of *Candidatus Scybalomonas excrementigallinarum* sp. nov.**

*Candidatus Scybalomonas excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 3201 and which is available via NCBI BioSample [SAMN15817095](#). The GC content of the type genome is 34.32% and the genome length is 3.2 Mbp.

**Description of *Candidatus Scybalosoma faecaviium* sp. nov.**

*Candidatus Scybalosoma faecaviium* (faec.a'vi.um. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *avis* bird; N.L. gen. n. *faecaviium* of bird faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej1B13-2233 and which is available via NCBI BioSample [SAMN15817224](#). This is a new name for the alphanumeric GTDB species sp900545085. The GC content of the type genome is 47.85% and the genome length is 1.6 Mbp.



Table 1 (continued)

**Description of *Candidatus Scybalousia intestinigallinarum* sp. nov.**

*Candidatus Scybalousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK193-12526 and which is available via NCBI BioSample [SAMN15817037](#). The GC content of the type genome is 31.54% and the genome length is 1.5 Mbp.

**Description of *Candidatus Scybalenecus* gen. nov.**

*Candidatus Scybalenecus* (Scy.bal.en.e'cus. Gr. neut. n. *skybalon* dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Scybalenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scybalenecus merdaviium*. This is a name for the alphanumeric GTDB genus UMG5905. 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 *Acutalibacteraceae*.

**Description of *Candidatus Scybalocola* gen. nov.**

*Candidatus Scybalocola* (Scy.ba.lo'co.la. Gr. neut. n. *skybalon* dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Scybalocola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scybalocola faecigallinarum*. This is a name for the alphanumeric GTDB genus UBA7096. 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 Scybalomonas* gen. nov.**

*Candidatus Scybalomonas* (Scy.ba.lo.mo'nas. Gr. neut. n. *skybalon* dung; L. fem. n. *monas* a monad; N.L. fem. n. *Scybalomonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scybalomonas excrementigallinarum*. This is a name for the alphanumeric GTDB genus UMG5680. 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 Scybalosoma* gen. nov.**

*Candidatus Scybalosoma* (Scy.ba.lo.so'ma. Gr. neut. n. *skybalon* dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Scybalosoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scybalosoma faecavium*. This is a name for the alphanumeric GTDB genus UMG5743. 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 *Christensenellales* and to the family *Christensenellaceae*.

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

*Candidatus Scybalousia* (Scy.bal.ou'si.a. Gr. neut. n. *skybalon* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Scybalousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Scybalousia intestinigallinarum*. This is a name for the alphanumeric GTDB genus UBA7057. 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 Sellimonas avistercoris* sp. nov.**

*Candidatus Sellimonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBccc13-3606 and which is available via NCBI BioSample [SAMN15816877](#). This is a new name for the alphanumeric GTDB species sp002161525. The GC content of the type genome is 46.79% and the genome length is 2.6 Mbp.

**Description of *Candidatus Sphingobacterium stercorigallinarum* sp. nov.**

*Candidatus Sphingobacterium 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK174-1108 and which is available via NCBI BioSample [SAMN15816705](#). The GC content of the type genome is 44.57% and the genome length is 2.9 Mbp.

(Continued)

Table 1 (continued)

**Description of *Candidatus Sphingobacterium stercoripullorum* sp. nov.**

*Candidatus Sphingobacterium stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1719 and which is available via NCBI BioSample [SAMN15816733](#). The GC content of the type genome is 39.36% and the genome length is 2.7 Mbp.

**Description of *Candidatus Sphingomonas excrementigallinarum* sp. nov.**

*Candidatus Sphingomonas excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 1562 and which is available via NCBI BioSample [SAMN15816779](#). The GC content of the type genome is 66.49% and the genome length is 3.7 Mbp.

**Description of *Candidatus Spyradenecus* gen. nov.**

*Candidatus Spyradenecus* (Spy.rad.en.e'cus. Gr. fem. n. *spyras* ball of dung; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Spyradenecus* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Spyradenecus faecavium*. This is a name for the alphanumeric GTDB genus W1P29-020. 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 *RFP12* and to the family *W1P29-020*.

**Description of *Candidatus Spyradenecus faecavium* sp. nov.**

*Candidatus Spyradenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 35461 and which is available via NCBI BioSample [SAMN15817160](#). The GC content of the type genome is 68.44% and the genome length is 1.8 Mbp.

**Description of *Candidatus Spyradocola* gen. nov.**

*Candidatus Spyradocola* (Spy.ra.do'co.la. Gr. fem. n. *spyras* ball of dung; L. suff. *-cola* inhabitant of; N.L. fem. n. *Spyradocola* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Spyradocola merdavium*. This is a name for the alphanumeric GTDB genus UBA7102. 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 *Christensenellales* and to the family *UBA1750*.

**Description of *Candidatus Spyradocola merdavium* sp. nov.**

*Candidatus Spyradocola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK191-18038 and which is available via NCBI BioSample [SAMN15817024](#). The GC content of the type genome is 66.20% and the genome length is 2.6 Mbp.

**Description of *Candidatus Spyradomonas* gen. nov.**

*Candidatus Spyradomonas* (Spy.ra.do.mo'nas. Gr. fem. n. *spyras* ball of dung; L. fem. n. *monas* a monad; N.L. fem. n. *Spyradomonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Spyradomonas excrementavium*. This is a name for the alphanumeric GTDB genus UMGS951. 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 *Gastranaerophilales* and to the family *Gastranaerophilaceae*.

**Description of *Candidatus Spyradomonas excrementavium* sp. nov.**

*Candidatus Spyradomonas 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK149-2741 and which is available via NCBI BioSample [SAMN15817232](#). This is a new name for the alphanumeric GTDB species sp900547155. The GC content of the type genome is 41.54% and the genome length is 2.0 Mbp.

Table 1 (continued)

**Description of *Candidatus* *Spyradosoma* gen. nov.**

*Candidatus* *Spyradosoma* (Spy.ra.do.so'ma. Gr. fem. n. *spyras* ball of dung; Gr. neut. n. *soma* a body; N.L. neut. n. *Spyradosoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* *Spyradosoma* merdigallarum. This is a name for the alphanumeric GTDB genus W0P29-029. 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 *Opiritales* and to the family *UBA953*.

**Description of *Candidatus* *Spyradosoma* merdigallarum sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 10669 and which is available via NCBI BioSample SAMN15817156. The GC content of the type genome is 62.43% and the genome length is 1.6 Mbp.

**Description of *Candidatus* *Stackebrandtia* excrementipullorum sp. nov.**

*Candidatus* *Stackebrandtia* 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej8B7-33794 and which is available via NCBI BioSample SAMN15816761. The GC content of the type genome is 64.17% and the genome length is 4.1 Mbp.

