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Genetic diversity of microbes and its impacts on host switching

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Abstract

Land use around forests, leading to habitat overlap, increases the risk of anthroponotic and zoonotic pathogen/microorganism transmission between humans, livestock, and wildlife. This scenario is exemplified by Buhoma, a village where most residents are primarily subsistence farmers who raise livestock and cultivate crops near the Bwindi Impenetrable National Park (BINP) in Southwestern Uganda, creating an ideal interface for understanding these dynamics. Given the significance of this geographic location and the underrepresentation of African populations in global microbiome research, this project aims to characterise the gut microbiome diversity and potential novel bacterial species, as well as microorganism sharing within a multi-host system in a rural area with documented interactions between humans, livestock, and wildlife. For microbial detection, DNA extracted from 553 faecal samples collected from humans, gorillas, and livestock was processed and sequenced to analyse microbial species communities in different hosts using shotgun high-throughput sequencing and bioinformatics tools. The analysis of 2,411 bacterial metagenome-assembled genomes (MAGs) confirmed the presence of numerous putative novel bacterial species in the gut microbiomes of the Ugandan hosts studied in this project. While many species were host-specific, others were detected across multiple host gut microbiomes from Buhoma and BINP, and in different host samples from other geographic locations (by comparing the MAGs generated in this thesis with other publicly available genomes). Among the bacterial MAGs assembled in this project, genera such as *Prevotella* and *Treponema*—considered markers of the gut microbiome in individuals with traditional agricultural lifestyles—and *Campylobacter*—which comprises species that are leading causes of bacterial gastroenteritis globally—were further investigated. These genera were found to contain numerous putative novel species, contributing to our knowledge of the human and animal gut microbiomes and enhancing our understanding of the species associated with them. The results of this study reveal a high diversity of previously unknown microbes recovered from human, gorilla, and livestock gut microbiomes collected simultaneously at the same wild rural interface.

The *Treponema* genus includes species that inhabit a wide range of hosts and types of microbiotas. In the Ugandan host samples, 75 *Treponema* MAGs were reconstructed, enabling the identification of sixteen intestinal species, including thirteen putative novel species. Three of the detected species were found in human samples from this study, as well as in publicly available *Treponema* genomes recovered from animals such as pigs, cattle, wild boars, roe

deer, and goats. This detection underscores the potential for interspecies transmission and the establishment of these bacteria in different hosts. Overall, these findings highlight the complex interplay between humans, animals, and their gut microbiomes, emphasising the need for further research to elucidate the implications for public health.

Prevotella species are prevalent and abundant components of microbial communities associated with mammals. This bacterial genus influences individual clinical and metabolic responses to dietary changes and overall health conditions. In humans, *Prevotella* species have been identified in various body sites such as the skin, oral cavity, vagina, and gastrointestinal tract. In the gut microbiome, they are commonly linked with diets abundant in plant-based foods and are particularly prevalent among agriculturalist populations, where they tend to dominate the microbiota. In the investigation of this genus, 37 MAGs were assembled, all belonging to yet-to-be-described species. Phylogenetic analysis revealed that they represented fifteen putative novel intestinal *Prevotella* species. The *nimJ* gene, which confers resistance to metronidazole (a nitroimidazole-class drug), was detected in one of the human intestinal *Prevotella* species. Given the widespread use of antibiotics like metronidazole for treating both humans and animals in regions of Uganda, including Buhoma, the presence of this gene provides evidence that *Prevotella* species can acquire resistance to commonly used nitroimidazole-class drugs in areas where their use is prevalent. Of the seven putative novel species identified in human gut microbiomes, two were also present in publicly available genomes in the gut microbiomes from pigs and rhesus macaques living in different geographic locations, providing evidence that the same *Prevotella* intestinal species can inhabit multiple hosts. Overall, these findings expand knowledge of intestinal *Prevotella* by introducing numerous previously unknown species, offering a species-level perspective for future studies on *Prevotella*'s impact on health.

Campylobacter species are leading causes of bacterial gastroenteritis worldwide, yet their diversity and transmission dynamics at wildlife–livestock–human interfaces remain poorly characterised. I investigated *Campylobacter* diversity among sympatric mountain gorillas, livestock, and humans in Uganda, assembling 44 *Campylobacter* MAGs representing seven species—including five putative novel taxa. Three novel species were found in mountain gorillas, livestock harboured *C. vicugnae* (goats) and *C. sp017646085* (cattle), while human gut microbiomes revealed *Candidatus* *Campylobacter* *infans* (not associated with disease) and *C. sp900539255*, which was significantly enriched in clinical samples ($p=0.001$) and displayed

unique sulfur and nitrogen metabolic pathways. Antimicrobial resistance genes, including *bla*_{OXA-471_1}, were detected in *Ca. C. infans* MAGs. Overall, our findings demonstrate high *Campylobacter* diversity at the human–animal interface in Buhoma and highlight the importance of expanding reference databases for accurate surveillance and effective public health interventions.

In summary, this thesis introduces a substantial amount of new information on gut microbiome bacterial species in gorillas, livestock, and humans living at a wild-livestock-human interface. It also provides detailed insights into three bacterial genera present in the gut microbiomes of human populations, as well as other mammals such as gorillas, cattle, and goats.

List of publications

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Glossary

Agriculturalist - A term describing individuals or societies that rely primarily on farming for food production, typically characterised by settled communities and the domestication of animals. Agriculturalists emerged during the Neolithic age, around 10,000 years ago, marking a shift from nomadic hunting and gathering lifestyles.

Alpha-diversity - A measure used in ecology to quantify the diversity of species within a single community or habitat. In the context of microbiology, alpha-diversity refers to the number of different microbial species present in a specific environment.

Beta-diversity - A measure used in ecology to quantify the diversity of species between different communities or habitats. In microbiology, beta-diversity describes the differences in microbial composition between different samples or environments.

Bootstrap – This is a resampling technique used to estimate the reliability of the branches in a phylogenetic tree. It involves creating multiple datasets by sampling from the original dataset with replacement, then constructing a phylogenetic tree for each resampled dataset. The support for each branch in the original tree is assessed by how often it appears in the bootstrap trees, with higher frequencies indicating greater confidence in the branch.

Dysbiosis - A term used to describe an imbalance in the microbial communities that normally inhabit a particular environment, such as the gut. Dysbiosis is often associated with negative health effects and can result in a disruption of the normal functions of the microbiome.

Gut microbiome - The collective genomes of the microorganisms that inhabit the gastrointestinal tract, including bacteria, archaea, viruses, and eukaryotes. The gut microbiome plays a crucial role in digestion, immunity, and overall health.

Hunter-gatherer - A term used to describe societies whose primary means of subsistence involve hunting wild animals and gathering wild plants. Hunter-gatherer lifestyles were prevalent among early human populations before the development of agriculture.

KEGG Orthology - A database that assigns orthologous genes to each gene in a genome, providing a functional annotation based on evolutionary relationships.

Metagenome - The collective genetic material of all the microorganisms present in a particular environment, such as the gut.

Metagenomics - The study of genetic material recovered directly from samples, allowing for the analysis of microbial communities without the need for isolation and cultivation of individual species.

Microbiome - The complete collection of microorganisms and their genomes in a particular environment, including bacteria, archaea, eukaryotes, and viruses, as well as their interactions with each other and the environment.

Microbiota - The community of microorganisms that inhabit a particular environment, such as the human body or soil.

Pathobionts - Microorganisms that are normally harmless or even beneficial but can become pathogenic under certain conditions, such as when the balance of the microbiome is disrupted.

Spillover - The transmission of a pathogen from one species to another, often resulting in the establishment of infection in the new host. Spillover events can occur between animals and humans, leading to the emergence of zoonotic diseases.

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Abbreviations

AIDS	- Acquired Immune Deficiency Syndrome
AGRF	- Australian Genome Research Facility Ltd
AMR	- Antimicrobial Resistance
ANI	- Average Nucleotide Identity
BINP	- Bwindi Impenetrable National Park
CTPH	- Conservation Through Public Health
DNA	- Deoxyribonucleic Acid
FASTQ	- Format for storing nucleotide sequences
gANI	- Genome-wide Average Nucleotide Identity
GTDB	- Genome Taxonomy Database
GTDB-Tk	- Genome Taxonomy Database Toolkit
HIV	- Human Immunodeficiency Virus
KO	- KEGG Orthology
MAG	- Metagenome-Assembled Genome
MSA	- Multiple Sequence Alignment
mEpiLab	- Massey Molecular Epidemiology and Public Health Laboratory
NHP	- Nonhuman Primates
NeSI	- New Zealand eScience Infrastructure
NCBI	- National Center for Biotechnology Information
PCoA	- Principal Coordinate Analysis
RNA	- Ribonucleic Acid
SCFA	- Short-Chain Fatty Acid
SSH	- Secure Shell
TB	- Tuberculosis
WHO	- World Health Organization

1 Chapter

1.1 Introduction

1.1.1 General background on gut microbiome

The microbiome refers to a characteristic microbial community occupying a reasonably well-defined habitat with distinct physio-chemical properties (Whipps et al., 1988). One well-known example of a microbiome is found in the gut which consists of trillions of microbial cells and thousands of bacterial species, eukaryotes, archaea, and viruses (Gentile & Weir, 2018). Advances in culture-independent technologies have revealed an enormous diversity in microbiomes (Berg et al., 2020; Turnbaugh et al., 2007; Ursell et al., 2012). The microorganisms in a microbiome encode over three million genes, producing thousands of metabolites that can replace and assist in many host functions (Bull & Plummer, 2014; Vyas & Ranganathan, 2012). These interactions have a considerable impact on the host, influencing fitness, phenotype, and overall health (Bull & Plummer, 2014; Rath & Dorrestein, 2012; Valdes et al., 2018; Vyas & Ranganathan, 2012).

A noticeable amount of research on microbiomes has focused on “Western” populations with industrialised backgrounds, revealing insights into how lifestyle, diet, and environmental factors affect gut microbiome composition (Makhalanyane et al., 2023; Rothschild et al., 2018a, 2018b; Schaan et al., 2021; Wang et al., 2012). However, there is limited knowledge about gut microbiome composition in non-Western and other understudied groups, such as those from South America, Africa, and parts of Asia, including India (Allali et al., 2021; Brewster et al., 2019; Makhalanyane et al., 2023). This gap in research is problematic because these groups exhibit genetic, ethnic, sociocultural, lifestyle, and dietary differences that can significantly influence their gut microbiomes. The bias in research focus results in an incomplete understanding of global microbiome variability and composition (Brewster et al., 2019).

It has been suggested that modern human populations have lost crucial gut microorganisms, potentially contributing to the increased incidence of various diseases in contemporary life (Fan & Pedersen, 2021; Lynch & Pedersen, 2016). Imbalances in the composition or function of intestinal microbes are associated with gastroenterological disorders, as well as disorders in other systems, including neurological, respiratory, metabolic, hepatic, and cardiovascular systems (Lynch & Pedersen, 2016). Diverse factors such as the increase in caesarean section practices, improvements in sanitation, the use of formula milk as a replacement for breast milk, diet, lifestyle, and exposure to

antibiotics have been associated with the loss of gut microorganisms, impacting the general health of humans (Blaser, 2017; Ramirez et al., 2020). The composition of the non-human primate (NHP) gut microbiome provides valuable insights into the evolutionary processes of the human gut microbiome. Comparing the genomes of intestinal bacteria between NHPs and human populations may help identify potentially beneficial microbes missing from modern human gut microbiomes (Amato et al., 2019).

1.1.2 Human–animal–environment interactions and microbial sharing

The human gut microbiome varies between populations, primarily reflecting ecological differences (Kuthyar & Reese, 2021), and may be influenced by contact with animals (Azad et al., 2013; Tun et al., 2017). The One Health approach to the microbiome considers that humans, animals, and the environment can exchange both pathogenic and non-pathogenic microbes (Trinh et al., 2018). Changes in human population density, activities, and behaviours have led to increased demands for domestic and wild animal products (Hassell et al., 2017). This expansion has boosted the consumption of animal-source protein and increased land use for raising animals, even in previously remote and seldom-visited regions that have now become areas for livestock and agricultural production (El-Sayed & Kamel, 2020; Machovina et al., 2015; White & Razgour, 2020). Proximity to livestock and wildlife industry activities such as transport, slaughtering, and meat processing contributes to increased microbial sharing and the risks of zoonotic transmission (Pal et al., 2013), particularly in certain African regions that have experienced the devastating impacts of successive epidemics, such as cholera, measles, and meningitis (Alinaitwe et al., 2019; Igawe et al., 2020). More than 60% of infections involve zoonotic pathogens that originated from wild or domestic animals (Karesh et al., 2012), which can then infect humans through a mechanism known as cross-species transmission (aka “spillover”) (Plowright et al., 2017a).

Domestic animals have historically been important sources of human infections, including pandemic viral diseases such as measles and smallpox, and they continue to be sources of bacterial zoonotic pathogens, such as *Campylobacter* and *Salmonella* (Wolfe et al., 2007). Animal production, particularly in areas with a wildlife-livestock-human interface and high farmworker contact rates, as seen in Buhoma, Uganda (Muylaert et al., 2021), serves as an important pathway for pathogens to transfer from wildlife to domestic animals and humans (Miller et al., 2017; Wolfe et al., 2007). For instance, new human strains of influenza A have emerged from domestic ducks and pigs infected by wild birds (Wolfe et al., 2007). The immediate source of human pathogens is more likely to be domestic animals rather than wild animals, as human contact with domestic animals is generally closer and more frequent (Wolfe et al., 2007). Multiple NHP species inhabit BINP (Muylaert et al.,

2021), and they might be important source of potential pathogens that may cause human disease due to their close phylogenetic relationship to humans which facilitate pathogen adaptation in the new host (Harper et al., 2013; Wolfe et al., 2007). It is estimated that primates have contributed to about 20% of major human infectious diseases such as acquired immunodeficiency syndrome (AIDS), dengue fever, malaria, yellow fever, and hepatitis B (Cohen, 2010; Liu et al., 2010; Sharp & Hahn, 2011; Wolfe et al., 2007; York, 2018).

BINP is home to nearly half of the world's critically endangered mountain gorilla individuals (*Gorilla beringei beringei*) (Guschanski et al., 2009). They share the forest ecosystem with an extensive diversity of small mammals and other animal species (Hamilton et al., 2000; Kasangaki et al., 2003), while livestock inhabit the populated rural areas surrounding the park (Kalema-Zikusoka et al., 2018; Nolan et al., 2017). Transmission of genetically similar gastrointestinal bacteria (Rwego et al., 2008) and protist parasites has been observed among gorillas, livestock, and humans in the habitat overlap area surrounding BINP and other African regions (Hogan et al., 2014; Kalema-Zikusoka et al., 2018; Nolan et al., 2017; Rwego et al., 2008). Due to their geographic and biological characteristics, those areas are considered global hotspots with a high predicted relative risk distribution of zoonotic emerging infectious disease events (Allen et al., 2017). The risk of zoonotic emerging infectious disease increases in areas with high mammal biodiversity and where anthropogenic land use for agricultural practices replaces formerly natural areas (Allen et al., 2017). Considering the increased necessity of surveillance programs to rapidly detect the emergence of pathogens with potential for zoonotic transmission, Wolfe, and collaborators (Wolfe et al., 2007) proposed a global effort to monitor for microorganisms emerging from animals to humans, especially in areas with increased risks (Allen et al., 2017). In addition, several research groups have been working to understand spillover events better, contributing to strategies that increase the successful chances of infectious disease preventions (Karesh et al., 2012; Plowright et al., 2017a; Sokolow et al., 2019).

1.1.3 Genome sequencing and bioinformatics for microbial surveillance and novel species detection

Genome sequencing and bioinformatics have revolutionised microbial surveillance, offering unprecedented precision in detecting, classifying, and monitoring pathogens (Gwinn et al., 2017, 2019). High-throughput sequencing technologies, particularly shotgun metagenomics, enable the comprehensive analysis of microbial communities directly from environmental or faecal samples (for example), bypassing the limitations of culture-dependent methods (Gwinn et al., 2017, 2019). These approaches have significantly enhanced our ability to identify novel and unculturable microorganisms and improve outbreak preparedness and response strategies (Campbell et al., 2020; Manara et al.,

2019; Miller et al., 2013; Morgan et al., 2013; Nayfach et al., 2019; Nayfach et al., 2021; Pasolli et al., 2019; Wibowo et al., 2021).

Effective use of sequencing data relies on robust bioinformatics pipelines that transform raw reads into meaningful biological insights (Besser et al., 2018; Chiu & Miller, 2019; Deurenberg et al., 2017). These workflows typically begin with quality control and preprocessing using tools such as FastQC (Andrews, 2010) and Trimmomatic (Bolger et al., 2014), which assess and clean the raw sequencing reads. Next, genome assembly is performed using de novo assemblers like MEGAHIT (Li et al., 2015) and SPAdes (Bankevich et al., 2012) to reconstruct microbial genomes without a reference. This is followed by binning, where tools such as MetaBAT2 (Kang et al., 2019) and MaxBin2 (Wu et al., 2016) group contigs into individual genome bins. This process enables the recovery of metagenome-assembled genomes (MAGs) from complex microbial communities, providing a foundation for downstream taxonomic and functional analyses.

Accurate taxonomic classification is crucial for identifying pathogens and assessing microbial diversity. GTDB-Tk is a tool that assigns taxonomy to bacterial and archaeal genomes in a standardised and objective way, using classifications from the Genome Taxonomy Database (GTDB) (Chaumeil et al., 2020). GTDB-Tk classifies genome bins (also called MAGs) by placing them within a reference tree and then evaluating their relative evolutionary divergence (RED) and average nucleotide identity (ANI) against reference genomes (Chaumeil et al., 2020). Other tools, such as MetaPhlAn 4 (Blanco-Míguez et al., 2023) and Kraken2 (Wood et al., 2019), use different strategies for taxonomic classification. MetaPhlAn 4 improves profiling by integrating metagenome assemblies and isolate genomes, using marker genes from over one million reference and metagenome-assembled genomes to classify species-level genome bins, including many uncultured taxa (Wood et al., 2019). Kraken2, in contrast, classifies sequences by breaking them into k-mers and querying a compact hash table that maps each k-mer to its lowest common ancestor (LCA) taxon (Wood et al., 2019).

In addition to computational tools, portable sequencing platforms are increasingly being used for real-time pathogen detection and surveillance (Bloemen et al., 2023). Oxford Nanopore Technologies' MinION device enables on-site metagenomic sequencing, offering rapid and comprehensive diagnostics outside of laboratory settings (Bloemen et al., 2023). These methods support reliable taxonomic profiling, even in field conditions, and enable recovery of long reads that can capture full-length antimicrobial resistance genes and link them to specific microbial hosts (Bloemen et al., 2023).

1.1.4 Project hypotheses and general objectives

The specific pathogen that will cause the next human infectious diseases, and when it will occur, remains unpredictable. However, characterising microbial diversity at wildlife–livestock–human interfaces is essential to better understand microbial sharing, identify emerging pathogens, and strengthen surveillance systems. The Buhoma region in Uganda presents a high-risk interface where humans, livestock, and critically endangered mountain gorillas live in close proximity, creating opportunities for cross-species microbial transmission. Due to the limited representation of African populations in microbiome studies and the complex human–animal–environment interactions in this area, the gut microbiomes of hosts from Buhoma are expected to harbour previously undescribed microorganisms and microbial taxa with zoonotic potential.

This research aimed to characterise gut microbiome diversity and assess microbial sharing within this multi-host system by analysing faecal samples from humans (including clinical and community individuals), livestock, and wild gorillas (both habituated and unhabituated) using shotgun metagenomic sequencing and bioinformatics tools.

Building on previous findings and literature (Kohl, 2020; Mallott & Amato, 2021; Muylaert et al., 2021; Ruuskanen et al., 2021), the study investigated the following hypotheses:

1. Microbial spillover: Identical or highly similar bacterial species are shared among humans, gorillas, and livestock, indicative of microbial spillover events at this interface.
2. Microbial novelty: A noticeable proportion of gut bacteria among Ugandan hosts represent putative novel species, some of which may have pathogenic or functional relevance.
3. Contact-driven microbiota variation: Variations in contact frequency and interaction types between hosts influence microbiota diversity (alpha diversity) and community dissimilarity (beta diversity) and are associated with specific taxonomic or functional microbial units.
4. *Prevotella*–*Treponema* diversity and host associations: The gut microbiomes of humans, livestock, and gorillas in Buhoma harbour diverse *Prevotella* and *Treponema* lineages, including putative novel taxa. Their distribution patterns are shaped by host lifestyle, diet, and ecology, with potential differences between commensal lineages providing insights into gut microbial adaptations in traditional and non-traditional hosts.

5. *Campylobacter* diversity, host range, and pathogenic potential: *Campylobacter* species in sympatric humans, livestock, and gorillas include putative novel lineages reflecting possible host adaptation and posing varying levels of public health risk.

1.1.5 Research objectives

This project seeks to deepen our understanding of microbial ecology and cross-species microbial transmission at a critical One Health interface. The primary objective is to characterise bacterial diversity and potential species sharing among human, livestock, and gorilla populations living in and around Bwindi Impenetrable National Park (BINP), with an emphasis on detecting novel microbial species and investigating potential zoonotic pathways.

The specific objectives of this study are:

1. Develop and implement a metagenomic analysis workflow to reconstruct and identify bacterial genomes (MAGs) from faecal metagenomes, including selection and optimisation of bioinformatics tools for estimating bacterial abundance, genome binning, and downstream taxonomic and phylogenetic analyses.
2. Characterise gut microbiome composition and diversity across host species (humans, gorillas, livestock), identifying differences in microbial structure and the presence of known and novel bacterial taxa. This includes quantifying alpha and beta diversity metrics and investigating associations with host type and contact level.
3. Given the significance of the *Prevotella* genus and its potential presence in the gut microbiomes of individuals living traditional lifestyles in Buhoma, as well as in the animals of this area, this study will investigate this genus in detail, analysing the possible *Prevotella* species present in the gut microbiomes of Ugandan hosts.
4. Examine the diversity of *Treponema* species in the gut microbiomes of the Ugandan studied hosts. Given the *Treponema* spp. and their reported presence in gorillas, this objective aims to explore the prevalence of both pathogenic and commensal lineages, with a focus on putative novel taxa in Buhoma region.
5. Assess the diversity, host distribution, and potential pathogenicity of *Campylobacter* species in the gut microbiomes of sympatric hosts. This includes assembling *Campylobacter* MAGs, identifying

putative novel taxa, evaluating their distribution among humans, gorillas, and livestock, and analysing their genomic features (e.g. antimicrobial resistance genes and unique metabolic pathways) to infer possible host adaptation and public health implications.

To address these objectives, the study is structured around three core components:

1. Bioinformatics pipeline development (**Chapter 3**): Develop a robust and efficient analytical pipeline to process previously generated metagenomic data, with the goal of recovering high-quality MAGs from faecal shotgun sequencing datasets. This included implementing quality control, assembly, binning, and classification steps to enable comprehensive taxonomic and functional characterisation of microbial communities across host species.
2. Microbiome composition and diversity analysis (**Chapter 4**): Evaluate gut microbiome structure across hosts, detect shared species and strain-level overlaps, and identify potential pathogens or zoonotic agents.
3. Genomic and phylogenetic studies of key genera (**Chapter 5**): Conduct in-depth taxonomic and phylogenetic analyses of *Prevotella* and *Treponema* MAGs, assess their novelty, detect resistance genes, and investigate their presence across multiple hosts and geographies.
4. Investigation of *Campylobacter* diversity and zoonotic potential (**Chapter 6**): Characterise *Campylobacter* species recovered from gorilla, livestock, and human gut microbiomes, including the identification of putative novel taxa. Examine species-specific host associations, antimicrobial resistance profiles, and functional genomic traits to better understand *Campylobacter* diversity and potential transmission pathways at the wildlife–livestock–human interface.

1.1.6 Thesis structure

Chapter 1 provides a comprehensive introduction to the gut microbiome and its relevance to host health, disease, and microbial ecology. It outlines the impacts of anthropogenic activities that promote overlap between wildlife, domestic animals, and human populations—conditions that enhance opportunities for microbial sharing and spillover events. This chapter frames the rationale for studying gut microbiomes in Buhoma, Uganda, where such interactions are intensified. It also introduces recent advances in metagenomic sequencing and bioinformatics as powerful tools for microbial surveillance and novel species discovery. The chapter concludes by presenting the research objectives and the structure of the thesis.

Chapter 2 presents a critical literature review, synthesising current knowledge on microbial diversity, cross-species transmission, and metagenomic methodologies. It also identifies existing research gaps in microbiome studies from African populations and wild–domestic–human interfaces, especially involving great apes.

Chapter 3 describes the foundational methods used in this project. It details the study area, sample collection and processing (conducted as part of a collaborative effort), and the development of a comprehensive bioinformatics workflow. This pipeline was applied to previously generated shotgun metagenomic data to recover and analyse MAGs for taxonomic and functional characterisation.

Chapter 4 investigates the composition and diversity of gut microbiomes across humans, livestock, and mountain gorillas. It explores how microbial communities differ by host species while also identifying host-specific and shared microbial taxa, including potential pathogens and novel species.

Chapter 5 focuses on *Prevotella* and *Treponema*. It presents the reconstruction and phylogenetic characterisation of MAGs within these genera, identifying multiple putative novel species, evaluating antimicrobial resistance potential, and exploring evidence of cross-host sharing and host adaptation.

Chapter 6 examines *Campylobacter* diversity across the same host species, identifying seven species, including five putative novel taxa. This chapter assesses host associations, antimicrobial resistance gene presence, and metabolic traits, contributing valuable insight into the zoonotic potential and public health relevance of this genus in a high-contact between humans and animals in a rural environment.

Chapter 7 provides a general discussion of the thesis findings, integrating key themes across chapters. It highlights the novelty and broader implications of the results. This chapter also outlines potential future research directions that could further elucidate microbiome evolution, pathogen emergence, and public health surveillance in One Health contexts.

Overall, this thesis advances our understanding of gut microbiome diversity and microbial exchange in a high-risk interface region. It uncovers a wealth of previously undescribed bacterial species and highlights the importance of including non-Western and wildlife-associated populations in microbiome research. The findings are directly relevant to the early detection of zoonotic risks and the design of evidence-based strategies for preventing future infectious disease outbreaks.

2 Chapter

2.1 Literature review

2.1.1 Concepts of microbiota, microbiome, and metagenome

Microbial communities are multispecies groups where microorganisms live and interact in a particular environment (Berg et al., 2020; Konopka, 2009). The term “microbiome” is a combination of the words “micro” and “biome”, which was first used in 1988 to describe communities associated with plants (Whipps et al., 1988). It was defined as a characteristic microbial community occupying a well-defined habitat (i.e., a habitat with a distinct physio-chemical property) (Berg et al., 2020; Whipps et al., 1988).

The living microorganisms in a specific environment, defined as microbiota, constitute all living organisms in the microbiome (Marchesi & Ravel, 2015). Since phages, viruses, plasmids, prions, viroids, and free DNA are typically not classified as living microorganisms (Dupré & O'Malley, 2009) they are not part of the microbiota (Berg et al., 2020), but they are included in the microbiome because they are members of the “theatre of activity”, the whole spectrum of molecules, presented by Whipps et al (1988). These microorganisms play a crucial role in environmental functioning. These communities engage in symbiotic interactions that influence microbial population dynamics and functional capacities (Berg et al., 2020; Fuhrman, 2009). In summary, **microbiota** refers to the assemblage of microorganisms present in a defined environment, while **microbiome** encompasses the entire habitat, including the microorganisms (bacteria, archaea, eukaryotes, and viruses), their genomes (i.e., genes), and the surrounding environmental conditions (Berg et al., 2020; Marchesi & Ravel, 2015). The **metagenome**, on the other hand, is the collection of genomes and genes from the members of a microbiota (Marchesi & Ravel, 2015).

2.1.2 Microbiome: Composition, taxonomic diversity, and functions

Research has been conducted on the origins of the gut microbiota, and the theory of heritability (transmissible from parent to offspring) remains controversial. While host genetics influence the composition of the human gut microbiome (Goodrich et al., 2014), other studies have shown that the environment plays a more meaningful role than host genetics in shaping the human gut microbiota (Rothschild et al., 2018c). These studies estimate that the overall heritability of the microbiome lies between 1.9% and 8.1% (Goodrich et al., 2016; Rothschild et al., 2018c). However, in another study,

nearly all gut microbiome taxa, both predominant and rare, were found to be heritable in baboons (Grieneisen et al., 2021).

The taxonomic diversity of the microbiome consists of two key elements: taxon richness and the relative abundance of different taxa within the community (Konopka, 2009). It was previously thought that the healthy human adult intestinal microbiome is dominated by the *Bacteroidetes* and *Firmicutes* (now *Bacteroidota* and *Bacillota*) phyla, with smaller proportions of *Actinobacteria*, *Proteobacteria*, and *Verrucomicrobia* (now *Actinomycetota*, *Pseudomonadota* and *Verrucomicrobiota*, respectively) (Eckburg et al., 2005). Additionally, it was expected to contain methanogenic archaea (mainly *Methanobrevibacter smithii*), eukaryotes (mainly yeasts), and viruses (primarily phage) (Lozupone et al., 2012; Reyes et al., 2010). However, in the field of gut microbiome research, defining the interrelationship of a healthy gut microbiome presents a complex challenge (McBurney et al., 2019). The microbiome, functioning as an ecological community, is shaped by numerous genetic, environmental, and clinical factors, as well as stochastic ecological processes (McBurney et al., 2019). These factors drive important interindividual variation and biogeographic differences in human populations, making it challenging to identify microbiome features that determine health (McBurney et al., 2019; Rothschild et al., 2018a; Wang et al., 2016). Moreover, microbiome features may influence the risk of disease years, if not decades, before pathologies arise (Fischbach, 2018; McBurney et al., 2019). Currently, neither the cause-and-effect relationships nor the molecular mechanisms are sufficiently understood (McBurney et al., 2019). Without this crucial information, progress in defining a healthy gut microbiome and translating this knowledge into tangible nutritional or pharmaceutical strategies, as well as regulatory policies, will be difficult (Fischbach, 2018; McBurney et al., 2019).

Microbial assemblages in each microbiome are unique, but, despite the taxonomic divergences, the functional capacity of the adult gut microbiota is reasonably consistent across healthy people (Huttenhower et al., 2012; Qin et al., 2010). These functions possess pathways implicated in lipopolysaccharide biosynthesis, oxidative phosphorylation (Hollister et al., 2015), fermentation and metabolism (Yatsunenko et al., 2012), which are essential activities that help the host organism to be balanced and healthy.

2.1.3 Gut microbiome influences in human health and diseases

A healthy human gut microbiome has yet to be defined at any profound taxonomic resolution (Fan & Pedersen, 2021). Nevertheless, increased taxa diversity, microbial gene richness, and regular microbiome functional cores indicate healthy gut microbial communities (Huttenhower et al., 2012).

Importantly, intestinal transit time impacts microbial richness (Falony et al., 2018), and a prolonged transit time may result in increased richness but not necessarily in a healthy gut microbiota (Fan & Pedersen, 2021).

The microbiota plays a fundamental role in the induction, training, and operation of the host immune system (Belkaid & Hand, 2014). The immune system, in turn, supports the maintenance of a symbiotic relationship with these highly diverse and evolving microbes (Belkaid & Hand, 2014). Host immune function is diminished in the intestines following antibiotic treatment, increasing susceptibility to intestinal infection (Buffie & Pamer, 2013). The microbiota also performs several other crucial physiological functions, such as immune maturation and intestinal endocrine functions necessary to maintain homeostasis in the host system (Buffie & Pamer, 2013). Consequently, it has been linked with various diseases affecting different organ systems (Lynch & Pedersen, 2016). For example, research has begun to associate microbial taxa with the microbiome profile of individuals with metabolic diseases and to link microbial phyla to specific metabolic functions and processes (Fan & Pedersen, 2021).

Stress on the gut microbiota may result in microbiome dysbiosis, which refers to an imbalance, dysfunction, or disturbance in the microbiota (Wei et al., 2021). Dysbiosis, a key term in microbiome research, has not been precisely defined. However, it is generally considered as a general modification in the microbiota composition (e.g., alteration, perturbation, abnormal composition, and loss of diversity), an imbalance in composition (almost always deemed to have negative effects), and changes to specific lineages in that composition (any named taxon change) (Hooks & O'Malley, 2017).

The gut microbiome also plays a central role in protecting the host from enteric bacterial infection. Several enteric pathogens have developed strategies to outcompete the intestinal community, leading to infection and/or chronic diseases (Rolhion & Chassaing, 2016). These pathogens induce more severe disease in mice lacking intestinal microbiota or following antibiotic treatments (Fukuda et al., 2011, 2012; Lawley et al., 2009). Given the constant temporal and spatial changes in the microbiota, responses to environmental perturbations, including the presence of enteric pathogens, occur continuously in the microbial community (Konopka, 2009; Lozupone et al., 2012; Sommer et al., 2017). Microbial community stability considers a longer-term perspective in which stress imposes selection for resistant taxa at low relative abundance. In this aspect, the resistance of the microbiota prevents an acute loss of function after the imposition of stress. Simultaneously, resilience indicates how functionality returns after the stress effect (Konopka, 2009; Lozupone et al., 2012; Pimm, 1984; Sommer et al., 2017).

The intestinal microbiota plays a crucial role in resisting colonisation by pathogenic species (Buffie & Pamer, 2013; Cameron & Sperandio, 2015; Sassone-Corsi & Raffatellu, 2015) which can be confirmed with experiments examining microbiome composition and proliferation of pathogenic species before and after using broad-spectrum antibiotic treatments (Baümle & Sperandio, 2016). Antibiotic therapy disrupts the native intestinal microbiota, increasing susceptibility to infection and proliferation of antibiotic-resistant intestinal pathogens (Buffie & Pamer, 2013).

The effectiveness of resistance against pathogenic bacteria can vary based on the composition of the host microbiota and the types of pathogens involved (Dicksved et al., 2014; Kampmann et al., 2016). For instance, the species composition of the human gut microbiome, particularly bacteria from the family *Lachnospiraceae*, including the genera *Dorea* and *Coprococcus*, plays an important role in resisting *Campylobacter* infection (Kampmann et al., 2016). Conversely, higher levels of *Bacteroides* and *Escherichia* species may increase susceptibility to *Campylobacter* infection in humans (Dicksved et al., 2014). Commensal bacteria that influence host immunity and provide resistance to intestinal pathogens are being discovered among the phyla that make up most of the intestinal microbiome (as reviewed by Buffie & Pamer, 2013).

The gut microbiota's composition varies among individuals and evolves over time, influenced by both host and environmental factors (Lozupone et al., 2012; Sommer et al., 2017). Despite facing diverse challenges, the gut microbiota and its function typically remain stable due to the resilience and resistance to change exhibited by microbial communities, unless they suffer from a strong and prolonged perturbation (Lozupone et al., 2012; Sommer et al., 2017).

2.1.4 Differences in gut microbiomes between Western and non-Western human populations

Many African agriculturalist and hunter-gatherer societies maintain subsistence practices similar to those predating the Neolithic era, which occurred over 10,000 years ago (Brewster et al., 2019; Tamburini et al., 2022). Comparing these traditional African groups with Western populations has provided insights into how changes in diet and environment accompanying industrialisation can significantly impact the gut microbiome (Brewster et al., 2019; Carter et al., 2023; Fragiadakis et al., 2019; Schnorr et al., 2014; Tamburini et al., 2022).

Prevotella is associated with a diet rich in plant-based foods, while a higher intake of animal fats and proteins, characteristic of industrialised populations, correlates with an increased relative abundance of *Bacteroides* (Brewster et al., 2019; De Filippo et al., 2010; Gomez et al., 2016; Schnorr et al.,

2014; Tamburini et al., 2022). Some African populations have diets rich in a variety of simple and complex carbohydrates from sources such as wild tubers, roots, and berries (De Filippo et al., 2010; Gomez et al., 2016; Tamburini et al., 2022). Their foraging lifestyle is linked to higher levels of *Prevotella*, *Treponema*, and *Succinivibrio*, which are known for their ability to degrade fibre and may play a role in breaking down starch, hemicellulose, and xylan (Angelakis et al., 2019; Brewster et al., 2019; Gomez et al., 2016; Schnorr et al., 2014). Agricultural societies, known for farming and domesticating animals, include a vegetarian diet rich in grains, vegetables, and legumes. This dietary pattern results in a gut microbiota where *Prevotella* and *Treponema*, capable of breaking down plant polysaccharides and fibres, are usually dominant. (Brewster et al., 2019; De Filippo et al., 2010; Gomez et al., 2016). Although the gut microbiome profiles of agriculturalist individuals more closely resemble those of hunter-gatherers, they also share some features with Western populations. This includes bacterial taxa and gene pathways related to the digestion of sugars (Brewster et al., 2019; Gomez et al., 2016; Hansen et al., 2019). Some agricultural communities also show an enrichment of xenobiotic-processing genes, likely due to antibiotic exposure, which results in the presence of genes conferring antibiotic resistance in their gut microbiomes (Dethlefsen & Relman, 2011; Fishbein et al., 2023; Kiguba et al., 2016; Ramirez et al., 2020). Microbial diversity in the gut microbiome varies among populations with different lifestyle practices (Yatsunenکو et al., 2012). Hunter-gatherer and agriculturalist groups tend to have higher gut microbiome alpha diversity compared to Western populations (Brewster et al., 2019; De Filippo et al., 2010; Gomez et al., 2016; Yatsunenکو et al., 2012). This observation supports the hypothesis that gut microbiome diversity decreases with industrialisation (Brewster et al., 2019; De Filippo et al., 2010; Gomez et al., 2016; Yatsunenکو et al., 2012).

Various factors such as the rise in caesarean deliveries, improved sanitation, cleaner water, formula feeding in place of breastfeeding, and exposure to antibiotics have been linked to the reduction of gut microbiota, affecting host physiology (Blaser, 2017; Blaser & Falkow, 2009; Ramirez et al., 2020). The loss of ancestral “indigenous” organisms is generally unfavourable and may contribute to the development of some “modern” diseases (Blaser, 2017; Blaser & Falkow, 2009; Ramirez et al., 2020). The microbiota is vital to many physiological activities, immunologic system maturation (Wu & Wu, 2012) and prevent the establishment of pathobionts (opportunistic microbes that emerge from perturbations in the healthy microbiome) (Fukuda et al., 2011, 2012) in the gut. The diminishing members of the gut microbiota have been linked to the development of several diseases (Chen et al., 2021). Therefore, it has been discussed that the consequence of missing gut microbes is increasing disease incidences (Blaser, 2017; Blaser & Falkow, 2009).

2.1.5 Human, animal, and environmental microbiomes in One Health perspectives

The One Health approach (aims to achieve a sustainable balance and optimise the health of humans, animals, and ecosystems) brings evidence that the human-animal interface environments may contribute substantially to microbiome variation (Kuthyar & Reese, 2021; Trinh et al., 2018). The microbiota can be influenced by contact with animals (Azad et al., 2013; Tun et al., 2017) and people (Trinh et al., 2018). Research conducted in Kenya has mentioned that the gut microbiome of children appears to be shared between children within the same household (Mosites et al., 2017). Some children may also share microbiome components with nearby animals, although this effect does not appear consistent across the population (Mosites et al., 2017). It has been discussed that different interactions with animals contribute to shaping the human microbiome globally (Kuthyar & Reese, 2021). These interactions include direct contact with animals (wildlife, livestock, and pets), sharing a common environment, and consuming or handling animal products (Kuthyar & Reese, 2021). Increasing anthropogenic disturbance and encroachment into wild habitats often intensify these interfaces and, consequently, increase the potential for the transmission of new microorganisms between hosts (Faust et al., 2018; Goldberg et al., 2008; Kuthyar & Reese, 2021).

2.1.6 Eukaryotes in the gut microbiome

The eukaryotic component of the gut microbiome has been relatively understudied using high-throughput sequencing technology due to the challenge of reconstructing eukaryotic genomes (Delmont et al., 2022). Initially, technical limitations restricted the capture of only a few genes, providing insights into a small portion of the eukaryotic genomes (Delmont et al., 2021). However, studies indicate progress in reconstructing high-quality eukaryotic MAGs from environmental communities (Lind & Pollard, 2021; Massana & López-Escardó, 2022; Parfrey et al., 2011; West et al., 2018; Yandell & Ence, 2012). Therefore, we can expect more information about the gut eukaryotic component in the coming years, including from this research project. Protozoans may play a role in intestinal dysbiosis (Ulusan Bagci & Caner, 2022). Therefore, a better understanding of the host-microbiota-parasite relationship will enhance our knowledge of protozoan diseases and could potentially lead to the development of novel treatment supports associated with microbiota intervention (Bär et al., 2015; Keselman et al., 2016; Yooseph et al., 2015).

Intestinal protozoan parasites continue to pose a notable public health challenge in Africa, where several factors facilitate transmission, particularly affecting children (Hajissa et al., 2022; Squire & Ryan, 2017). Gorilla faecal samples have shown the presence of eukaryotic pathogens that also can infect humans (Hamad et al., 2014; Nolan et al., 2017) including pathogenic fungi such as *Candida*

tropicalis, *C. parapsilosis*, *C. rugosa*, *Malassezia globosa*, *M. restricta*, *Trichosporon* sp., and *Trichosporon asahii* (Hamad et al., 2014) and intestinal protozoans like *Cryptosporidium* and *Giardia* have been detected in gorillas living in BINP, Uganda and Rwanda (Hogan et al., 2014; Kalema-Zikusoka et al., 2018).

2.1.7 Viral fraction of the gut microbiome

In the past decade, there has been a growing interest in the viral fraction of the intestinal microbiota, which mainly consists of phages that infect bacteria (Sausset et al., 2020; Zuppi et al., 2022). This interest has led to the discovery of numerous new phage families, thanks to the advancement of viral metagenomics (Sausset et al., 2020; Zuppi et al., 2022). Phages, or bacteriophages, are viruses that target and infect bacteria specifically (Zuppi et al., 2022). They are abundant within the human microbiomes and are potential modulators of the gut ecosystem (Zuppi et al., 2022). Phages can influence the human gut microbiome by either affecting bacteria or promoting bacterial survival through gene transfer that enhances bacterial fitness after infection (Zuppi et al., 2022). Our knowledge of how phages affect the structure of the gut microbiota is still limited (Sausset et al., 2020). Shifts in viral community composition have been noted in various diseases, but whether these changes indicate a direct role of phages in disease development or simply arise from alterations in bacterial composition remains unclear (Sausset et al., 2020).

2.1.8 Spillover of microorganisms between hosts

Spillover is promoted by successive processes that enable an animal pathogen/microorganism to establish infection in a human and *vice versa* (Plowright et al., 2017b). Interfaces represent a critical point for cross-species spillover and the emergence of pathogens into new host populations and should be studied as complex, multi-host communities with interferences of ecological and anthropological factors (Hassell et al., 2017). Even though wildlife and domesticated animals are important reservoirs for pathogens, the anthropogenic influence on ecological systems drives the risk at the interface between humans and animals in zoonotic disease emergence (Hassell et al., 2017). To mitigate the risk of disease emergence, interfaces must be studied as complex, multi-host communities whose structure and form are dictated by both ecological and anthropological factors (Hassell et al., 2017).

Urbanisation, rapid agricultural intensification, socioeconomic shifts, and ecological fragmentation can generate a variety of interfaces among wildlife, livestock, and humans, often linked to the emergence of diseases (Hassell et al., 2017). Increased interactions between humans, animals, and

the environment in these situations can lead to a more substantial volume and diversity of pathogenic and commensal microbes moving between different host species (Kuthyar & Reese, 2021). Some pathogens are transmitted via wild or domesticated animals at human-animal interfaces (Kuthyar & Reese, 2021). For example, *Mycobacterium tuberculosis* could be directly transmitted through contact with wild animals in Africa (Alexander et al., 2002). The initial cases of human infections with the Nipah virus primarily affected adult males engaged in pig farming or pork production activities (Lo & Rota, 2008). Fragmenting of natural habitats can influence the wild animal species to move in high densities near humans and vectors resulting in increased contact (Bloomfield et al., 2020), thereby increasing the potential for transmission (Glidden et al., 2021). That might have happened during the transmission of *Plasmodium knowlesi* in Malaysia when forest loss due to agricultural activities drove primary reservoir hosts, long-tailed macaques, and pig-tailed macaques close to the farming areas inhabited by people and anthropogenic vectors (Brant et al., 2016; Davidson et al., 2019; Fornace et al., 2016; Manin et al., 2016). Similarly, agricultural conversion has limited the availability of winter resources for elk, which reduced their migration and promoted high-density aggregations, thereby increasing the spread of *Brucella* among these animals and potential spillover to livestock (Brennan et al., 2017; Jones et al., 2014).

Other routes are also considered for the occurrence of microbial spillover. Animal markets, which host high densities of humans interacting with live and carcass animals, can lead to exposure to novel pathogens, as observed in the case of SARS-CoV-2 (Holmes et al., 2021; Pekar et al., 2022). Additionally, consuming undercooked meat and other animal products that harbour microorganisms and pathogens can serve as routes for host cross-species transmission, as demonstrated in the case of the zoonotic transmission of the hepatitis E virus from deer to humans (Tei et al., 2003). The novel direct and indirect transmission of microbes between animals and humans is expected to increase as hosts move across the globe due to growing trade and travel (Kuthyar & Reese, 2021).

Zoonotic pathogens and microorganisms must overcome multiple barriers to spillover between different host species. These include ecological factors, the capacity for microbiological survival, epidemiological factors, behavioural determinants of pathogen/microorganism's exposure, and the within host characteristics that affect vulnerability to infection/transmission (Plowright et al., 2017b).

Tropical regions in North America, Asia, Central Africa, and parts of South America have large areas predicted to experience emerging infectious diseases (Allen et al., 2017). There is a higher risk of zoonotic emerging infectious diseases in forested tropical regions undergoing anthropogenic land-use changes (such as agricultural practices) and where wildlife biodiversity (mammal species richness) is high (Allen et al., 2017; Morse, 1995). As an example, African animal trypanosomiasis

affects both livestock and wildlife, carrying a considerable risk of spillover and cross-transmission of species and strains between populations (Kasozi et al., 2021). In 2001, a study mentioned that the Ugandan outbreak was introduced by cattle infected with *Trypanosoma brucei rhodesiense* (Fèvre et al., 2001). Many African wild animals carry *Trypanosoma* species (Kasozi et al., 2021), spreading the protozoan between hosts in the community (Clément et al., 2020). Moreover, bats may play an important role in dispersing these protozoan parasites between countries and continents (Clément et al., 2020).

In parts of Central Africa and Asia, wildlife is an important source of meat and income for millions of people living in rural areas (Devaux et al., 2019). Some rural groups depend on wildlife and are frequently exposed to the risk of NHP pathogen transmission through animal hunting and wild meat consumption (Devaux et al., 2019). Together with anthropogenic land-use changes and high wildlife biodiversity, the NHPs were involved in the origins of some zoonotic emerging infectious diseases like AIDS (Sharp & Hahn, 2011), Dengue fever (Hanley et al., 2013) and vivax malaria (Escalante et al., 2005).

In addition, African apes harbour at least twelve *Plasmodium* species, some of which have been a source of human infection (Sharp et al., 2020). It is now well established that *Plasmodium falciparum*, responsible for the deadliest form of human malaria, emerged following the transmission of a gorilla parasite, possibly within the last 10,000 years (Sharp et al., 2020). Humans are believed to be an important or central host for *Mycobacterium leprae*, which causes leprosy. However, the infection has occurred in other mammals like red squirrels (Avanzi et al., 2016), captive nonhuman primates (Gormus et al., 1988; Meyers et al., 1985), armadillos (Balamayooran et al., 2015) and two wild populations of Western chimpanzees (*Pan troglodytes verus*) in West Africa that are now considered as maintenance hosts (Hockings et al., 2021). Leprosy was most likely introduced into West Africa by infected explorers, traders, or colonialists of European or North African descent (Monot et al., 2005), it has been suggested that *M. leprae* may be circulating in more wild animals than suspected, either because of exposure to humans or other unknown environmental sources (Hockings et al., 2021).

2.2 Infectious diseases

2.2.1 Important pathogens causing world pandemics throughout history

Infectious diseases with pandemic potential have occurred continually throughout history and have impacted humanity. Most of those diseases, such as COVID-19, Ebola virus disease, AIDS,

leptospirosis, brucellosis, toxoplasmosis, and Chagas disease, have origins in the wild or wild domestic animals (Karesh et al., 2012).

It is discussed that humanity had three epidemiologic transitions (Barrett et al., 1998). The first one related to a rise in infectious diseases associated with the Neolithic period marked by a transition from a lifestyle of hunting and gathering to one of agriculture and settlement, making an increasingly large population possible (Barrett et al., 1998). The second involved the shift from infectious to chronic disease mortality associated with industrialisation (Barrett et al., 1998; Lindahl & Grace, 2015). The third and current one is characterised by newly emerging, re-emerging, and antibiotic-resistant pathogens in the globalisation of human disease ecologies (Barrett et al., 1998; Lindahl & Grace, 2015). Contributing to the last one, climate changes have been influencing the transmission of pathogens by expanding the habitats of common zoonotic disease-carrying hosts (Caminade et al., 2019; Rocklöv & Dubrow, 2020).

2.2.2 Examples of bacterial diseases and their impacts on human health worldwide

Some of the most critical world pandemics were caused by bacteria, such as *Yersinia pestis* (plague) and *Mycobacterium tuberculosis* (tuberculosis) (Piret & Boivin, 2021). The plague, caused by the flea-borne bacterium *Y. pestis*, is responsible for at least three major human plague pandemics: the plague of Justinian (5th Century - Egypt), the Black Death (14th Century - Europe), and the ongoing third plague (1885–ongoing - China) (Piret & Boivin, 2021). It is estimated that this pathogen caused more than 300 million deaths during these outbreaks (Piret & Boivin, 2021). It is proposed that *Y. pestis* may have persevered in rodent reservoirs in Europe and regularly re-emerged in people (Seifert et al., 2016). Another explanation could be the repeated climate-driven reintroductions of the pathogen into European harbours from reservoirs in Asia (Schmid et al., 2015). Probably due to the fact that plague is endemic in a variety of wildlife rodent species worldwide in a wide range of natural habitats (Stenseth et al., 2008), it remains endemic in some countries such as Madagascar, Congo, and Peru (Glatter & Finkelman, 2021), and it is still considered as a neglected human threat due to its rapid spread, its high fatality rate without early treatment and its capacity to disrupt social and healthcare systems (Vallès et al., 2020).

Tuberculosis (TB), caused by *M. tuberculosis*, is another example of a bacterium that has had a striking impact on the world (Paulson, 2013; Vitale, 2020). It is one of the world's most lethal infectious diseases, estimated to have caused 1 billion deaths in the last 200 years (Paulson, 2013). TB remains a global health problem, with a total of 1.5 million human casualties in 2020 (WHO, 2020). Africa is the only continent where all *M. tuberculosis* complex lineages are present, suggesting

that the disease emerged from a common ancestor internally and then expanded to the rest of the world following human migrations (Comas et al., 2013). It was thought that *M. tuberculosis* in humans arose from *Mycobacterium bovis* that infected domesticated cattle. However, genome sequencing studies have revealed that *M. bovis* is likely derived from a human-adapted mycobacterium (Galagan, 2014). The molecular events that accompanied this emergence remain unknown in 2020 (Ngabonziza et al., 2020).

Another important bacterium that raises public health concerns is *Campylobacter*. Species of the genus *Campylobacter* are the leading global cause of bacterial colon infections and are associated with post-infection irritable bowel syndrome in humans (Peters et al., 2021). More than 90% of human *Campylobacter* infections are caused by *C. jejuni* or *C. coli*, mainly transmitted through the consumption of contaminated meat and poultry (Dai et al., 2020; Mughini-Gras et al., 2021). *C. jejuni* infection was considered one of the most widespread infectious diseases of the last century (Kaakoush et al., 2015).

Campylobacter infection is endemic and common in some parts of Africa, especially among young people (Mason et al., 2013; Ouko et al., 2021; Platts-Mills et al., 2014; Samie et al., 2022). The high prevalence among children under five years of age in Ethiopia is significantly associated with domestic animal contact, illiterate mothers, and consumption of animal products (Ouko et al., 2021). In Malawi, *Campylobacter* species were detected in 415 out of 1,941 (21%) diarrheic children (median age of 11 months), with *C. jejuni* accounting for 85% of all cases (Mason et al., 2013). In Tanzania, from 138 children's stool samples, 42% were positive for *C. jejuni* and or *C. coli* (Platts-Mills et al., 2014). These findings indicate that *Campylobacter* affects children's health and nutritional development on the continent.

Another important example of bacteria impacting human health is certain species from the *Treponema* genus. The results of this project concerning this genus will be presented in **Chapter 5** of this thesis. The *Treponema* species detected in this study are intestinal species, and currently, very little information about them is available in the literature. Most of the existing information on *Treponema* species pertains to treponematoses, including *T. pallidum*, the causative agent of syphilis.

Human treponematoses are caused by four closely related members of the genus *Treponema*: Three subspecies of *Treponema pallidum* plus *Treponema carateum*. *T. pallidum* subsp. *pallidum* causes venereal syphilis, while *T. pallidum* subsp. *pertenue*, *T. pallidum* subsp. *endemicum*, and *T. carateum* are the agents of the endemic treponematoses yaws, bejel (or endemic syphilis), and pinta, respectively (Mitjà et al., 2013). These infections share similarities but can be differentiated based on

clinical (Table 2.2) (Mitjà et al., 2013), epidemiological, and geographical criteria (Giacani & Lukehart, 2014).

Syphilis was first recognised in Europe in the late 15th century (Harper et al., 2011), its cause was identified four centuries later (Rothschild & Rothschild, 1996). Treponemal disease appears to have had its origins with the first hominids to walk out of Africa (Rothschild & Rothschild, 1996). Over the last few years, the incidence of this disease is increasing, and exactly how *T. pallidum* is transmitted sexually from person to person is still unclear (Towns et al., 2021). Much attention is directed towards *T. pallidum*, while very little is known about *Treponema* species residing in the gut microbiomes of humans and other animals. Some of these species contribute to the gut microbiota of traditional rural populations but are absent in urban individuals (Angelakis et al., 2019). Sequencing surveys of the human intestinal microbiota have revealed dissimilarities among individuals with varying lifestyles and origins (Schnorr et al., 2014; Yatsunenko et al., 2012). One study found that *Spirochaetota* (the phylum to which the *Treponema* genus belongs) were more prevalent in the gut microbiota of traditional rural populations, particularly enriched with *Treponema succinifaciens* (Angelakis et al., 2019) and, together with other microbiota members, may enhance the ability to digest and extract valuable nutrition from fibrous plant foods (Schnorr et al., 2014). *T. succinifaciens* and *T. berlinense* are two intestinal species found in the gut microbiomes of traditional rural populations (Angelakis et al., 2019). Recently, a new intestinal *Treponema* species, *T. peruense*, was isolated from the faeces of humans living in a remote Amazonian community in Peru (Belkhou et al., 2021). Despite their significance, there is little information available about these intestinal *Treponema* species. This indicates that these organisms are still under-studied, and their activities and interactions with the microbiota require more attention.

2.2.3 Intestinal *Treponema* and *Prevotella* species in the gut microbiomes of traditional rural populations

Fibrinolytic bacterial species, such as *Prevotella* and *Treponema*, are highly prevalent in the gut microbiomes of agriculturalist societies characterised by subsistence farming and animal domestication, such as the Buhoma rural population in Uganda (Brewster et al., 2019; Gomez et al., 2016; Muylaert et al., 2021). The gut microbiomes of hosts living in Africa, which have a higher likelihood of containing these microorganisms compared to industrialised populations, are underrepresented in this research landscape (Brewster et al., 2019; Littlejohn & Glover, 2023; Makhalanyane et al., 2023). Additionally, the available literature typically does not mention taxonomic classification beyond the genus level, leaving a vast amount of new information about

intestinal *Treponema* and *Prevotella* species unclear (Angelakis et al., 2019; Brewster et al., 2019; Littlejohn & Glover, 2023; Makhalanyane et al., 2023).

The Gram-negative anaerobic bacteria, *Prevotella*, is a diverse genus with numerous species. The genus is particularly intriguing due to its frequent association with both health and disease (Gorvitovskaia et al., 2016; Könönen & Gursoy, 2022; Mehmood et al., 2014; Tett et al., 2021; Webb et al., 2022). Most *Prevotella* characterised species (over 50), are associated with human microbiomes, although they are found in varied natural habitats (Amat et al., 2020; Betancur-Murillo et al., 2023; Könönen & Gursoy, 2022; Mehmood et al., 2014; Shinkai et al., 2022; Tett et al., 2021; Webb et al., 2022). While *Prevotella copri* is often the main focus within this genus, there is a growing interest in cataloguing and characterising other *Prevotella* species found in the gut (Tett et al., 2021; Yeoh et al., 2022). **Chapter 6** of this thesis studies the *Prevotella* genus and introduces over 10 potentially novel species within this genus.

2.3 Key bioinformatics methods

The advent of high-throughput genome sequencing has transformed how microbial pathogens are detected, classified, and monitored across clinical, environmental, and public health settings (Pronyk et al., 2023). These technologies generate vast amounts of data, necessitating the use of sophisticated bioinformatics tools to extract meaningful insights (Satam et al., 2023). Advances in computational biology have led to the development of integrated analytical pipelines capable of processing raw sequencing reads, assembling genomes, performing taxonomic and functional classification, and supporting epidemiological investigations (Satam et al., 2023).

This section outlines key bioinformatics methods commonly used in genome-based microbial surveillance, encompassing the major analytical stages: quality control, genome assembly and binning, taxonomic classification, functional annotation, and comparative genomics.

2.3.1 Genome sequencing and bioinformatics as surveillance tools

Metagenomics has emerged as a powerful and culture-independent approach for microbial surveillance, allowing researchers to analyse the entire microbial content of a sample (Pronyk et al., 2023; Satam et al., 2023). Unlike conventional diagnostic techniques, metagenomics enables the simultaneous detection of multiple microorganisms—including unculturable and previously undescribed species—from a single sample (Yen & Johnson, 2021). This approach, when combined with bioinformatic workflows, allows for the detection of pathogens, monitoring of antimicrobial

resistance genes, and the tracking of microbial population dynamics (Sherry et al., 2025; Urbaniak et al., 2022). In addition, long-read sequencing technologies, such as Oxford Nanopore Technologies, are increasingly being integrated into microbial genomics (Wang et al., 2021). Nanopore sequencing enables the generation of whole genomes with fewer contigs and improved resolution of repetitive regions (Wang et al., 2021). Its portability and speed offer advantages for on-site diagnostics and outbreak surveillance, particularly in resource-limited or remote settings (Oehler et al., 2025).

2.3.2 Quality control and preprocessing

The initial step in most sequencing-based workflows involves the quality control and cleaning of raw sequence data. High-throughput technologies can introduce sequencing artefacts such as base-calling errors, adapter contamination, and low-quality reads (Andrews, 2010; Bolger et al., 2014). To address these issues, several preprocessing tools are routinely employed. FastQC provides a visual overview of sequence quality metrics (Andrews, 2010), while Trimmomatic (Bolger et al., 2014) remove adapters and trim low-quality bases. Effective preprocessing ensures that only high-quality reads proceed to downstream steps, thereby reducing analytical biases and improving accuracy.

2.3.3 Genome assembly and binning

Following quality filtering, sequencing reads are assembled into longer contiguous sequences, or contigs, which are then grouped to reconstruct microbial genomes, commonly referred to as metagenome-assembled genomes (MAGs) (Goussarov et al., 2022). Assemblies may be conducted using *de novo* methods, which do not rely on a reference genome, or reference-guided approaches for well-characterised species (Lischer & Shimizu, 2017). For metagenomic data, MEGAHIT (Li et al., 2015) and metaSPAdes (Nurk et al., 2017) are widely used for short-read assemblies, while tools like Flye (Kolmogorov et al., 2019) and Canu (Koren et al., 2017) are effective for long-read data.

Once assembled, contigs are grouped into genome bins through a process known as binning, which is essential for recovering MAGs from complex microbial communities. Binning tools such as MetaBAT2 (Kang et al., 2019), MaxBin2 (Wu et al., 2016), and CONCOCT (Alneberg et al., 2014) rely on features like GC content, k-mer frequencies, tetranucleotide frequencies, and differential coverage across samples to assign contigs to distinct microbial genomes.

2.3.4 Taxonomic classification

Accurate taxonomic identification of microbial genomes is critical for understanding community composition and tracking pathogenic or zoonotic species. Classification tools employ a variety of

strategies to assign taxonomy. Marker gene-based classifiers, such as MetaPhlAn (Blanco-Míguez et al., 2023), rely on species-specific genetic markers, while k-mer-based approaches, including Kraken2 (Wood et al., 2019) and Centrifuge match short sequence motifs to reference databases for rapid classification. More robust taxonomic placement can be achieved using phylogenomic methods, such as GTDB-Tk (Chaumeil et al., 2020), which construct genome-wide alignments to classify novel organisms within an evolutionary framework.

2.3.5 Functional annotation

In addition to taxonomic classification, functional annotation provides insight into the metabolic and pathogenic potential of microbial communities. Tools such as KEGG (Kanehisa & Sato, 2020) and EggNOG-mapper (Cantalapiedra et al., 2021) assign gene functions based on sequence similarity to curated databases. Prokka (Seemann, 2014) is commonly used for rapid annotation of bacterial genomes, while DRAM (Shaffer et al., 2020) supports pathway-level analysis of microbial metabolism and ecology. Functional annotation is particularly important for detecting virulence factors, AMR genes, and genes involved in host-microbe or microbe-microbe interactions (Stromberg et al., 2023).

2.3.6 Comparative genomics and phylogenetic analysis

Comparative genomics enables researchers to explore evolutionary relationships, assess genomic variation, and track the spread of microbial strains across hosts and geographic regions (Zhang et al., 2025). For broader evolutionary analyses, phylogenomics uses genome-wide data—typically concatenated alignments of conserved marker genes—to infer deep phylogenetic relationships (Zhu et al., 2019). Tools like PhyloPhlAn (Asnicar et al., 2020) and IQ-TREE2 (Minh et al., 2020) facilitate the reconstruction of robust maximum-likelihood trees from such alignments, with IQ-TREE2 offering flexible model selection, ultrafast bootstrapping, and partitioned analyses. In parallel, tools like Roary (Page et al., 2015) enable pangenome analysis by identifying shared (core) and variable (accessory) genes across multiple strains. Together, these approaches are particularly valuable for investigating microbial transmission dynamics, host-specific adaptations, and evolutionary diversification across environments.

2.3.7 Future directions in bioinformatics for microbial surveillance

As sequencing platforms become faster and more affordable, the demand for scalable, accurate, and reproducible bioinformatics workflows continues to grow (Satam et al., 2023). Emerging technologies, including machine learning-based classifiers and artificial intelligence, are likely to

reshape the future of microbial surveillance (Onyeaka et al., 2024; Suster et al., 2024). In addition, standardised, reproducible workflows such as those built using Nextflow and nf-core offer scalable solutions for consistent and collaborative analyses (Langer et al., 2025). Looking ahead, these tools and bioinformatics platforms will be critical for responding swiftly to emerging threats and strengthening global surveillance networks.

2.3.8 Bioinformatics challenges in the era of big data

The increasing scale of metagenomic sequencing presents notable challenges for bioinformatics, particularly in the era of big data (Escobar-Zepeda et al., 2015; Papageorgiou et al., 2018; Pop & Salzberg, 2008; Yohe & Thyagarajan, 2017). Managing and storing vast volumes of genomic information demands high-performance computing infrastructure and efficient data compression strategies to avoid bottlenecks in analysis (Papageorgiou et al., 2018). In metagenomic microbiome studies, the ability to process data accurately is essential (Kumar et al., 2024). However, biological datasets are frequently noisy, incomplete, or error-prone, which may compromise the reliability of downstream analyses and interpretations (Kumar et al., 2024). Additionally, bridging the skills gap between biological sciences and computational analytics remains a persistent barrier, particularly as modern bioinformatics increasingly relies on expertise in software development, statistical modelling, and machine learning (Lin et al., 2025; Suster et al., 2024). As sequencing technologies continue to evolve, overcoming these challenges will be essential to fully harness the potential of big data in microbial surveillance and genomics (Lin et al., 2025; Suster et al., 2024).

3 Chapter

3.1 Research methodology

The “Genetic diversity of enteric microbes and its impacts on host switching” is a long-term project that began four years before I joined it. Therefore, substantial work had been done before the start of my PhD. These details will be described at the beginning of the following subsections.

3.1.1 Ethics and importation approval

Ethics approval was obtained by Professor David Hayman and the team.

Ethical approval for this study was obtained from the Massey University Human Ethics Committee (Application Number: Southern A Application-14-44). Additional consultation was conducted with the New Zealand Ministry of Health and Disability Committee and the Massey University Animal Ethics Committee. Official approval was not deemed necessary due to the anonymous nature of the samples and the absence of animal manipulations. Consultation with the Ministry for Primary Industries Animal Welfare Senior Policy Advisor was undertaken regarding the involvement of gorillas; however, no further discussion was required for the same reasons.

3.1.2 Study area

Uganda, located in eastern Africa, is characterised by its fertile land and abundant water resources, including Lake Victoria, the largest lake in Africa. The country's diverse geography, biodiversity, and land use make it a hotspot for emerging and re-emerging infectious diseases. The likelihood of pathogen/microorganism transmissions is heightened in areas where humans, domestic animals, and wildlife come into frequent contact, known as landscape interfaces. This study adopts a holistic One Health approach, collaborating closely with the local partner Conservation Through Public Health (CTPH) and communities to promote optimal health outcomes for people, animals, and the environment.

3.1.3 Bwindi Impenetrable National Park

Bwindi Impenetrable National Park (BINP) (Weber et al., 2020) is a 331 km² forest located in southwest Uganda (0°53'–1°08' S; 29°35'–29°50'E). The park is renowned for its rich biodiversity,

home to at least 135 mammal species (including 10 primate species), 381 bird species, 34 reptile species, 29 amphibian species, and 393 tree species (Plumptre et al., 2007).

Around 43% of the world's remaining 1,063 Mountain gorillas (*Gorilla beringei beringei*) are found in BINP (Weber et al., 2020).

The people living in Buhoma, around BINP in Uganda are primarily subsistence farmers, raising livestock and cultivating crops up to the forest edge. This environment creates a functional interface where pathogens can cross between humans, their domestic animals, and wildlife (Muylaert et al., 2021). The presence of wildlife-associated microbes entering livestock production increases the likelihood of new emerging pathogens (Bengis et al., 2004).

The sampling collection was conducted by Conservation Through Public Health (CTPH) and collaborators in Bwindi – Buhoma and BINP, Uganda.

In total, 553 faecal samples were collected from various hosts in the region of BINP. These samples included habituated (N = 100) and unhabituated (N = 100) mountain gorillas, cattle (N = 83), goats (N = 73), anonymous human faecal samples provided at hospitals or clinics, and samples collected from people in the community who agreed to join the study and completed questionnaires. The human faecal sample groups were described as human – hospital (N = 99) for samples collected in hospitals and/or clinics, and human – community for samples collected during visits in the community (N = 98). The sample collection was conducted between June and August 2018 by collaborators in Uganda for the larger project, CTPH, of which this research is a part. Further details, including the metadata file for the samples, are provided in the [appendices](#).

To minimise the risk of contamination during faecal sample collection, standardised biosafety and contamination prevention protocols were followed across all host groups. Field teams wore new disposable gloves for the collection of each individual sample, and collectors avoided direct contact with faecal matter by using sterile instruments and cryovials pre-filled with RNAlater® (Sigma, MO, USA). For gorilla samples, collectors followed Conservation Through Public Health (CTPH) protocols, which always included the use of face masks and gloves. Samples were collected immediately after the groups had vacated their night nests to minimise environmental contamination. Faeces were sampled from the internal portion of the bolus to avoid contamination from surface material. For livestock and community human samples, collectors were trained in aseptic technique and instructed to collect only freshly deposited faeces, using sterile spatulas and avoiding contact with surrounding surfaces. Human samples obtained from clinics were placed in RNAlater® within

24 hours of collection by medical personnel trained in biological sample handling. All samples were clearly labelled, stored in sterile cryovials, and kept cold during transport. These precautions were implemented to minimise the introduction of human skin flora or environmental contaminants and to preserve the microbial integrity of the samples for downstream metagenomic analysis.

CTPH routinely collects habituated mountain gorilla faecal samples from the night nests, together with gorilla names and ages when known for surveillance purposes. Habituated gorilla groups are tracked daily. Samples collected from June to August 2018 were categorised as infant, juvenile, sub-adult, adult, or silverback based on the size of the sample and presence of hair samples; faeces were then stored in 5 mL cryovials containing RNAlater® (Sigma, MO, USA). Samples from unhabituated wild gorillas were collected during the bi-decadal population survey from March to May 2018 using the same methods.

Cattle and goat faeces were collected using convenience sampling from community livestock in the region surrounding Bwindi Impenetrable Forest from June to August 2018. The faecal samples were collected and placed into 5 mL cryovials containing RNAlater®.

Samples from anonymous clinic patients were collected from the local health centres in the region, Kanungu District Medical Office, and Kasese District. Samples were placed in RNAlater® within 24 hours of collection and stored in a -20°C freezer until shipment to New Zealand, made in refrigerated conditions.

Samples from people (81 male, 19 female participants, from 19 to 70 years old (median = 35 years old) in the community were collected from June to August 2018. Participants were non-randomly recruited as part of a broad study on human behaviour and infectious disease transmission risk. Participants answered 27 background survey questions and 49 questions in self-reported diaries, completed daily, to investigate the participant's health, such as symptoms and 28 behaviours, human and animal contact patterns, direct contacts, and sightings over a week. Full details are described in (Muyllaert et al., 2021).

All faecal samples arrived on October 1st, 2018, under the Ministry for Primary Industries permit number 2018068860. They were stored at -20°C until analysis at freezer in a PC2 containment facility at the Hopkirk Research Institute, Massey University, New Zealand.

3.1.4 Nucleic acid extraction

The nucleic acid extraction and amplification were conducted by Dr. Matthew Knox, who also assisted in describing the methods provided below.

Approximately 150 mg of faecal sample and 750 µl BashingBead™ Buffer were added to a ZR BashingBead™ Lysis tube (0.1 & 0.5 mm). Then, the DNA was extracted using the Zymo Quick-DNA™ Faecal/Soil Microbe Miniprep Kit following the manufacturer's instructions. Detailed information on the DNA extraction protocol and the sample metadata is provided in the appendices (see [here](#) and [here](#)).

3.1.5 DNA processing

The nucleic acid processing was conducted by Dr. Matthew Knox, who kindly helped to write this methods subsection.

From the extracted DNA, multiple displacement amplification was undertaken to bring the DNA yield up to the amount required for sequencing using the Illustra GenomiPhi V3 DNA Amplification Kit (GE Healthcare Life Sciences, Illinois, USA) as per the manufacturer's instructions. Quantification of DNA was performed using the dsDNA HS Qubit kit (ThermoFisher, Massachusetts, USA) with the Qubit® 2.0 Fluorometer (ThermoFisher, Massachusetts, USA).

3.1.6 Library preparation and genome sequencing of individual files

The sequencing data associated with this thesis are available under BioProject accession number PRJNA1213876 on NCBI. The DNA FASTQ files were divided into six groups composed of humans in the community (98), hospitalized humans (99), habituated gorillas (100), wild gorillas (100), cattle (83), and goats (73). This data was used to assess the relative abundances of the host gut microbiomes at the phylum level, as described in **Chapter 4**. More results regarding genera and species, including the Kraken taxonomic classification outputs, can be found in the supplementary section.

The library preparation and shallow genome sequencing were conducted by Orion Integrated Biosciences Inc. (Manhattan, Kansas, USA), who also assisted in describing the methodology below.

Aliquots of 5µg of whole genome and whole transcriptome amplified nucleic acids were dried down in a hooded cabinet under negative pressure at room temperature overnight in a DNASTable® plate (Biomatrica, California, USA) and sent at ambient temperature conditions via courier to Orion

Integrated Biosciences Inc. (Manhattan, Kansas, USA) for next-generation sequencing. Next-generation sequencing (NGS) was performed on an Illumina® MiSeq with Nextera XT DNA Library Prep (Illumina®, California, USA). For NGS, a procedural negative control of RNAlater® alone was included in the nucleic acid extraction and DNA amplification methods.

Sequencing reads were demultiplexed and parsed into individual sample files, then imported into CLC Genomic Workbench 7.5 for analysis. Reads were trimmed to remove ambiguous bases at the 5' terminus and trimmed based on a quality score of > Q25. Reads shorter than 50 nucleotides were removed. The trimmed and filtered reads were used for downstream analysis.

3.1.7 Library preparation and genome sequencing of pooled files

For the deep sequencing approach, the samples were pooled in groups containing 20 samples each for gorilla and human groups. For example, the first 20 wild gorilla samples were included in the first pool, generating the UG_DNA_01 pool and so on. The exceptions were UG_DNA_13 from hospitalised humans, and the two pools, UG_DNA_16 and UG_DNA_18, from humans in the community, each containing 19 samples. Livestock had fewer samples collected; therefore, the cattle pools contained 17 samples, except UG_DNA_24 containing 16. For goats, the pools contained 15 samples, with the exceptions of UG_DNA_29 and UG_DNA_23, both containing 14 samples. A metadata file containing further details about the pooled samples is provided in the appendices (see [here](#)). The pooled samples were subsequently sent to AGRF for sequencing.

The library preparation and deep genome sequencing were conducted by Australian Genome Research Facility Ltd (AGRF), who also provided information described in the methodology below.

A total of 31 paired-end FASTQ files were generated, including one used as a blank sample. The data yield was as follows: 150bp Paired End - Flowcell ID: H3CGTDSX3. In total, 2,978,787,317 reads were generated, totalling 899.59Gb of data.

The library preparation was conducted using the xGen™ cfDNA & FFPE DNA Library Preparation Kit. Image analysis was performed in real time by the NovaSeq Control Software (NCS) v1.7.5 and Real Time Analysis (RTA) v3.4.4, running on the instrument computer. RTA performs real-time base calling on the NovaSeq instrument computer. Then the Illumina bcl2fastq 2.20.0.422 pipeline was used to generate the sequence data. The data generated here meet the AGRF quality standards.

The checksum information of the files included has been generated using Exactfile. Two files were included in the directory, “checksums.exf”, which contains the MD5 hashes of the original files on AGRF’s data server and “TestFiles.exe”, an applet created by the Exactfile program to check files against the hashes listed in “checksums.exf”. The file integrities were confirmed by using the following command: `md5sum -c checksums.md5`

The AGRF next-generation sequencing service report is provided in the appendices (see [here](#)).

3.2 Bioinformatic pipeline

All bioinformatic work from section 3.4 onwards was carried out by the author of this thesis, including data science analyses, quality control, data management, and data visualisations.

3.2.1 High-throughput computing cluster and raw data

All the files provided by both Orion (genome sequencing of individual samples/files) and AGRF (deep sequencing pooled sample files) were transferred to the NeSI Mahuika supercomputer for high-throughput computing under the NeSI project Massey03212 allocation (project of the author of this thesis). The files were transferred using a Unix-like operating system, Mac OS (local machine) by establishing a Secure Shell (SSH) connection with the NeSI Mahuika cluster. The transfer was made via the terminal using command lines based on these patterns: **`scp <path/filename> mahuika:<path/filename>`** to move files from my local machine to Mahuika and **`scp mahuika:<path/filename> <path/filename>`** to move output and result files from Mahuika to my local machine for further analysis steps. During the transfer process, a 100% indication displayed in the terminal ensured that the files were successfully transferred to the cluster and *vice versa*.

The allocation was divided into two different directories: one permanent (regularly backed up) and one non-backup. Together, they had sufficient storage capacity to accommodate the files and subsequent output result files. Additionally, to ensure data integrity, the original files (raw data) were triply backed up and stored on personal hard drives and in the Massey Molecular Epidemiology and Public Health Laboratory (mEpiLab) backup system. The bioinformatics workflow used software that were selected based on the genome sequencing strategy (shallow or deep sequencing). The codes and scripts, along with software details, are documented and shared in the repository ‘Uganda-cross-species-transmission’ on my GitHub page (ValterAlmeida - [link](#)) and will be further explained in the following sections.

3.2.2 Deep sequencing approach analysis – Applied in Chapters 4, 5, and 6

From this section onwards, footnotes provide individual links to examples of the software scripts I created on my GitHub page. The scripts include details of the computational resources and software versions used.

To identify possible issues involving adapter/barcode sequences, low-quality regions, and quality drop-off towards the end of each read-pair sequence, each sequence read was quality-checked using FastQC (v.0.11.9)¹ (Andrews, 2010). Adapter sequences were removed, and reads were trimmed with Trimmomatic (v.0.39)² (Bolger et al., 2014). Reads with a quality score of at least 30 and a length of 80 bp were retained, and BBDuk (v.38.95)³ (Bushnell, 2014) was used to remove host contamination before assembling.