**Description of *Candidatus* *Stackebrandtia* faecavium sp. nov.**

*Candidatus* *Stackebrandtia* 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej4B4-770 and which is available via NCBI BioSample SAMN15816782. The GC content of the type genome is 62.84% and the genome length is 3.4 Mbp.

**Description of *Candidatus* *Stercoripulliclostridium* gen. nov.**

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

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus* *Stercoripulliclostridium* merdipullorum. 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 *Christensenellales* and to the family *DTU072*.

**Description of *Candidatus* *Stercoripulliclostridium* merdigallarum sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 18911 and which is available via NCBI BioSample SAMN15816986. The GC content of the type genome is 48.67% and the genome length is 1.5 Mbp.

**Description of *Candidatus* *Stercoripulliclostridium* merdipullorum sp. nov.**

*Candidatus* *Stercoripulliclostridium* 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 23406 and which is available via NCBI BioSample SAMN15816995. The GC content of the type genome is 53.33% and the genome length is 1.7 Mbp.

**Description of *Candidatus* *Stercoripulliclostridium* pullicola sp. nov.**

*Candidatus* *Stercoripulliclostridium* 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 517 and which is available via NCBI BioSample SAMN15816997. The GC content of the type genome is 52.41% and the genome length is 1.6 Mbp.

(Continued)

**Table 1 (continued)****Description of *Candidatus Stercorousia* gen. nov.**

*Candidatus Stercorousia* (Ster.cor.ou'si.a. L. neut. n. *stercus* dung; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Stercorousia* a microbe associated with the intestines)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Stercorousia faecigallinarum*. This is a name for the alphanumeric GTDB genus Zag1. 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 *Gastranaerophilales* and to the family *Gastranaerophilaceae*.

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

*Candidatus Stercorousia faecigallinarum* (fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *faecigallinarum* of hen faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK154-323 and which is available via NCBI BioSample SAMN15817192. This is a new name for the alphanumeric GTDB species sp000438175. The GC content of the type genome is 34.85% and the genome length is 2.1 Mbp.

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

*Candidatus Streptococcus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiBcolR9-63 and which is available via NCBI BioSample SAMN15816845. This is a new name for the alphanumeric GTDB species sp002300045. The GC content of the type genome is 40.90% and the genome length is 1.4 Mbp.

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

*Candidatus Sutterella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiGjej6B6-11950 and which is available via NCBI BioSample SAMN15816882. This is a new name for the alphanumeric GTDB species sp900543805. The GC content of the type genome is 62.35% and the genome length is 2.1 Mbp.

**Description of *Candidatus Tetragenococcus pullicola* sp. nov.**

*Candidatus Tetragenococcus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK175-10598 and which is available via NCBI BioSample SAMN15816709. The GC content of the type genome is 36.35% and the genome length is 2.6 Mbp.

**Description of *Candidatus Tidjanibacter faecipullorum* sp. nov.**

*Candidatus Tidjanibacter faecipullorum* (fae.ci.pul.lo'rum. L. fem. n. *faex*, *faecis* excrement; L. masc. n. *pullus* a young chicken; N.L. gen. n. *faecipullorum* of young chicken faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej11B10-19426 and which is available via NCBI BioSample SAMN15816696. The GC content of the type genome is 60.46% and the genome length is 1.8 Mbp.

**Description of *Candidatus Tidjanibacter gallistercoris* sp. nov.**

*Candidatus Tidjanibacter 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiSxjej4B16-7142 and which is available via NCBI BioSample SAMN15816746. The GC content of the type genome is 58.50% and the genome length is 2.0 Mbp.

**Description of *Candidatus Treponema excrementipullorum* sp. nov.**

*Candidatus Treponema 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID Gambia15-2214 and which is available via NCBI BioSample SAMN15816896. Although GTDB has assigned this species to the genus it calls *Treponema\_F*, 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 39.91% and the genome length is 2.3 Mbp.



Table 1 (continued)

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

*Candidatus Treponema 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID USASDec8-330 and which is available via NCBI BioSample [SAMN15816910](#). Although GTDB has assigned this species to the genus it calls *Treponema\_F*, 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 53.41% and the genome length is 2.2 Mbp.

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

*Candidatus Ureaplasma intestinipullorum* (in.tes.ti.ni.pul.lo'rum. L. neut. n. *intestinum* gut; L. masc. n. *pullus* a young chicken; N.L. gen. n. *intestinipullorum* of the gut of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID A5-1222 and which is available via NCBI BioSample [SAMN15816777](#). The GC content of the type genome is 24.43% and the genome length is 0.6 Mbp.

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

*Candidatus Ventrenecus* (Ventr.en.e'cus. L. masc. n. *venter* the belly; Gr. masc. *enoikos* inhabitant; N.L. masc. n. *Ventrenecus* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Ventrenecus avicola*. This is a name for the alphanumeric GTDB genus UMG51217. 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-1000*.

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

*Candidatus Ventrenecus 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiW22-487 and which is available via NCBI BioSample [SAMN15817076](#). The GC content of the type genome is 31.09% and the genome length is 1.3 Mbp.

**Description of *Candidatus Ventrenecus stercoripullorum* sp. nov.**

*Candidatus Ventrenecus stercoripullorum* (ster.co.ri.pul.lo'rum. L. neut. n. *stercus* dung; L. masc. n. *pullus* a young chicken; N.L. gen. n. *stercoripullorum* of the faeces of young chickens)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK197-17881 and which is available via NCBI BioSample [SAMN15817010](#). The GC content of the type genome is 30.90% and the genome length is 1.4 Mbp.

**Description of *Candidatus Ventricola* gen. nov.**

*Candidatus Ventricola* (Ven.tri'co.la. L. masc. n. *venter* the belly; L. suff. *-cola* inhabitant of; N.L. fem. n. *Ventricola* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Ventricola intestinavium*. This is a name for the alphanumeric GTDB genus SFFH01. 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 *Christensenellales* and to the family *CAG-74*.

**Description of *Candidatus Ventricola gallistercoris* sp. nov.**

*Candidatus Ventricola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcec16-310 and which is available via NCBI BioSample [SAMN15817100](#). The GC content of the type genome is 60.63% and the genome length is 2.4 Mbp.

**Description of *Candidatus Ventricola intestinavium* sp. nov.**

*Candidatus Ventricola 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 8987 and which is available via NCBI BioSample [SAMN15817130](#). The GC content of the type genome is 59.95% and the genome length is 2.2 Mbp.