The reads from individual samples and concatenated group files were assembled using MEGAHIT (v.1.1.4) (Li et al., 2015) with standard parameters. Seqmagick (v.0.7.0)⁴ ([github](#)) was used to select contigs longer than 1.0 kb.

A mapping index file was generated from the assembly using Bowtie2 (v.2.4.5)⁵ (Langmead & Salzberg, 2012) for read mapping with the same software. Following read mapping, SAMtools (v.1.15.1)⁶ (Li et al., 2009) was used to sort and compress the resulting file.

Contigs longer than 1.0 kb were binned using MetaBAT 2 (v.2.15)⁷ (Kang et al., 2019), MaxBin⁸ (v.2.2.6) (Wu et al., 2016), and CONCOCT (v.1.1.0)⁹ (Alneberg et al., 2014). MetaBAT and MaxBin require a text-based representation of the coverage data to perform binning. To meet this requirement, bash commands were used to reformat the MetaBAT output file (*metabat.txt*) into the format required by MaxBin. Specifically, only the *contigName* and coverage columns were retained, while the *contigLen*, *totalAvgDepth*, and *variance* columns were excluded. The base command was:

```
cut -f1,4,6,8,10 metabat.txt > maxbin.txt
```

This step was done using bash commands as described below.

¹ FASTQC (0.11.9) – (GitHub – [script](#))

² Trimmomatic (0.39) – (GitHub – [script](#))

³ BBDuk (38.95) – (GitHub – [script](#))

⁴ Seqmagick (0.7.0) – (GitHub – [script](#))

⁵ Bowtie2 (2.4.1) – (GitHub – [script](#))

⁶ SAMtools (1.15.1) – (GitHub – [script](#))

⁷ MetaBAT (2.15) – (GitHub – [script](#))

⁸ MaxBin (2.2.6) – (GitHub – [script](#))

⁹ CONCOCT (1.1.0) – (GitHub – [script](#))

MetaBAT:

```
for bin_path in metabat/*.fa;
do
    bin_name=$(basename ${bin_path} .fa)

    grep ">" ${bin_path} | sed 's/> //g' | sed "s/\t/${bin_name}/g" >> metabat_associations.txt
done
```

Maxbin:

```
for bin_path in maxbin/*.fasta;
do
    bin_name=$(basename ${bin_path} .fasta)

    grep ">" ${bin_path} | sed 's/> //g' | sed "s/\t/${bin_name}/g" >> maxbin_associations.txt
done
```

CONCOCT:

```
for bin_path in concoct_cattle_output/fasta_bins/*.fa;
do
    bin_name=$(basename ${bin_path} .fa)

    grep ">" ${bin_path} | sed 's/> //g' | sed "s/\t/${bin_name}/g" >> concoct_associations.txt
done
```

Then, the highest quality nonredundant prokaryotic bins were selected using DAS_Tool (v.1.1.1)¹⁰ (Yue et al., 2020), and CheckM (v.1.0.13)¹¹ (Parks et al., 2015) was used to estimate genome completeness and contamination. The contamination was reduced by diminishing the percentage of strain heterogeneity from the contamination, resulting in a new contamination value. MAG dereplication was performed using dRep (v. 2.3.2) (Olm et al., 2017) and the parameters `-str 100 -pa 0.95 -sa 0.99`.

¹⁰ DAS_Tool (1.1.1) – (GitHub – [script](#))

¹¹ CheckM (1.0.13) – (GitHub – [script](#))

The bin taxonomic classifications were performed using GTDB-Tk (v.2.1.0)¹² (Chaumeil et al., 2020). The GTDB-Tk output file containing concatenated alignments of 120 single-copy core marker genes was used to construct phylogenetic trees with IQ-TREE 2 (v.2.2.0.5)¹³ (Minh et al., 2020). The tree visualisations were generated on the iTOL website, accessible [here](#) (Letunic & Bork, 2019).

Additional software, including Prodigal (v.2.6.3)¹⁴ (Hyatt et al., 2010), Prokka (v.1.14.5)¹⁵ (Seemann, 2014), and Roary (v.3.13.0)¹⁶ (Page et al., 2015) was utilised for genomic annotation and comparisons. In addition, ANIcalculator (v.1.0) (Varghese et al., 2015) was used with default settings to calculate the average nucleotide identity (ANI) of the genomes or species based on their alignment fractions. The Seqkit (v.2.4.0) (Shen et al., 2016) software default commands were used to extract information from the FASTA files, such as genome sizes and other relevant details.

ANIcalculator default commands: ANIcalculator -genome1fna <fna file of the first query genome> -genome2fna <fna file of the second query genome> -outfile <the output file>

Seqkit default commands (example): seqkit stats *.fna

3.2.3 Bioinformatic tools exclusively applied in Chapter 4

Considering the pre-processed interleaved paired-end Illumina FASTQ files that had already been trimmed by Orion Integrated Biosciences Inc., I did not use Trimmomatic with this shallow sequencing approach. Since the files were ready to start the workflow, I performed a quality control check using FastQC (Andrews, 2010), and then used BBMap (v.38.95) (Bushnell, 2014), with the same parameters and codes contained in the script example provided in the previous section, to reduce host contamination in the files. The reference genomes used to deplete host contamination were Gorilla ([GCF_008122165.1](#)), Human (a masked version of hg19 by Brian Bushnell [[link](#)]), Cattle ([GCF_002263795.1](#)), and Goat ([GCF_001704415.1](#)). This step resulted in a depletion of host reads from the files for downstream analysis. In the sequence, Kraken2 (v.2.1.1) and Bracken (v.2.6.0) were used for the taxonomic classification (Lu et al., 2017; Wood et al., 2019). Both software tools were used in the same shell script¹⁷. Additionally, a Python (v.2.7.18) script¹⁸ was utilised to combine the report output files (Wood et al., 2019). Human faecal sample reference genomes were downloaded

¹² GTDB-Tk (2.1.0) – (GitHub – [script](#))

¹³ IQ-TREE 2 (2.2.0.5) – (GitHub – [script](#))

¹⁴ Prodigal (2.6.3) – (GitHub – [script](#))

¹⁵ Prokka (1.14.5) – (GitHub – [script](#))

¹⁶ Roary (3.13.0) – (GitHub – [script](#))

¹⁷ Kraken 2 (2.1.1) and Bracken 2 (2.6.0) – (GitHub – [script](#))

¹⁸ Kraken 2 (2.1.1) – (GitHub - Python [script](#) to combine reports)

to compare the relative abundances between human samples from Uganda, Republic of the Congo (NCBI – [Bioproject link](#)), Mexico (NCBI – [Bioproject link](#)), Italy (NCBI – [Bioproject link](#)) and the US (NCBI – [Bioproject link](#)). The accession numbers of the samples used in this comparison are provided in the supplementary section of this thesis.

The Kraken2 workflow described above, used for shallow sequencing, was also applied to the deep sequencing data for more detailed analysis and comparison.

The β -diversity was analysed using a Python (v.3.10.5) script¹⁹ (Lu et al., 2022) and a Bray-Curtis dissimilarity matrix. The script was applied using bash commands as shown below:

```
python beta_diversity.py -i *_hostFilt_bracken.report --type bracken --level S > beta_diversity_uganda.tsv
```

With the matrix data, the PCoA analysis was performed using weighted classical (metric) multidimensional scaling (cmdscale) with the R package vegan (v.2.6-4)²⁰ (Oksanen et al., 2020) in R Studio (v.2023.12.1+402), R version (v.4.3.1).

The α -diversity (Shannon's diversity) was calculated using a Python script²¹ following the Kraken suite protocol (Lu et al., 2022). The script was applied using bash commands as shown below:

```
module load Python/3.10.5-gimkl-2022a
```

```
#!/bin/bash
```

```
for file in *_bracken.report; do
```

```
base=$(basename -- "$file")
```

```
    prefix=${base%.*}
```

```
    python alpha_diversity.py -f "$file" -a Sh > "${prefix}_alpha_diversity.txt"
```

```
done
```

Statistical analyses were performed with the statistical tests Tukey HSD (Honestly Significant Difference) ANOVA²² using R Studio, R version (v.4.3.1). The following R packages were utilised for plot visualisations and data handling: ggplot2 (v.3.5.0) (Wilkinson, 2011), dplyr (v.1.1.4) (Wickham et al., 2019), ggpubr (v.0.6.0) (Kassambara, 2020), ggridges (v.0.5.6) (Claus O. Wilke,

¹⁹ Kraken 2 (2.1.1) – (GitHub – Python [script](#) - β -diversity)

²⁰ Vegan (2.6-4) – (GitHub – R [script](#) – β -diversity - PCoA)

²¹ Kraken 2 (2.1.1) – (GitHub – Python [script](#) - α -diversity)

²² R Studio (2023.12.1+402) – (GitHub – R [script](#) - α -diversity)

2022), reshape2 (v.1.4.4) (Wickham, 2014), RColorBrewer (v.1.1-3) (Neuwirth, 2014), viridis (v.0.6.5) (Garnier, 2018) and plotly (v.4.10.4) (Shalabh, 2021). Additionally, in Python, the used libraries were: pandas (McKinney & Team, 2015), numpy (Van Der Walt et al., 2011), matplotlib (Hunter et al., 2020), seaborn (Ravikiran A, 2023) and plotly (W. Zhang, 2022) for the plot showing the assignment/classification of the MAGs²³.

3.2.4 Bioinformatic tools applied in Chapters 5 and 6

Genes conferring resistance to antibiotics and virulence genes were assessed using ABRicate (v. 1.0.0)²⁴ (<https://github.com/tseemann/ABRicate>) using ResFinder database (Bortolaia et al., 2020; Clausen et al., 2018).

3.2.5 Bioinformatic tools applied in Chapter 6

Genome coverage and read-based mapping to assess abundances were performed using MetaBAT2 (v. 2.15)⁹ (Kang et al., 2019), Bowtie2 (v. 2.5.4)⁷ (Langmead & Salzberg, 2012) and SAMtools (v. 1.21)⁸ (Li et al., 2009). Gene prediction was carried out using Prodigal (v. 2.6.3)¹⁶ (Hyatt et al., 2010) and genome annotation with DRAM²⁵ (v. 1.3.5) (Shaffer et al., 2020) and HMMER²⁶ (v. 3.4) (Pfam database) (Finn et al., 2011). Average nucleotide identity comparisons were performed with FastANI (v. 1.33)²⁷ (Jain et al., 2018). Seqkit (v. 2.4.0) (Shen et al., 2016) was used to extract genome information. Comparative alignments to the *Campylobacter jejuni* reference genome (GCA_000009085.1) were conducted using MUMmer (v. 4.0.0)²⁸ (Marçais et al., 2018). Genome quality and general information was assessed using CheckM2 (v. 1.0.1)²⁹ (Chklovski et al., 2023). Genomes were dereplicated using dRep (v. 2.3.2)³⁰ (Olm et al., 2017) and the parameters `-str 100 -pa 0.95 -sa 0.99`.

For a second taxonomic classification, abundance strategy and microbial composition analysis, Kraken 2 (standard database 12/2024)¹⁹ and Bracken¹⁹ were used (Lu et al., 2017; Wood et al., 2019). Statistical analyses were conducted in RStudio (v. 2025.05.0+496), including ANOVA and Tukey's HSD. A logistic regression model assessed the association between host age and *Ca. C. infans* detection.

²³ Python (3.9.5) – (GitHub – Python [script](#) – Plot)

²⁴ ABRicate (1.0.0) – (GitHub – [script](#))

²⁵ DRAM (v. 1.3.5) – (GitHub – [script](#))

²⁶ HMMER (v 3.4) – (GitHub – [script](#))

²⁷ FastANI (v. 1.33) – (GitHub – [script](#))

²⁸ MUMmer (v. 4.0.0) – (GitHub – [script](#))

²⁹ CheckM2 (v. 1.0.1) – (GitHub – [script](#))

³⁰ dRep (v. 2.3.2) – (GitHub – [script](#))

4 Chapter

4.1 Gut microbiomes from sympatric humans, mountain gorillas and livestock reveal novel bacterial diversity and signs of microbial sharing

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4.1.1 Abstract

The emergence of zoonotic infectious diseases is a growing concern, with areas where humans come into contact with wildlife and domestic animals being hotspots for this emergence. Why certain microbes switch hosts remains elusive, although factors such as microbe-host contact rates are believed to play a role. To better comprehend the influence of spatiotemporal overlap on microbial sharing, we examined over 500 samples, and 2,400 bacterial metagenome-assembled genomes obtained from the gut microbiomes of mountain gorillas, humans, and livestock in Uganda. Our study suggests that closer physical proximity within a shared environment may correlate with greater gut microbiome similarity. Moreover, it reveals the presence of hundreds of putative novel bacteria, addressing a critical gap in our understanding of microbial interactions, particularly in high-intensity human-animal interfaces in African settings.

4.1.2 Introduction

The mechanisms for the sharing of certain microorganisms and pathogens among host species are still not fully understood. However, factors such as microbial prevalence, co-evolution, co-adaptation, contact rates between multiple host species, and specific traits of host-pathogen interactions are believed to play a role (Groussin et al., 2020; Plowright et al., 2017b). For example, the presence of identical bacterial species across multiple host species may be explained by historical host phylogenetic connections, i.e., common host ancestry, followed by minimal microorganism evolution in their gut microbiomes (Gaulke et al., 2018; Groussin et al., 2020). On the other hand, high contact rates between multiple host species increase the likelihood of microbe sharing through on-going transmission (Davies & Pedersen, 2008).

The gut microbiome plays a vital role in maintaining the health of both humans and animals by influencing physiological processes and immune responses (Bull & Plummer, 2014). Understanding its composition, diversity, and functional dynamics is important for deciphering its impact on health and disease (Bull & Plummer, 2014). There have been important advances in describing the composition of the gut microbiome across multiple host species, including hosts from diverse locations and with various characteristics, such as those related to lifestyle, age and diet (Campbell et al., 2020; Pasolli et al., 2019). However, there remains a knowledge gap in relation to NHP species, such as mountain gorillas (*Gorilla beringei beringei*), and geographic sites characterised by wildlife-livestock-human interfaces (Muylaert et al., 2021; Plowright et al., 2021; Wilkinson et al., 2018), as seen at Bwindi Impenetrable National Park (BINP), Uganda (Muylaert et al., 2021). These interface regions are of particular importance as they facilitate increased inter-species interactions, potentially leading to an elevated exchange of both commensal and pathogenic microbes among multiple host species (Kuthyar & Reese, 2021).

Species from genera that reside in the gut microbiome of different hosts in wildlife-livestock-human interfaces, such as *Treponema* and *Prevotella*, might offer valuable insights for analysing microbial sharing in relation to host phylogenetic relatedness and contact rates among multiple host species. These bacterial genera are commonly present in the gut microbiomes of human populations with traditional agricultural lifestyles (Angelakis et al., 2019; de Goffau et al., 2022), including members of the community in Buhoma, Uganda (Muylaert et al., 2021). In contrast, *Prevotella* and *Treponema* are generally absent from or significantly reduced in the gut microbiota of people living in industrialised countries (Angelakis et al., 2019; Brewster et al., 2019; de Goffau et al., 2022; Obregon-Tito et al., 2015). Additionally, bacteria from these genera are commonly found in the gut microbiomes of livestock (Betancur-Murillo et al., 2023) and NHPs (Davies & Pedersen, 2008;

Obregon-Tito et al., 2015). Of these, livestock are more likely to have higher contact rates with humans, while NHPs, being more closely related to humans, are more likely to share microorganisms when inhabiting the same geographical region (Davies & Pedersen, 2008).

Next-generation metagenomic sequencing has revolutionised our capacity to comprehensively investigate the gut microbiota, allowing for the identification of rare, novel or uncultivable taxa across diverse host species and populations (Quince et al., 2017). Microbial surveillance via metagenome-assembled genomes (MAGs) (Ko et al., 2022) has enhanced knowledge of both established commensal and pathogenic microorganisms (Miller et al., 2013). It has become a fundamental approach for identifying infectious agents causing outbreaks (Quince et al., 2017), and uncovered essential insights from microbiomes (Ko et al., 2022; Quince et al., 2017). However, there have been few gut microbiome metagenomic analyses from multiple host species in the same time and regional context, leading to gaps in our comprehension of how spatiotemporal overlap influences microbial sharing among different host species (Faust et al., 2018).

Therefore, our study aims to comprehensively characterise the gut microbiomes of sympatric host species in a region viewed as high-risk for pathogen emergence. Specifically, we investigated habituated and unhabituated wild mountain gorillas (apes, family Hominidae), humans (also Hominidae), and domestic goats and cattle (both bovids, family Bovidae), each exhibiting distinct dietary preferences (herbivores except for omnivorous humans). Given the overlapping habitat scenario of humans, livestock, and gorillas living in BINP and the Buhoma area, our objective was to analyse microbial communities to identify potentially shared microbial taxa among multiple host species, giving insights into possible pathways of cross-species transmission, and uncover putative novel bacterial species within their gut microbiomes.

4.1.3 Results

4.1.3.1 Diverse collection of putative novel bacterial species across different hosts

This study analysed 553 faecal samples collected from gorillas, humans, and livestock living in the BINP and the surrounding Buhoma area in Uganda. It aimed to explore the gut microbiomes of these host species, which inhabit overlapping environments within close proximity. The limited research on gut microbiomes across this diverse range of hosts in the region highlights the need for a better understanding of microbial diversity within these populations. To investigate the bacterial species present, a deep sequencing approach was applied to 30 pooled samples (five each for wild gorillas, habituated gorillas, humans in the community, hospitalised humans, cattle, and goats). The pools consisted of 20 individual faecal samples from gorillas, 19 or 20 samples from humans, 16 or 17 samples from cattle, and 14 or 15 samples from goats. Using the pooled approach, a total of 3,185 MAGs were reconstructed. MAGs that were less than 50% complete or more than 5% contaminated were removed, resulting in 2,411 MAGs being retained for further analysis. Most of these retained MAGs were over 80% complete and less than 3% contaminated (Fig. 4.1a,b). Over half of the MAGs retained for further analysis originated from gorilla samples (61.6%, totalling 1,485). Human samples accounted for 28.7% (691), while goats and cattle contributed 7.3% (175) and 2.5% (60), respectively (Fig. 4.1c). MAG dereplication to identify groups of organisms that share similar DNA content in terms of Average Nucleotide Identity (ANI) reduced the total number of MAGs by 417 (from 2,411 to 1,994) (Supplementary Fig. 4.5). We retained the full 2,411 MAGs for analysis so as not to lose information on auxiliary gene variability among representatives from the same species (Evans & Denef, 2020). According to the classification performed using GTDB-Tk (Chaumeil et al., 2020), only 212 (8.8%) could be assigned a described species name, while 902 (37.4%) were classified at the genus level, but remained unidentified at the species level (Fig. 4.1c). The majority of the MAGs, totalling 1,297 (53.8%), were classified at the family level or higher, with no genera or species described (Fig. 4.1c). Of these, 927 originated from gorilla samples, meaning 71.5% of the MAGs from gorillas were novel bacterial genera and species. Most of the known bacterial species, along with described genera with putative novel species, were detected in human samples, while gorillas had the highest number of putative novel species within unknown genera (Fig. 4.1c). At the phylum level, more than half of the total MAGs belonged to the *Bacillota* phylum (Fig. 4.1d).

Figure 4.1: Assessment and classification of gut microbiome MAGs from human, gorilla, and livestock at the BINP border rural-wildlife interface.

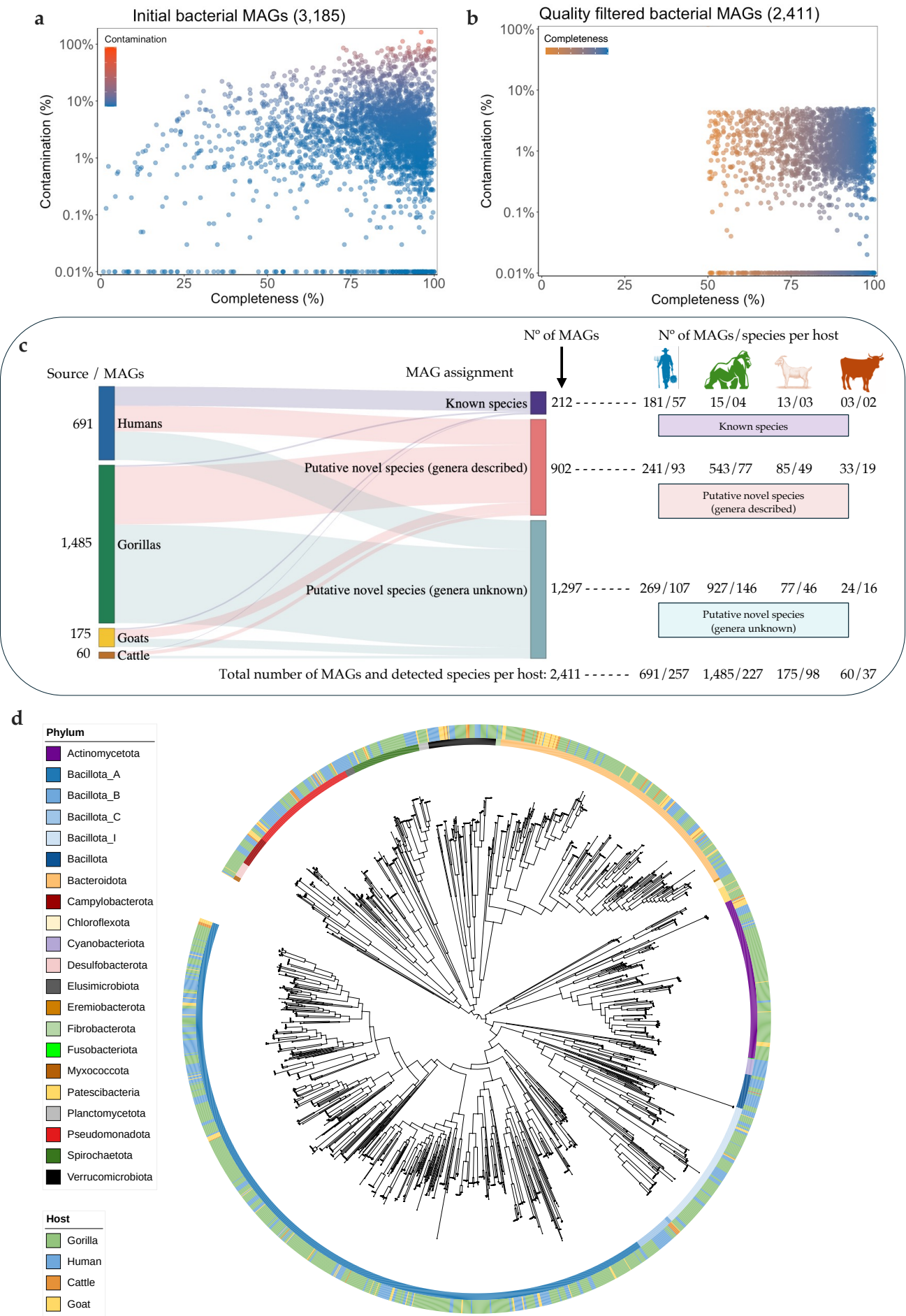


Figure 4.1 – a, Completeness and contamination of the total 3,185 gut microbiome MAGs reconstructed. **b,** Bacterial MAGs that were retained for further analysis based on their completeness and contamination scores. **c,** Number of MAGs assigned to known or putative novel bacterial species based on the taxonomic classification database from GTDB-Tk software (left). Number of known and putative novel bacterial species detected in the host gut microbiomes (right). Due to the novelty of the putative novel species and the lack of similar reference genomes assigned to a particular genus, the actual number of putative novel species is likely higher than stated here. Consequently, the number of putative genera and species may increase once we confirm that these represent distinct novel species, based on alignment with additional reference genomes included in the GTDB-Tk workflow. A similar figure showing the numbers after MAG dereplication can be found in (Supplementary Fig. 4.5). **d,** Phylogenetic tree showing the MAG phyla classification distributions. *The inner ring represents phyla, while the outer ring represents hosts.

4.1.3.2 Microbial community similarities among the different groups

To further assess the gut microbiome diversities, we compared the unassembled gut metagenomes from individual samples, which comprised 98 from wild gorillas, 100 from habituated gorillas, 98 samples from humans who had faecal samples examined in clinics or hospitals, 97 from humans in the community, 83 from cattle and 73 from goats. The species accumulation curve indicated that the sample size was sufficient for this study (Supplementary Fig. 4.6). β -diversity analysis based on Principal Coordinate Analysis (PCoA) of a Bray-Curtis dissimilarity matrix showed three distinct clusters of samples, with microbiome community compositions exhibiting the highest similarity according to host species (Fig. 4.2a). Closely related host communities from most samples co-clustered: goats and cattle, two groups of humans, and two groups of gorillas. However, some habituated gorilla samples clustered more closely to livestock and human samples than to wild gorilla samples. Similarly, a few hospitalised human samples were located at the centre of the plot, separate from most of the human cluster. Further analysis of the β -diversity plot showed that humans had a higher number of classified reads compared to the other hosts (Supplementary Fig. 4.7a,b), reflecting results based on the taxonomic classification of sequences.

Cattle and goats had higher α -diversity values compared to all other host groups (ANOVA and Tukey's HSD test p-values: <0.01, and <0.01, respectively). Considering the MAGs strategy, these host groups had fewer bacterial species assembled—37 and 98, respectively (Fig. 4.1c). In contrast, humans, particularly those who provided samples at the hospital or clinic, showed lower α -diversity compared to the other hosts (ANOVA and Tukey's HSD test p-values: <0.01) (Fig. 4.2b).

Figure 4.2: Analysis of microbial α -diversity and β -diversity across host groups.

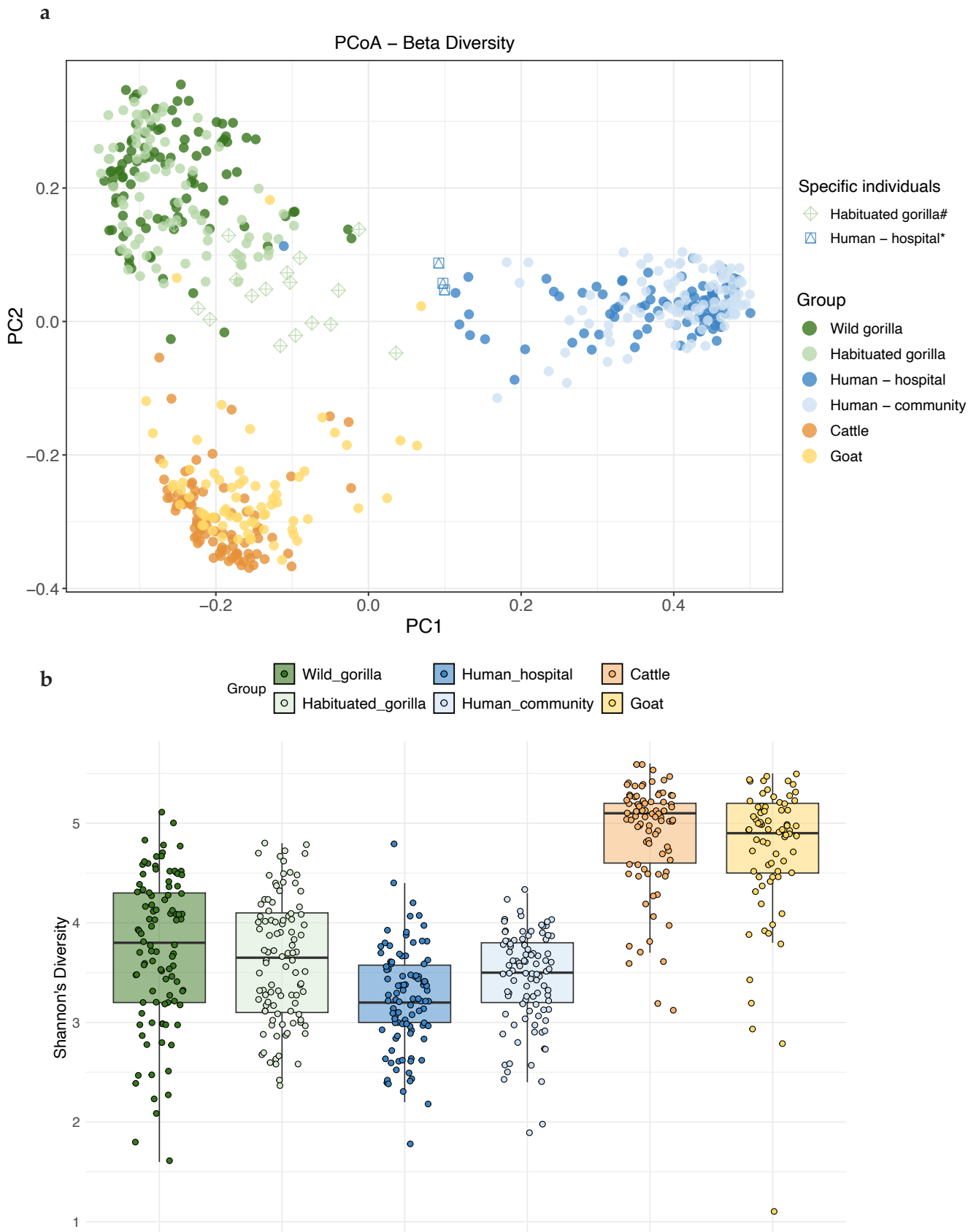


Figure 4.2 – a, PCoA results illustrating the β -diversity between different host groups. The distinct symbols for three human samples* indicate that they were collected from a clinic in Mushorero, a village experiencing ongoing human-gorilla conflict in the Buhoma region. The distinct symbols for some gorilla samples# indicate that these came from gorilla families living near the boundary between the forest and the village, with easier access to overlapping habitats shared with humans and livestock. The human-hospital gut microbiome sample, which clusters among the gorilla clusters, was the only human sample with fewer than 20,000 sequences classified (see Supplementary Fig. 4.7). This suggests an increased number of unclassified microorganisms, a phenomenon also observed in gorilla gut microbiome samples. **b**, Alpha diversity (Shannon's diversity index) across gut microbiome samples from habituated gorillas, wild gorillas, humans (hospital and community), cattle, and goats.

4.1.3.3 Relative abundance variations in composition among hosts and groups

For gorillas, the Kolmogorov-Smirnov (KS) test comparing wild and habituated individuals indicated a significant difference in their gut microbiome β -diversities (D-value of 0.135, p-value <0.01). Similarly, for human samples, the KS test comparing samples collected from the hospital and the community revealed a substantial difference in β -diversity between these two groups (D-value of 0.215, p-value <0.01). Comparing the gut microbiomes of individual habituated and wild gorillas revealed significant differences in the relative abundances of *Actinomyces*, *Pseudomonadota*, and *Spirochaetota*. Wild gorillas were found to have higher abundances of these phyla compared to habituated gorillas (Wilcoxon rank sum exact test, p-value: <0.001). Significant differences were also found when comparing hospital-derived human samples, which contained a higher proportion of *Pseudomonadota* and *Spirochaetota*, whereas humans in the community had higher relative abundances of *Bacillota* bacteria (Wilcoxon rank-sum exact test, p-value: <0.001 for *Pseudomonadota* and *Bacillota*, and <0.01 for *Spirochaetota*) (Fig. 4.3).

Figure 4.3: Most abundant phyla proportions among the host groups.

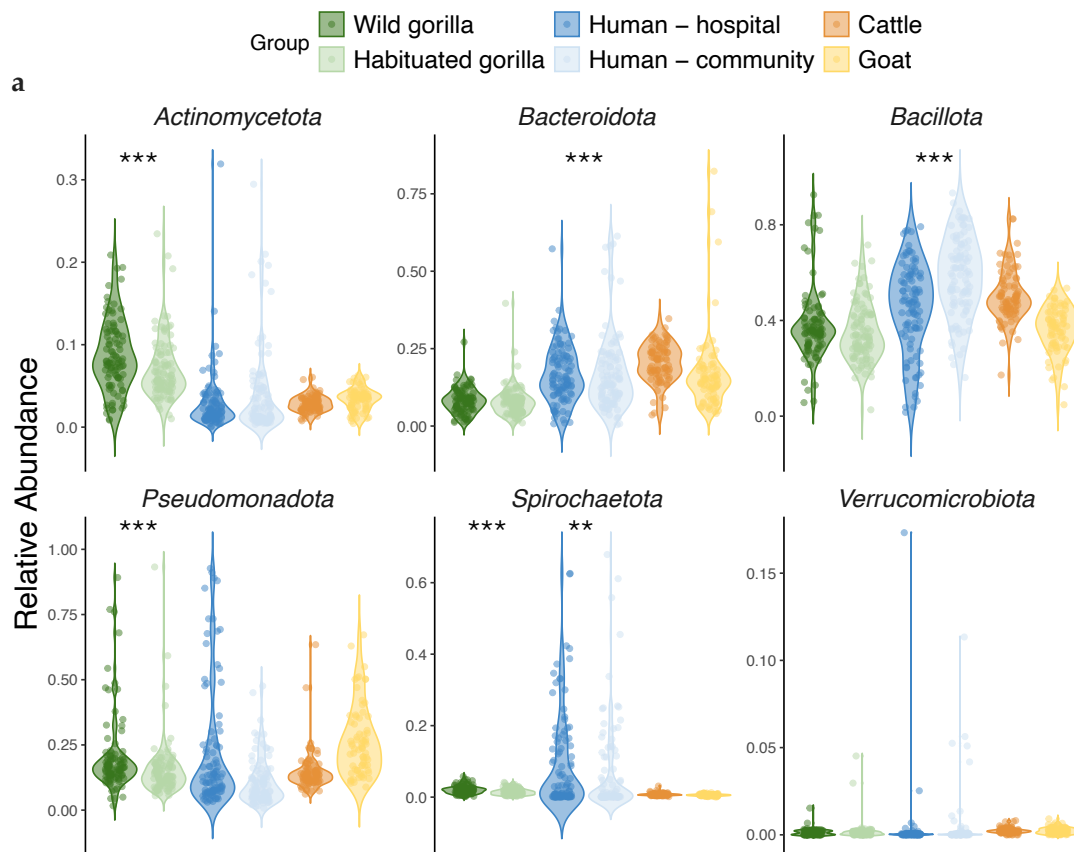


Figure 4.3 - a, The relative abundances of the gut microbiomes of habituated and wild gorillas, as well as hospital-derived and community humans, varied significantly (** for p-values < 0.01, and *** for p-values < 0.001).

Overall, three distinct phyla abundance patterns were observed: one for gorillas, another for humans, and a third for ruminant livestock (Fig. 4.4a). For example, the analysis of human samples in this study revealed higher levels of *Spirochaetota* abundance in their gut microbiomes compared to other studied hosts and human populations from different locations (Fig. 4.4b). *Spirochaetota* are commonly found in the gut microbiomes of several mammal species such as human (Belkhou et al., 2021; Thingholm et al., 2021), cattle (Lin et al., 2023), goat (Cao et al., 2023) and gorillas (Bittar et al., 2014). In humans, they are regularly detected in rural populations but notably scarce or absent in individuals living an industrialised lifestyle (Angelakis et al., 2019; Belkhou et al., 2021). Here, we illustrate that the gut microbiome of humans living in Uganda, like those living in Congo basin (Campbell et al., 2020), have higher relative abundances of this phylum, which was absent or rarely present in human gut microbiomes from Mexico, Italy, and the USA (Wilcoxon rank sum exact test p-value: <0.01) (Fig. 4.4b).

Figure 4.4: Dominant phyla relative abundances in the gut microbiomes of the studied Ugandan hosts.

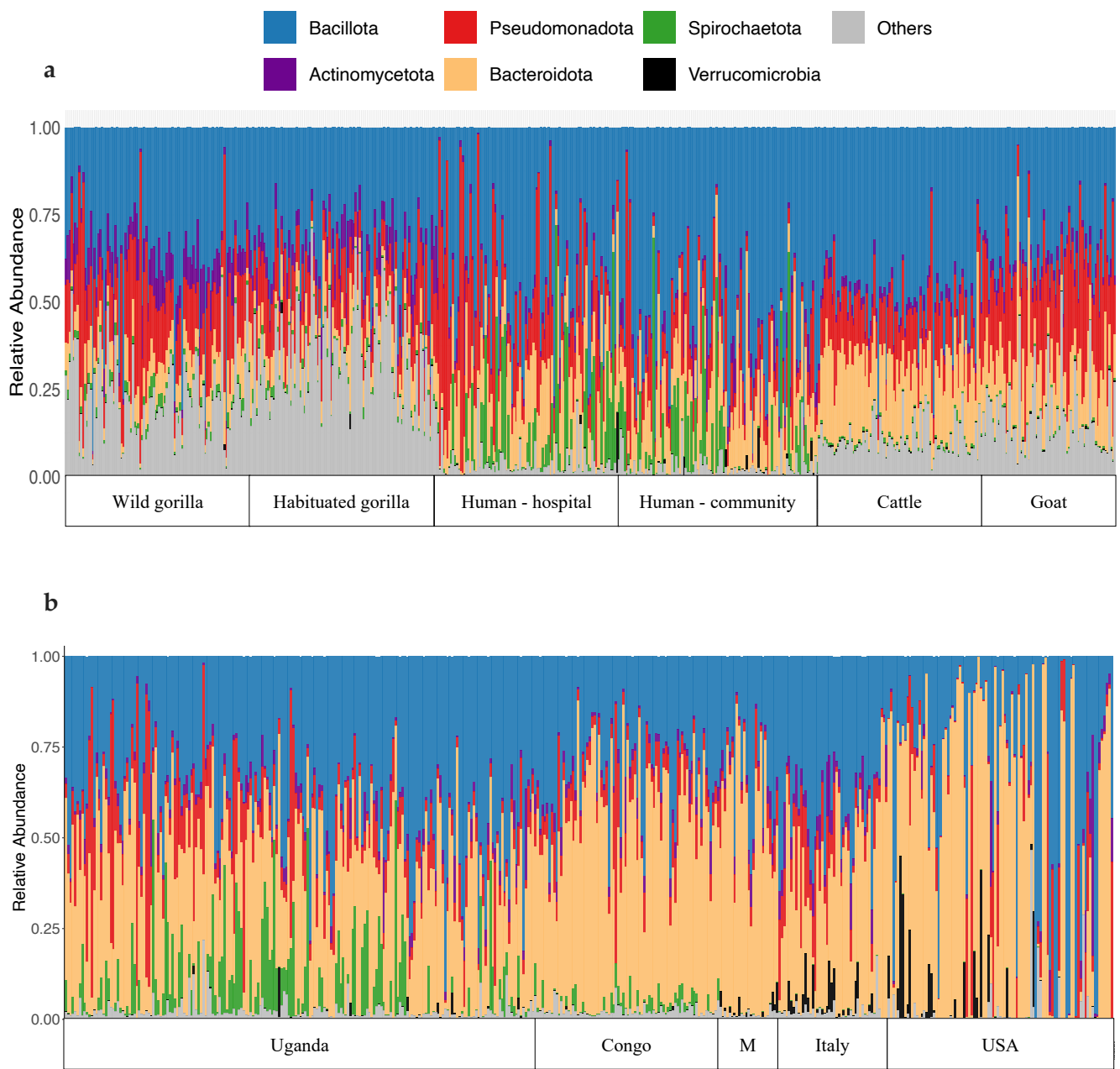


Figure 4.4 - a, Relative abundance of the dominant phyla in the gut microbiomes of Ugandan studied hosts. **b**, Comparative analysis of the Ugandan human gut microbiome relative abundances from this study with those of people from other countries, with 'M' representing human samples from Mexico and 'Congo' referring to the Republic of the Congo.