(Continued)



Table 1 (continued)

**Description of *Candidatus Ventrimonas* gen. nov.**

*Candidatus Ventrimonas* (Ven.tri.mo'nas. L. masc. n. *venter* the belly; L. fem. n. *monas* a monad; N.L. fem. n. *Ventrimonas* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Ventrimonas merdaviium*. This is a name for the alphanumeric GTDB genus UBA9502.

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 Ventrimonas merdaviium* sp. nov.**

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

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID USAMLcec2-739 and which is available via NCBI BioSample SAMN15817118.

The GC content of the type genome is 57.43% and the genome length is 3.0 Mbp.

**Description of *Candidatus Ventrisoma* gen. nov.**

*Candidatus Ventrisoma* (Ven.tri.so'ma. L. masc. n. *venter* the belly; Gr. neut. n. *soma* a body; N.L. neut. n. *Ventrisoma* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Ventrisoma faecale*. This is a name for the alphanumeric GTDB genus UC5-1-2E3. 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 Ventrisoma faecale* sp. nov.**

*Candidatus Ventrisoma faecale* (fae.ca'le. L. neut. adj. *faecale* of faeces)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHcolR19-5415 and which is available via NCBI BioSample SAMN15817173.

This is a new name for the alphanumeric GTDB species sp001304875. The GC content of the type genome is 55.91% and the genome length is 2.8 Mbp.

**Description of *Candidatus Ventrousia* gen. nov.**

*Candidatus Ventrousia* (Ventr.ou'si.a. L. masc. n. *venter* the belly; Gr. fem. n. *ousia* an essence; N.L. fem. n. *Ventrousia* a microbe associated with faeces)

A bacterial genus identified by metagenomic analyses. The genus includes all bacteria with genomes that show  $\geq 60\%$  average amino acid identity (AAI) to the type genome from the type species *Candidatus Ventrousia excrementavium*. This is a name for the alphanumeric GTDB genus SCN-57-10.

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 *Butyrivibrionaceae*.

**Description of *Candidatus Ventrousia excrementavium* sp. nov.**

*Candidatus Ventrousia 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID CHK191-8634 and which is available via NCBI BioSample SAMN15817048.

The GC content of the type genome is 57.61% and the genome length is 2.1 Mbp.

**Description of *Candidatus Yaniella excrementavium* sp. nov.**

*Candidatus Yaniella 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  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID ChiHjej13B12-778 and which is available via NCBI BioSample SAMN15816702.

The GC content of the type genome is 55.30% and the genome length is 2.5 Mbp.

**Description of *Candidatus Yaniella excrementigallinarum* sp. nov.**

*Candidatus Yaniella excrementigallinarum* (ex.cre.men.ti.gal.li.na'rum. L. neut. n. *excrementum* excrement; L. fem. n. *gallina* hen; N.L. gen. n. *excrementigallinarum* of hen excrement)

A bacterial species identified by metagenomic analyses. This species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the type genome, which has been assigned the MAG ID 4905 and which is available via NCBI BioSample SAMN15816764. The GC content of the type genome is 53.17% and the genome length is 2.6 Mbp.

**Table 2** Protologues for new taxa cultured from chicken faeces.**Description of *Acinetobacter pecorum* sp. nov.**

(pe.co'rum. L. gen. pl. n. *pecorum* of flocks of sheep, birds etc., as this species has been isolated from chickens and sheep)

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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014837015.1](#). The GC content of the type strain is 42.9% and the genome size is 3.2 Mbp. GTDB has given this species the alphanumerical designation sp001647535 and the two other genomes assigned to this species are derived from sheep isolates (RefSeq assembly accessions [GCF\\_001647535.1](#), [GCF\\_001647575.1](#)) (Gupta et al., 2016). The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1BUA6.

**Description of *Arthrobacter gallicola* sp. nov.**

(gal.li'co.la. L. masc. n. *gallus* a cock; N.L. suff. *-cola* an inhabitant of; N.L. masc. or fem. n. *gallicola* an inhabitant of the chicken)

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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836775.1](#). The GC content of the type strain is 65.5% and the genome size is 3.7 Mbp. Although GTDB has assigned this species to the genus it calls *Arthrobacter\_B*, this genus designation cannot be incorporated into a well-formed binomial, so in naming this species, we have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2CUA1.

**Description of *Arthrobacter pullicola* sp. nov.**

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

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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836875.1](#). The GC content of the type strain is 65.7% and the genome size is 3.7 Mbp. Although GTDB has assigned this species to the genus it calls *Arthrobacter\_B*, this genus designation cannot be incorporated into a well-formed binomial, so in naming this species, we have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2BUA2.

**Description of *Bacillus norwichensis* sp. nov.**

(nor.wich.en'sis. N.L. masc. adj. *norwichensis* pertaining to English city of Norwich, where the organism was isolated)

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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836955.1](#). The GC content of the type strain is 40.2% and the genome size is 4.7 Mbp. Although GTDB has assigned this species to the genus it calls *Bacillus\_AM*, this genus designation cannot be incorporated into a well-formed binomial, so in naming this species, we have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1BUA2

(Continued)

Table 2 (continued)

**Description of *Brevibacterium 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 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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836885.1](#). The GC content of the type strain is 67.0% and the genome size is 3.2 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the 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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836335.1](#). The GC content of the type strain is 29.8% and the genome size is 4.3 Mbp. GTDB has given this species the alphanumerical designation sp007115085. One other isolate from this species (RefSeq accession [GCA\\_007115085.1](#)) has been cultured from zha-chili, a Chinese fermented food. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa3CVN1.

**Description of *Clostridium 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 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 (Fig. S3).

**Table 2 (continued)**

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836325.1](#). The GC content of the type strain is 27.2% and the genome size is 3.4 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa3CUN1.

**Description of *Clostridium faecium* sp. nov.**

(fae'ci.um. N.L. gen. pl. n. *faecium*, of faeces, as this species has been isolated from chicken and human 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 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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836835.1](#). The GC content of the type strain is 28.7% and the genome size is 3.9 Mbp. Although GTDB has assigned this species to the genus it calls *Clostridium\_J*, this genus designation cannot be incorporated into a well-formed binomial, so in naming this species, we have used the basonym for the genus. GTDB has given this species the alphanumerical designation sp900547625, which includes a gut isolate from a preterm human infant (GenBank accession [GCA\\_900547625.1](#)). The type strain has been deposited in NCTC and DSMZ, where it 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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  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. GTDB has assigned this species to the genus it calls *Bacillus\_AA*, which cannot be incorporated into a well-formed binomial. However, according to ([Patel & Gupta, 2020](#)), the newly named genus *Cytobacillus* encompasses other species classified by GTDB within the genus designation *Bacillus\_AA* and therefore *Cytobacillus* is treated as a synonym of GTDB *Bacillus\_AA*. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa5YUA1.

(Continued)

Table 2 (continued)

**Description of *Escherichia whittamii* sp. nov.**

(whit.tam'i.i. N.L. gen. n. *whittamii*, named in honour of American microbiologist Thomas S. Whittam)

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 reference genomes from the genus (Fig. 4).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836715.1](#). The GC content of the type strain is 50.6% and the genome size is 4.6 Mbp. GTDB has given this species the alphanumerical designation sp001660175 and has assigned two other cultured isolates to this species, both of which come from birds (RefSeq assembly accessions [GCF\\_001660175.1](#), [GCF\\_002965485.1](#)) (Clermont et al., 2011; Gangiredla et al., 2018). The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2BVA5.

**Description of *Fictibacillus norfolkensis* sp. nov.**

(nor.folk.en'sis. N.L. masc. adj. *norfolkensis* pertaining to the English county of Norfolk)

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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836645.1](#). The GC content of the type strain is 39.5% and the genome size is 4.0 Mbp. Although GTDB has assigned this species to the genus it calls *Fictibacillus\_B*, this genus designation cannot be incorporated into a well-formed binomial, so in naming this species, we have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2CUA10

**Description of *Kaistella pullorum* sp. nov.**

(pul.lo'rum. L. gen. pl. n. *pullorum* of chickens)

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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014837035.1](#). The GC content of the type strain is 42.9% and the genome size is 2.6 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1CVA4

**Description of *Limosilactobacillus 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 brain-heart infusion 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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836425.1](#). The GC content of the type strain is 39.9% and the genome size is 1.8 Mbp. GTDB has assigned this species to the genus it calls *Lactobacillus\_H*, which cannot be incorporated into a well-formed binomial. However, according to (Zheng et al., 2020) *Limosilactobacillus* encompasses other species classified by GTDB within the genus designation *Lactobacillus\_H* and therefore *Limosilactobacillus* is treated as a synonym for GTDB designation *Lactobacillus\_H*. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa3CUN2



**Table 2 (continued)****Description of *Luteimonas colneyensis* sp. nov.**

(col.ney.en'sis. N.L. fem. adj. *colneyensis* pertaining to the English village of Colney, home to the Quadram Institute, where the species was first described)

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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836665.1](#). The GC content of the type strain is 71.0% and the genome size is 3.0 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2BVA3

**Description of *Microbacterium commune* sp. nov.**

(com.mu'ne. L. neut. adj. *commune* common, referring to diverse habitats, as this species has been isolated from mosquitos and chicken)

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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836945.1](#). The GC content of the type strain is 70.3% and the genome size is 3.3 Mbp. GTDB has given this species the alphanumerical designation sp001878835, which also contains a mosquito isolate (RefSeq accession [GCF\\_001878835.1](#)). The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Re1.

**Description of *Microbacterium 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 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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014837165.1](#). The GC content of the type strain is 69.4% and the genome size is 2.8 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1CUA4

**Description of *Microbacterium pullorum* sp. nov.**

(pul.lo'rum. L. gen. pl. n. *pullorum* of chickens)

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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836535.1](#). The GC content of the type strain is 70.1% 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 Sa4CUA7

**Description of *Oceanitalea stevensii* sp. nov.**

(ste.ven'si.i. N.L. gen. n. *stevensii*, named in honour of British microbiologist Mark Stevens)

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 (Fig. S3).

(Continued)

**Table 2 (continued)**

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014837105.1](#). The GC content of the type strain is 73.4% and the genome size is 3.5 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1BUA1.

**Description of *Ochrobactrum 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 brain-heart infusion 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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836735.1](#). The GC content of the type strain is 53.5% and the genome size is 5.0 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2BUA5

**Description of *Oerskovia douganii* sp. nov.**

(dou.ga'ni.i. N.L. gen. n. *douganii* named in honour of British microbiologist Gordon Dougan)

The type strain for this bacterial species has been cultured from chicken faeces after overnight incubation on brain-heart infusion 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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_015142735.1](#). The GC content of the type strain is 72.5% and the genome size is 4.3 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1BUA8

**Description of *Oerskovia gallyi* sp. nov.**

(gal'ly.i. N.L. gen. n. *gallyi* named in honour of British microbiologist David Gally)

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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836745.1](#). The GC content of the type strain is 72.5% and the genome size is 4.3 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2CUA8

**Description of *Oerskovia merdaviium* sp. nov.**

(merd.a'vi.um. L. fem. n. *merda* faeces; L. fem. n. *avis* bird; N.L. gen. n. *merdaviium* 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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836755.1](#). The GC content of the type strain is 72.1% and the genome size is 4.5 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2CUA9.

**Description of *Oerskovia rustica* sp. nov.**

(rus'ti.ca. L fem adj. *rustica* of the countryside, as isolates have been obtained from soil and chickens)

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 ([Fig. S3](#)).

**Table 2 (continued)**

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836555.1](#). The GC content of the type strain is 72.5% and the genome size is 4.4 Mbp. GTDB has given this species the alphanumerical designation sp005937995, which includes a soil isolate (RefSeq accession [GCF\\_005937995.2](#)). The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa4CUA1.

**Description of *Paenibacillus 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 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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836635.1](#). The GC content of the type strain is 41.2% and the genome size is 5.4 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2BVA9

**Description of *Phocaeicola faecium* sp. nov.**

(fae'ci.um L. gen. pl. n. *faecium*, of faeces)

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 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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014837055.1](#). The GC content of the type strain is 45.6% and the genome size is 3.5 Mbp. GTDB has given this species the alphanumerical designation sp900540105, which includes a gut isolate from an infant human (GenBank accession [GCA\\_900540105.1](#)). The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1YUN3

**Description of *Phocaeicola intestinalis* sp. nov.**

(in.tes.ti.na'lis. N.L. masc./fem. adj. *intestinalis*, pertaining to the intestines)

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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014837065.1](#). The GC content of the type strain is 45.7% and the genome size is 4.1 Mbp. GTDB has given this species the alphanumerical designation sp002161565, which includes isolates from the human and chicken guts (GenBank accession numbers [GCA\\_000432695.1](#), [GCA\\_900540165.1](#), [GCF\\_002159615.1](#), [GCF\\_002159755.1](#), [GCF\\_002160215.1](#), [GCF\\_002161565.1](#)). The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1CVN1.