A total of 212 MAGs were from 63 known species detected across ten phyla (*Actinomyces*, *Bacillota*, *Bacillota A*, *Bacillota C*, *Bacillota I*, *Bacteroidota*, *Campylobacterota*, *Pseudomonadota*, *Spirochaetota*, and *Verrucomicrobiota*), of which 56 were found in humans, three in gorillas, two in goats, and one in cattle gut microbiomes. *Escherichia coli* was the only described species detected in

all host gut microbiomes, completing the list of known species. The remaining MAGs, assigned to eleven additional phyla, were identified as putative novel species. Of the 21 *Spirochaetota* species identified, 17 were novel, and for the most part differed across hosts. The MAGs recovered from the gut microbiome from humans living in Buhoma confirmed the presence of the *Spirochaetota* species *Treponema berlinense*, *T. succinifaciens*, and *T. peruense*, two putatively novel *Treponema* species, *Brachyspira aalborgi*, and a species from the *Sphaerochaetaceae* family. In the gorilla gut microbiomes, at least thirteen *Spirochaetota* species were present, including nine novel *Treponema* species. The remaining species belonged to the genera *Brachyspira*, *Ornithospirochaeta*, and two other yet-to-be-described genera from the families *Sphaerochaetaceae* and *Treponemataceae*. Our analysis identified at least four putative novel species shared between humans and gorillas, with at least one individual from each group carrying them (since the MAGs were derived from pooled samples). Furthermore, at least one individual from the cattle and goat groups harboured the same *Treponema* species in their gut microbiomes. In addition, another putative novel *Treponema* species was detected in goat samples, along with a species that could only be classified at the phylum level as *Spirochaetota*.

4.1.3.4 Evidence of bacterial species shared among different hosts

Geographic locations characterised by wildlife-livestock-human interfaces (Faust et al., 2018; Muylaert et al., 2021; Plowright et al., 2017b; Wilkinson et al., 2018), such as those seen at BINP in Uganda (Muylaert et al., 2021), have overlapping habitats that facilitate increased inter-species interactions. These interactions elevate the chances for the exchange of both commensal and pathogenic microbes among the multiple host species (Kuthyar & Reese, 2021). Some MAGs from different host species were given the same GTDB designations, suggesting that bacterial species present across different host gut microbiomes exhibited a high level of genomic relatedness. Analysis based on genome-wide Average Nucleotide Identity (ANI) using a species threshold of 95% (Varghese et al., 2015), along with the Alignment Fraction (AF), further illustrates that at least five bacterial species were part of the gut microbiomes of multiple host species. Four putative novel bacterial species, detected in MAGs recovered from human and gorilla samples, belong to three different genera within the phylum *Bacillota* and (Supplementary Fig. 4.8). Additionally, one putative *Treponema* species was detected in the gut microbiomes of both cattle and goats (Supplementary Fig. 4.8).

4.1.4 Discussion

The gut microbiota plays a crucial role in both health and disease. However, investigations into the gut microbiota among African populations are notably limited (Littlejohn & Glover, 2023;

Makhalanyane et al., 2023). In this study, we examined the gut microbiome of humans, gorillas, and livestock living at the rural-wildlife interface on the BINP border, Uganda. Based on MAGs, this research identified numerous putative novel bacteria, contributing to the African gut microbiome data. The relevance of these findings is heightened as they were recovered from a region that is a wildlife-livestock-human interface, where the risk for emerging infectious diseases is elevated due to overlapping habitats and increased contact between different hosts (Karmacharya et al., 2024; Magouras et al., 2020; Meurens et al., 2021). As of 2024 there are no closely related references for many novel bacterial species recovered from mountain gorilla gut microbiomes in this study. The high phylogenetic similarities between different host species, including humans and other NHPs, increase the chances of microorganisms and pathogens being shared between them (Davies & Pedersen, 2008). Given that we sampled only one of the two extant populations of mountain gorillas, the gorilla gut microbiome might contain additional bacterial species that could potentially be shared with human hosts (and *vice versa*) due to overlapping habitats, as the four examples described in this work demonstrate.

We have shown that habituated gorillas, which have more exposure to humans and livestock, had significant differences in the abundance of gut microbiome phyla compared to wild gorillas that typically reside deeper in BINP without human contact (Fig. 4.3). In addition, some habituated gorilla gut community compositions were more similar to those of livestock and humans than those of wild gorillas, possibly reflecting the greater exposure of habituated gorillas to these other host group members (Fig. 4.2a). Some samples from habituated gorillas were obtained from families living closer to Buhoma (Fig. 4.2a). These disparities may have emerged from variations in diet (Beam et al., 2021; Fragiadakis et al., 2019; Hicks et al., 2018), influenced by the availability of different foods near human interfaces and farms, or from microbial contaminants or sharing in habitats where there was overlap between gorillas, livestock, and humans (Karmacharya et al., 2024; Muylaert et al., 2021; Sharma et al., 2020). Likewise, cattle and goat gut communities were compositionally similar. They shared the *Treponema* putative novel species, and together with other similar taxa, this resulted in higher gut microbiome resemblance between these hosts (Fig. 4.2a). Cattle and goats had higher α -diversity values in the read-based strategy compared to all other host groups (Fig. 4.2b), but fewer bacterial species were assembled in the MAG strategy (Fig. 4.1c). These contrasting results might be explained by the greater complexity of these host samples, which might contain more similar or overlapping DNA sequences, increasing computational complexity (Alneberg et al., 2014; Quince et al., 2017). In addition, cattle and goat samples were not only fewer in number but also produced lower DNA yields compared to the other groups, possibly reflecting lower-quality samples. These factors might make it more difficult to recover, sort, and group sequences into individual genomes, reducing the quantity and quality of MAGs.

As observed in habituated and wild gorillas, human samples from hospitals versus communities exhibited significant differences in their gut microbiome similarities and phyla abundances (Fig. 4.3). In particular, the gut communities of a few hospitalised humans were compositionally distinct from most other human communities (Fig. 4.2a). Three of these samples from the hospitalised human group were collected from a clinic in Mushorero, a village experiencing ongoing human-gorilla conflict, where gorillas escape the BINP to raid crops planted by local communities near the park. Members of the village chase the gorillas away from the community, suggesting a higher level of human-gorilla direct and indirect contact than in other villages. However, the most likely reason for the observed gut microbiome disparities between the two human groups is due to the widespread use of antibiotics in Buhoma village clinics (Dixon et al., 2021; Fishbein et al., 2023; Kiggundu et al., 2022; Mukonzo et al., 2013; Ramirez et al., 2020), or to other illness-related causes of dysbiosis. Indeed, the samples from patients in the hospital or clinics showed lower α -diversity, indicating reduced gut microbiome diversity compared to other hosts.

The results described here show that the human hosts had prominent amounts of *Spirochaetota* in their gut microbiomes. Bacteria from this phylum are typically absent in the gut microbiomes of individuals in industrialised populations (Angelakis et al., 2019; Thingholm et al., 2021), but they are commonly found in those of people living agricultural lifestyles, as described in previous studies (Angelakis et al., 2019; Brewster et al., 2019; Thingholm et al., 2021). Comparisons of the human gut microbiome analysis with samples from people living in other countries have corroborated previous observations, showing a higher abundance of *Spirochaetota* in individuals living traditional lifestyles in Buhoma, Uganda. In our study, we expanded on these findings by recovering MAGs and identifying specific *Spirochaetota* species. We detected seven species in humans, five of which are *Treponema* species (including two putative novel species), a genus particularly involved in metabolising plant polysaccharides and fibres (Brewster et al., 2019), thirteen species in gorillas, and two in livestock. These findings could be relevant for future research focused on understanding the roles and functions of these newly identified taxa in both animal and human health, highlighting the metabolic functions of these species in physiology and/or disease pathophysiology.

Here, we also described evidence of multiple host species sharing the same bacterial species. Although people from this study had more contact with livestock than with gorillas (Muylaert et al., 2021), we did not directly detect shared bacterial species between humans and livestock. However, we did find bacterial species shared between humans and gorillas, and between cattle and goats. Microorganisms are more frequently transmitted between hosts that are closely related phylogenetically and live in the same geographical area (Davies & Pedersen, 2008). The degree of

host relatedness is the most reliable indicator of whether two host species can share the same pathogens (Davies & Pedersen, 2008). Infection of a new host may be facilitated by the proximity of the new host to the reservoir host, a scenario promoted by the wildlife-livestock-human interface due to frequent contact among multiple host species (Hamilton et al., 2000; Karmacharya et al., 2024; Magouras et al., 2020; Muylaert et al., 2021; Rwego et al., 2008). The close phylogenetic relatedness of the hosts might have helped the microorganisms to transmit between these specific hosts (Davies & Pedersen, 2008; Karmacharya et al., 2024). However, for this microbial transmission (a.k.a. spillover) to have occurred from animals to humans and *vice versa*, the microorganisms needed to go through multiple barriers to be successful in their new host species (Faust et al., 2018; Glidden et al., 2021; Plowright et al., 2017b). The presence of the four putative novel species detected in both human and gorilla gut microbiomes suggests that the conditions at the Buhoma wildlife-human interface and overlapping habitats may have facilitated this bacterial spillover. However, further sampling in other regions is needed to confirm whether this pattern is consistent across similar settings. Alternatively, or perhaps additionally, this occurrence could be attributed to the high versatility and adaptability of these bacteria, which enable them to jump between numerous intermediate and definitive hosts (Moradali et al., 2017; Pokharel et al., 2023; Scheuerl et al., 2020; Soni et al., 2024).

The results and analysis presented in this study confirm the presence of numerous understudied microbes and hundreds of putative novel bacteria within the gut microbiomes of gorillas, cattle, goats, and humans living in the BINP and around Buhoma region in Uganda. Here, while most bacterial species were host-specific (Fig. 4.2a), the identification of a small number of novel species across multiple hosts cohabiting in the same regional space raises questions about whether these hosts maintain the same bacterial species over generations, experience accidental microorganism presence in their guts, or undergo cross-species transmission. The study also confirmed the presence of *Spirochaetota*, which are commonly found in the gut microbiomes of people living an agricultural lifestyle, and show members of this phylum were common to all host species sampled, including gorillas.

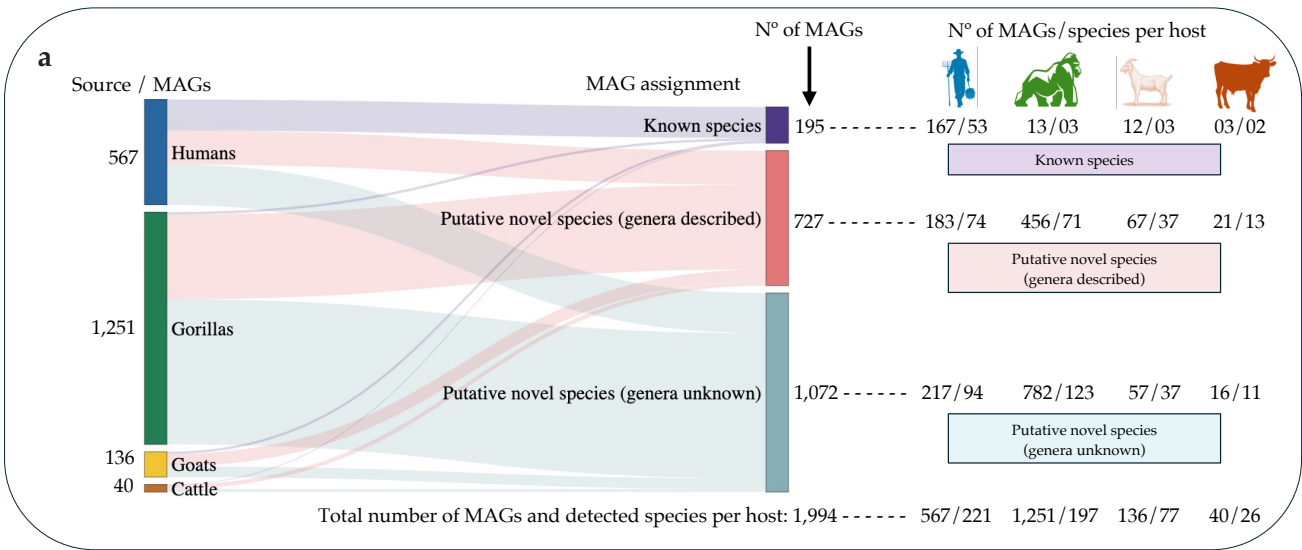
4.1.5 Code availability

The codes, scripts, and software details are comprehensively documented and shared in the 'Uganda-cross-species-transmission' repository - GitHub [link](#): ([ValterAlmeida](#)).

4.1.6 Supplementary information

The full results of quality assessments (CheckM) and MAG classifications (GTDB-Tk) are provided in the appendices (see [here](#) and [here](#)).

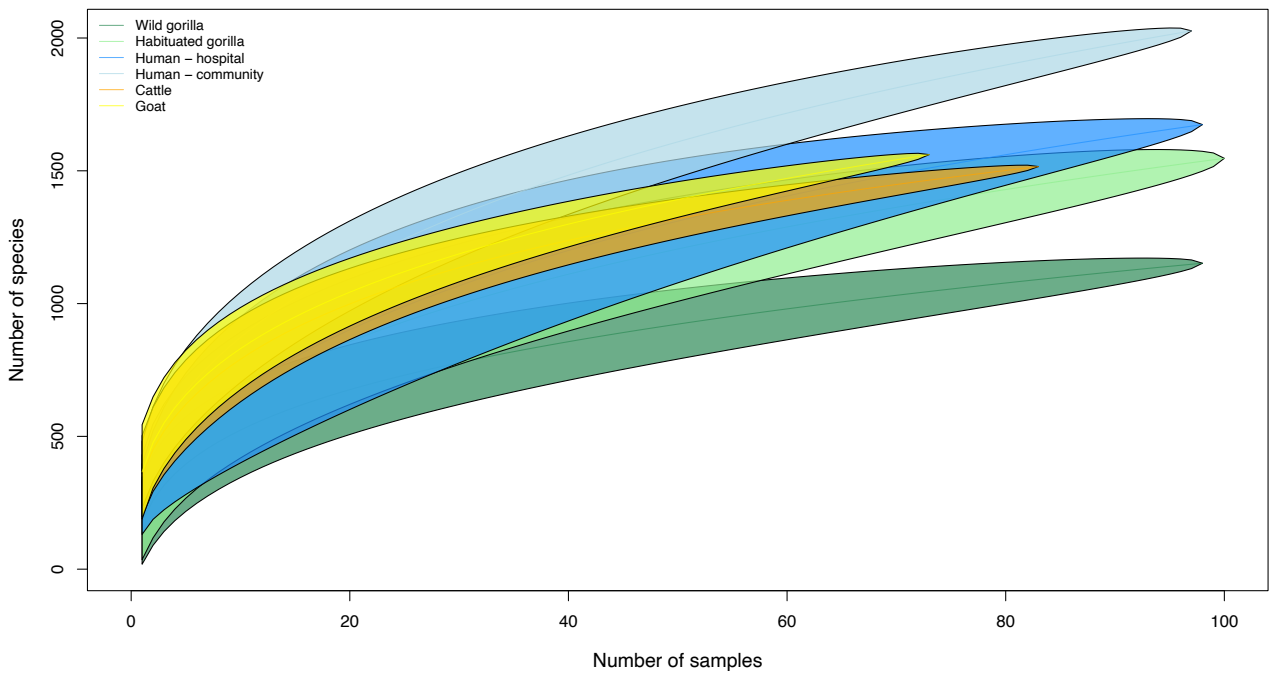
Supplementary Fig 4.5: Dereplication of MAGs by Average Nucleotide Identity (ANI) reduces total MAG count



a, Number of MAGs and species detected after dereplication. Some species detected in different hosts were removed during the dereplication process and are not included in the numbers shown in this figure.

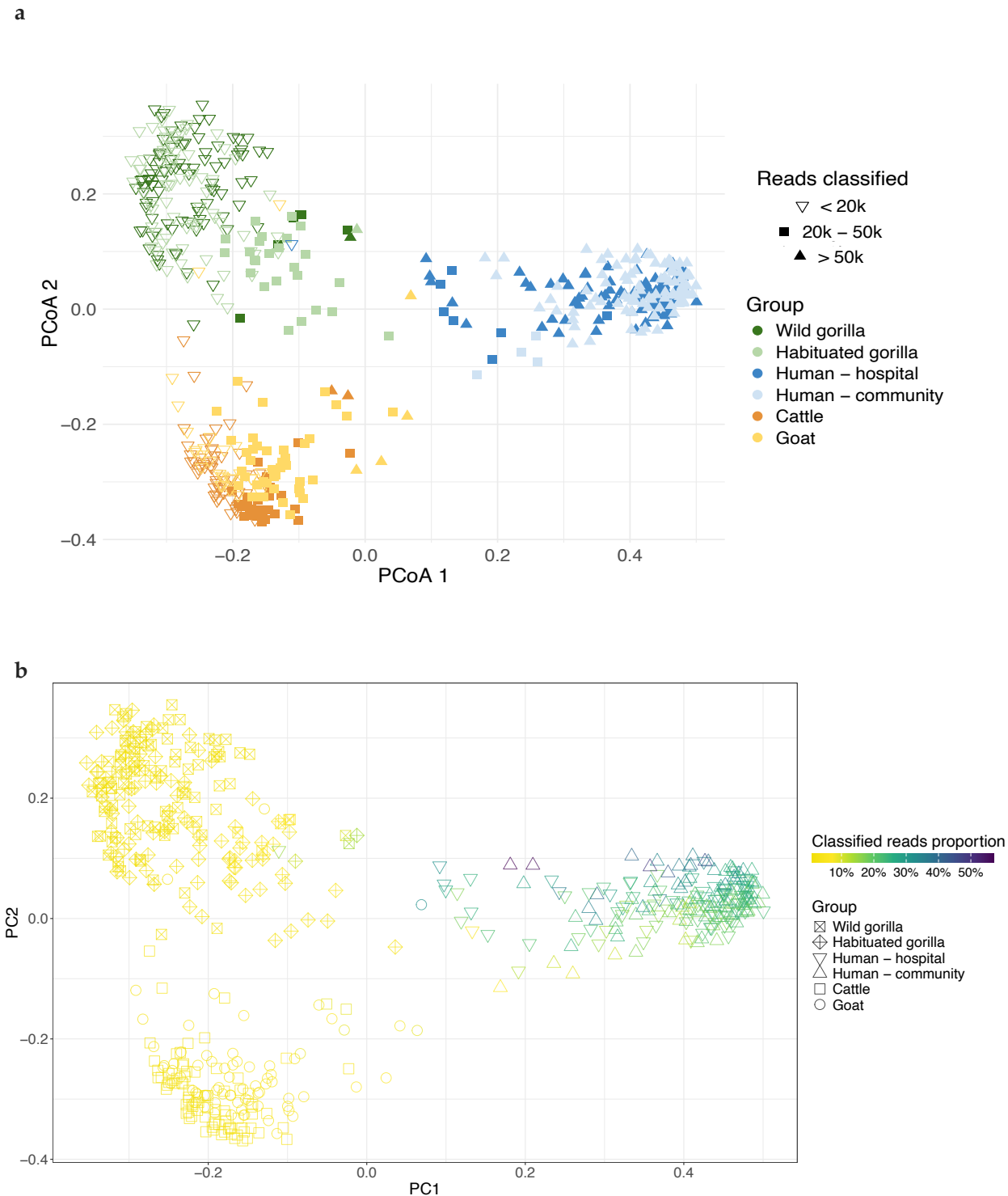
Supplementary Fig 4.6: Species accumulation curve indicating low likelihood of detecting additional species

a



a, The species accumulation curve shows that further sampling is unlikely to discover many new species in the dataset.

Supplementary Fig 4.7: Variation in classified microbial reads among humans, gorillas, cattle, and goats

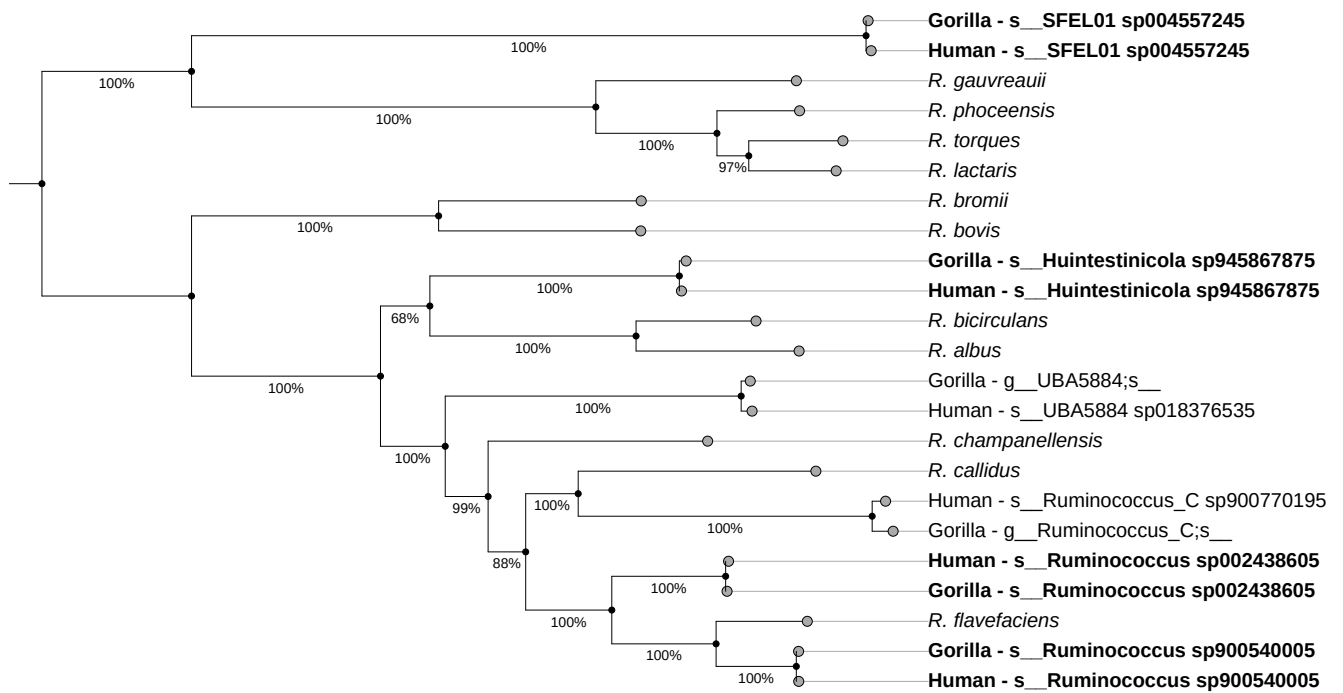


a,b, The analysis revealed that the number of classified reads was significantly higher in human samples compared to those from the other hosts. This suggests that the microbial diversity in humans was more thoroughly characterised due to more comprehensive classification of sequences. In contrast, the other hosts, such as gorillas, cattle, and goats, had fewer classified reads, which could

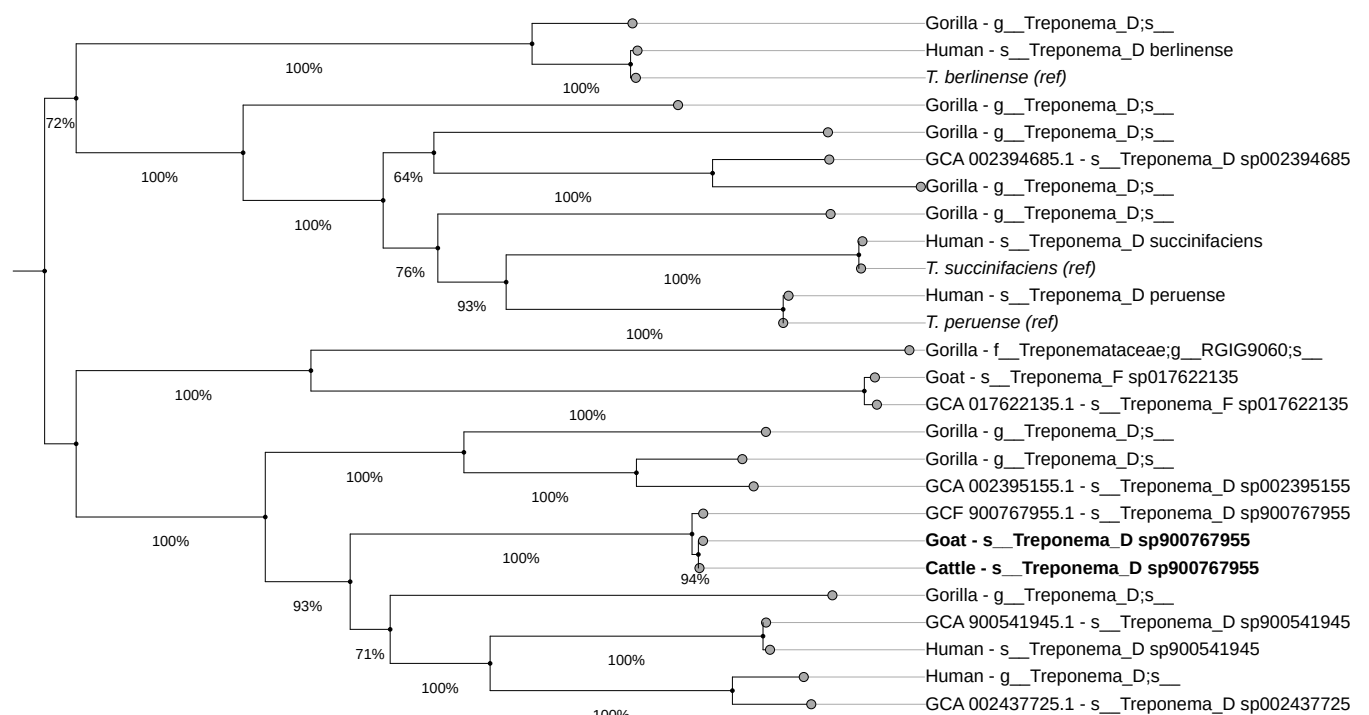
indicate either a less well-studied microbial communities, or a greater presence of novel or unclassified species in their samples.

Supplementary Fig 4.8: Putative novel bacterial species shared between different host species at the rural-wildlife interface near the BINP border, Uganda.

a



b



a, The phylogenetic tree presents reference genomes from *Ruminococcus* species alongside putative novel species, shown in bold, that were detected in both human and gorilla gut microbiomes. **b**, Phylogenetic tree showing the detected *Treponema* species present in different hosts (bold) and their phylogenetic relationship with other species detected in this work, *Treponema* reference genomes, and the closest related species that have yet to be described. Both phylogenetic trees (a and b) were constructed using an alignment file from GTDB-Tk containing 42 amino acids from each of the 120 concatenated marker genes and were inferred with IQ-TREE2, incorporating 1,000 bootstrap replicates for enhanced robustness, all using default settings. The final alignments comprised a total of 5,035 and 5,036 amino acids after trimming using default settings.

A Statement of Contribution for this chapter is provided in the [Appendices](#).

5 Chapter

5.1 Diverse and putative novel *Prevotella* and *Treponema* species in the gut microbiome from humans, gorillas, and livestock at a wildlife–livestock–human interface in Uganda

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5.1.1 Abstract

The gut microbiome of non-industrialised populations remained understudied and contained a considerable number of unexplored bacterial species. This study investigated the diversity of the *Treponema* and *Prevotella* genera at a wildlife–livestock–human interface in Uganda. Analysing 75 metagenome-assembled genomes (MAGs), sixteen distinct *Treponema* species were identified from the gut microbiomes of humans, gorillas, and livestock. Three of these species, found in human samples, were also present in other host species, suggesting close contact may have facilitated bacterial sharing. The study also explored *Prevotella* diversity, a genus that often dominates the gut microbiome in non-Westernised populations. No previously identified species were found, but fifteen putative novel species were phylogenetically identified from human (7), gorilla (7), and goat (1) gut microbiomes. One of the human-derived MAGs contained the *nimJ* gene, indicating resistance to a nitroimidazole-class drug common in the region. These findings not only expanded the taxonomic knowledge of *Treponema* and *Prevotella* but also provided a species-level perspective for future studies on their impact on health.

5.1.2 Introduction

Most commensal intestinal organisms coexist peacefully with their hosts, occupying microenvironmental niches that might otherwise be filled by harmful pathogens (Abt & Pamer, 2014; Costello et al., 2009). The *Treponema* and *Prevotella* genera are both prevalent in mammalian microbial communities, particularly in non-industrialised human populations with traditional lifestyles (Brewster et al., 2019; De Filippo et al., 2010; Gomez et al., 2016; Tamburini et al., 2022). However, there is a notable lack of microbiome research conducted in Africa (Allali et al., 2021; Makhalanyane et al., 2023), and the species diversity and function of these bacteria in such settings remain poorly understood.

Several *Treponema* species inhabit different microbiomes in humans and animals, with some causing lesions that lead to diseases (Giacani & Lukehart, 2014; Mitjà et al., 2013; Radolf et al., 2016; Šmajš et al., 2018). For example, *Treponema pallidum* causes syphilis in humans and non-human primate (NHP) hosts (Chuma et al., 2019; Radolf et al., 2016). The genus also includes oral species associated with dental plaques and periodontal diseases in both humans and animals (Asai et al., 2002; Yousefi et al., 2020; Zeng et al., 2021). Some of these oral species are also linked to digital dermatitis in ruminants (Dias et al., 2024; Edwards et al., 2003; Zinicola et al., 2015), and the gastrointestinal tracts of these animals are considered a potential source of the associated treponemes (Sullivan et al., 2015). Reports of potential exchange of pathogenic and commensal treponemes between animals and humans highlight the adaptability of this genus species (Chuma et al., 2019; Harper et al., 2011, 2013; Paciência et al., 2019). Despite the genus's relevance to health and disease, there remains a considerable gap in knowledge regarding intestinal *Treponema* species and their importance in the gut microbiome of humans and animals (Angelakis et al., 2019; Brewster et al., 2019; Littlejohn & Glover, 2023).

Similarly, while *Prevotella* species are prevalent in the gut microbiome of non-industrialised human populations and are associated with a diet rich in plant-based foods, their specific species diversity remains understudied (Brewster et al., 2019; Pasolli et al., 2019; Tamburini et al., 2022; Tett et al., 2021). The ecology of urban environments, characterised by diets high in animal fats and proteins and greater antibiotic usage, contributes to a reduction in *Prevotella* and an increase in *Bacteroides* (Brewster et al., 2019; Dethlefsen & Relman, 2011; Eckburg et al., n.d.; Tamburini et al., 2022). The widespread use of antibiotics can also lead to the presence of antibiotic-resistant genes, which have been found in *Prevotella* species in the oral microbiota and airways (Castillo et al., 2022; Webb et al., 2022). Little is known about the presence of these resistance genes in rural populations like those in Buhoma, Uganda, where antibiotics are widely accessible (Mukonzo et al., 2013).

The proximity of humans, livestock, and wildlife at a shared interface presents a unique opportunity to study the transfer of microorganisms and pathogens (Amato et al., 2019; Cooper & Nunn, 2013; Gomez et al., 2016; Muylaert, et al., 2021). Given this context, this study aimed to investigate the diversity of intestinal *Treponema* and *Prevotella* species using shotgun metagenomics on faecal samples from a rural Ugandan location with documented human–livestock–gorilla contact. The findings of this study revealed several putative novel *Prevotella* species, including those with antibiotic resistance genes, and identified putative novel *Treponema* species, including species that are found in both human and animal hosts. The comparisons with publicly available genomes highlighted a closer phylogenetic relationship between the human intestinal treponemes and those found in livestock than to those in non-human primates (NHPs).

5.1.3 Results

5.1.3.1 Diverse collection of putative novel *Treponema* and *Prevotella* species across studied Ugandan hosts

This study involved the analysis of 553 gut microbiomes collected from humans, gorillas, and livestock at the rural-wildlife interface of Bwindi Impenetrable National Park (BINP) in Uganda. A deep sequencing approach was applied to 30 pooled samples, which included five pools each from wild gorillas, habituated gorillas, community humans, hospitalised humans, cattle, and goats. These pools comprised a varying number of individual faecal samples. A total of 75 *Treponema* metagenome-assembled genomes (MAGs) and 37 *Prevotella* MAGs were assembled. Most of the *Treponema* MAGs were obtained from gorilla faecal samples (46), followed by humans (25), goats (3), and cattle (1). For the *Prevotella* MAGs, the majority originated from human faecal samples (20), followed by gorillas (14), and goats (3), with no *Prevotella* MAGs recovered from cattle.

Phylogenetic analysis of the assembled MAGs revealed a diverse collection of bacterial species. For the *Treponema* genus, sixteen distinct species were identified: nine from gorillas, five from humans, one from a goat, and one found in both goat and cattle gut microbiomes. Of the human-derived species, three were previously described (*T. succinifaciens*, *T. berlinense*, and *T. peruense*), while the remaining two were putative novel species. One was assigned as *Treponema* sp900541945, and the second is yet to be given an assignment (Fig. 5.1).

Figure 5.1: Phylogenetic relationships of *Treponema* species, including putative novel species from this study, and publicly available genomes

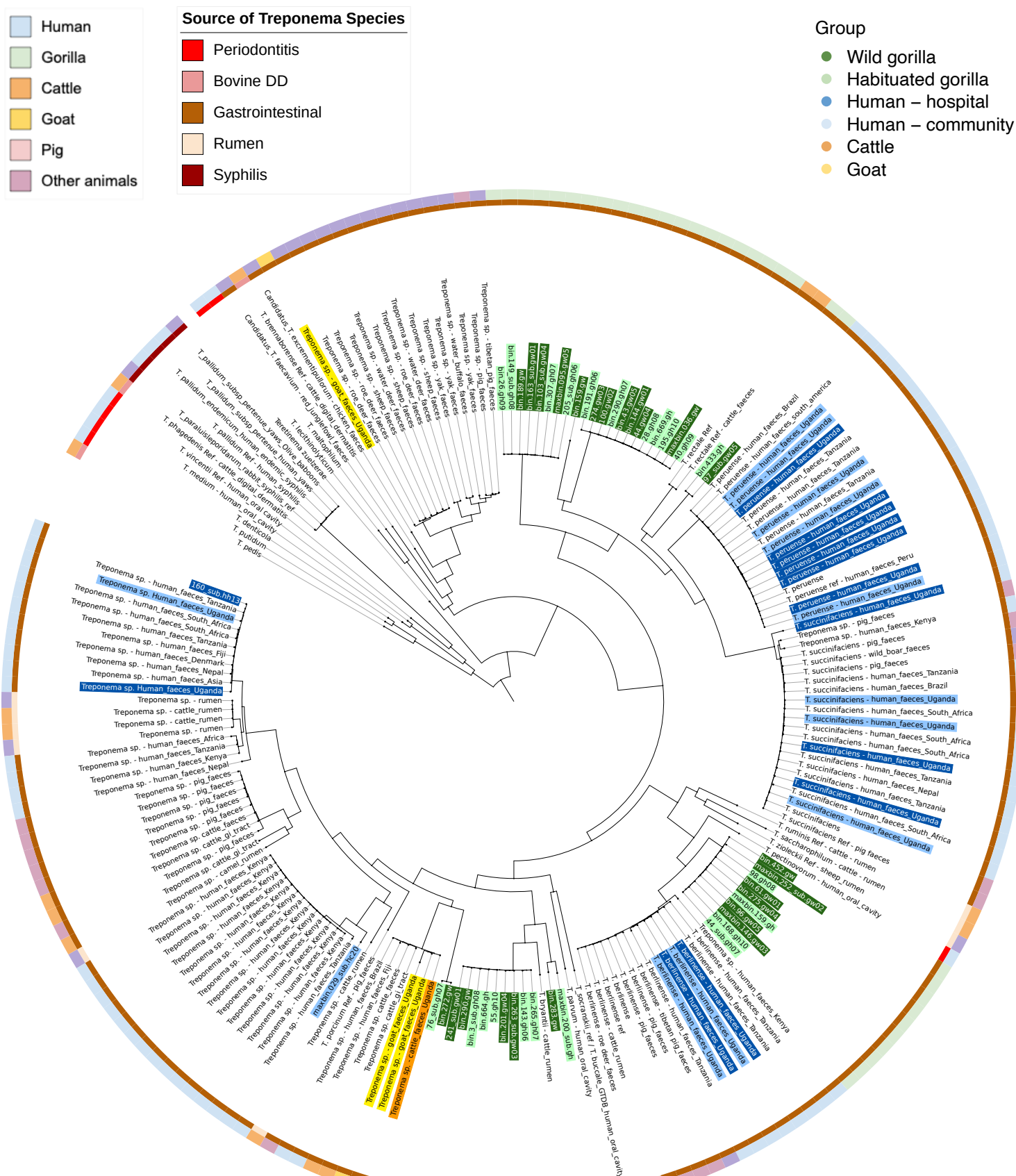


Figure 5.1 – The phylogenetic tree illustrates the relationships between *Treponema* species, putative novel species from host gut microbiome samples analysed in this study, and various other hosts and sources from publicly available genomes. The highlighted text in the genome names represents the MAGs from this study. The inner ring indicates the source of the *Treponema* genomes, and the outer ring shows the host species from which the samples originated. A multiple sequence alignment (MSA) of 120 bacterial marker genes (approximately 5,000 amino acids) was used for phylogenetic inference. The described and putative novel *Treponema* MAGs identified in this study are highlighted. *The phylogenetic tree was constructed using GTDB-Tk v2.4 to identify and extract the 120 bacterial marker genes from each MAG and reference genome. These marker genes were concatenated and aligned using GTDB-Tk's integrated alignment pipeline, which applies FastTree-compatible trimming to remove poorly aligned regions. The resulting concatenated MSA (~5,000 amino acid positions) was then used as input for IQ-TREE 2, which inferred the phylogeny using the maximum likelihood method under the default substitution model selection procedure (ModelFinder). The final tree was visualised and annotated using iTOL website.