**Description of *Planococcus wigleyi* sp. nov.**

(wig'ley.i. N.L. masc. gen. n. *wigleyi* named in honour of British microbiologist Paul Wigley)

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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836985.1](#). The GC content of the type strain is 45.0% and the genome size is 3.8 Mbp. Although GTDB has assigned a genus name with an alphabetic suffix *Planococcus\_A*, this genus designation cannot be incorporated into a well-formed binomial, so in naming this species, we have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1BUA13

(Continued)

Table 2 (continued)

**Description of *Psychrobacillus faecigallinarum* sp. nov.**

(fae.ci.gal.li.na'rum. L. fem. n. *faex*, *faecis* faeces; L. fem. n. *gallina* a hen; N.L. gen. n. *faecigallinarum* 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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836595.1](#). The GC content of the type strain is 36.5% and the genome size is 4.0 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2BUA9

**Description of *Psychrobacter communis* sp. nov.**

(com.mu'nis. L. masc. adj. *communis* common, referring to diverse habitats from which this species has been isolated, including chickens and soil)

The type strain for this bacterial species has been cultured from chicken faeces after overnight incubation on xyz medium 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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836505.1](#). The GC content of the type strain is 43.7% and the genome size is 3.0 Mbp. GTDB has given this species the alphanumerical designation sp001652315, which contains six environmental isolates from a variety of sources including soil ([GCA\\_002332465.1](#), [GCA\\_002439405.1](#), [GCA\\_003524605.1](#), [GCA\\_007280595.1](#), [GCF\\_001652315.1](#), [GCF\\_002836335.1](#)) The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa4CVA2

**Description of *Serpens 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 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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836765.1](#). The GC content of the type strain is 61.0% and the genome size is 3.9 Mbp. Although GTDB has assigned a genus name with an alphabetic suffix *Pseudomonas\_H*, which cannot be incorporated into a well-formed binomial. However, GDTB genus *Pseudomonas\_H* includes *Pseudomonas flexibilis*, where the basonym is *Serpens* (Hespell, 1977), so we have used this genus name. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2CUA2

**Description of *Solibacillus faecavium* sp. nov.**

(faec.a'vi.um. L. fem. n. *faex*, *faecis* faeces; L. fem. n. *avis* bird; N.L. gen. n. *faecavium* of bird 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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836905.1](#). The GC content of the type strain is 37.1% and the genome size is 3.8 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference A46

**Description of *Solibacillus merdavium* sp. nov.**

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

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 (Fig. S3).

**Table 2 (continued)**

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836935.1](#). The GC content of the type strain is 37.0% and the genome size is 3.8 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa1YVA6

**Description of *Sporosarcina gallistercoris* sp. nov.**

(gal.li.ster'co.ris. L. masc. n. *gallus* a cock; L. neut. n. *stercus* dung; N.L. gen. n. *gallistercoris* of faeces of a cock)

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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836415.1](#). The GC content of the type strain is 44.1% and the genome size is 3.1 Mbp. Although GTDB has assigned a genus name with an alphabetic suffix *Sporosarcina\_A*, this genus designation cannot be incorporated into a well-formed binomial, so in naming this species, we have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa3CUA8

**Description of *Sporosarcina quadrami* sp. nov.**

(qua.dra'mi. N.L. gen. n. *quadrami*, of the Quadram Institute, where the species was first cultured.)

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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836615.1](#). The GC content of the type strain is 41.4% and the genome size is 3.6 Mbp. Although GTDB has assigned a genus name with an alphabetic suffix *Sporosarcina\_B*, this genus designation cannot be incorporated into a well-formed binomial, so in naming this species, we have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa2YVA2

**Description of *Stenotrophomonas pennii* sp. nov.**

(pen'ni.i. N.L. gen. n. *pennii*, named in honour of British microbiologist Charles W. Penn)

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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836545.1](#). The GC content of the type strain is 66.4% and the genome size is 3.9 Mbp. GTDB has given this species the alphanumerical designation sp002836635, which includes four environmental isolates (RefSeq accessions [GCF\\_000834105.1](#), [GCF\\_002836635.1](#), [GCF\\_002836645.1](#), [GCF\\_002836675.1](#)). The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa5BUN4

**Description of *Ureibacillus galli* sp. nov.**

(gal'li. L. masc. gen. n. *galli* of a chicken)

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 ([Fig. S3](#)).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836845.1](#). The GC content of the type strain is 35.2% and the genome size is 3.7 Mbp. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Re31.

(Continued)



Table 2 (continued)

**Description of *Xanthomonas surreyensis* sp. nov.**

(sur.rey.en'sis. N.L. fem. adj. surreyensis pertaining to the English county of Surrey, where the samples were obtained)

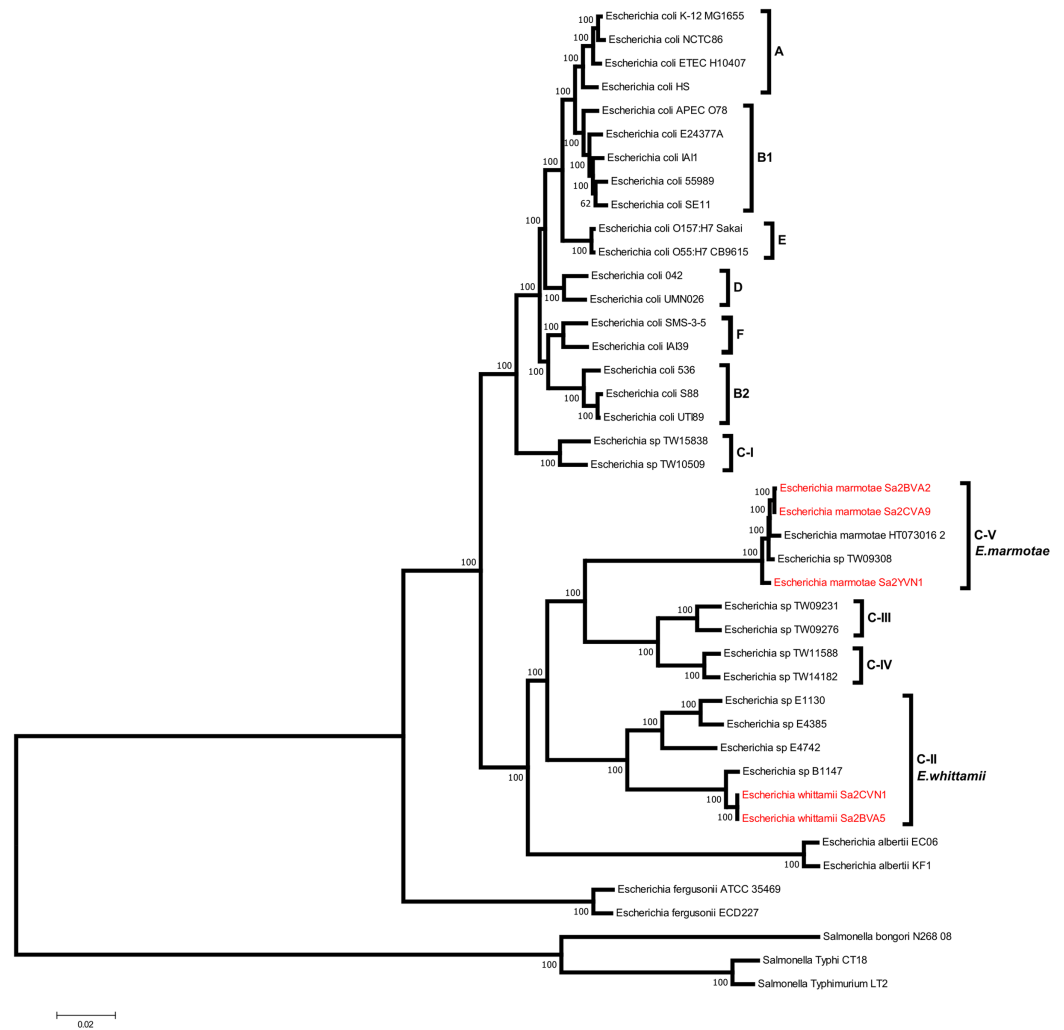
The type strain for this bacterial species has been cultured from chicken faeces after overnight incubation on brain-heart infusion agar at 37 °C under aerobic conditions. The species has been assigned to this genus by the software tool GTDB-Tk v1.3.0 applied to the Genome Taxonomy Database (GTDB) Release 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 (Fig. S3).

The species includes all bacteria with genomes that show  $\geq 95\%$  average nucleotide identity (ANI) to the genome of the type strain, which is available via GenBank accession [GCA\\_014836395.1](https://genbank.ncbi.nlm.nih.gov/GenBank/FASTA/entry.fcgi?accession=GCA_014836395.1). The GC content of the type strain is 68.8% and the genome size is 5.4 Mbp. Although GTDB has assigned a genus name with an alphabetic suffix *Xanthomonas\_A*, this genus designation cannot be incorporated into a well-formed binomial, so in naming this species, we have used the basonym for the genus. The type strain has been deposited in NCTC and DSMZ, where it can be identified via the original strain reference Sa3BUA13.

recently described in Himalayan marmots (Liu et al., 2015)). As previously reported, the *E. marmotae* strains cluster closely with the *Escherichia* Clade V (Liu et al., 2019; Walk, 2015), so all members of this clade should be considered members of this species (Fig. 5; Table S18). Further analysis of the GTDB species designated *Escherichia* sp001660175 (<https://gtdb.ecogenomic.org/searches?s=al&q=sp001660175>) confirmed that this species forms a monophyletic lineage that corresponds to Clade II, among the cryptic environmental clades described by Walk et al. (2009), which has subsequently been documented in birds (Clermont et al., 2011). As Clade II is comparable in divergence to the other *Escherichia* spp. and cryptic clades, we have therefore assigned the Linnaean binomial *Escherichia whittamii* to designate a new species (Table 2), honouring the outstanding contribution of Thomas S. Whittam to the study of *Escherichia* spp. (Walk & Feng, 2011).

We found that only 16 species were common to our cultured isolates and our MGS. Subsequent sequence mapping allowed us to detect a further two cultured species at  $\geq 1\times$  coverage in at least one metagenomic sample (Fig. 6A; Table S19). The genomes from cultured isolates were on average 20% larger than the corresponding MAG sequences retrieved from the same source sample (Table S20), which is in line with the completeness threshold of 80% we adopted in quality assurance of the MAGs. However, when we performed detailed gene content analyses on three abundant species in both cultured and metagenomic datasets—*Lactobacillus reuteri* (with the synonym *Limosilactobacillus reuteri*), *Escherichia coli* (including the synonym *Escherichia flexneri*) and *Enterococcus faecium*—we found that  $>99\%$  of the genes from the core genomes and nearly half of the genes in the accessory genomes of cultured species were represented in at least one MAG. These observations suggest that our high-quality MAGs are sufficiently complete to warrant *Candidatus* names.

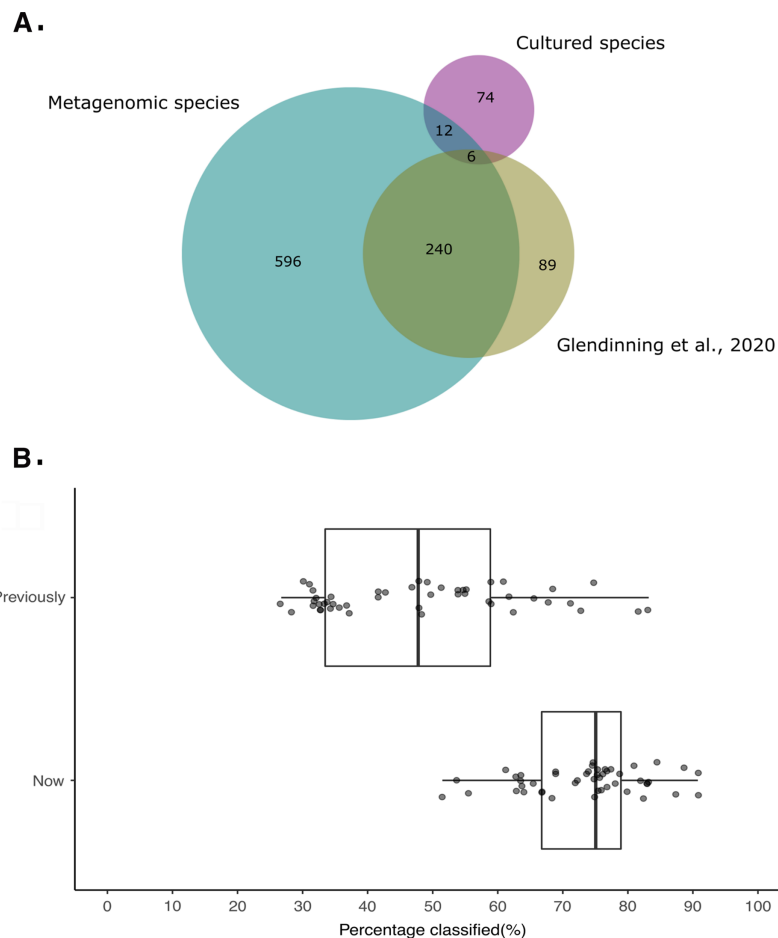
We analysed our chicken faecal metagenomes with a Kraken 2 database derived from genomes representing our candidate metagenomic and cultured species; this yielded a considerable improvement in the number of reads that can be classified through rapid phylogenetic profiling (Fig. 6B).