The general characteristics of the *Treponema* MAGs assembled in this study were compared with reference genomes for context (Table 5.1). Among the human-derived MAGs, three corresponded to previously described species: *T. succinifaciens* (2.61 Mb, 38.9% G+C), *T. berlinense* (2.22 Mb, 39.9% G+C), and *T. peruense* (2.10 Mb, 42.4% G+C). The remaining two putative novel species identified in human gut microbiomes had genome sizes of 2.71 Mb and 2.75 Mb, and G+C contents of 34.8% and 41.4%, respectively. The gorilla gut microbiomes revealed eleven putative novel *Treponema* MAGs, with genome sizes from 1.95 Mb to 2.47 Mb and G+C contents from 33.8% to 44.4%. One putative novel *Treponema* species was identified from a goat sample (2.55 Mb, 53.4% G+C), and another from a cattle sample (2.11 Mb, 31.9% G+C). Completeness of the novel MAGs ranged from 88.9% to 98.6%, indicating medium to high-quality assemblies (Table 5.1).

Table 5.1 - Overview of the characteristics of *Treponema* MAGs assembled in this study and publicly available genomes.

	General features of <i>Treponema</i> species							
	Known species	Host	Source	Genome size (bp)	G + C content (%)	Genes	Location	Accession
References / MAGs	<i>T. pedis</i>	Bovine	DD	2,889,325	37	2,652	Sweden	GCF_000447675.1
	<i>T. denticola</i>	Human	Oral	2,843,201	37.9	2838	n/a	GCF_000008185.1
	<i>T. pallidum</i>	Human	STI	1,139,633	52.8	1065	n/a	GCF_000410535.2
	<i>T. medium</i>	Human	Oral	2,721,998	44.3	2409	n/a	GCA_017161265.1
	<i>T. succinifaciens</i>	Pig	GI	2,897,425	39	2581	n/a	GCF_000195275.1
	<i>T. succinifaciens</i> *	Human	GI	2,605,881	38.9	2341	Uganda	=
	<i>T. berlinense</i>	Human	GI	2,521,032	39.5	2155	Germany	GCF_900167025.1
	<i>T. berlinense</i> *	Human	GI	2,222,088	39.9	1874	Uganda	=
	<i>T. peruense</i>	Human	GI	2,738,066	41	2425	Peru	GCF_016117655.1
	<i>T. peruense</i> *	Human	GI	2,095,015	42.4	1778	Uganda	=
	Novel species	Host	Source	Genome size (bp)	G + C content (%)	Genes	Location	Completeness (%)
	<i>Treponema</i> sp. 1	Human	GI	2,708,717	34.8	2377	Uganda	94
	<i>Treponema</i> sp. 2	Human	GI	2,750,372	41.4	2488		95.7
	<i>Treponema</i> sp. 3	Gorilla	GI	2,427,054	38.8	1937		97.9
	<i>Treponema</i> sp. 4	Gorilla	GI	2,097,615	37	1828		92.9
	<i>Treponema</i> sp. 5	Gorilla	GI	2,401,622	36.5	1868		91.3
	<i>Treponema</i> sp. 6	Gorilla	GI	2,147,537	36.1	1821		98.6
	<i>Treponema</i> sp. 7	Gorilla	GI	2,012,786	44.4	1706		96.5
	<i>Treponema</i> sp. 8	Gorilla	GI	2,001,977	37.8	1680		96.9
	<i>Treponema</i> sp. 9	Gorilla	GI	1,950,765	33.8	1703		94.1
	<i>Treponema</i> sp. 10	Gorilla	GI	2,391,419	37.8	1988		88.9
	<i>Treponema</i> sp. 11	Gorilla	GI	2,468,557	39	2022		98.6
	<i>Treponema</i> sp. 12	Goat	GI	2,553,654	53.4	2393		94.9
	<i>Treponema</i> sp. 13	Cattle	GI	2,111,257	31.9	1769		97.9

* Species sequenced in this work. * DD – Digital dermatitis / GI – Gastrointestinal / STI - Sexually transmitted infections. n/a – not available.

For the *Prevotella* genus, fifteen distinct intestinal species were identified. Seven of these originated from human gut microbiomes, seven from gorilla samples, and one from goat faecal samples. All of these were putative novel *Prevotella* species yet to be described. The general characteristics of the *Prevotella* MAGs assembled in this study were compared with publicly available reference genomes (Table 5.2). Human gut samples yielded seven novel species, with genome sizes ranging from 1.76 Mb to 2.65 Mb and G+C contents from 43.7% to 56.4%. The gorilla gut microbiomes contained seven novel species with genome sizes between 1.92 Mb and 3.41 Mb and G+C contents from 48.6% to 59.0%. One novel species was identified from a goat sample (3.09 Mb, 44.6% G+C). Completeness of the novel MAGs ranged from 70.2% to 96.6%, and contamination levels were low (0.0–3.8%).

Table 5.2 - Overview of the characteristics of *Prevotella* reference genomes and species identified in the studied Ugandan host samples from this thesis.

General features of <i>Prevotella</i> species								Accession
Known species (Ref.)	Host	Source	Assembly size (bp)	Completeness (%)	Genes	G + C content (%)	Location	
<i>P. copri</i>	Human	GI	3,756,461	99.0	3,115	45	US	GCF_019127725.1
<i>P. intermedia</i>	Human	Oral	2,730,073	99.0	2,334	43.5	KP	GCF_002762425.1
<i>P. ruminicola</i>	n/a	n/a	3,961,687	99.6	3,408	46.3	n/a	GCF_900142525.1
<i>P. bivia</i>	Human	Vagina	2,386,762	99.7	1,993	39.5	US	GCF_001065995.1
<i>P. denticola</i>	Human	Vagina, Oral	2,937,589	99.3	2,349	50.4	n/a	GCF_000193395.1
<i>P. bryantii</i>	Ruminant	Rumen	2,790,226	79.9	2,476	37.9	IR	GCA_016287715.1
<i>P. melaninogenica</i>	Human	Vagina, Oral	3,090,326	99.3	2,407	40.8	JPN	GCF_003609775.1
Novel species (MAGs)	Host	Source	Assembly size (bp)	Completeness (%)	Genes	G + C content (%)	Location	Contamination (%)
<i>Prevotella</i> sp. 1	Human	GI	1,763,471	84.1	1,434	56.4	Uganda	1.3
<i>Prevotella</i> sp. 2	Human	GI	1,856,360	84.2	1,566	45.3		0.4
<i>Prevotella</i> sp. 3	Human	GI	2,621,605	93.5	2,054	43.7		1.5
<i>Prevotella</i> sp. 4	Human	GI	2,035,341	70.2	1,520	53.1		3.8
<i>Prevotella</i> sp. 5	Human	GI	2,269,540	87.7	1,793	52.7		3.0
<i>Prevotella</i> sp. 6	Human	GI	2,653,024	92.0	2,094	46.7		1.9
<i>Prevotella</i> sp. 7	Human	GI	2,257,926	78.3	1,850	50.5		2.3
<i>Prevotella</i> sp. 8	Gorilla	GI	2,536,175	93.2	1,853	59		2.0
<i>Prevotella</i> sp. 9	Gorilla	GI	1,915,124	91.1	1,525	50.9		0.0
<i>Prevotella</i> sp. 10	Gorilla	GI	3,405,209	93.7	2,583	51.5		3.4
<i>Prevotella</i> sp. 11	Gorilla	GI	2,846,326	90.8	2,201	51.2		2.4
<i>Prevotella</i> sp. 12	Gorilla	GI	2,911,130	93.5	2,247	49.6		1.0
<i>Prevotella</i> sp. 13	Gorilla	GI	2,455,133	81.0	1,822	53.7		0.1
<i>Prevotella</i> sp. 14	Gorilla	GI	2,574,040	96.6	2,091	48.6		2.0
<i>Prevotella</i> sp. 15	Goat	GI	3,091,302	90	2,422	44.6		1.7

* GI – Gastrointestinal; Ref. – References; US – United States; KP – South Korea; n/a - Not available; IR – Iran; JPN – Japan.

5.1.3.2 Genomic relatedness and host-sharing of *Treponema* and *Prevotella* Species

For *Treponema*, analysis of 46 MAGs from mountain gorillas revealed nine distinct species, none of which had a close relative in the GTDB, suggesting they are putative novel species without closely related publicly available genomes in databases. In contrast, three of the species identified in human samples were also found in livestock, including the previously described *T. succinifaciens* and *T. berlinense* from swine, and a putative novel species shared with cattle and goats. This highlights that human intestinal treponemes have a close phylogenetic relationship to those found in livestock (Fig. 5.1).

For *Prevotella*, two of the seven putative novel species identified in human samples were also found in other hosts: one was shared with pigs and another with rhesus macaques. The remaining human-derived species were present in human gut microbiomes from other countries. In contrast, none of the seven putative novel *Prevotella* species recovered from gorilla faecal samples had closely related genomes in publicly available databases. The single putative novel *Prevotella* species from goat samples was similar to the one recovered from goat gut microbiomes in China (Fig. 5.2).

Figure 5.2: *Prevotella* MAGs and cross-host phylogenetic relationships

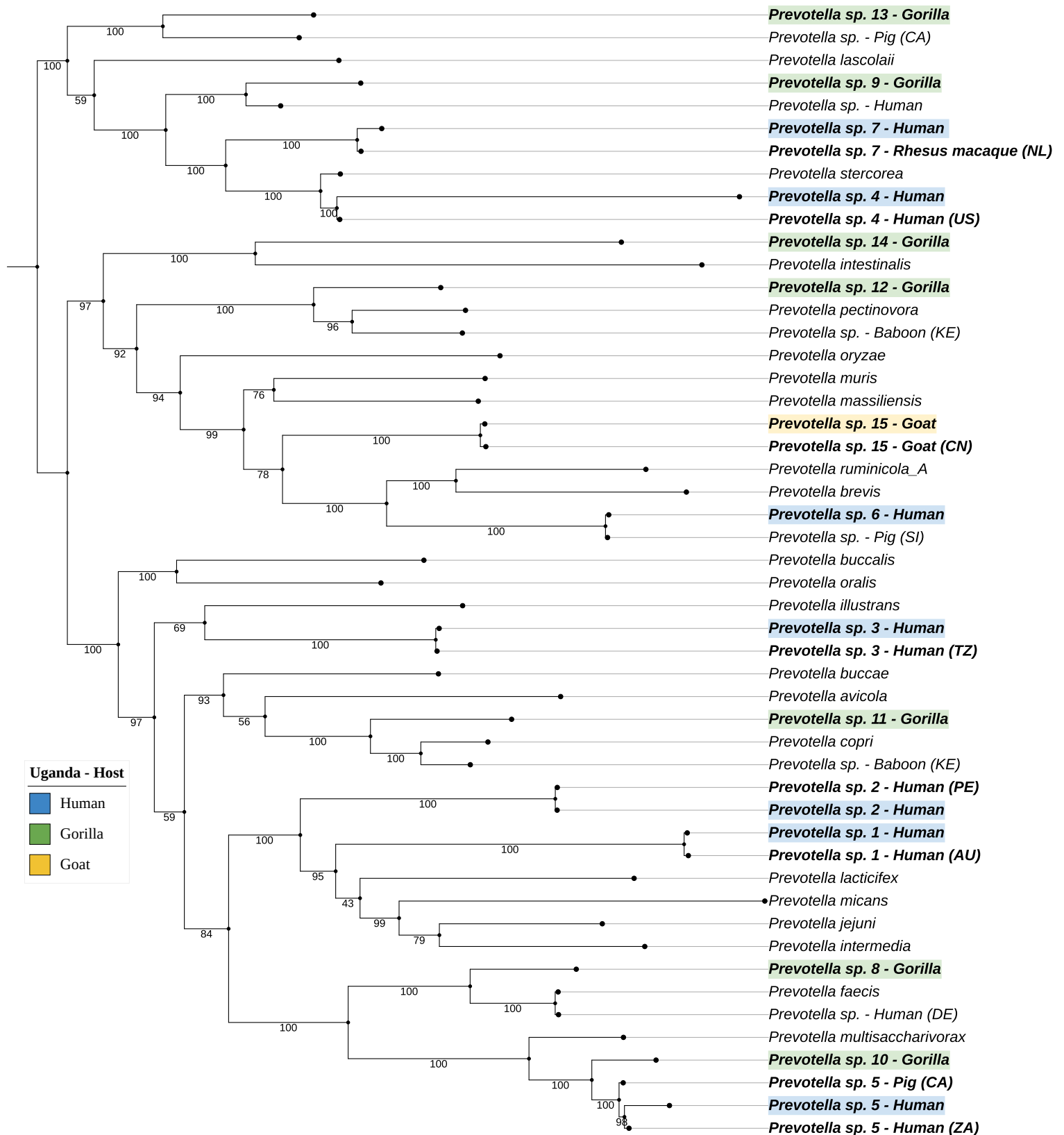


Figure 5.2 – Representative MAGs of *Prevotella* species in the studied host gut microbiomes in Uganda and their phylogenetic relationships, indicating same species across different hosts (*Prevotella* sp. 5 and sp.7). *The phylogenetic tree was constructed using a maximum likelihood approach. First, GTDB-Tk v2.4 was used to identify and extract 120 bacterial marker genes from each MAG and publicly available genome. These marker genes were then concatenated and

aligned, with poorly aligned regions removed. The resulting concatenated multiple sequence alignment, which contained approximately 5,000 amino acid positions, was used as input for IQ-TREE 2. This software inferred the phylogeny using the maximum likelihood method, with the best-fit substitution model automatically selected by ModelFinder. The final tree was visualised and annotated using the iTOL website. The labels on the tree (CA – Canada; NL – Netherlands; US – United States; KE – Kenya; CN – China; SI – Slovenia; TZ – Tanzania; PE – Peru; AU – Australia; DE – Germany; ZA – South Africa) correspond to the geographic origins of the reference genomes used for comparison, providing context for the observed phylogenetic relationships.

5.1.3.3 Antimicrobial resistance (AMR) genes

No AMR genes were found in any of the *Treponema* MAGs from the Ugandan samples. However, AMR genes were present in three publicly available genomes used for comparison, conferring resistance to tetracycline, lincosamide, macrolide, streptogramin B, and aminoglycosides. In contrast, the *nimJ* resistance gene was present in a putative novel *Prevotella* species MAG (*Prevotella* sp. 7) from human gut microbiomes. This gene, which was 99.40% identical with 100% coverage, confers resistance to metronidazole and other nitroimidazole-class drugs commonly used in the region. It was absent in the reference genome of the same species from a rhesus macaque.

5.1.4 Discussion

Gut microbiome evolution is a dynamic process shaped by both vertical transmission from mother to offspring and horizontal transmission through social interactions, shared environments, and diet (Amato et al., 2019; Davenport et al., 2017). This study investigated the diversity of *Treponema* and *Prevotella* at a wildlife–livestock–human interface in Uganda, revealing insights into host-sharing and bacterial diversity. The findings contribute to a deeper understanding of these bacterial genera across different host populations in a shared environment.

The *Treponema* genus, though scarce in many human populations, is characteristic of traditional gut microbiomes (Angelakis et al., 2019; Obregon-Tito et al., 2015). This study identified five species in humans, including three previously described ones (*T. succinifaciens*, *T. berlinense*, and *T. peruense*) and two putative novel species. One novel species showed a high genetic similarity to a genome from an Asian human sample (Almeida et al., 2019), suggesting a wide geographic range. None of the nine putative novel species from mountain gorillas were closely related to the human-derived species.

Three of the human intestinal *Treponema* species were also found in livestock, detected in publicly available genomes but not in the livestock studied in this work. These include two species originally described in swine (*T. succinifaciens* and *T. berlinense*) and a putative novel species shared with cattle and goats (Nayfach et al., 2019). Phylogenetic analyses confirmed a close relationship between human intestinal *Treponema* and those found in livestock. One novel *Treponema* species from a goat

was phylogenetically distinct and had a higher GC content (53.4%) (Table 5.1). The absence of these species in industrialised populations could be linked to antibiotic use, as AMR genes were found in publicly available genomes from pigs and other sources, although not in the Ugandan samples (Cwyk & Canale-Parola, 1979). The use of antibiotics such as penicillin G and chloramphenicol may affect the growth of *Treponema* species in the intestine (Cwyk & Canale-Parola, 1979), contributing to their disappearance in these settings.

The study's findings on the *Prevotella* genus challenged the idea that *P. copri* and *P. stercorea* are the dominant species in humans (Yeoh et al., 2022). None of the seven putative novel species identified in this study were closely related to these two. Human intestinal *Prevotella* species showed evidence of host-sharing, with two putative novel species also found in pigs and rhesus macaques in publicly available genomes. The remaining species matched those found in human samples from Australia, Peru, Tanzania, and the USA (Bowerman et al., 2020; Fragiadakis et al., 2019; Nayfach et al., 2019). Conversely, all seven of the putative novel *Prevotella* species from gorillas appeared to be unique to that host, with no closely related reference genomes in public databases (GTDB and NCBI accessed in February 2024), suggesting they represent host-specific lineages. A single putative novel *Prevotella* species from goats was found to be similar as that in a goat reference genome from China (Xie et al., 2021).

The *nimJ* resistance gene was detected in a human-derived *Prevotella* MAG (*Prevotella* sp. 7). This gene confers resistance to metronidazole, a nitroimidazole-class drug widely used in Uganda (Mukonzo et al., 2013; Nayiga et al., 2020). Its absence in the same species genomes assembled from rhesus macaque gut microbiomes suggests that its acquisition is linked to selective pressure from extensive antibiotic use in the human population.

The high diversity of species in both *Treponema* and *Prevotella* genera, especially in gorillas, highlights the importance of studying diverse, non-industrialised populations to fully understand microbial biodiversity in the gut microbiome. Although evidence of *Prevotella* and *Treponema* host-sharing between humans and animals was not fully detected in the gut microbiomes in this study, this further emphasises the interconnectedness of microbiomes and provides a foundation for future research into the dynamics of microbial transmission and the evolution of host–microbiome relationships.

5.1.5 Code availability

The codes, scripts, and software details are comprehensively documented and shared in the 'Uganda-cross-species-transmission' repository - GitHub [link](#): ([ValterAlmeida](#)).

The quality assessment of *Treponema* and *Prevotella* MAGs can be accessed [here](#), and other phylogenetic tree formats can be found in the appendices (see [here](#)).

A Statement of Contribution for this chapter is provided in the [Appendices](#).

6 Chapter

Formatting note

The following chapter was developed to be submitted to a journal in *The Lancet* portfolio. It retains the journal's original structure, formatting, and subheadings, which may differ from the standard thesis formatting used in other chapters.

6.1 Metagenomic analysis of *Campylobacter* at a wildlife–livestock–human interface in Uganda reveals novel species associated with human disease

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6.1.1 Summary

6.1.1.1 Background

Campylobacter species are leading causes of bacterial gastroenteritis globally, but their diversity and transmission dynamics at wildlife–livestock–human interfaces are poorly understood. We investigated *Campylobacter* diversity across sympatric mountain gorillas, livestock, and humans in Uganda, and assessed its clinical relevance in human samples.

6.1.1.2 Methods

We analysed 553 faecal samples from mountain gorillas (N=200), cattle (N=83), goats (N=73), and humans (N=197) collected in Buhoma, Uganda. DNA was extracted and subjected to Illumina shotgun sequencing. Metagenome-assembled genomes (MAGs) were reconstructed, dereplicated, and classified using GTDB-Tk. Phylogenetic and functional analyses of *Campylobacter* were performed, and its abundance was compared across host groups. Clinical associations in humans were assessed via read-based mapping and statistical analysis in R.

6.1.1.3 Findings

We assembled 44 *Campylobacter* MAGs representing seven species, including five putative novel taxa. Mountain gorillas harboured three of these novel species, while livestock carried *C. vicugnae* (goats) and *C. sp017646085* (cattle). Human gut microbiomes revealed *Candidatus* *Campylobacter* *infans*, which was not associated with disease, and *C. sp900539255*, which was significantly enriched in clinical samples ($p=0.001$). Functional profiling revealed sulfur and nitrogen metabolic pathways unique to *C. sp900539255*. Antimicrobial resistance genes, including *bla*_{OXA-471_1}, were detected in *C. C. infans* MAGs.

6.1.1.4 Interpretation

Campylobacter diversity is high at the human–animal interface in Buhoma, with novel species identified, including one significantly associated with human clinical samples. Expanding reference databases is critical for accurate surveillance and improved public health interventions.

6.1.1.5 Funding

Royal Society Te Apārangi, Percival Carmine Chair in Epidemiology and Public Health, Massey University.

6.1.2 Introduction

Campylobacter species are among the leading causes of bacterial gastroenteritis and diarrhoea worldwide, with *C. jejuni* and *C. coli* being the most prevalent etiological agents in human infections (Burnham & Hendrixson, 2018; Kaakoush et al., 2015). Several other *Campylobacter* species, including *C. fetus* (Wagenaar et al., 2014), *C. lari* (Gourmelon et al., 2022), *C. hyointestinalis* (Edmonds et al., 1987), *C. concisus* (Kaakoush & Mitchell, 2012), *C. showae* (Hsu et al., 2019), *C. upsaliensis* (Bourke et al., 1998), *C. lanienae* (Lévesque et al., 2016), and *C. vicugnae* (Jehanne et al., 2024) have also been implicated in human diseases, highlighting the genus's ongoing species

evolution and adaptation to infect human hosts. The frequent occurrence of sporadic human infections is mainly linked to contaminated food, water, and its widespread presence as a zoonotic pathogen in both livestock and wildlife populations (Burnham & Hendrixson, 2018).

Diarrhoea continues to pose a notable public health challenge, contributing substantially to childhood morbidity and mortality, particularly in developing countries (Kyu et al., 2025). Diarrhoeal disease mortality rates vary significantly across regions, with striking disparities between high-income areas and some countries in Africa (Kyu et al., 2025). For example, in high-income regions, fewer than one child under five per 100,000 dies from diarrhoea, whereas in sub-Saharan Africa, the rate surpasses 130 deaths per 100,000 (Kyu et al., 2025). In Uganda, diarrhoea is one of the top five causes of under-five mortality, responsible for over 140,000 deaths annually, accounting for 7.1% of all under-five deaths in the country (Nantege et al., 2022).

Research in context

Evidence before this study

Campylobacter diversity and interspecies transmission dynamics at wildlife–livestock–human interfaces remained poorly characterised. *Ca. C. infants* had been mentioned in a limited number of studies, but evidence for its association with human disease was inconclusive. Data on its close phylogenetic relationship with *Campylobacter* species found in gorillas and other non-human primates were scarce. No studies had reported the presence or clinical relevance of *C. sp900539255* in humans. Additionally, the potential for misclassification or under detection of novel *Campylobacter* species by standard metagenomic diagnostic approaches in complex, multi-host samples had not been explored.

Added value of this study

This study provides the first comprehensive metagenomic characterisation of *Campylobacter* diversity at a high-intensity human–animal interface in Uganda, identifying seven species, including five putative novel taxa. We demonstrate a significant association between *C. sp900539255* and human clinical samples, while *Ca. C. infants* was widely detected across age groups but not associated with disease. Functional genomic analysis revealed distinct metabolic pathways between these two species detected in human gut microbiomes with potentially linked to pathogenicity and host adaptation. Importantly, we show that current metagenomic diagnostic pipelines can misidentify novel *Campylobacter* species, with implications for clinical surveillance and public health responses.

Implications of all the available evidence

This study, alongside existing evidence, highlights the considerable and underexplored diversity of *Campylobacter* species at human–animal interfaces, especially in regions with frequent wildlife–livestock–human contact. The discovery of novel taxa with zoonotic potential and their misclassification by current diagnostic tools underscores the urgent need to improve reference genome databases. Enhanced metagenomic surveillance across diverse populations and hosts is essential to strengthen diagnostic accuracy, guide public health responses, and monitor the emergence of previously unrecognised *Campylobacter* pathogens within a One Health framework.

In Africa, studies across several countries indicate that *Campylobacter* species are highly prevalent, particularly among children (Kaakoush et al., 2015). However, the presence of *Campylobacter*, even when the most common pathogenic species, *C. jejuni* and *C. coli*, are reportedly detected, is not

always associated with diarrhoea symptoms (Kaakoush et al., 2015; Platts-Mills et al., 2014). For instance, a study in Madagascar found a higher rate of *Campylobacter* in children without diarrhoea symptoms (Randremanana et al., 2014). These findings suggest that the bacterium is endemic in some African populations and can colonise the gut without always causing symptomatic disease (Bian et al., 2020). In 2020, a novel species was identified in the faecal microbial compositions of infants less than one year old (Bian et al., 2020). The same study stated that although *C. jejuni* and *C. coli* are prevalent among these infants, the second most abundant *Campylobacter* species was this new species, which they named *Candidatus Campylobacter infans* (Bian et al., 2020). Subsequently the detection of *Ca. C. infans* was not associated with diarrhoea symptoms in children under age of two in Peru (Garcia Bardales et al., 2022).

The majority of emerging infectious diseases in humans have animal origins, and the frequency of new infections transferring from wildlife and livestock to humans is expected to increase (Allen et al., 2017). However, *Campylobacter* research involving non-human primates (NHPs) remains limited. When investigated, *C. upsaliensis*, *C. jejuni*, and several novel *Campylobacter* species have been detected or isolated, some associated with disease in both captive (Clayton et al., 2019) and wild NHPs (Whittier et al., 2010). While an increase in *Campylobacter* detection in mountain gorillas in Uganda has suggested the possibility of anthroponotic transmission due to rising ecotourism in the region (Bosco Nizeyi et al., 2001), another study speculated that the high prevalence of *Campylobacter* spp. in gorilla faecal samples primarily reflects a previously uncharacterised, non-pathogenic component of their intestinal flora (Whittier et al., 2010).

Despite growing human encroachment into more natural habitats such as tropical forests and urban development in various countries in the world, our understanding of how associated environmental and socioeconomic changes influence pathogen transmission and emergence among urban wildlife, livestock, and human populations remains limited. In addition, given that zoonotic diseases are an increasingly concern, particularly in regions where humans, wildlife, and domestic animals share overlapping habitats and interact closely, our study aimed to investigate interspecies transmission of *Campylobacter* species by analysing its presence in faecal samples from habituated and unhabituated mountain gorillas, livestock, and humans living at a wildlife-livestock-human interface in Buhoma, Uganda. To better characterise *Campylobacter* transmission risk at densely connected human–animal interfaces in African contexts, we employed metagenomic sequencing to quantify microbial abundance, reconstruct MAGs, and infer evolutionary relationships, offering a high-resolution view of *Campylobacter* species diversity in underrepresented ecological settings.

6.1.3 Methods

6.1.3.1 Ethical and regulatory approvals

This study received ethical approval from the Massey University Human Ethics Committee (Southern A Application-14-44) and the Mbarara University of Science and Technology Research Ethics Committee (via Conservation Through Public Health [CTPH]).

6.1.3.2 Study area and sample collection

Fieldwork was conducted in and around Bwindi Impenetrable National Park (BINP), southwestern Uganda, a region of high biodiversity and zoonotic disease emergence risk due to close human-livestock-wildlife contact. BINP is home to approximately 43% of the world's remaining mountain gorillas (*Gorilla beringei beringei*). Communities surrounding the park engage in subsistence farming and livestock rearing adjacent to forest margins.

Between June and August 2018, CTPH and collaborators collected 553 faecal samples from six host groups near BINP: habituated mountain gorillas (N=100), wild (non-habituated) gorillas (N=100), cattle (N=83), goats (N=73), anonymous human patients from local health centres (N = 99), and community members (N=98; 81 male, 19 female; aged 19–70 years, median = 35 years) (Ethnicities: Bakiga (N=93), Banyankole (N=2), Basonga (N=1), Mukonzo (N=1), and Batwa (N=1)). Samples from habituated gorillas were obtained from night nests, with age category and individual identity recorded when possible. Non-habituated gorilla samples were collected during the 2018 population census. Livestock samples were obtained from local farms using convenience sampling. Clinical samples were from anonymous patients at healthcare facilities, while non-clinical samples were provided voluntarily by community members as part of a wider study described elsewhere (Muylaert, Davidson, Ngabirano, Kalema-Zikusoka, MacGregor, et al., 2021). The differential diagnosis for patients that provided stool samples at healthcare facilities was not available, but they are typically to diagnose the cause of gastrointestinal symptoms such as diarrhoea and abdominal pain.

Faecal samples were placed in RNAlater® (Sigma, MO, USA) and stored at –20°C. Samples from Uganda were imported to New Zealand under Ministry for Primary Industries permit 2018068860 and stored at the Hopkirk Research Institute, Massey University, in a PC2 containment facility until analysis.

6.1.3.3 DNA extraction and amplification

Approximately 150 mg of faeces was processed using the Zymo Quick-DNA™ Faecal/Soil Microbe Miniprep Kit (Zymo Research, CA, USA). For downstream sequencing, whole genome amplification was performed using the illustra™ GenomiPhi V3 DNA Amplification Kit (GE Healthcare). DNA quantity was measured with the Qubit® 2.0 Fluorometer using the dsDNA HS Qubit kit (ThermoFisher, MA, USA).

6.1.3.4 Genome sequencing

Two sequencing strategies were used: pooled and individual. Detailed metadata and yield information are provided in the data availability section.

Pooled sample sequencing: Samples were pooled by host type (e.g., 20 samples per gorilla or human pool), with final pool sizes ranging from 14 to 20. Sequencing was conducted at the Australian Genome Research Facility (AGRF, Melbourne, Australia) using the xGen™ cfDNA & FFPE DNA Library Preparation Kit on an Illumina® NovaSeq platform (2 × 150 bp). Demultiplexed reads yielded 31 paired-end FASTQ files, totalling ~900 Gb and ~3 billion reads.

Individual sample sequencing: A total of 553 DNA samples were sequenced at Orion Integrated Biosciences (Kansas, USA) using the Illumina® MiSeq platform with Nextera XT library preparation. RNAlater® procedural blanks were included as negative controls. Sequences were demultiplexed, trimmed (Q > 25, minimum length 50 bp), and quality-filtered in CLC Genomic Workbench (QIAGEN, Denmark). Host reads were removed using BBDMap (v. 38.95).

6.1.3.5 Bioinformatics pipeline

Reads were quality-checked (FastQC), adapter-trimmed (Trimmomatic), and filtered (Q ≥ 30, ≥ 80 bp). Host reads were reduced using BBDMap. MEGAHIT was used for metagenomic assembly. Bowtie2 and SAMtools were used for read mapping, sorting and file compression.

Assembled contigs >1 kb were binned using MetaBAT2, MaxBin, and CONCOCT, with bin refinement via DAS_Tool. Genome quality and general information was assessed using CheckM2. Genomes were dereplicated using dRep. Taxonomic assignment was conducted using GTDB-Tk. Phylogenetic trees were constructed using IQ-TREE 2 based on GTDB-Tk alignments of 120 single-copy core genes. Tree visualisation was performed using the iTOL platform.

Genome coverage and read-based mapping to assess abundances were performed using MetaBAT2, Bowtie2 and SAMtools. Gene prediction was carried out using Prodigal (v. 2.6.3) and genome annotation with DRAM and HMMER (Pfam). Average nucleotide identity comparisons were performed with FastANI. Seqkit was used to extract genome information. Genes conferring resistance to antibiotics and virulence genes were assessed using Abricate. Comparative alignments to the *Campylobacter jejuni* reference genome (GCA_000009085.1) were conducted using MUMmer.

For a second taxonomic classification, abundance strategy and microbial composition analysis, Kraken 2 (standard database 12/2024) and Bracken were used. Statistical analyses were conducted in RStudio (v. 2025.05.0+496), including ANOVA and Tukey's HSD. A logistic regression model assessed the association between host age and *Ca. C. infans* detection.

6.1.4 Results

6.1.4.1 Study location, host populations, and sampling overview

This study analysed 553 faecal samples collected from mountain gorillas, livestock, and humans in BINP and the adjacent Buhoma community, Uganda, to assess *Campylobacter* presence, prevalence and potential interspecies transmission. Samples included habituated (n=100) and non-habituated (n=100) gorillas; 83 cattle and 73 goats (total livestock n=156); and 197 humans, categorised as clinical (n=99) or non-clinical (n=98). Seven non-clinical participants reported diarrhoea symptoms. Two sequencing approaches—individual and pooled—were used at different stages of the study.

6.1.4.2 Diversity and phylogenetic structure of *Campylobacter* in host gut microbiomes

A total of 44 *Campylobacter* MAGs were reconstructed: 19 from gorilla, 17 from human, two from cattle, and six from goat faecal samples. *Campylobacter* MAGs from gorilla gut microbiomes revealed three species that could not be assigned to known species with GTDB-Tk, indicating the potential presence of novel *Campylobacter* taxa. In contrast, *Ca. C. infans* and *C. sp900539255* were identified in human, *C. sp017646085* in cattle, and *C. vicugnae* in goat gut microbiomes. Subsequently, 23 dereplicated *Campylobacter* MAGs were retained for genomic and phylogenetic analyses: thirteen from human, four from gorilla, five from goat, and one from cattle gut microbiomes. For comparative purposes, genomes of *Campylobacter* species along with *Helicobacter pylori* (outgroup) were downloaded from the GTDB, classified, aligned with a MAG assembled for each *Campylobacter* species identified in this study, and analysed phylogenetically (figure 6.1).

Figure 6.1: Phylogenomics and characteristics of *Campylobacter* genomes

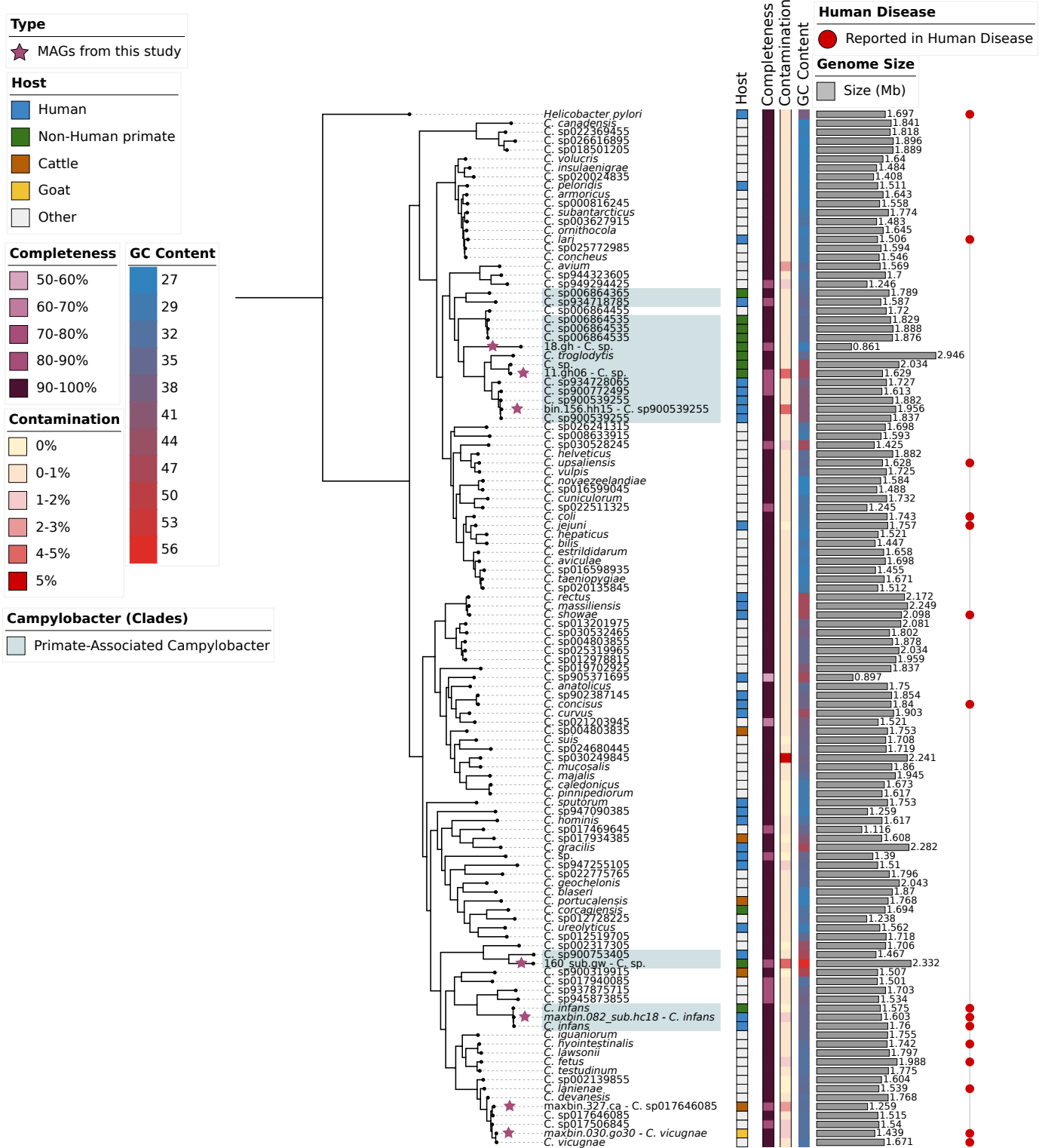


Figure 6.1 Phylogenomic relationships and general characteristics of study-derived and publicly available *Campylobacter* genomes

The resulting phylogenetic tree depicts the placement of *Campylobacter* MAGs from seven species assembled in this study (indicated by stars) and their relationships to publicly available *Campylobacter* genomes, including both described and undescribed species. The phylogenetic tree was constructed from a concatenated alignment of 120 bacterial marker genes generated by GTDB-Tk (v2.4). Sequence alignment and core gene concatenation followed the standard GTDB-Tk pipeline. Phylogenetic inference was performed with IQ-TREE2 under standard parameters, including model selection using the ModelFinder algorithm to determine the best-fitting substitution model. The resulting tree was visualised using iTOL

(Interactive Tree of Life). Highlighted clades include *Campylobacter* species from human and NHP gut microbiomes that cluster together, suggesting host-specific adaptation and shared evolutionary trajectories among primates. Genome completeness, contamination, and estimated size were assessed using CheckM2, which employs artificial neural networks and gradient boosting.

Phylogenetic inference based on MAGs assembled here and public *Campylobacter* genomes supported the species classifications of our MAGs (figure 6.1). Distinct clades include MAGs (indicated by stars) assigned to three putative novel species: two gorilla-derived (lacking species-level assignment) and one human-derived (*C. sp900539255*). These novel species cluster within a clade containing three other putative novel human-associated species, comprising four novel human-associated species: *C. sp934718785*, *C. sp934728065*, *C. sp900772495*, and *C. sp900539255* (identified here). This clade also encompasses described NHP-associated species (e.g., *C. troglodytis*) and includes public genomes classified as *C. sp006864535* and *C. sp0068664365*, derived from NHP hosts. Separately, the *Ca. C. infans* MAG derived from a human gut microbiome in this study clustered with publicly available *Ca. C. infans* genomes from other human and gorilla sources (figure 6.1). Livestock-derived MAGs clustered phylogenetically with *C. vicugnae* (goat-derived MAG) and *C. sp017646085* (cattle-derived MAG). This livestock-associated clade was positioned in close phylogenetic proximity to species previously linked to human disease, *C. vicugnae* and *C. lanienae* (figure 6.1). Average nucleotide identity (ANI) values among *Ca. C. infans* genomes from both human and NHP hosts supported their close genomic relatedness. In contrast, ANI values for other *Campylobacter* species from primates varied between human and NHP sources. The species identified in livestock gut microbiomes exhibited ANI values consistent with their phylogenetic clustering within a clade comprising *C. sp017506845*, *C. sp017646085* (identified here), *C. vicugnae*, and *C. lanienae* (Supplementary figure 6.7).

6.1.4.3 Coverage assessment of dereplicated MAGs

To assess *Campylobacter* species abundances and genome coverage across the dataset, sequencing reads from the pooled samples were mapped against the concatenated MAGs and their coverage was evaluated. Livestock samples consistently contributed to the *Campylobacter* species MAGs assembled from livestock gut microbiomes. Similarly, gorilla gut microbiomes, including those from both habituated and non-habituated groups, contributed equally to the formation of the three putative novel *Campylobacter* species MAGs. Samples derived from non-clinical and clinical human groups contributed to the assembly of both *Ca. C. infans* and *C. sp900539255* MAGs. However, a distinct pattern of differential contribution was observed: non-clinical samples predominantly contributed to the *Ca. C. infans* MAGs, whereas clinical samples showed a greater contribution to the *C. sp900539255* MAGs (figure 6.2).

Figure 6.2: Coverage of *Campylobacter* MAGs

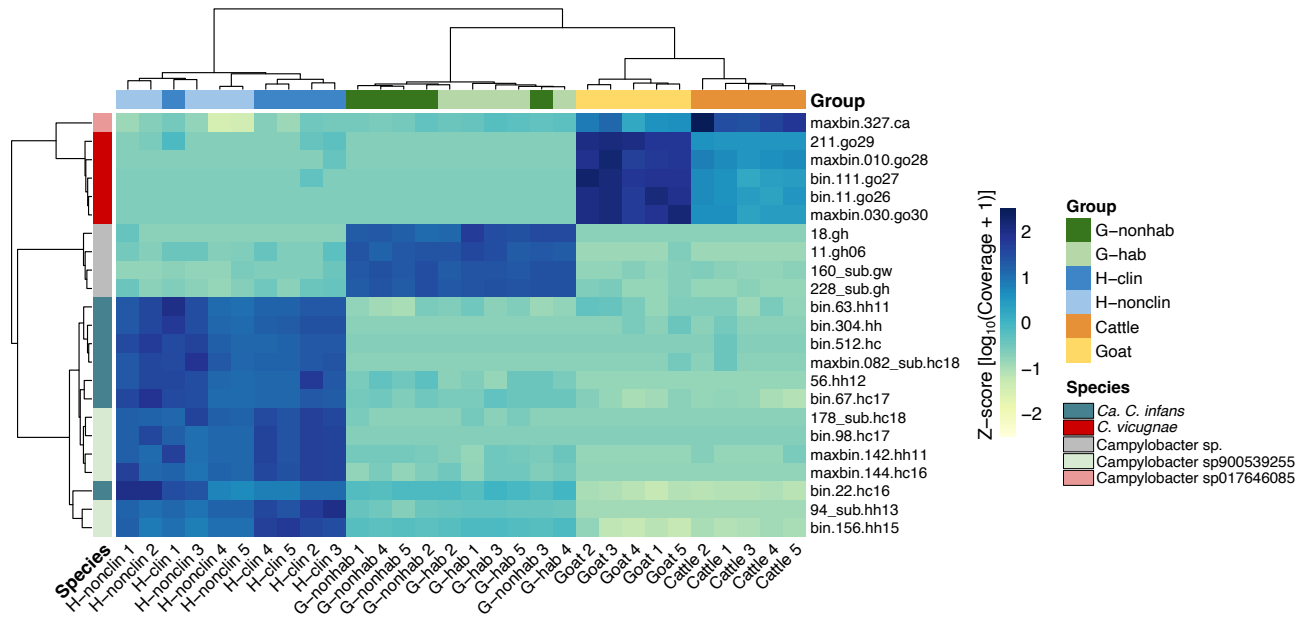


Figure 6.2 Coverage heatmap of *Campylobacter* MAGs across host-associated samples

The heatmap illustrates the coverage of each *Campylobacter* MAG across samples, indicating the host species gut microbiomes from which the MAGs were assembled. To account for sequencing depth variability, coverage values were normalised per MAG based on the average read depth across all samples. Values were subsequently log-transformed ($\log_{10}[x + 1]$) and scaled using z-scores to highlight relative abundance differences. MAG identifiers indicate the sample group of origin: gw (G-nonhab), gh (G-hab), hh (H-clin), hc (H-nonclin), ca (Cattle), and go (Goat).

6.1.4.4 Clinical relevance of *Campylobacter* species in the human gut microbiome

To further investigate the association of *Campylobacter* species assembled from human gut microbiomes with disease, individual sequencing reads were mapped using two distinct strategies. First, reads were mapped against the single best-quality MAG for each *Campylobacter* species (figure 6.3 a,b). Second, reads were mapped against a concatenated reference comprising all dereplicated MAGs for each respective species (figure 6.3 c,d).

Read alignments to *C. sp900539255* were significantly higher in clinical samples compared to non-clinical samples, whether mapping was performed against the highest-quality MAG ($p=0.001$) or a concatenated of dereplicated MAGs reference ($p=0.007$) (figure 6.3a,c). In contrast, normalised read alignments to *Ca. C. infans* were similarly distributed across clinical and non-clinical samples ($p=0.052$, and $p=0.14$) (figure 6.3b,d). Notably, a distinct non-clinical sample (highlighted in red), derived from an individual reporting severe diarrhoea, exhibited co-occurrence of both *Ca. C. infans* and *C. sp900539255* (figure 6.3). Using a normalised threshold of 100 aligned reads, co-occurrence was detected in 7 clinical and 4 non-clinical individuals with best-quality MAGs, increasing to 21 and 16, respectively, with concatenated dereplicated MAGs.

Figure 6.3: Mapping metagenomic reads to *Campylobacter* MAGs in human samples

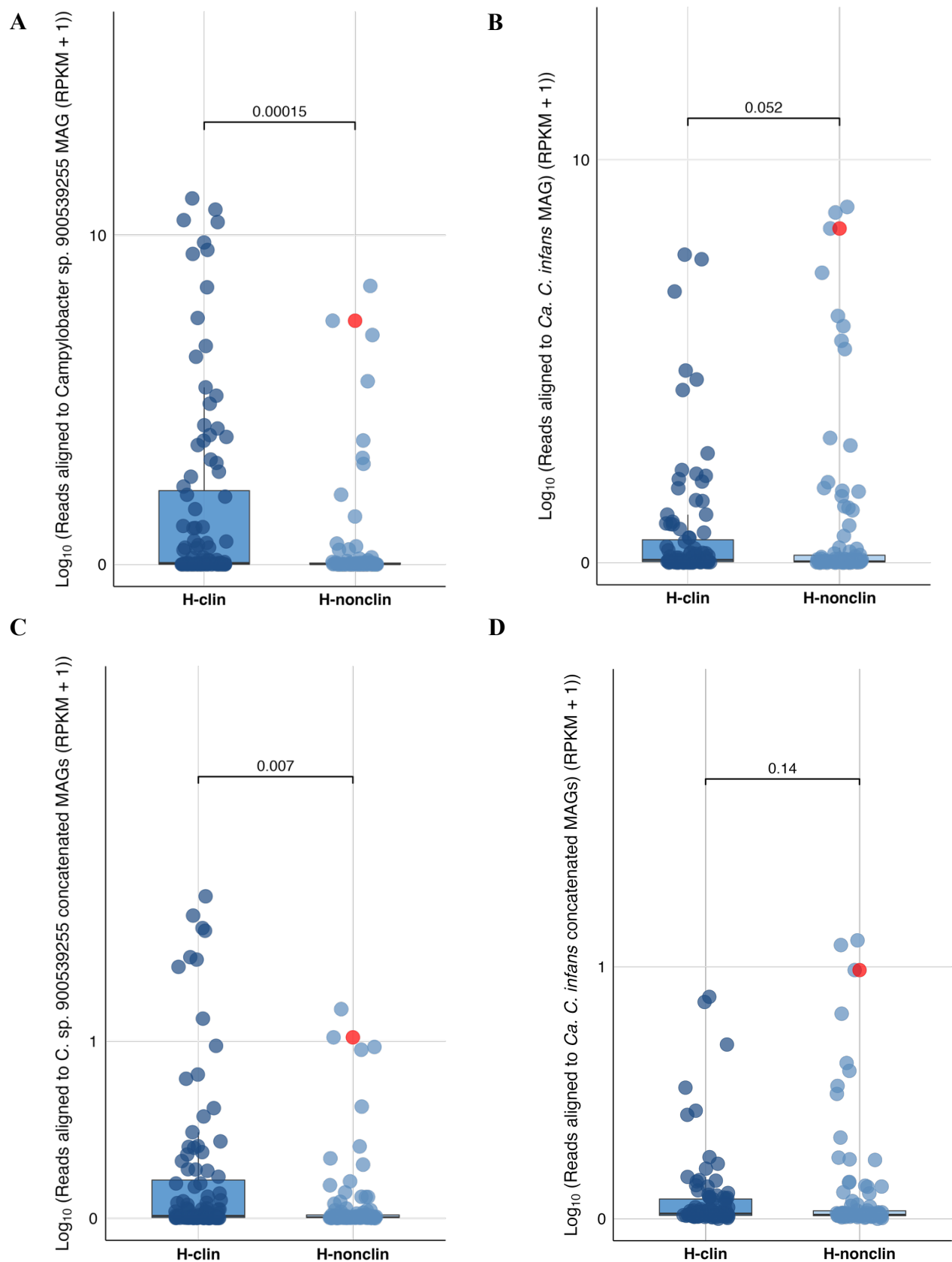


Figure 6.3 Mapping of metagenomic reads to *Campylobacter* MAGs across human clinical and non-clinical samples

Campylobacter abundance differences between clinical and non-clinical human gut microbiomes. Reads Per Kilobase per Million (RPKM) values were calculated for each sample, normalised for sequencing library size and MAG genome length. All RPKM values were $\log_{10}(x+1)$ -transformed (pseudo-

count = 1) for visualisation. **A)** *C. sp900539255* abundance mapped to highest-quality MAG. **B)** *Ca. C. infans* abundance mapped to highest-quality MAG. **C)** *C. sp900539255* abundance mapped to concatenated dereplicated MAGs. **D)** *Ca. C. infans* abundance mapped to concatenated dereplicated MAGs. Red points highlight sample ug347 (non-clinical donor reporting severe diarrhoea). Statistical comparisons by Wilcoxon rank-sum test.

6.1.4.5 Functional genomic divergence of human-associated *Campylobacter* species

To investigate genomic factors underlying the association of *C. sp900539255* with human disease and the absence of such association in *Ca. C. infans*, we performed comparative proteomic and metabolic profiling of dereplicated MAGs and publicly available genomes for both species. Sulfur metabolism via thiosulfate oxidation to sulfite was present in 17/18 *C. sp900539255* genomes but absent in all *Ca. C. infans* genomes ($p < 0.0001$). Similarly, a nitrogen metabolism pathway (nitrous oxide reduction to N_2) was detected in 16 *C. sp900539255* genomes and undetected in *Ca. C. infans* ($p < 0.0001$). In contrast, polyphenolic degradation functions were identified in 11/21 *Ca. C. infans* genomes but were completely absent from *C. sp900539255* ($p < 0.00023$) (figure 6.4a). In addition, an investigation into the presence of general virulence-associated Pfam domains across both human-associated *Campylobacter* species revealed that the majority of genomes encoded these domains, with no significant differences observed between *Ca. C. infans* and *C. sp900539255* (figure 6.4b). However, analysis of specific functional elements, particularly individual glycoside hydrolase (GH) families, highlighted distinct patterns. The GH73 normalised hits was significantly higher in *C. sp900539255* compared to *Ca. C. infans* ($p < 0.0001$) (figure 6.4c). Conversely, GH23 hits showed no statistically significant difference ($p = 0.626$) between the two species. This last it seems to be a peculiar GH family for almost all other *Campylobacter* species analysed (Supplementary figure 6.8).

Figure 6.4: Metabolic functions of *Campylobacter* species from human samples

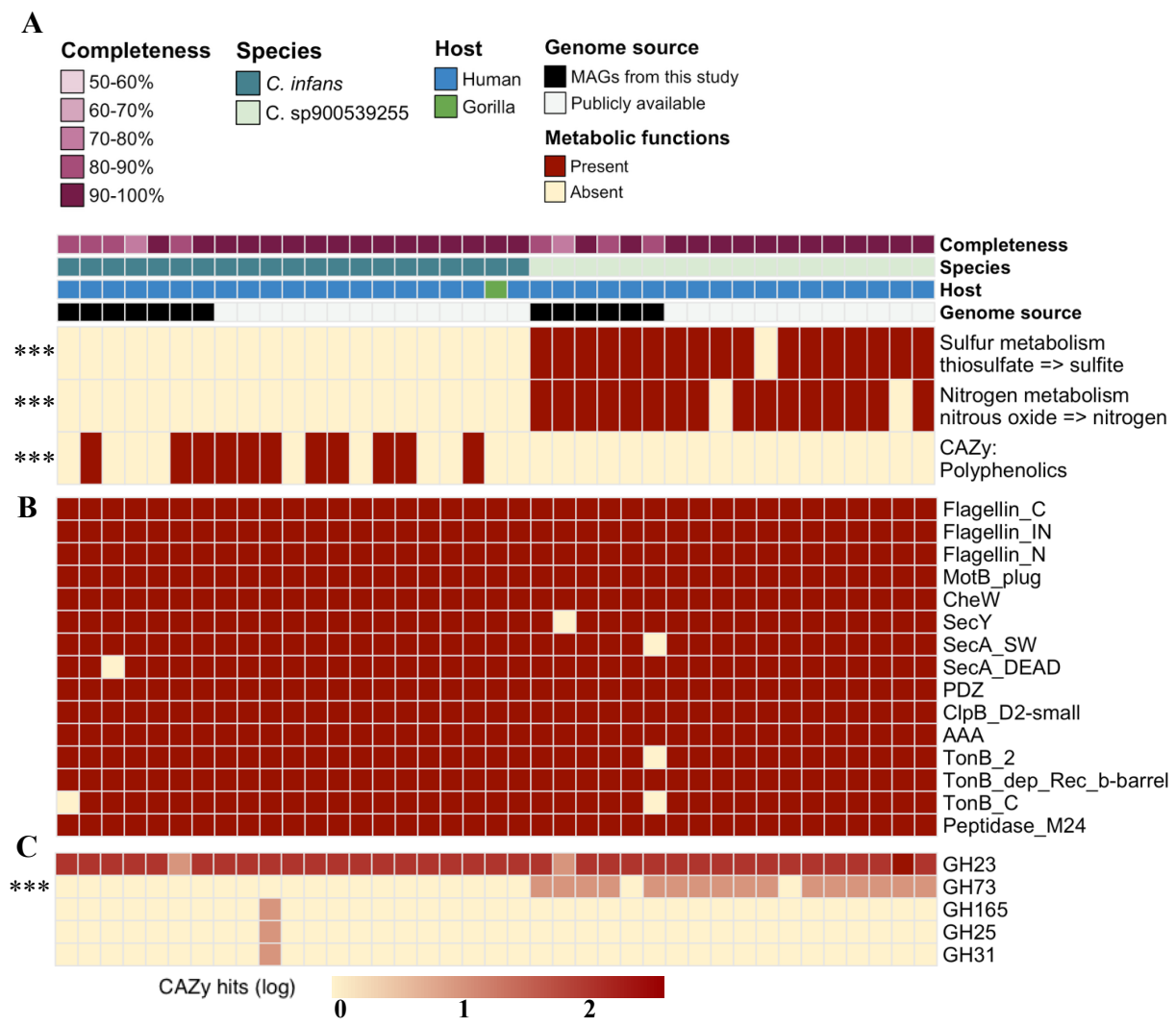


Figure 6.4 Genomic factors contributing to differential human disease association of *C. sp900539255* and *Ca. C. infans*

Heatmaps illustrate the distribution of predicted functions across *Ca. C. infans* and *C. sp900539255* genomes. Columns represent individual genomes, ordered by species and genome source. **A)** Metabolic pathway presence/absence predicted by DRAM. **B)** Presence/absence of selected virulence-associated Pfam domains. **C)** Log-transformed abundance of GH families (CAZy). Cell colours for **(A)** and **(B)** indicate presence (dark red) or absence (light yellow); for **(C)**, they represent log-transformed counts from low (light yellow) to high (dark red).

6.1.4.6 Read-based metagenomic profiling of *Campylobacter* species abundance and prevalence

An independent read-based metagenomic analysis (Kraken2 v2.1.3; Standard_12_2024 database), performed without an abundance threshold, offered an alternative view of *Campylobacter* presence in human gut microbiomes. *Ca. C. infans* and *C. jejuni* were the dominant species, while *C. coli* appeared at lower prevalence in only a few individuals (Supplementary figure 6.9a). No statistically significant differences were observed in *Campylobacter* abundance ($p=0.817$) or species prevalence between clinical and non-clinical samples (Supplementary figure 6.9a) (Supplementary table 1). *C. jejuni* was detected in 47.5% (47/99) of clinical and 58.8% (57/97) of non-clinical samples ($p=0.12$;

OR = 0.64, 95% CI: 0.36–1.14). For *Ca. C. infans*, detection was 41.4% in clinical and 33.0% in non-clinical samples (OR = 1.43, 95% CI: 0.77–2.68); however, neither association was statistically significant. A similar pattern was observed across other host gut microbiomes, with *C. jejuni* detected in numerous individual samples, leading to all pooled samples testing positive for the species (Supplementary figure 6.9b). To explore this widespread detection, MAGs from this study were aligned against a *C. jejuni* reference genome. Alignment lengths ranged from 823 to 15,563 base pairs, with average identity between 80.8% and 95.2% (Supplementary table 2), suggesting that *C. jejuni* hits may have originated from genetically similar, but distinct, novel species absent from the reference database.

Among the 156 livestock samples (83 cattle, 73 goats), *Campylobacter* abundance was significantly higher in goats ($p < 0.001$). Nine *Campylobacter* species were detected, with *C. devanensis*, *C. lanienae*, *C. porcelli*, and *C. vicugnae* being the dominant *Campylobacter* species in the gut microbiome of cattle and goats (Supplementary table 3). Focusing on these four dominant species in livestock-positive faecal samples, microbial profiling revealed host-specific colonisation patterns. *C. vicugnae* was predominantly associated with goats, whereas in cattle, it comprised nearly 50% of the *Campylobacter* community and frequently co-occurred with *C. devanensis* in positive samples (figure 6.5a). While *C. devanensis* and *C. vicugnae* were detected in cattle gut microbiomes, the corresponding MAGs were classified as *C. sp.* 017646085, indicating that this potentially novel species harbours genomic regions shared with both taxa.

Figure 6.5 *Campylobacter* species detected in livestock samples

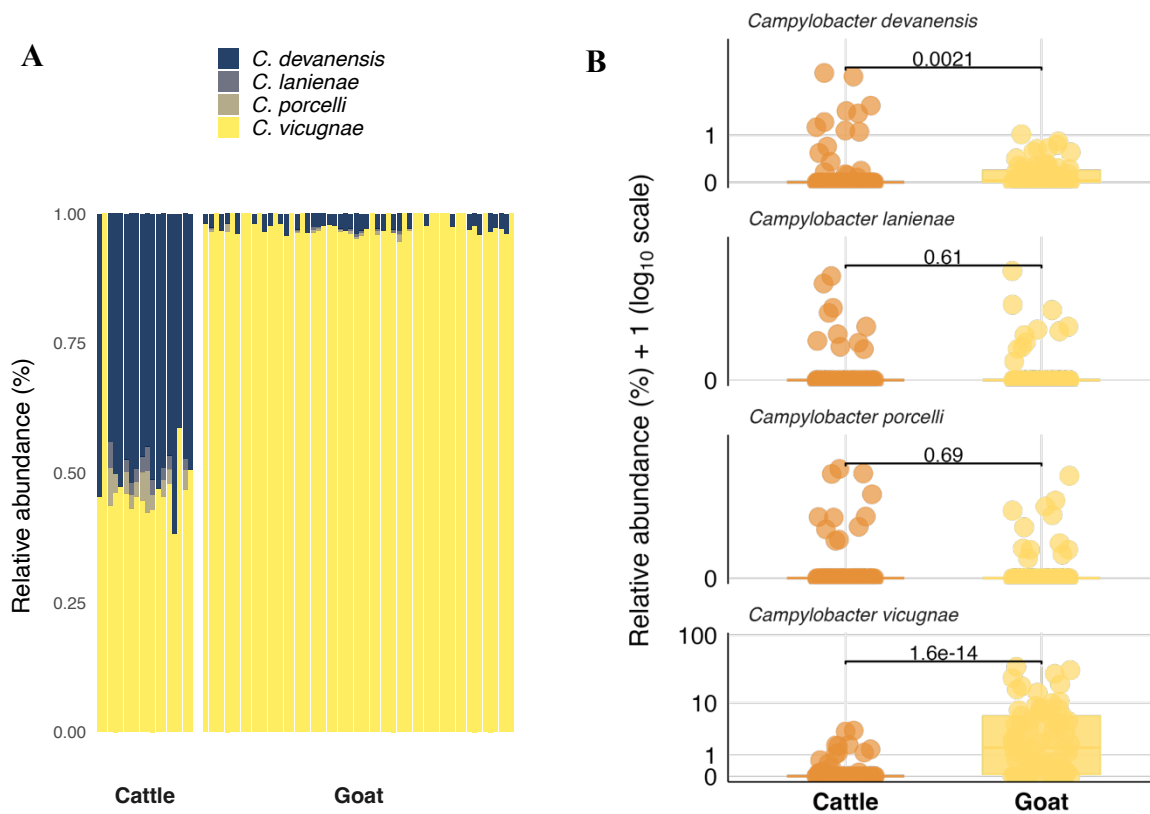


Figure 6.5 *Campylobacter* species abundances comparisons in livestock gut microbiomes

A) Dominant *Campylobacter* community in livestock samples show different pattern between cattle and goats. B) *C. lanienae* and *C. porcelli* show similar distribution patterns in both cattle and goats. In contrast, *C. vicugnae* is significantly more common and occurs at higher levels in goats (Fisher's exact test and Wilcoxon $W=2295.5$, $p<0.001$), while *C. devanensis* is more frequently detected and more abundant in cattle (Fisher's exact test and Wilcoxon $W=1018.5$, $p=0.002$; $p<0.001$, respectively).

6.1.4.7 Prevalence and abundance of *Ca. C. infants* in humans across different age groups

Age data were recorded for individuals providing faecal samples at healthcare facilities and for donors of non-clinical samples group. Of the 192 samples analysed with age registers, 73 contained detectable relative abundances of *Ca. C. infants* (Supplementary table 1). Logistic regression indicated no significant association between age and the presence of *Ca. C. infants* ($p=0.324$) (figure 6.6a). Notably, however, the samples with the highest *Ca. C. infants* levels originated from individuals aged over 30 years (figure 6.6b). Linear regression analysis revealed that age was a significant predictor of relative abundance among positive cases ($\beta=0.071$, $SE=0.016$, $t=4.38$, $p<0.001$), indicating that relative abundance increased with age (figure 6.6b). Outliers (in red) had some influence, but the relationship remained significant after their removal ($p<0.01$).

Figure 6.6: Prevalence of *Ca. C. infants* by age group

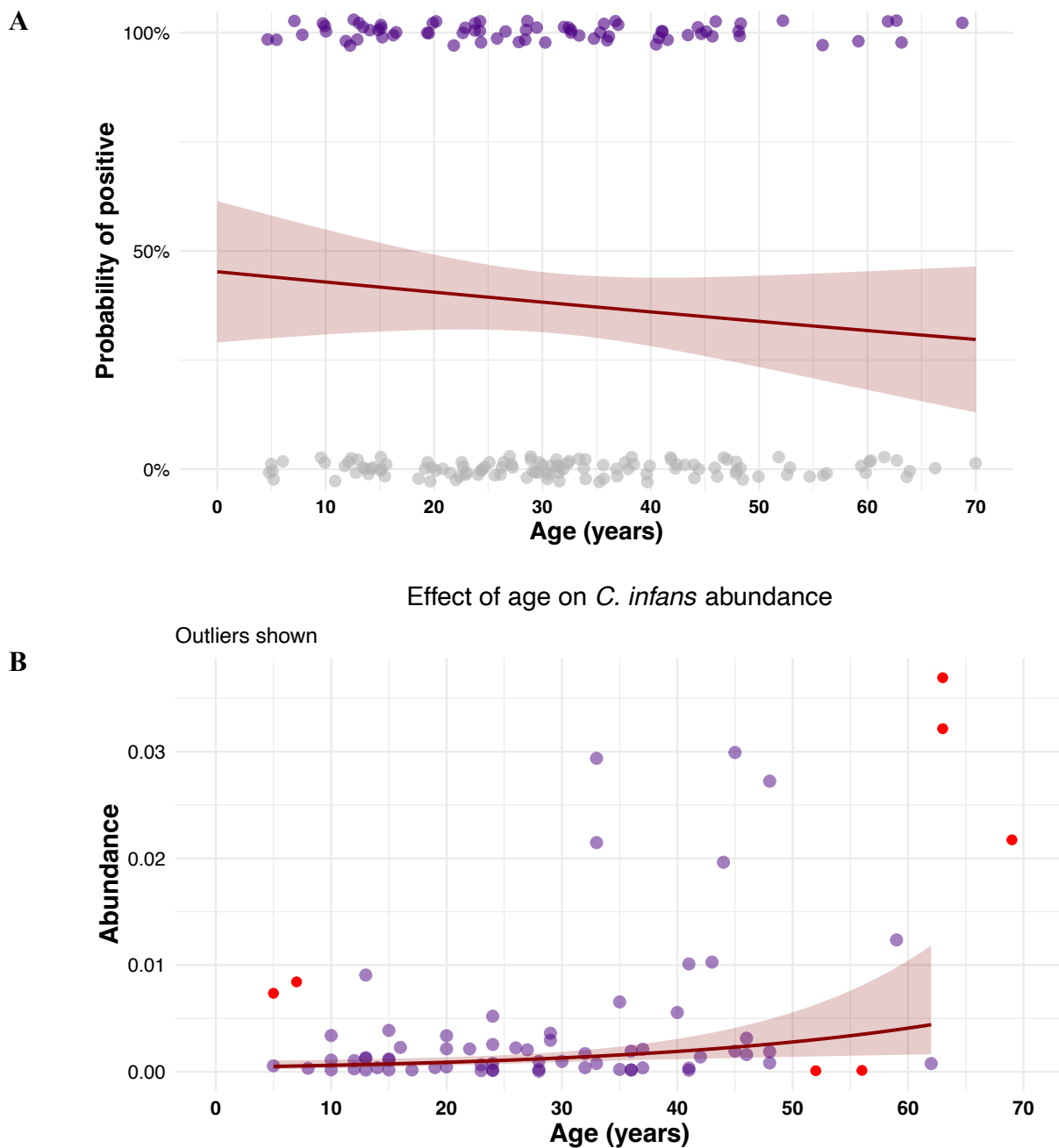


Figure 6.6 Age-stratified detection of *Ca. C. infants* in human gut microbiomes

A) *Ca. C. infants* was detected across a wide age range, with individuals over 30 years exhibiting the highest abundance. Although prevalence declined with age, no significant association was found between age and *Ca. C. infants* presence. **B)** Among positive cases, age significantly predicted relative abundance of *Ca. C. infants*, which increased with age. This association remained significant after excluding outliers (red dots) ($p < 0.01$).

6.1.4.8 Antimicrobial resistance and virulence genes detected in the *Campylobacter* MAGs

The β -lactam resistance genes *bla*_{OXA-471_1} and *bla*_{OXA-489_1} was detected in *Ca. C. infants* MAGs. The virulence gene *cheY* (chemotaxis regulatory protein) was identified in *Ca. C. infants* and *C. vicugnae* MAGs, while *fliM* (flagellar motor switch protein) was found in *C. sp900539255* MAGs from human gut microbiomes. These genes showed alignment coverage of 83.7–91.6% and sequence identities of

80.1–81.6%. To contextualise these findings, genomes closely related to *Ca. C. infans*, *C. sp900539255*, and *C. vicugnae* were retrieved from the GTDB and screened for antimicrobial resistance and virulence genes. Among fourteen *Ca. C. infans* genomes, six carried *bla*_{OXA-471_1}, two *bla*_{OXA-193_1}, and one *tet*(*W*)₅, which confers tetracycline resistance; all harboured *cheY*. None of the twelve *C. sp900539255* genomes encoded resistance genes, although one carried the virulence gene *fliN*. Similarly, none of the 21 *C. vicugnae* genomes encoded resistance genes, and all but one carried *cheY*.

6.1.5 Discussion

Campylobacter species are a leading cause of human bacterial gastroenteritis and diarrhoeal diseases worldwide (Burnham & Hendrixson, 2018; Kaakoush et al., 2015). In Uganda, diarrhoea remains a major cause of mortality among children under five, responsible for over 140,000 deaths annually and accounting for 7.1% of all under-five mortality (Nantege et al., 2022). While *Campylobacter* species are widespread across Africa, particularly among children, the presence of *C. jejuni* and/or *C. coli* does not always correlate with diarrhoeal symptoms, suggesting a complex interplay between carriage and disease (Kaakoush et al., 2015; J. Mason et al., 2013; Platts-Mills et al., 2014; Rendremanana et al., 2014). In this study, comparative analysis of clinical and non-clinical human faecal samples revealed no statistically significant differences in overall *Campylobacter* prevalence or abundance, indicating a limited role for overall *Campylobacter* load in symptomatic infection within this setting. However, *C. sp900539255* was significantly enriched in clinical samples, whereas *Ca. C. infans* was widespread and not associated with illness, strongly supporting their divergent ecological and pathogenic roles. Traditionally, human *Campylobacter* infections have been attributed to livestock sources (Burnham & Hendrixson, 2018). However, our phylogenetic analyses revealed that the *Campylobacter* species identified in the gut microbiome of humans living in a wildlife–livestock–human interface were more closely related to those from NHPs than to livestock. These findings underscore the potential importance of understanding human–wildlife microbial exchange and highlight complex ecological connections that may influence microorganisms transmission.

Strikingly, read-based taxonomic approaches detected *C. jejuni* more frequently in non-clinical samples (58.8%) than in clinical ones (47.5%), despite no *C. jejuni* or *C. coli* MAGs being recovered from any sample. These findings raise important questions regarding the reliability of read-based *Campylobacter* classifications in metagenomic studies, particularly in settings where novel *Campylobacter* species might be present. This discrepancy likely arises from the reliance on short k-mer sequences, which may be conserved across related taxa, leading to misclassification of novel or unrepresented species as *C. jejuni* or *C. coli*. Direct evidence from MAG alignments to the *C. jejuni*

reference genome supported this, as multiple MAGs (e.g., *Ca. C. infans*, *C. sp900539255*, *C. vicugnae*) showed partial sequence similarity and encoded *C. jejuni*-annotated virulence genes such as *cheY* and *fliM*. These genes shared 83·7–91·6% coverage and 80·1–81·6% identity with known *C. jejuni* genes, underscoring the considerable potential for false positives when using short-read classification tools without genome-resolved validation.

Comparative functional analysis revealed important differences between *C. sp900539255* and *Ca. C. infans*. These included the presence of sulfur and nitrogen metabolic pathways in the former, and polyphenolic degradation pathways in the latter. These distinctions may help explain the observed association of *C. sp900539255* with clinical disease, as these pathways may confer adaptive advantages for colonisation, persistence, or energy acquisition within the host gut, particularly under anaerobic or specific nutrient conditions relevant to infection (Kies & Hammer, 2022; Lensmire & Hammer, 2019). In addition, GH73 enzymes, which aid in nutrient acquisition from host glycans or mucins, were significantly more abundant in *C. sp900539255* genomes, potentially facilitating host tissue degradation or colonisation (Lipski et al., 2014). Conversely, *Ca. C. infans*, exhibited polyphenolic degradation functions, suggesting adaptation to plant-rich environments or a more generalist, commensal gut lifestyle (Rodríguez-Daza et al., 2021). Furthermore, *Ca. C. infans* was detected across all age groups, and its relative abundance increased with age among positive cases, suggesting possible long-term colonisation or age-related shifts in microbiota composition. Together, these genomic differences support the epidemiological patterns and offer functional insights into host adaptation and pathogenic potential.

Antimicrobial resistance (AMR) genes were identified in *Ca. C. infans* MAGs, including *bla_{OXA-471}_1* and *bla_{OXA-489}_1*, while *C. sp900539255* MAGs carried no AMR genes but did include virulence-associated genes such as *fliM*. Among livestock-associated MAGs, *C. vicugnae* carried *cheY*, consistent with public reference genomes, though AMR genes were largely absent. The presence of β -lactam resistance genes in *Ca. C. infans* highlights the potential for under-recognised resistance reservoirs even in species not currently linked to disease.

Collectively, these findings highlight the critical need for cautious interpretation of diagnostic and metagenomic results using read-based approaches, especially in underrepresented regions of the world and populations. They support expanding reference genome databases and adopting genome-resolved approaches to improve pathogen detection, characterisation of virulence and AMR profiles, and diagnostic accuracy for *Campylobacter* and other enteric bacteria in Africa.

6.1.6 Data availability

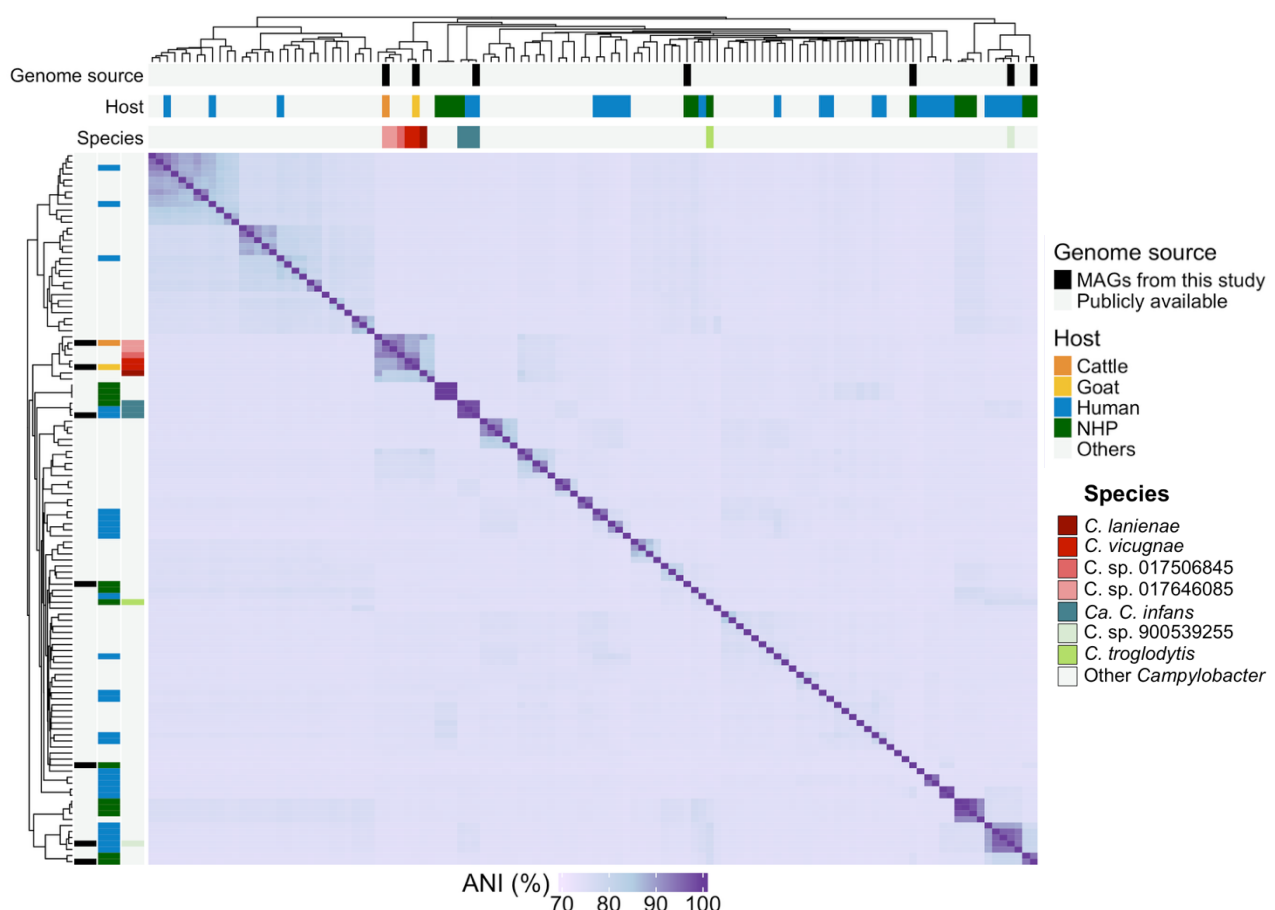
The sequencing data generated in this study have been deposited in the NCBI Sequence Read Archive (SRA) under the BioProject accession code PRJNA1213876.

6.1.7 Code availability

The code, scripts, and software details are comprehensively documented and shared in the 'Uganda-cross-species-transmission' repository on GitHub link: (ValterAlmeida).