**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. [Full-size !\[\]\(1663bb69f307a960345edb0e712f8c02\_img.jpg\) DOI: 10.7717/peerj.10941/fig-5](https://doi.org/10.7717/peerj.10941/fig-5)

## Distribution of microbial species

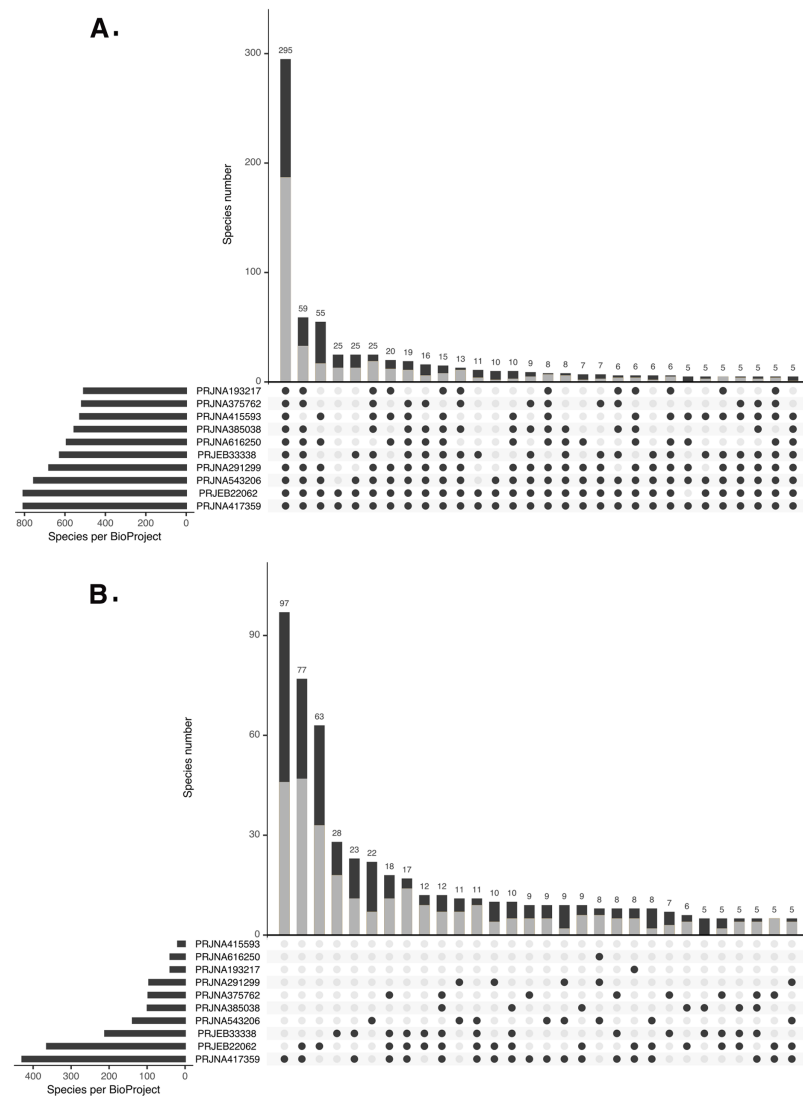
An analysis of the distribution of 820 MGSs across the entire metagenomic dataset revealed marked variation between samples, with not a single species present at  $\geq 1\times$  coverage in all samples and only 39 species present in  $>90\%$  of samples—although 441 species were present in  $>50\%$  of samples at  $\geq 1\times$  coverage (Table S21). At  $\geq 1\times$  coverage, co-occurrence of nearly 300 species ( $n = 295$ ) was identified across all 10 BioProjects (Fig. 7A), with no species identified in all BioProjects at  $\geq 10\times$  coverage (Fig. 7B). Focusing on samples from distinct anatomical or physiological sites (faeces, caecum etc.), we found no species present in all faecal samples at  $>1\times$  coverage and only two species were



**Figure 6 Sequence novelty.** (A) Venn diagram showing shared and unique taxonomic species among three data sources; cultured isolates derived from six 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)*. (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 2,344 genomic and metagenomic sequences derived from this study (Now). [Full-size !\[\]\(ba1b80118482ccef74a5d718ca4d7242\_img.jpg\) DOI: 10.7717/peerj.10941/fig-6](https://doi.org/10.7717/peerj.10941/fig-6)

found in all caecal samples at  $>1\times$  coverage: both of them newly named in this study: *Candidatus* Paraprevotella stercorarium and *Candidatus* *Blautia pullistercoris* (the latter identified but not named by *Glendinning et al. (2020)*). These findings rule out the concept of a core chicken gut microbiome. Studies on the human gut microbiome provide a useful comparison in that, in a recent study, only 14 genera were found to be shared across 95% of samples from the human gut (*Falony et al., 2016*).

Among the species with high coverage, frequency is clearly linked to Bioproject. Although species quantification curves showed that the number of species identified increased rapidly with the number of samples, species discovery appeared to plateau at approximately 230 species after including only 50 metagenomes (*Fig. S2A*). Only two species appeared to be restricted (at  $\geq 1\times$  coverage) to just a single sample: *Aliarcobacter thereius* and *Candidatus* Avibacteroides faecarium. Correlation clustering confirmed



**Figure 7** UpSet plots depicting presence of 820 metagenomic species across all BioProjects included within this study. (A) 1× coverage b. (B) 10× 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 five or more species are shown.

Full-size DOI: 10.7717/peerj.10941/fig-7

structure in the data linked to BioProject (Fig. S2B)—for example, the BioProject from the study by *Glendinning et al. (2020)* clearly shows enhancement of clostridial species compared to other BioProjects, which reflects the fact that samples in that study were sourced from chicks with no post-hatching contact with an adult bird. However, the BioSamples do not appear to cluster by country (Fig. S2C) and show only limited clustering by anatomical/physiological sample site (Fig. S2D). Unfortunately, there is insufficient metadata for other potentially important factors, such as breed, age or diet to draw conclusions on how these might influence clustering.

## DISCUSSION

Given the dominance of chickens in the planetary biomass, the chicken gut microbiome ranks as one of the most abundant microbial communities on the planet. Here, we have exploited two complementary approaches—metagenomics and culture—to create an extensive catalogue of genes, genomes and isolates from this important ecosystem. Our work illustrates the value of combining culture-dependent and culture-independent approaches in analysing microbiomes.

We have clearly demonstrated the advantages of shotgun metagenomic sequencing when applied to the chicken gut microbiome, providing catalogues of genes and genome sequences that takes us well beyond what can be achieved using 16S ribosomal RNA gene sequences. Similarly, the current study is much wider in scope than the previous study by [Glendinning et al. \(2020\)](#), not just including analyses of viral genomes and cultured isolates, while also incorporating MAGs built from data not just from that study but from all publicly available metagenomic datasets. Furthermore, the limited overlap between bacterial species represented among our cultured isolates and in our MGS reinforces the utility of the combined approach. Nonetheless, the substantial co-linearity between genomes obtained by the two approaches—and with those from another similar metagenomic study ([Glendinning et al., 2020](#))—confirms the reliability of our binning approaches.

We were surprised to find such a remarkable phylogenetic diversity within this commonplace livestock ecosystem—diversity that rivals that associated with the human gut. Our work has more than doubled the number of bacterial species known to reside in the chicken gut and has resulted in the creation of an unprecedented number of new *Candidatus* species. By including well-formed Latin binomials with the genomes we have uploaded into public repositories, we have ensured that the new proposed names and associated sequences will be integrated into commonly used online taxonomies and databases and will provide a stable taxonomic nomenclature for future studies. In addition, we have provided proof-of-principle for a scalable approach to Linnaean nomenclature that could be applied to species recovered from other metagenomic assembly projects.

Given that we did not recover by culture some of the organisms that appear most abundant by metagenomics, there is clearly scope for additional culture-based investigations, using a wider range of cultural conditions—perhaps drawing on the precedent of the Human Microbiome Project to create and target a list of the ‘most-wanted-for-culture’ organisms documented by metagenomics ([Fodor et al., 2012](#)). The fact that novel metagenomic species are still being recovered from human gut datasets that include tens of thousands of metagenomes ([Almeida et al., 2019](#))—twinned with the promise of novel long-read and proximity-capture approaches to metagenome analyses ([Stewart et al., 2018](#))—make it clear that our attempts here to analyse all currently available chicken gut metagenomes provide far from the last word on microbial diversity in this abundant and important ecosystem. Nonetheless, the availability of so many novel genes, genome and species represents a substantial step forward.



## CONCLUSIONS

The extensive catalogue of genes, genomes and isolates we have created here substantially improves the coverage of the chicken gut microbiome in the public databases and will make it possible to profile sequences from the chicken gut much more rapidly, easily and comprehensively, providing a valuable resource that lays the ground-work for future comparative and intervention studies. This study also sets a provocative precedent—relevant not just to animal microbiomes, but to studies on all microbiomes—assigning well-formed Latin binomials to hundreds of metagenomic species in a scalable alternative to the automated use of bland, unstable, user-unfriendly alphanumeric designations. Drawing on the precedent set by the current study, we have recently extended this approach to encompass creation of more than a million new names for Bacteria and Archaea (*Pallen, Telatin & Oren, 2020*). Thus, the time is now ripe to bring Linnaeus right into the heart of microbiome studies.

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## ADDITIONAL INFORMATION AND DECLARATIONS

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### Competing Interests

Arss Secka is employed by the West Africa Livestock Innovation Centre.

### Author Contributions

- Rachel Gilroy analysed the data, prepared figures and/or tables, authored or reviewed drafts of the paper, and approved the final draft.

- Anuradha Ravi analysed the data, authored or reviewed drafts of the paper, and approved the final draft.
- Maria Getino performed the experiments, authored or reviewed drafts of the paper, and approved the final draft.
- Isabella Pursley performed the experiments, authored or reviewed drafts of the paper, and approved the final draft.
- Daniel L. Horton performed the experiments, authored or reviewed drafts of the paper, and approved the final draft.
- Nabil-Fareed Alikhan analysed the data, authored or reviewed drafts of the paper, and approved the final draft.
- Dave Baker performed the experiments, authored or reviewed drafts of the paper, and approved the final draft.
- Karim Gharbi conceived and designed the experiments, performed the experiments, authored or reviewed drafts of the paper, and approved the final draft.
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- Evelien M. Adriaenssens conceived and designed the experiments, analysed the data, authored or reviewed drafts of the paper, and approved the final draft.
- Ebenezer Foster-Nyarko performed the experiments, analysed the data, authored or reviewed drafts of the paper, and approved the final draft.
- Sheikh Jarju performed the experiments, authored or reviewed drafts of the paper, and approved the final draft.
- Arss Secka performed the experiments, authored or reviewed drafts of the paper, and approved the final draft.
- Martin Antonio conceived and designed the experiments, authored or reviewed drafts of the paper, and approved the final draft.
- Aharon Oren analysed the data, prepared figures and/or tables, authored or reviewed drafts of the paper, and approved the final draft.
- Roy R. Chaudhuri analysed the data, authored or reviewed drafts of the paper, and approved the final draft.
- Roberto La Ragione conceived and designed the experiments, authored or reviewed drafts of the paper, and approved the final draft.
- Falk Hildebrand conceived and designed the experiments, analysed the data, prepared figures and/or tables, authored or reviewed drafts of the paper, and approved the final draft.
- Mark J. Pallen conceived and designed the experiments, analysed the data, prepared figures and/or tables, authored or reviewed drafts of the paper, and approved the final draft.

### **Data Availability**

The following information was supplied regarding data availability:

Data are available at BioProject ID [PRJNA543206](#) and Figshare:

- Gilroy, Rachel (2020): Gene catalogue and MAGs. figshare. Dataset. DOI [10.6084/m9.figshare.13116809.v4](https://doi.org/10.6084/m9.figshare.13116809.v4).
- Gilroy, Rachel (2020): Cultured isolates. figshare. Dataset. DOI [10.6084/m9.figshare.13234556.v3](https://doi.org/10.6084/m9.figshare.13234556.v3).
- Gilroy, Rachel (2020): Gene catalogue and MAGs. figshare. Dataset. DOI [10.6084/m9.figshare.13116809.v4](https://doi.org/10.6084/m9.figshare.13116809.v4).
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- Gilroy, Rachel (2020): MAGs. figshare. Dataset. DOI [10.6084/m9.figshare.13187396.v1](https://doi.org/10.6084/m9.figshare.13187396.v1).
- Gilroy, Rachel (2020): MAGs10. figshare. Dataset. DOI [10.6084/m9.figshare.13234478.v1](https://doi.org/10.6084/m9.figshare.13234478.v1).

### New Species Registration

The following information was supplied regarding the registration of a newly described species:

Hundreds of new candidatus taxa and dozens of new cultured bacterial taxa are detailed in the article and [Supplemental Material](#).

### Supplemental Information

Supplemental information for this article can be found online at <http://dx.doi.org/10.7717/peerj.10941#supplemental-information>.

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