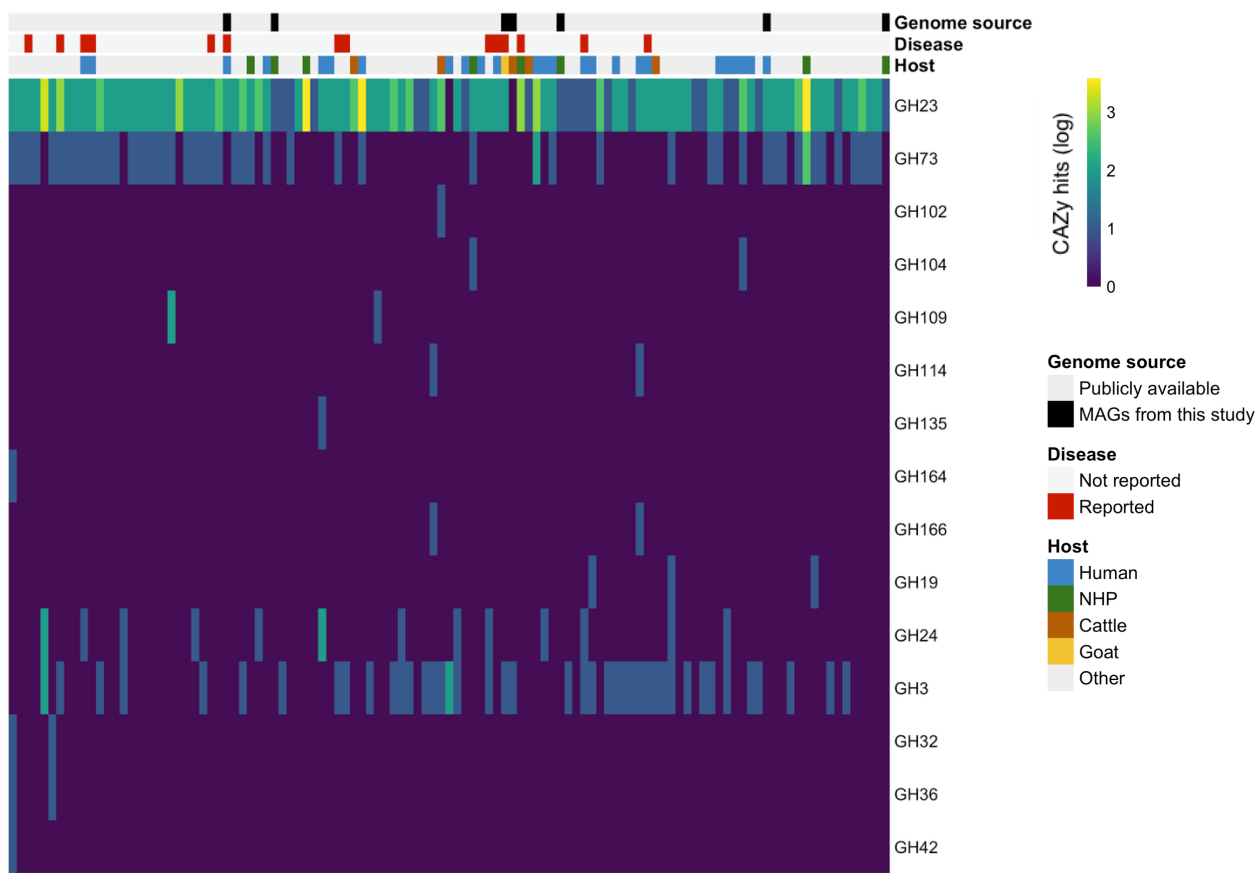
6.1.8 Supplementary information

Supplementary Fig 6.7: Average nucleotide identity (ANI) heatmap showing genome-wide similarities among *Campylobacter* species



Ca. C. infans genomes from human and gorilla hosts showed high ANI values, suggesting cross-species transmission or shared evolutionary history. Other primate-derived *Campylobacter* species showed more variable ANI values across hosts. The livestock-associated species also exhibited genomic similarity to *Campylobacter* taxa previously associated with human disease.

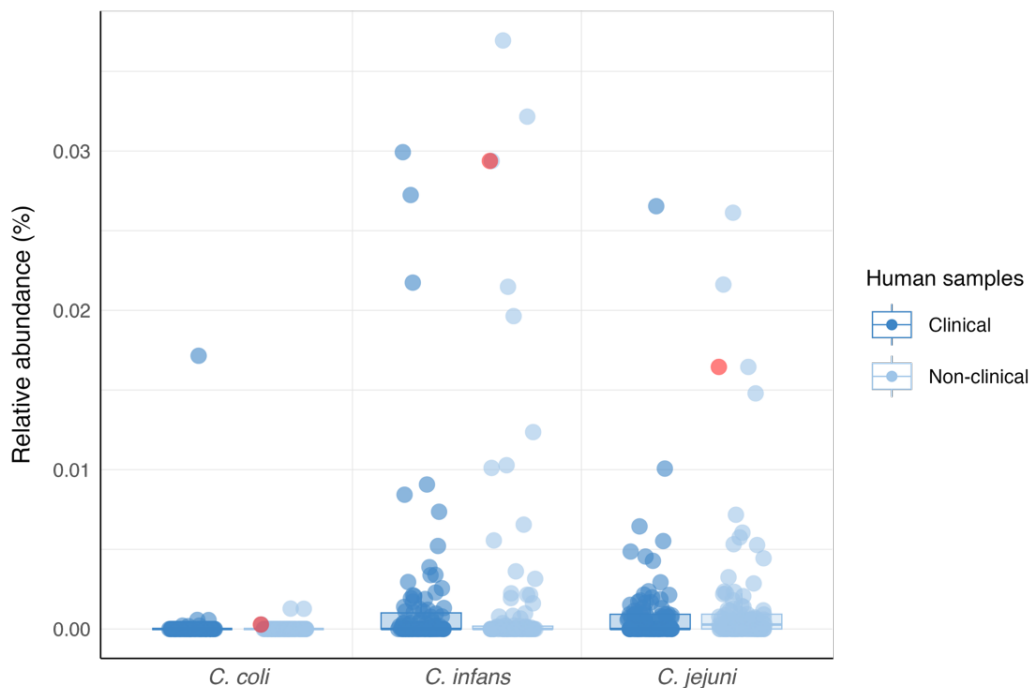
Supplementary Fig 6.8: Functional diversity of glycoside hydrolase families across *Campylobacter* genomes



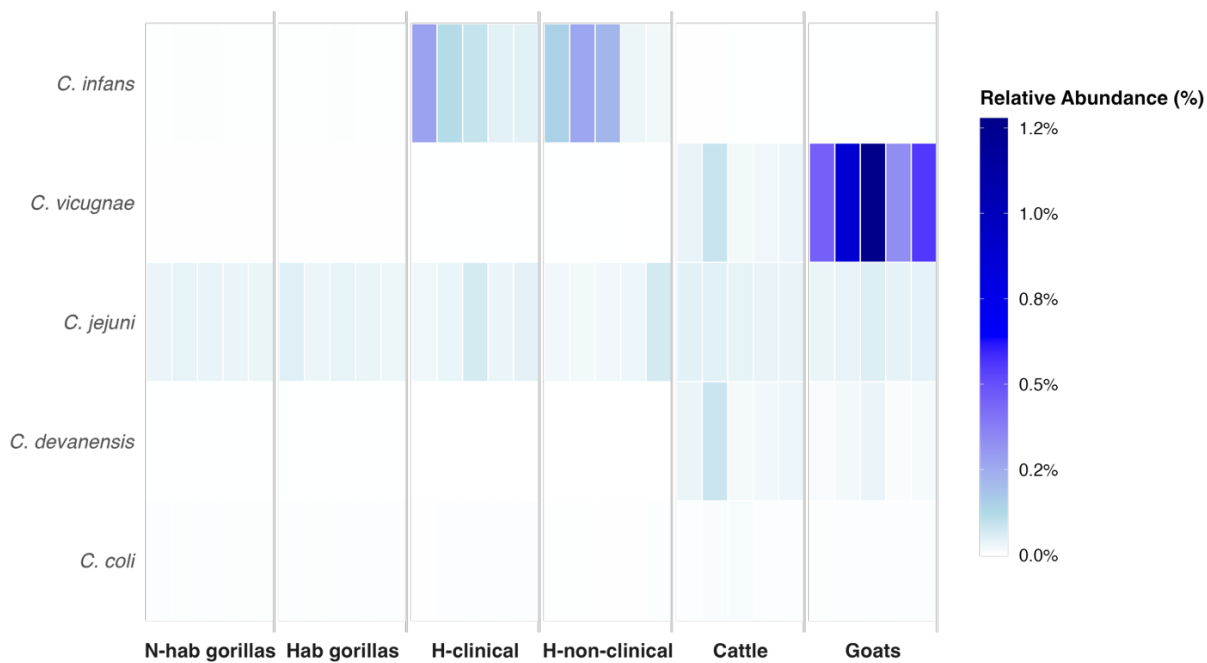
Heatmap showing the presence and absence of GH families across *Campylobacter* MAGs assembled in this study and publicly available genomes. Three GH families (GH23, GH73, and GH3) were present in MAGs, indicating conserved capacity for lysozyme-mediated peptidoglycan degradation (GH23), peptidoglycan hydrolysis (GH73), and broad-specificity β -glucosidase activity (GH3). A total of fifteen GH families were identified across all genomes, reflecting functional diversity in CAZy profiles within the genus.

Supplementary Fig 6.9: Metagenomics diagnosis based on additional read-based analysis strategy human individual samples

A



B



A) Read-based metagenomic analysis (e.g., Kraken2) revealed a different *Campylobacter* species distribution pattern in human samples compared to the MAG-based classification strategy. Specifically, this analysis identified *C. jejuni* as one of the predominant *Campylobacter* species in human gut microbiomes. Notably, the highlighted sample, which showed high abundance of *C. sp900539255* in the MAG-based analysis, exhibited a similarly high proportion of *C. jejuni* in the read-based analysis. This suggests that reads originating from *C. sp900539255* may have been erroneously assigned to *C. jejuni* by the read-based software due to the likely absence of this novel species from its database. **B)** The panel

highlights species for which MAGs were successfully recovered in this study. It also illustrates the detectable presence of *C. jejuni* across samples, despite no corresponding MAG for *C. jejuni* being assembled during this study.

Supplementary Table 6.1 - Prevalence and associations of *Campylobacter* species between human clinical and non-clinical samples

Species	Clinical		Non-clinical		p-value	OR (95% CI)
	Positive	Prevalence	Positive	Prevalence		
<i>C. coli</i>	06/99	6.1%	03/97	3.1%	0.50	2.01 (0.42-12.81)
<i>C. jejuni</i>	47/99	47.5%	57/97	58.8%	0.12	0.64 (0.35-1.16)
<i>C. infans</i>	41/99	41.4%	32/97	33.0%	0.24	1.43 (0.77-2.68)

Statistical tests: Two-sided Fisher's exact tests compared prevalence between groups, with odds ratios (OR) and 95% confidence intervals (CI) as effect measures.

Supplementary Table 6.2 - Alignment of MAGs to *C. jejuni* reference genome

Host	MAG species	Aligned to <i>C. jejuni</i> (bp)	Average identity (%)	Genes with sequence alignments
Human	<i>C. infans</i>	7,227	85.5	<i>tuf</i> , <i>dsbI</i> , <i>dba</i> , <i>nifJ</i> , <i>tRNA</i> (Leu, Arg, His, Pro)
	<i>C. sp. 900539255</i>	2,310	83.3	<i>tuf</i> , <i>tRNA</i> (Thr, Tyr, Gly, Leu, Met)
Gorilla	<i>Campylobacter sp. 1</i>	823	95.2	<i>rRNA</i> -5S, <i>tRNA</i> (Ser, Arg, Thr)
	<i>Campylobacter sp. 2</i>	1,374	85.5	<i>tuf</i> , <i>tRNA</i> (Thr, Leu, Lys, Asp)
	<i>Campylobacter sp. 3</i>	11,782	80.8	<i>ribE</i> , <i>kdsA</i> , <i>napA</i> , <i>gatA</i> , <i>accD</i> , <i>dnaK</i> , <i>tuf</i> , <i>rpmG</i> , <i>secE</i> , <i>nusG</i> , <i>rplK</i> , <i>rplA</i> , <i>rplP</i> , <i>rpmC</i> , <i>rpsC</i> , <i>rplV</i> , <i>nifJ</i> , <i>rpsU</i> , <i>tRNA</i> (Thr, Trp, Leu, Cys, Ser, His, Pro)
				<i>tuf</i> , <i>secE</i> , <i>rpmG</i> , <i>rpsI</i> , <i>rplM</i> , <i>gyrB</i> , <i>rRNA</i> - 23S <i>tRNA</i> (Trp, Thr, Gly, Pro, His, Arg, Lys, Val, Ser)
Cattle	<i>C. sp. 017646085</i>	12,607	89.4	<i>aspA</i> , <i>fusA</i> , <i>ssrA</i> , <i>rplO</i> , <i>secY</i> , <i>rpsI</i> , <i>rplM</i> , <i>tRNA</i> (Arg, Gly, Leu, Cys, Ser, Phe, Val, Glu, Lys, Asp, His, Pro, Asn)

Supplementary Table 6.3 - *Campylobacter* species prevalence in livestock samples

Species	Cattle		Goat	
	Positive	Prevalence	Positive	Prevalence
<i>C. concisus</i>	03/83	3.6%	01/73	1.4%
<i>C. devanensis</i>	17/83	20.5%	37/73	50.7%
<i>C. fetus</i>	02/83	2.4%	12/73	16.4%
<i>C. hyointestinalis</i>	04/83	4.8%	08/73	11.0%
<i>C. jejuni</i>	01/83	1.2%	0/73	0.0%
<i>C. lanienae</i>	10/83	12.0%	11/73	15.1%
<i>C. pinnipediorum</i>	02/83	2.4%	02/73	2.7%
<i>C. porcelli</i>	11/83	13.3%	12/73	16.4%
<i>C. vicugnae</i>	18/83	21.7%	58/73	79.5%

A Statement of Contribution for this chapter is provided in the [Appendices](#).

7 Chapter

7. Synthesis / General discussion

7.1 Overview, challenges, gaps, and future perspectives

7.1.1.1 Relative abundances and novel species in Ugandan gut microbiomes

This thesis commenced with the analysis of approximately 550 shallow sequencing individual files, detailed in Chapter 3 and 4. These files enabled the determination of bacterial relative abundances, α -diversity, and β -diversity for the individual samples, shedding light on the most abundant phyla and species read hits and providing a preliminary understanding of the dataset. In terms of β -diversity, microbiome community compositions showed the highest similarity according to host species. Cattle and goats exhibited higher α -diversities, while humans, especially those who were hospitalised, had lower microbial diversity compared to other hosts. The relative abundances of the most prevalent phyla in the gut microbiome varied significantly among the sampled Ugandan hosts in this study. Notably, there was a high number of *Spirochaetota* reads, indicating a potentially important presence of this bacterial group in the gut microbiomes studied. Subsequent analysis revealed described and putative novel *Spirochaetota* species from genera such as *Treponema* and *Brachyspira*. *Treponema*, along with *Prevotella* (*Bacteroidota*), are two important genera more commonly found in the gut microbiomes of humans living an agricultural lifestyle, as observed in non-industrialised populations like those in Uganda (Brewster et al., 2019). In the initial stage of the project, *Prevotella copri*, *Treponema peruense*, and *T. succinifaciens* were among the top three species hits identified by the taxonomic software Kraken2 (Lu et al., 2022; Wood et al., 2019) in the gut microbiomes of the human samples. Subsequently, these genera were analysed in more detail in Chapter 5, revealing that *Prevotella copri* was not included in the detected *Prevotella* species from the Ugandan hosts studied. On the other hand, using MAGs in the second phase of the project, it was possible to identify seven different *Prevotella* species in the human gut microbiomes, all of them being putative novel species from this genus.

7.1.1.2 Future directions and challenges in Ugandan gut microbiome research

There is a substantial amount of future work to be done using the first shallow sequencing dataset. For instance, further exploration of individual information (e.g., symptoms and habits from non-hospitalised humans compared to their gut microbiomes) and comparisons between the studied hosts within different categories, such as hospitalised and non-hospitalised humans, as well as habituated

and non-habituated gorillas, could contribute to more intriguing results. The sequencing dataset consists of hundreds of samples, and its weakness is the fact that with shallow sequencing, it was not possible to recover good quality MAGs (with more than 50% completion and less than 5% contamination) to obtain a more reliable classification containing complete or near-complete MAGs. However, performing deep sequencing for hundreds of samples individually would be incredibly expensive for the 553 samples in this project (30 samples cost around NZ\$12,000 at the time of writing), highlighting a gap in this initial phase of the project.

To address the gaps left during the initial phase of this PhD project, the second phase involved deep sequencing of pooled samples, resulting in a substantial amount of genomic data for analysis. Using a metagenomics pipeline, it was possible to reconstruct 3,185 MAGs, with 2,411 meeting the criteria for good quality (more than 50% completeness or less than 5% contamination), as detailed in Chapter 4. Considering the analysis of 37 *Prevotella* and 75 *Treponema* MAGs in Chapters 5 and 6 of this thesis, which revealed many putative novel species, these represent only 112 (4.6%) of the 2,411 MAGs reconstructed in this work. Therefore, there is still a vast amount of data to explore from both datasets, indicating the potential for further bacterial research in this project. Considering the context of gut microbiomes in non-industrialised populations, which are common among agriculturists like in Ugandan populations, Chapters 5 and 6 showed 28 putative novel species of *Treponema* and *Prevotella*, their general characteristics, shared species between hosts and functional analysis. These findings will contribute for a better understanding of the general characteristics and functions of these two common genera in non-industrialised societies. Despite having some analysed data about the functions of putative novel species of *Prevotella* and *Treponema* based on their KO codes in this work, there is much more functional analysis, including their metabolic pathways, to explore and integrate with known data and functions of already described species of these genera. Since pathways and functions of gut microbiota metabolism impact host physiology (Krishnan et al., 2015), the novel putative species identified in these genera will contribute to a more complete understanding of gut microbiome metabolism and answer more questions related to its impact on host physiology. These genera are commonly associated with diets abundant in plant-based foods, focusing on complex carbohydrate metabolism, propionate short-chain fatty acid (SCFA) production, and xenobiotic metabolism (Brewster et al., 2019).

7.1.1.3 Exploring collaborative opportunities in probiotic research

Given the significance of gut microbiota in health, there has been growing research and commercial interest in various aspects of probiotic functional foods and drugs (Latif et al., 2023; Yoha et al., 2022). The increase in gut microbiome-related diseases could be partially attributed to reduced

exposure to, or loss of, microbes that have co-evolved with humans, commonly associated with an industrialised lifestyle (Ursell et al., 2013; Wieërs et al., 2020). Considering that humans living in Buhoma (and elsewhere) with traditional lifestyles have a gut microbiome less affected by industrialisation, the results in Chapters 5 and 6 of my thesis show nine putative novel species of two important genera (*Treponema* and *Prevotella*) in their gut microbiomes that are not normally found in the gut microbiomes of industrialised human populations (Angelakis et al., 2019; Tett et al., 2021; Yeoh et al., 2022). Given that these findings represent only a small fraction of the MAGs recovered in this study, future projects may provide additional valuable information regarding beneficial microbes and their role in complex microbial communities. For instance, one or more of the novel species described here may have a particularly important metabolic function associated with the system homeostasis. This function could potentially prevent gut microbiome-related disease pathogenesis, a condition more commonly associated with industrialised human populations. This makes it a potential new probiotic constituent that collaborative institutions might consider if laboratory cultivation of the microorganism is feasible and worthwhile.

7.1.1.4 Cross-species bacterial sharing and potential zoonotic organism in Buhoma gut microbiomes from the studied hosts

Chapters 4, 5, and 6 presented results showing the same bacterial species shared between different hosts: *Ruminococcus* between humans and gorillas, *Treponema* between cattle, goats, pigs, and humans, and *Prevotella* between rhesus macaques, pigs, and humans. Pigs from other countries have been found to harbor *T. succinifaciens* and *T. berlinense*, along with one putative novel *Prevotella* species also found in the gut microbiomes of humans from Uganda. Additional funding for this project could enable another round of species-focused deep sequencing, providing more comprehensive information and possible complete genomes, thereby enhancing the confidence in the genetic characteristics and the general bacterial information discussed here. Furthermore, contact rates and proximity may play an important role in species sharing between different hosts. The participants in this study reported a notable number of sightings and contacts with pigs, baboons, and chickens (Muylaert et al., 2021) due to their frequent presence around residential areas in Buhoma. Poultry is an important reservoir and source of human campylobacteriosis (Skarp et al., 2016), and baboons may harbour infectious pathogens that are of zoonotic concern, acting as a reservoir of gastrointestinal diseases transmissible to humans and domestic animals (Alqumber, 2014; Mafuyai et al., 2013; Nakayima et al., 2014). Therefore, investigating the gut microbiomes of these hosts from Uganda and comparing them to those of the hosts in this study would be highly interesting. However, this would involve additional costs for another round of sampling and genome sequencing.

7.1.1.5 Putative novel *Campylobacter* species in Ugandan gut microbiomes: Future works in a one health perspective

A total of 44 *Campylobacter* MAGs were recovered from humans, livestock, and mountain gorilla gut microbiomes in Buhoma, Uganda, representing seven species, of which five were putative novel taxa. Three of these novel species were identified in gorillas, while livestock carried *C. vicugnae* (goats) and *C. sp017646085* (cattle). In humans, *Candidatus Campylobacter infans* was detected, which was not associated with disease but carried antimicrobial resistance genes such as *bla*_{OXA-489_1}, and *C. sp900539255*, which was significantly enriched in clinical samples and possessed unique sulphur and nitrogen metabolic pathways. These findings highlighted a previously unrecognised diversity of *Campylobacter* at the human–animal interface and suggested that certain novel taxa might have clinical relevance. From a One Health perspective, future work should focus on expanding *Campylobacter* reference genome databases to improve detection accuracy, undertaking longitudinal and source-tracking studies to clarify transmission pathways, and integrating genomic surveillance with clinical and epidemiological data. Such efforts would be essential to assess the pathogenic potential, antimicrobial resistance dynamics, and ecological roles of these novel species, ultimately informing targeted public health interventions in rural, multi-host environments.

7.1.1.6 Take-home messages and implications to Buhoma - Bwindi area of study

The results of this thesis held important implications for the Buhoma community and the surrounding Bwindi Impenetrable National Park. As reported previously, frequent interactions between gorillas and individuals such as ranger guides, trackers, poachers, tourists, veterinarians, and researchers had the potential to increase the risk of anthroponozoonotic and zoonotic transmission of *Campylobacter* spp. in the region (Nizeyi et al., 2001). Three *Campylobacter* novel species were detected in gorillas, and two species were present in human gut microbiomes, including *Candidatus Campylobacter infans* and *C. sp900539255*, the latter significantly enriched in clinical samples. These two species were closely related to *Campylobacter* genomes assembled from NHP gut microbiomes, suggesting possible sharing of species of this genus between humans and NHPs over a long term of co-existence at the wildlife–human interface. Despite this diversity, no strong phylogenetic evidence was found to indicate recent transmission between gorillas and humans. This suggested that *Campylobacter* occurrences in the area might not have been directly linked to increased contact between these hosts; however, undetected shared species could not be ruled out. The identification of novel taxa, one with potential clinical relevance, underscored the importance of targeted surveillance, particularly in communities living in close contact with wildlife and livestock.

The putative novel *Treponema* species detected in livestock samples in this study was also found in the gut microbiomes of humans from Brazil and Fiji, but not in the people from Buhoma who participated in this study. It is unclear whether this species might cause disease or confer benefits to humans, and this hypothesis could also be investigated in future research. It might potentially be shared with human hosts who are in close contact with livestock carcasses containing this species.

While *Prevotella* species are not usually the focus of antibiotic therapies, one of the newly identified intestinal *Prevotella* species (Chapter 6) found in human samples from Buhoma was found to carry the *nimJ* resistance gene. This gene confers resistance to metronidazole and potentially other similar antibiotics (Florensa et al., 2022). The use of antibiotics, including metronidazole, is widespread for treating both humans and animals in certain regions of Uganda (Dixon et al., 2021; Mukonzo et al., 2013; Nayiga et al., 2020). Metronidazole is one of the treatment options for amoebiasis and giardiasis (Bassily et al., 1987; Welch et al., 1978), which have a noticeable prevalence in Ugandan communities (McElligott et al., 2013; Ngowi, 2020). This finding raises concerns about the consequences of widespread antibiotic usage. It is important to highlight this additional message to underscore that metronidazole resistance genes are present in microbes from human gut microbiomes in the region. Moreover, the widespread use of antibiotics should be reevaluated to avoid the emergence of additional genes conferring resistance to antibiotics, which could be detrimental to future and necessary antibiotic therapies.

7.1.2 Conclusions

In conclusion, this study shed light on the intricate microbial interactions within the gut microbiomes of humans, livestock, and gorillas at the interface of land usage around forests in Uganda. The findings revealed a great number of putative novel bacterial species, including more detailed information within the *Prevotella*, *Treponema*, and *Campylobacter* genera, highlighting the complexity of microbial communities in this multi-host system. In *Campylobacter*, two species in human gut microbiomes were closely related to *Campylobacter* genomes from NHP gut microbiomes, suggesting possible long-term sharing of *Campylobacter* species between humans and wildlife. C. sp900539255 was significantly enriched in human clinical samples, indicating potential public health relevance. These findings underscored the importance of targeted genomic surveillance at the wildlife–livestock–human interface.

This thesis has provided valuable insights into the bacterial composition of host gut microbiomes in Uganda, particularly emphasising the prevalence of *Spirochaetota*, including described and putative novel species from genera such as *Treponema* across different host species. It also brings important

novel information regarding *Prevotella*, an important bacteria genus in the gut microbiome especially for agriculturalist societies. The detection of drug resistance genes in human *Prevotella* species suggests the potential for *Prevotella* to acquire resistance genes in environments with frequent antibiotic use. Moreover, it raises concerns about the use of antibiotics in the region and emphasises the need for further research into the implications of these findings.

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7.1.4 Appendices section

7.1.4.1 Appendices – Chapter 3

7.1.4.1.1 Uganda samples metadata

LAB METADATA							SAMPLE METADATA									
Mepi Number	CTPH_FAR		CTPH_NU		Position	Note	Species	Sampling Class	Date		Location	Measure ment				
	M_ID	MBER_ID	Location	MBER_ID					Sampled	SECTOR		Nest	(cm)	GRP	Age	Gender
UG001	FARM_G		Box_01	A1			Gorilla	Gorilla_Wild	27/4/2018	SECTOR_BB		6a		BB1	MED	
UG002	FARM_G		Box_01	A2			Gorilla	Gorilla_Wild	27/4/2018	SECTOR_BB		7		BB1	UNK	
UG003	FARM_G		Box_01	A3			Gorilla	Gorilla_Wild	27/4/2018	SECTOR_BB		12		BB1	MED	
UG004	FARM_G		Box_01	A4			Gorilla	Gorilla_Wild	27/4/2018	SECTOR_BB		9		BB1	MED	
UG005	FARM_G		Box_01	A5			Gorilla	Gorilla_Wild	27/4/2018	SECTOR_BB		8		BB1	MED	
UG006	FARM_G		Box_01	A6			Gorilla	Gorilla_Wild	27/4/2018	SECTOR_BB		11		BB1	MED	
UG007	FARM_G		Box_01	A7			Gorilla	Gorilla_Wild	26/4/2018	SECTOR_BB		1		BB2	SB	
UG008	FARM_G		Box_01	A8			Gorilla	Gorilla_Wild	27/4/2018	SECTOR_BB		4		BB1	MED	
UG009	FARM_G		Box_01	A9			Gorilla	Gorilla_Wild	27/4/2018	SECTOR_BB		3		BB1	MED	
UG010	FARM_G		Box_01	A10			Gorilla	Gorilla_Wild	27/4/2018	SECTOR_BB		13		BB1	MED	
UG011	FARM_G		Box_01	B1			Gorilla	Gorilla_Wild	16/4/2018	SECTOR_CC		H5		CC4	JUV	
UG012	FARM_G		Box_01	B2			Gorilla	Gorilla_Wild	16/4/2018	SECTOR_CC		1		CC4	MED	
UG013	FARM_G		Box_01	B3			Gorilla	Gorilla_Wild	16/4/2018	SECTOR_CC		H7		CC4	MED	
UG014	FARM_G		Box_01	B4			Gorilla	Gorilla_Wild	16/4/2018	SECTOR_CC		H6		CC4	MED	
UG015	FARM_G		Box_01	B5			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_CC		H2		CC2	MED	
UG016	FARM_G		Box_01	B6			Gorilla	Gorilla_Wild	16/4/2018	SECTOR_CC		H3		CC4	JUV	
UG017	FARM_G		Box_01	B7			Gorilla	Gorilla_Wild	30/4/2018	SECTOR_EE		1		EE5	UNK	
UG018	FARM_G		Box_01	B8			Gorilla	Gorilla_Wild	3/5/2018	SECTOR_FF		1b		FF2	UNK	
UG019	FARM_G		Box_01	B9			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_FF		2		FF4	MED	
UG020	FARM_G		Box_01	B10			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_FF		1		FF4	MED	
UG021	FARM_G		Box_01	C1			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_FF		3		FF4	SB	
UG022	FARM_G		Box_01	C2			Gorilla	Gorilla_Wild	3/5/2018	SECTOR_FF		2a		FF2	MED	
UG023	FARM_G		Box_01	C3			Gorilla	Gorilla_Wild	2/5/2018	SECTOR_FF		1b		FF2	INF	
UG024	FARM_G		Box_01	C4			Gorilla	Gorilla_Wild	7/5/2018	SECTOR_GG		3		GG2	UNK	
UG025	FARM_G		Box_01	C5			Gorilla	Gorilla_Wild	7/5/2018	SECTOR_GG		1		GG2	MED	
UG026	FARM_G		Box_01	C6			Gorilla	Gorilla_Wild	7/5/2018	SECTOR_GG		4		GG2	UNK	
UG027	FARM_G		Box_01	C7			Gorilla	Gorilla_Wild	12/4/2018	SECTOR_P		1b		P1	INF	
UG028	FARM_G		Box_01	C8			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		1		P3	MED	
UG029	FARM_G		Box_01	C9			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		1		P1	MED	
UG030	FARM_G		Box_01	C10			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		10		P3	MED	
UG031	FARM_G		Box_01	D1			Gorilla	Gorilla_Wild	13/4/2018	SECTOR_P		1		P3	MED	
UG032	FARM_G		Box_01	D2			Gorilla	Gorilla_Wild	13/4/2018	SECTOR_P		5		P3	UNK	
UG033	FARM_G		Box_01	D3			Gorilla	Gorilla_Wild	12/4/2018	SECTOR_P		8		P1	SB	
UG034	FARM_G		Box_01	D4			Gorilla	Gorilla_Wild	12/4/2018	SECTOR_P		4		P1	SB	
UG035	FARM_G		Box_01	D5			Gorilla	Gorilla_Wild	12/4/2018	SECTOR_P		2		P1	MED	
UG036	FARM_G		Box_01	D6			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		3a		P3	JUV	
UG037	FARM_G		Box_01	D7			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		5		P2	MED	
UG038	FARM_G		Box_01	D8			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		13		P3	MED	
UG039	FARM_G		Box_01	D9			Gorilla	Gorilla_Wild	12/4/2018	SECTOR_P		10		P1	MED	
UG040	FARM_G		Box_01	D10			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		2		P2	MED	
UG041	FARM_G		Box_01	E1			Gorilla	Gorilla_Wild	13/4/2018	SECTOR_P		2		P3	MED	
UG042	FARM_G		Box_01	E2			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		8b		P3	INF	
UG043	FARM_G		Box_01	E3			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		1		P3	MED	
UG044	FARM_G		Box_01	E4			Gorilla	Gorilla_Wild	12/4/2018	SECTOR_P		1a		P1	UNK	
UG045	FARM_G		Box_01	E5			Gorilla	Gorilla_Wild	12/4/2018	SECTOR_P		5		P1	JUV	
UG046	FARM_G		Box_01	E6			Gorilla	Gorilla_Wild	12/4/2018	SECTOR_P		3		P1	JUV	
UG047	FARM_G		Box_01	E7			Gorilla	Gorilla_Wild	13/4/2018	SECTOR_P		H7		P3	UNK	
UG048	FARM_G		Box_01	E8			Gorilla	Gorilla_Wild	13/4/2018	SECTOR_P		4		P2	MED	
UG049	FARM_G		Box_01	E9			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		3b		P3	INF	
UG050	FARM_G		Box_01	E10			Gorilla	Gorilla_Wild	14/4/2018	SECTOR_P		4		P3	MED	
UG051	FARM_G		Box_01	F1			Gorilla	Gorilla_Wild	19/4/2018	SECTOR_Q		4		Q3	MED	
UG052	FARM_G		Box_01	F2			Gorilla	Gorilla_Wild	18/4/2018	SECTOR_Q		5a		Q1	UNK	
UG053	FARM_G		Box_01	F3			Gorilla	Gorilla_Wild	19/4/2018	SECTOR_Q		5b		Q3	INF	
UG054	FARM_G		Box_01	F4			Gorilla	Gorilla_Wild	19/4/2018	SECTOR_Q		2a		Q3	MED	
UG055	FARM_G		Box_01	F5			Gorilla	Gorilla_Wild	18/4/2018	SECTOR_Q		2a		Q1	MED	
UG056	FARM_G		Box_01	F6			Gorilla	Gorilla_Wild	18/4/2018	SECTOR_Q		2b		Q1	INF	
UG057	FARM_G		Box_01	F7			Gorilla	Gorilla_Wild	19/4/2018	SECTOR_Q		3		Q3	UNK	
UG058	FARM_G		Box_01	F8			Gorilla	Gorilla_Wild	18/4/2018	SECTOR_Q		1a		Q1	MED	
UG059	FARM_G		Box_01	F9			Gorilla	Gorilla_Wild	18/4/2018	SECTOR_Q		5b		Q1	INF	
UG060	FARM_G		Box_01	F10			Gorilla	Gorilla_Wild	19/4/2018	SECTOR_Q		1a		Q3	MED	
UG061	FARM_G		Box_01	G1			Gorilla	Gorilla_Wild	18/4/2018	SECTOR_Q		4		Q1	SB	
UG062	FARM_G		Box_01	G2			Gorilla	Gorilla_Wild	16/4/2018	SECTOR_U		H4		U4	SB	
UG063	FARM_G		Box_01	G3			Gorilla	Gorilla_Wild	29/4/2018	SECTOR_V		6		V1	SB	
UG064	FARM_G		Box_01	G4			Gorilla	Gorilla_Wild	29/4/2018	SECTOR_V		2b		V1	UNK	
UG065	FARM_G		Box_01	G5			Gorilla	Gorilla_Wild	29/4/2018	SECTOR_V		1		V1	MED	
UG066	FARM_G		Box_01	G6			Gorilla	Gorilla_Wild	28/4/2018	SECTOR_V		3		XMAS	JUV	
UG067	FARM_G		Box_01	G7			Gorilla	Gorilla_Wild	29/4/2018	SECTOR_V		5		V1	MED	
UG068	FARM_G		Box_01	G8			Gorilla	Gorilla_Wild	29/4/2018	SECTOR_V		7		V1	MED	
UG069	FARM_G		Box_01	G9			Gorilla	Gorilla_Wild	29/4/2018	SECTOR_V		3a		V1	JUV	
UG070	FARM_G		Box_01	G10			Gorilla	Gorilla_Wild	28/4/2018	SECTOR_V		1		XMAS	JUV	
UG071	FARM_G		Box_01	H1			Gorilla	Gorilla_Wild	29/4/2018	SECTOR_V		4		V1	MED	
UG072	FARM_G		Box_01	H2			Gorilla	Gorilla_Wild	22/4/2018	SECTOR_W		1		W4	JUV	
UG073	FARM_G		Box_01	H3			Gorilla	Gorilla_Wild	22/4/2018	SECTOR_W		1b		W4	INF	
UG074	FARM_G		Box_01	H4			Gorilla	Gorilla_Wild	25/4/2018	SECTOR_W		3		W2	SB	
UG075	FARM_G		Box_01	H5			Gorilla	Gorilla_Wild	21/4/2018	SECTOR_W		4		W2	UNK	
UG076	FARM_G		Box_01	H6			Gorilla	Gorilla_Wild	22/4/2018	SECTOR_W		4		W4	SB	
UG077	FARM_G		Box_01	H7			Gorilla	Gorilla_Wild	25/4/2018	SECTOR_W		1		W2	UNK	
UG078	FARM_G		Box_01	H8			Gorilla	Gorilla_Wild	21/4/2018	SECTOR_W		1		W2	UNK	
UG079	FARM_G		Box_01	H9			Gorilla	Gorilla_Wild	2/5/2018	SECTOR_X		4		X2	UNK	
UG080	FARM_G		Box_01	H10			Gorilla	Gorilla_Wild	2/5/2018	SECTOR_X		5		X3	UNK	
UG081	FARM_G		Box_01	I1			Gorilla	Gorilla_Wild	2/5/2018	SECTOR_X		2		X2	SB	
UG082	FARM_G		Box_01	I2			Gorilla	Gorilla_Wild	2/5/2018	SECTOR_X		3		X2	UNK	
UG083	FARM_G		Box_01	I3			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		10a		Y1	MED	
UG084	FARM_G		Box_01	I4			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		11		Y1	MED	
UG085	FARM_G		Box_01	I5			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		6		Y1	MED	
UG086	FARM_G		Box_01	I6			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		8a		Y1	MED	
UG087	FARM_G		Box_01	I7			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		3		Y1	UNK	
UG088	FARM_G		Box_01	I8			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		8b		Y1	UNK	
UG089	FARM_G		Box_01	I9			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		5		Y1	UNK	
UG090	FARM_G		Box_01	I10			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		4		Y1	MED	
UG091	FARM_G		Box_01	J1			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		9		Y1	MED	
UG092	FARM_G		Box_01	J2			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		1		Y1	UNK	
UG093	FARM_G		Box_01	J3			Gorilla	Gorilla_Wild	4/5/2018	SECTOR_Y		10b		Y1	UNK	
UG094	FARM_G		Box_01	J4			Gorilla	Gorilla_Wild	9/5/2018	SECTOR_Z		6		Z1	MED	
UG095	FARM_G		Box_01	J5			Gorilla	Gorilla_Wild	9/5/2018	SECTOR_Z		2		Z2	MED	
UG096	FARM_G		Box_01	J6			Gorilla	Gorilla_Wild	9/5/2018	SECTOR_Z		4		Z2	JUV	
UG097	FARM_G		Box_01	J7			Gorilla	Gorilla_Wild	9/5/2018	SECTOR_Z		3a		Z2	MED	

UG098	FARM_G	Box_01	J8	Gorilla	Gorilla_Wild	9/5/2018	SECTOR_Z		5	Z2	MED
UG099	FARM_G	Box_01	J9	Gorilla	Gorilla_Wild	9/5/2018	SECTOR_Z		3b	Z2	UNK
UG100	FARM_G	Box_01	J10	Gorilla	Gorilla_Wild		UNMARKED_TUBE				
UG101	FARM_G ^H	Box_02	A1	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	15a		UNK
UG102	FARM_G ^H	Box_02	A2	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	12a		MED
UG103	FARM_G ^H	Box_02	A3	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	1a		MED
UG104	FARM_G ^H	Box_02	A4	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	10b		UNK
UG105	FARM_G ^H	Box_02	A5	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	16		UNK
UG106	FARM_G ^H	Box_02	A6	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	12b		UNK
UG107	FARM_G ^H	Box_02	A7	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	3		MED
UG108	FARM_G ^H	Box_02	A8	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	9		UNK
UG109	FARM_G ^H	Box_02	A9	Gorilla	Gorilla_Habituated	21/4/2018	SECTOR_U	Bushaho	3		MED
UG110	FARM_G ^H	Box_02	A10	Gorilla	Gorilla_Habituated	21/4/2018	SECTOR_U	Bushaho	2a		MED
UG111	FARM_G ^H	Box_02	B1	Gorilla	Gorilla_Habituated	21/4/2018	SECTOR_U	Bushaho	6		MED
UG112	FARM_G ^H	Box_02	B2	Gorilla	Gorilla_Habituated	21/4/2018	SECTOR_U	Bushaho	8b		JUV
UG113	FARM_G ^H	Box_02	B3	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	15b		INF
UG114	FARM_G ^H	Box_02	B4	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	2a		MED
UG115	FARM_G ^H	Box_02	B5	Gorilla	Gorilla_Habituated	21/4/2018	SECTOR_U	Bushaho	7		MED
UG116	FARM_G ^H	Box_02	B6	Gorilla	Gorilla_Habituated	21/4/2018	SECTOR_U	Bushaho	2b		INF
UG117	FARM_G ^H	Box_02	B7	Gorilla	Gorilla_Habituated	21/4/2018	SECTOR_U	Bushaho	8a		MED
UG118	FARM_G ^H	Box_02	B8	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	5		JUV
UG119	FARM_G ^H	Box_02	B9	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	7b		INF
UG120	FARM_G ^H	Box_02	B10	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	4		UNK
UG121	FARM_G ^H	Box_02	C1	Gorilla	Gorilla_Habituated	5/7/2017		Bikyingi			ADF
UG122	FARM_G ^H	Box_02	C2	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	13		MED
UG123	FARM_G ^H	Box_02	C3	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	2b		INF
UG124	FARM_G ^H	Box_02	C4	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	6		MED
UG125	FARM_G ^H	Box_02	C5	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	1b		INF
UG126	FARM_G ^H	Box_02	C6	Gorilla	Gorilla_Habituated	21/4/2018	SECTOR_U	Bushaho	1		SB
UG127	FARM_G ^H	Box_02	C7	Gorilla	Gorilla_Habituated	21/4/2018	SECTOR_U	Bushaho	4		MED
UG128	FARM_G ^H	Box_02	C8	Gorilla	Gorilla_Habituated	21/4/2018	SECTOR_U	Bushaho	5		MED
UG129	FARM_G ^H	Box_02	C9	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	14		MED
UG130	FARM_G ^H	Box_02	C10	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	7a		MED
UG131	FARM_G ^H	Box_02	D1	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	11a		MED
UG132	FARM_G ^H	Box_02	D2	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	11b		INF
UG133	FARM_G ^H	Box_02	D3	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	8		UNK
UG134	FARM_G ^H	Box_02	D4	Gorilla	Gorilla_Habituated	20/4/2018	SECTOR_U	Bikyingi	10a		SB
UG135	FARM_G ^H	Box_02	D5	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura		5.5	
UG136	FARM_G ^H	Box_02	D6	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura	4		
UG137	FARM_G ^H	Box_02	D7	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura	5.8		
UG138	FARM_G ^H	Box_02	D8	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura	3.5		
UG139	FARM_G ^H	Box_02	D9	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura	5.2		
UG140	FARM_G ^H	Box_02	D10	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura	4.5		
UG141	FARM_G ^H	Box_02	E1	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	3		MED
UG142	FARM_G ^H	Box_02	E2	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	7		UNK
UG143	FARM_G ^H	Box_02	E3	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	4		UNK
UG144	FARM_G ^H	Box_02	E4	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	5b		UNK
UG145	FARM_G ^H	Box_02	E5	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura		6.5	
UG146	FARM_G ^H	Box_02	E6	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	6		UNK
UG147	FARM_G ^H	Box_02	E7	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura		5.1	
UG148	FARM_G ^H	Box_02	E8	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura		6.4	
UG149	FARM_G ^H	Box_02	E9	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	1		MED
UG150	FARM_G ^H	Box_02	E10	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura		4.4	
UG151	FARM_G ^H	Box_02	F1	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	8a		MED
UG152	FARM_G ^H	Box_02	F2	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	8b		UNK
UG153	FARM_G ^H	Box_02	F3	Gorilla	Gorilla_Habituated	26/8/2017	SECTOR_GG	Rushegura		5.4	
UG154	FARM_G ^H	Box_02	F4	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	2		MED
UG155	FARM_G ^H	Box_02	F5	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	9		UNK
UG156	FARM_G ^H	Box_02	F6	Gorilla	Gorilla_Habituated	10/5/2018	SECTOR_GG	Rushegura	5a		MED
UG157	FARM_G ^H	Box_02	F7	Gorilla	Gorilla_Habituated	17/6/2017	MUBARE				ADF
UG158	FARM_G ^H	Box_02	F8	Gorilla	Gorilla_Habituated	1/11/2017	MUBARE				ADF
UG159	FARM_G ^H	Box_02	F9	Gorilla	Gorilla_Habituated	17/6/2017	MUBARE				INF
UG160	FARM_G ^H	Box_02	F10	Gorilla	Gorilla_Habituated	17/6/2017	MUBARE				INF
UG161	FARM_G ^H	Box_02	G1	Gorilla	Gorilla_Habituated	17/6/2017	MUBARE				ADF
UG162	FARM_G ^H	Box_02	G2	Gorilla	Gorilla_Habituated	18/5/2017	MUBARE				INF
UG163	FARM_G ^H	Box_02	G3	Gorilla	Gorilla_Habituated	26/8/2017	MUBARE				SB
UG164	FARM_G ^H	Box_02	G4	Gorilla	Gorilla_Habituated	18/5/2017	MUBARE				ADF
UG165	FARM_G ^H	Box_02	G5	Gorilla	Gorilla_Habituated	17/6/2017	MUBARE				ADF
UG166	FARM_G ^H	Box_02	G6	Gorilla	Gorilla_Habituated	26/8/2017	MUBARE				ADF
UG167	FARM_G ^H	Box_02	G7	Gorilla	Gorilla_Habituated	26/8/2017	MUBARE				ADF
UG168	FARM_G ^H	Box_02	G8	Gorilla	Gorilla_Habituated	18/5/2017	MUBARE				ADF
UG169	FARM_G ^H	Box_02	G9	Gorilla	Gorilla_Habituated	26/8/2017	MUBARE				ADF
UG170	FARM_G ^H	Box_02	G10	Gorilla	Gorilla_Habituated	17/6/2017	MUBARE				INF
UG171	FARM_G ^H	Box_02	H1	Gorilla	Gorilla_Habituated	18/5/2017	MUBARE				ADF
UG172	FARM_G ^H	Box_02	H2	Gorilla	Gorilla_Habituated	17/6/2017	MUBARE				ADF
UG173	FARM_G ^H	Box_02	H3	Gorilla	Gorilla_Habituated	17/6/2017	MUBARE				SAD
UG174	FARM_G ^H	Box_02	H4	Gorilla	Gorilla_Habituated	17/6/2017	MUBARE				ADF
UG175	FARM_G ^H	Box_02	H5	Gorilla	Gorilla_Habituated	26/8/2017	MUBARE				INF
UG176	FARM_G ^H	Box_02	H6	Gorilla	Gorilla_Habituated	17/6/2017	MUBARE				SB
UG177	FARM_G ^H	Box_02	H7	Gorilla	Gorilla_Habituated	18/5/2017	MUBARE				ADF
UG178	FARM_G ^H	Box_02	H8	Gorilla	Gorilla_Habituated	#####	M				ADF
UG179	FARM_G ^H	Box_02	H9	Gorilla	Gorilla_Habituated	#####	M				SB
UG180	FARM_G ^H	Box_02	H10	Gorilla	Gorilla_Habituated	#####	M				ADF
UG181	FARM_G ^H	Box_02	I1	Gorilla	Gorilla_Habituated	26/8/2017	M				ADF
UG182	FARM_G ^H	Box_02	I2	Gorilla	Gorilla_Habituated	#####	M				ADF
UG183	FARM_G ^H	Box_02	I3	Gorilla	Gorilla_Habituated	#####	M				INF
UG184	FARM_G ^H	Box_02	I4	Gorilla	Gorilla_Habituated	#####	R				ADF
UG185	FARM_G ^H	Box_02	I5	Gorilla	Gorilla_Habituated	15/1/2018	R				INF
UG186	FARM_G ^H	Box_02	I6	Gorilla	Gorilla_Habituated	#####	R				INF
UG187	FARM_G ^H	Box_02	I7	Gorilla	Gorilla_Habituated	#####	R				BB
UG188	FARM_G ^H	Box_02	I8	Gorilla	Gorilla_Habituated	15/1/2018	R				JUV
UG189	FARM_G ^H	Box_02	I9	Gorilla	Gorilla_Habituated	15/1/2018	R				BB
UG190	FARM_G ^H	Box_02	I10	Gorilla	Gorilla_Habituated	1/8/2017	H				ADF
UG191	FARM_G ^H	Box_02	J1	Gorilla	Gorilla_Habituated	#####	H				ADF
UG192	FARM_G ^H	Box_02	J2	Gorilla	Gorilla_Habituated	1/8/2017	H				ADF
UG193	FARM_G ^H	Box_02	J3	Gorilla	Gorilla_Habituated	#####	H				ADF
UG194	FARM_G ^H	Box_02	J4	Gorilla	Gorilla_Habituated	1/8/2017	H				INF
UG195	FARM_G ^H	Box_02	J5	Gorilla	Gorilla_Habituated	#####	H				ADF
UG196	FARM_G ^H	Box_02	J6	Gorilla	Gorilla_Habituated	1/8/2017	H				ADF
UG197	FARM_G ^H	Box_02	J7	Gorilla	Gorilla_Habituated	16/4/2018	SECTOR_P	Busimgye	3		UNK
UG198	FARM_G ^H	Box_02	J8	Gorilla	Gorilla_Habituated	16/4/2018	SECTOR_P	Busimgye	2		MED
UG199	FARM_G ^H	Box_02	J9	Gorilla	Gorilla_Habituated	16/4/2018	SECTOR_P	Busimgye	4		MED

UG200	FARM_G ^H	Box_02	J10	Gorilla	Gorilla_Habituated	16/4/2018	SECTOR_P	Busimgye	1	MED
UG201	FARM_H	NO:001	Box_03	A1	Human	hospitalised humans	6/6/2018	Kacerere		31 M
UG202	FARM_H	NO:002	Box_03	A2	Human	hospitalised humans	6/6/2018	Rypemirama		22 F
UG203	FARM_H	NO:003	Box_03	A3	Human	hospitalised humans	6/6/2018	Byumba		14 M
UG204	FARM_H	NO:004	Box_03	A4	Human	hospitalised humans	6/6/2018	Nyakahanga		23 F
UG205	FARM_H	NO:005	Box_03	A5	Human	hospitalised humans	6/6/2018	Nyakahanga		48 F
UG206	FARM_H	NO:006	Box_03	A6	Human	hospitalised humans	6/6/2018	Rugando		38 F
UG207	FARM_H	NO:007	Box_03	A7	Human	hospitalised humans	6/6/2018	Nyakahanga		41 M
UG208	FARM_H	NO:008	Box_03	A8	Human	hospitalised humans	6/6/2018	Rugando		48 F
UG209	FARM_H	NO:009	Box_03	A9	Human	hospitalised humans	6/6/2018	Rugando		5 F
UG210	FARM_H	NO:010	Box_03	A10	Human	hospitalised humans	6/6/2018	Rugando		7 F
UG211	FARM_H	NO:011	Box_03	B1	Human	hospitalised humans	6/6/2018	Kabirizi		17 F
UG212	FARM_H	NO:012	Box_03	B2	Human	hospitalised humans	6/6/2018	Mushorero		14 F
UG213	FARM_H	NO:013	Box_03	B3	Human	hospitalised humans	6/6/2018	Kabirizi		23 F
UG214	FARM_H	NO:014	Box_03	B4	Human	hospitalised humans	6/6/2018	Nyakahanga		15 F
UG215	FARM_H	NO:015	Box_03	B5	Human	hospitalised humans	6/6/2018	Nyakahanga		15 F
UG216	FARM_H	NO:016	Box_03	B6	Human	hospitalised humans	6/6/2018	Byumba		13 M
UG217	FARM_H	NO:017	Box_03	B7	Human	hospitalised humans	6/6/2018	Kabirizi		12 F
UG218	FARM_H	NO:018	Box_03	B8	Human	hospitalised humans	6/6/2018	Byumba		15 M
UG219	FARM_H	NO:019	Box_03	B9	Human	hospitalised humans	6/6/2018	Rurangara		69 F
UG220	FARM_H	NO:020	Box_03	B10	Human	hospitalised humans	6/6/2018	Mushorero		10 F
UG221	FARM_H	NO:021	Box_03	C1	Human	hospitalised humans	6/6/2018	Mushorero		14 F
UG222	FARM_H	NO:022	Box_03	C2	Human	hospitalised humans	6/6/2018	Kishegyure		56 M
UG223	FARM_H	NO:023	Box_03	C3	Human	hospitalised humans	6/6/2018	Bugarura		45 F
UG224	FARM_H	NO:024	Box_03	C4	Human	hospitalised humans	6/6/2018	Nulemgye		5 F
UG225	FARM_H	NO:025	Box_03	C5	Human	hospitalised humans	6/6/2018	Nulemgye		24 F
UG226	FARM_H	NO:026	Box_03	C6	Human	hospitalised humans	6/6/2018	Kishegyure		37 F
UG227	FARM_H	NO:027	Box_03	C7	Human	hospitalised humans	7/6/2018	Myamiyaga		15 F
UG228	FARM_H	NO:028	Box_03	C8	Human	hospitalised humans	7/6/2018	Bikuto		36 M
UG229	FARM_H	NO:029	Box_03	C9	Human	hospitalised humans	7/6/2018	Kamoni		10 F
UG230	FARM_H	NO:030	Box_03	C10	Human	hospitalised humans	7/6/2018	Myamiyaga		15 F
UG231	FARM_H	NO:031	Box_03	D1	Human	hospitalised humans	7/6/2018	Myanja		29 M
UG232	FARM_H	NO:032	Box_03	D2	Human	hospitalised humans	7/6/2018	Pugarura		32 M
UG233	FARM_H	NO:033	Box_03	D3	Human	hospitalised humans	7/6/2018	Myamiyaga		5 M
UG234	FARM_H	NO:034	Box_03	D4	Human	hospitalised humans	7/6/2018	Myamiyaga		13 F
UG235	FARM_H	NO:035	Box_03	D5	Human	hospitalised humans	7/6/2018	Myamiyaga		15 F
UG236	FARM_H	NO:036	Box_03	D6	Human	hospitalised humans	7/6/2018	Kanoni		11 F
UG237	FARM_H	NO:037	Box_03	D7	Human	hospitalised humans	7/6/2018	Kabirizi		42 F
UG238	FARM_H	NO:038	Box_03	D8	Human	hospitalised humans	7/6/2018	Kacerere		5 F
UG239	FARM_H	NO:039	Box_03	D9	Human	hospitalised humans	7/6/2018	Kacerere		24 F
UG240	FARM_H	NO:040	Box_03	D10	Human	hospitalised humans	7/6/2018	Nyarututo		13 M
UG241	FARM_H	NO:041	Box_03	E1	Human	hospitalised humans	7/6/2018	Ryemirama		13 M
UG242	FARM_H	NO:042	Box_03	E2	Human	hospitalised humans	7/6/2018	Kishanda		13 M
UG243	FARM_H	NO:043	Box_03	E3	Human	hospitalised humans	7/6/2018	Nyarututo		12 F
UG244	FARM_H	NO:044	Box_03	E4	Human	hospitalised humans	7/6/2018	Nyarututo		8 F
UG245	FARM_H	NO:045	Box_03	E5	Human	hospitalised humans	7/6/2018	Nyarututo		10 F
UG246	FARM_H	NO:046	Box_03	E6	Human	hospitalised humans	7/6/2018	Kishegyure		5 M
UG247	FARM_H	NO:047	Box_03	E7	Human	hospitalised humans	8/6/2018	Kishegyure		45 F
UG248	FARM_H	NO:048	Box_03	E8	Human	hospitalised humans	8/6/2018	Kishegyure		37 F
UG249	FARM_H	NO:049	Box_03	E9	Human	hospitalised humans	8/6/2018			21 M
UG250	FARM_H	NO:050	Box_03	E10	Human	hospitalised humans	8/6/2018			48 M
UG251	FARM_H	NO:051	Box_03	F1	Human	hospitalised humans	8/6/2018			27 F
				Sample NO:052 was missing, replaced with sample NO:101						
UG252	FARM_H	NO:101	Box_03	F2	Human	hospitalised humans	9/6/2018			19 F
UG253	FARM_H	NO:053	Box_03	F3	Human	hospitalised humans	8/6/2018			24 F
UG254	FARM_H	NO:054	Box_03	F4	Human	hospitalised humans	8/6/2018			62 M
UG255	FARM_H	NO:055	Box_03	F5	Human	hospitalised humans	8/6/2018			9 M
UG256	FARM_H	NO:056	Box_03	F6	Human	hospitalised humans	8/6/2018	Health Centre		62 F
UG257	FARM_H	NO:057	Box_03	F7	Human	hospitalised humans	8/6/2018			42 F
UG258	FARM_H	NO:058	Box_03	F8	Human	hospitalised humans	8/6/2018			10 F
UG259	FARM_H	NO:059	Box_03	F9	Human	hospitalised humans	8/6/2018			36 M
UG260	FARM_H	NO:060	Box_03	F10	Human	hospitalised humans	8/6/2018			30 F
UG261	FARM_H	NO:061	Box_03	G1	Human	hospitalised humans	8/6/2018			27 F
UG262	FARM_H	NO:062	Box_03	G2	Human	hospitalised humans	8/6/2018			30 F
UG263	FARM_H	NO:063	Box_03	G3	Human	hospitalised humans	8/6/2018			60 F
UG264	FARM_H	NO:064	Box_03	G4	Human	hospitalised humans	8/6/2018			20 F
UG265	FARM_H	NO:065	Box_03	G5	Human	hospitalised humans	9/6/2018			40 F
UG266	FARM_H	NO:066	Box_03	G6	Human	hospitalised humans	9/6/2018			19 F
UG267	FARM_H	NO:061	Box_03	G7	Human	hospitalised humans	9/6/2018			20 F
UG268	FARM_H	NO:068	Box_03	G8	Human	hospitalised humans	9/6/2018			15 M
UG269	FARM_H	NO:069	Box_03	G9	Human	hospitalised humans	9/6/2018			20 F
UG270	FARM_H	NO:070	Box_03	G10	Human	hospitalised humans	9/6/2018			40 M
UG271	FARM_H	NO:071	Box_03	H1	Human	hospitalised humans	9/6/2018			24 F
UG272	FARM_H	NO:072	Box_03	H2	Human	hospitalised humans	9/6/2018			13 M
UG273	FARM_H	NO:073	Box_03	H3	Human	hospitalised humans	9/6/2018			26 F
UG274	FARM_H	NO:074	Box_03	H4	Human	hospitalised humans	9/6/2018			12 M
UG275	FARM_H	NO:075	Box_03	H5	Human	hospitalised humans	9/6/2018			14 F
UG276	FARM_H	NO:076	Box_03	H6	Human	hospitalised humans	9/6/2018			30 F
UG277	FARM_H	NO:077	Box_03	H7	Human	hospitalised humans	9/6/2018			14 F
UG278	FARM_H	NO:078	Box_03	H8	Human	hospitalised humans	9/6/2018			12 F
UG279	FARM_H	NO:079	Box_03	H9	Human	hospitalised humans	9/6/2018			10 F
UG280	FARM_H	NO:080	Box_03	H10	Human	hospitalised humans	9/6/2018			6 F
UG281	FARM_H	NO:081	Box_03	I1	Human	hospitalised humans	9/6/2018			30 F
UG282	FARM_H	NO:082	Box_03	I2	Human	hospitalised humans	9/6/2018			13 M
UG283	FARM_H	NO:083	Box_03	I3	Human	hospitalised humans	9/6/2018			15 F
UG284	FARM_H	NO:084	Box_03	I4	Human	hospitalised humans	9/6/2018			40 F
UG285	FARM_H	NO:085	Box_03	I5	Human	hospitalised humans	9/6/2018			19 F
UG286	FARM_H	NO:086	Box_03	I6	Human	hospitalised humans	9/6/2018			5 M
UG287	FARM_H	NO:087	Box_03	I7	Human	hospitalised humans	9/6/2018			12 M
UG288	FARM_H	NO:088	Box_03	I8	Human	hospitalised humans	9/6/2018			16 F
UG289	FARM_H	NO:089	Box_03	I9	Human	hospitalised humans	9/6/2018			20 F
UG290	FARM_H	NO:090	Box_03	I10	Human	hospitalised humans	9/6/2018			29 F
UG291	FARM_H	NO:091	Box_03	J1	Human	hospitalised humans	9/6/2018			16 M
UG292	FARM_H	NO:092	Box_03	J2	Human	hospitalised humans	9/6/2018			63 M
UG293	FARM_H	NO:093	Box_03	J3	Human	hospitalised humans	9/6/2018			29 F
UG294	FARM_H	NO:094	Box_03	J4	Human	hospitalised humans	9/6/2018			20 F
UG295	FARM_H	NO:095	Box_03	J5	Human	hospitalised humans	9/6/2018			32 F
UG296	FARM_H	NO:096	Box_03	J6	Human	hospitalised humans	9/6/2018			42 F
UG297	FARM_H	NO:097	Box_03	J7	Human	hospitalised humans	9/6/2018			46 M
UG298	FARM_H	NO:098	Box_03	J8	Human	hospitalised humans	9/6/2018			32 M
UG299	FARM_H	NO:099	Box_03	J9	Human	hospitalised humans	9/6/2018			26 F
UG300	FARM_H	NO:100	Box_03	J10	Human	hospitalised humans	9/6/2018			36 M

UG345	FARM_H	missing	Box_04	E5	missing sample	Human_community
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UG403	FARM_B	NO:003	Box_05	A3		Cow	Livestock_Cattle	8/6/2018
UG404	FARM_B	NO:004	Box_05	A4		Cow	Livestock_Cattle	11/6/2018
UG405	FARM_B	NO:005	Box_05	A5		Cow	Livestock_Cattle	22/6/2018
UG406	FARM_B	NO:006	Box_05	A6		Cow	Livestock_Cattle	22/6/2018
UG407	FARM_B	NO:007	Box_05	A7		Cow	Livestock_Cattle	22/6/2018
UG408	FARM_B	NO:008	Box_05	A8		Cow	Livestock_Cattle	22/6/2018
UG409	FARM_B	NO:009	Box_05	A9		Cow	Livestock_Cattle	22/6/2018
UG410	FARM_B	NO:010	Box_05	A10		Cow	Livestock_Cattle	22/6/2018
UG411	FARM_B	NO:011	Box_05	B1		Cow	Livestock_Cattle	22/6/2018
UG412	FARM_B	NO:012	Box_05	B2		Cow	Livestock_Cattle	22/6/2018
UG413	FARM_B	NO:013	Box_05	B3		Cow	Livestock_Cattle	27/6/2018
UG414	FARM_B	NO:014	Box_05	B4		Cow	Livestock_Cattle	27/6/2018
UG415	FARM_B	NO:015	Box_05	B5		Cow	Livestock_Cattle	27/6/2018
UG416	FARM_B	NO:016	Box_05	B6		Cow	Livestock_Cattle	27/6/2018
UG417	FARM_B	NO:017	Box_05	B7		Cow	Livestock_Cattle	27/6/2018
UG418	FARM_B	NO:018	Box_05	B8		Cow	Livestock_Cattle	27/6/2018
UG419	FARM_B	NO:019	Box_05	B9		Cow	Livestock_Cattle	27/6/2018
UG420	FARM_B	NO:020	Box_05	B10		Cow	Livestock_Cattle	27/6/2018
UG421	FARM_B	NO:021	Box_05	C1		Cow	Livestock_Cattle	27/6/2018
UG422	FARM_B	NO:022	Box_05	C2		Cow	Livestock_Cattle	27/6/2018
UG423	FARM_B	NO:023	Box_05	C3		Cow	Livestock_Cattle	27/6/2018
UG424	FARM_B	NO:024	Box_05	C4		Cow	Livestock_Cattle	27/6/2018
UG425	FARM_B	NO:025	Box_05	C5		Cow	Livestock_Cattle	27/6/2018
UG426	FARM_B	NO:026	Box_05	C6		Cow	Livestock_Cattle	27/6/2018
UG427	FARM_B	NO:027	Box_05	C7		Cow	Livestock_Cattle	27/6/2018
UG428	FARM_B	NO:028	Box_05	C8		Cow	Livestock_Cattle	27/6/2018
UG429	FARM_B	NO:029	Box_05	C9		Cow	Livestock_Cattle	27/6/2018
UG430	FARM_B	NO:030	Box_05	C10		Cow	Livestock_Cattle	27/6/2018
UG431	FARM_B	NO:031	Box_05	D1		Cow	Livestock_Cattle	27/6/2018
UG432	FARM_B	NO:032	Box_05	D2		Cow	Livestock_Cattle	27/6/2018
UG433	FARM_B	NO:033	Box_05	D3		Cow	Livestock_Cattle	27/6/2018
UG434	FARM_B	NO:034	Box_05	D4		Cow	Livestock_Cattle	27/6/2018
UG435	FARM_B	NO:035	Box_05	D5		Cow	Livestock_Cattle	27/6/2018
UG436	FARM_B	NO:036	Box_05	D6		Cow	Livestock_Cattle	27/6/2018
UG437	FARM_B	NO:037	Box_05	D7		Cow	Livestock_Cattle	27/6/2018
UG438	FARM_B	NO:038	Box_05	D8		Cow	Livestock_Cattle	27/6/2018
UG439	FARM_B	NO:039	Box_05	D9		Cow	Livestock_Cattle	27/6/2018
UG440	FARM_B	NO:040	Box_05	D10		Cow	Livestock_Cattle	27/6/2018
UG441	FARM_B	NO:041	Box_05	E1		Cow	Livestock_Cattle	27/6/2018
UG442	FARM_B	NO:042	Box_05	E2		Cow	Livestock_Cattle	27/6/2018
UG443	FARM_B	NO:043	Box_05	E3		Cow	Livestock_Cattle	27/6/2018
UG444	FARM_B	NO:044	Box_05	E4		Cow	Livestock_Cattle	27/6/2018
UG445	FARM_B	NO:046	Box_05	E5	Duplicate CTPH_NUMBER_ID	Cow	Livestock_Cattle	27/6/2018
UG446	FARM_B	NO:046	Box_05	E6	Duplicate CTPH_NUMBER_ID	Cow	Livestock_Cattle	27/6/2018
UG447	FARM_B	NO:047	Box_05	E7		Cow	Livestock_Cattle	27/6/2018
UG448	FARM_B	NO:048	Box_05	E8		Cow	Livestock_Cattle	28/6/2018
UG449	FARM_B	NO:049	Box_05	E9		Cow	Livestock_Cattle	28/6/2018
UG450	FARM_B	NO:050	Box_05	E10		Cow	Livestock_Cattle	28/6/2018
UG451	FARM_B	NO:051	Box_05	F1		Cow	Livestock_Cattle	28/6/2018
UG452	FARM_B	NO:052	Box_05	F2		Cow	Livestock_Cattle	28/6/2018
UG453	FARM_B	NO:053	Box_05	F3		Cow	Livestock_Cattle	28/6/2018
UG454	FARM_B	NO:054	Box_05	F4		Cow	Livestock_Cattle	28/6/2018
UG455	FARM_B	NO:055	Box_05	F5		Cow	Livestock_Cattle	28/6/2018
UG456	FARM_B	NO:056	Box_05	F6		Cow	Livestock_Cattle	28/6/2018
UG457	FARM_B	NO:057	Box_05	F7		Cow	Livestock_Cattle	28/6/2018
UG458	FARM_B	NO:058	Box_05	F8		Cow	Livestock_Cattle	28/6/2018
UG459	FARM_B	missing	Box_05	F9	missing sample			
UG460	FARM_B	NO:060	Box_05	F10		Cow	Livestock_Cattle	28/6/2018
UG461	FARM_B	NO:061	Box_05	G1		Cow	Livestock_Cattle	28/6/2018
UG462	FARM_B	NO:062	Box_05	G2		Cow	Livestock_Cattle	28/6/2018
UG463	FARM_B	NO:063	Box_05	G3		Cow	Livestock_Cattle	28/6/2018
UG464	FARM_B	NO:064	Box_05	G4		Cow	Livestock_Cattle	28/6/2018
UG465	FARM_B	NO:065	Box_05	G5		Cow	Livestock_Cattle	28/6/2018
UG466	FARM_B	NO:066	Box_05	G6		Cow	Livestock_Cattle	28/6/2018
UG467	FARM_B	NO:067	Box_05	G7		Cow	Livestock_Cattle	28/6/2018
UG468	FARM_B	NO:068	Box_05	G8		Cow	Livestock_Cattle	28/6/2018
UG469	FARM_B	NO:069	Box_05	G9		Cow	Livestock_Cattle	28/6/2018
UG470	FARM_B	NO:070	Box_05	G10		Cow	Livestock_Cattle	28/6/2018
UG471	FARM_B	NO:071	Box_05	H1		Cow	Livestock_Cattle	28/6/2018
UG472	FARM_B	NO:072	Box_05	H2		Cow	Livestock_Cattle	28/6/2018
UG473	FARM_B	NO:073	Box_05	H3		Cow	Livestock_Cattle	28/6/2018
UG474	FARM_B	NO:074	Box_05	H4		Cow	Livestock_Cattle	28/6/2018
UG475	FARM_B	NO:075	Box_05	H5		Cow	Livestock_Cattle	28/6/2018
UG476	FARM_B	NO:076	Box_05	H6		Cow	Livestock_Cattle	28/6/2018
UG477	FARM_B	NO:077	Box_05	H7		Cow	Livestock_Cattle	28/6/2018
UG478	FARM_B	NO:078	Box_05	H8		Cow	Livestock_Cattle	28/6/2018
UG479	FARM_B	NO:079	Box_05	H9		Cow	Livestock_Cattle	28/6/2018
UG480	FARM_B	NO:080	Box_05	H10		Cow	Livestock_Cattle	28/6/2018
UG481	FARM_B	NO:081	Box_05	I1		Cow	Livestock_Cattle	28/6/2018
UG482	FARM_B	NO:082	Box_05	I2		Cow	Livestock_Cattle	28/6/2018
UG483	FARM_B	NO:083	Box_05	I3		Cow	Livestock_Cattle	28/6/2018
UG484	FARM_B	NO:084	Box_05	I4		Cow	Livestock_Cattle	28/6/2018
UG485			Box_05	I5				
UG486			Box_05	I6				
UG487			Box_05	I7				
UG488			Box_05	I8				
UG489			Box_05	I9				
UG490			Box_05	I10				
UG491			Box_05	J1				
UG492			Box_05	J2				
UG493			Box_05	J3				
UG494			Box_05	J4				
UG495			Box_05	J5				
UG496			Box_05	J6				
UG497			Box_05	J7				
UG498			Box_05	J8				
UG499			Box_05	J9				
UG500			Box_05	J10				
UG501	FARM_C	NO:001	Box_06	A1		Goat	Livestock_Goat	8/6/2018
UG502	FARM_C	NO:002	Box_06	A2		Goat	Livestock_Goat	8/6/2018
UG503	FARM_C	NO:003	Box_06	A3		Goat	Livestock_Goat	8/6/2018
UG504	FARM_C	NO:004	Box_06	A4		Goat	Livestock_Goat	8/6/2018

UG505	FARM_C	NO:005	Box_06	A5	Goat	Livestock_Goat	8/6/2018
UG506	FARM_C	NO:006	Box_06	A6	Goat	Livestock_Goat	8/6/2018
UG507	FARM_C	NO:007	Box_06	A7	Goat	Livestock_Goat	8/6/2018
UG508	FARM_C	NO:008	Box_06	A8	Goat	Livestock_Goat	8/6/2018
UG509	FARM_C	NO:009	Box_06	A9	Goat	Livestock_Goat	8/6/2018
UG510	FARM_C	NO:010	Box_06	A10	Goat	Livestock_Goat	8/6/2018
UG511	FARM_C	NO:011	Box_06	B1	Goat	Livestock_Goat	8/6/2018
UG512	FARM_C	NO:012	Box_06	B2	Goat	Livestock_Goat	8/6/2018
UG513	FARM_C	NO:013	Box_06	B3	Goat	Livestock_Goat	8/6/2018
UG514	FARM_C	NO:014	Box_06	B4	Goat	Livestock_Goat	8/6/2018
UG515	FARM_C	NO:015	Box_06	B5	Goat	Livestock_Goat	8/6/2018
UG516	FARM_C	NO:016	Box_06	B6	Goat	Livestock_Goat	8/6/2018
UG517	FARM_C	NO:017	Box_06	B7	Goat	Livestock_Goat	8/6/2018
UG518	FARM_C	NO:018	Box_06	B8	Goat	Livestock_Goat	8/6/2018
UG519	FARM_C	NO:019	Box_06	B9	Goat	Livestock_Goat	8/6/2018
UG520	FARM_C	NO:020	Box_06	B10	Goat	Livestock_Goat	8/6/2018
UG521	FARM_C	NO:021	Box_06	C1	Goat	Livestock_Goat	8/6/2018
UG522	FARM_C	NO:022	Box_06	C2	Goat	Livestock_Goat	11/6/2018
UG523	FARM_C	NO:023	Box_06	C3	Goat	Livestock_Goat	11/6/2018
UG524	FARM_C	NO:024	Box_06	C4	Goat	Livestock_Goat	11/6/2018
UG525	FARM_C	NO:025	Box_06	C5	Goat	Livestock_Goat	11/6/2018
UG526	FARM_C	NO:026	Box_06	C6	Goat	Livestock_Goat	11/6/2018
UG527	FARM_C	NO:027	Box_06	C7	Goat	Livestock_Goat	11/6/2018
UG528	FARM_C	NO:028	Box_06	C8	Goat	Livestock_Goat	11/6/2018
UG529	FARM_C	NO:029	Box_06	C9	Goat	Livestock_Goat	11/6/2018
UG530	FARM_C	NO:030	Box_06	C10	Goat	Livestock_Goat	11/6/2018
UG531	FARM_C	NO:031	Box_06	D1	Goat	Livestock_Goat	11/6/2018
UG532	FARM_C	NO:032	Box_06	D2	Goat	Livestock_Goat	11/6/2018
UG533	FARM_C	NO:033	Box_06	D3	Goat	Livestock_Goat	11/6/2018
UG534	FARM_C	NO:034	Box_06	D4	Goat	Livestock_Goat	11/6/2018
UG535	FARM_C	NO:035	Box_06	D5	Goat	Livestock_Goat	11/6/2018
UG536	FARM_C	NO:036	Box_06	D6	Goat	Livestock_Goat	11/6/2018
UG537	FARM_C	NO:037	Box_06	D7	Goat	Livestock_Goat	11/6/2018
UG538	FARM_C	NO:038	Box_06	D8	Goat	Livestock_Goat	11/6/2018
UG539	FARM_C	NO:039	Box_06	D9	Goat	Livestock_Goat	11/6/2018
UG540	FARM_C	NO:040	Box_06	D10	Goat	Livestock_Goat	11/6/2018
UG541	FARM_C	NO:041	Box_06	E1	Goat	Livestock_Goat	11/6/2018
UG542	FARM_C	NO:042	Box_06	E2	Goat	Livestock_Goat	11/6/2018
UG543	FARM_C	NO:043	Box_06	E3	Goat	Livestock_Goat	11/6/2018
UG544	FARM_C	NO:044	Box_06	E4	Goat	Livestock_Goat	11/6/2018
UG545	FARM_C	NO:045	Box_06	E5	Goat	Livestock_Goat	11/6/2018
UG546	FARM_C	NO:046	Box_06	E6	Goat	Livestock_Goat	11/6/2018
UG547	FARM_C	NO:047	Box_06	E7	Goat	Livestock_Goat	11/6/2018
UG548	FARM_C	NO:048	Box_06	E8	Goat	Livestock_Goat	11/6/2018
UG549	FARM_C	NO:049	Box_06	E9	Goat	Livestock_Goat	11/6/2018
UG550	FARM_C	NO:050	Box_06	E10	Goat	Livestock_Goat	11/6/2018
UG551	FARM_C	NO:051	Box_06	F1	Goat	Livestock_Goat	11/6/2018
UG552	FARM_C	NO:052	Box_06	F2	Goat	Livestock_Goat	11/6/2018
UG553	FARM_C	NO:053	Box_06	F3	Goat	Livestock_Goat	11/6/2018
UG554	FARM_C	NO:054	Box_06	F4	Goat	Livestock_Goat	11/6/2018
UG555	FARM_C	NO:055	Box_06	F5	Goat	Livestock_Goat	11/6/2018
UG556	FARM_C	NO:056	Box_06	F6	Goat	Livestock_Goat	11/6/2018
UG557	FARM_C	NO:057	Box_06	F7	Goat	Livestock_Goat	11/6/2018
UG558	FARM_C	NO:058	Box_06	F8	Goat	Livestock_Goat	11/6/2018
UG559	FARM_C	NO:059	Box_06	F9	Goat	Livestock_Goat	11/6/2018
UG560	FARM_C	NO:060	Box_06	F10	Goat	Livestock_Goat	11/6/2018
UG561	FARM_C	NO:061	Box_06	G1	Goat	Livestock_Goat	11/6/2018
UG562	FARM_C	NO:062	Box_06	G2	Goat	Livestock_Goat	11/6/2018
UG563	FARM_C	NO:063	Box_06	G3	Goat	Livestock_Goat	11/6/2018
UG564	FARM_C	NO:064	Box_06	G4	Goat	Livestock_Goat	11/6/2018
UG565	FARM_C	NO:065	Box_06	G5	Goat	Livestock_Goat	11/6/2018
UG566	FARM_C	NO:066	Box_06	G6	Goat	Livestock_Goat	11/6/2018
UG567	FARM_C	NO:067	Box_06	G7	Goat	Livestock_Goat	12/6/2018
UG568	FARM_C	NO:068	Box_06	G8	Goat	Livestock_Goat	12/6/2018
UG569	FARM_C	NO:069	Box_06	G9	Goat	Livestock_Goat	12/6/2018
UG570	FARM_C	NO:070	Box_06	G10	Goat	Livestock_Goat	12/6/2018
UG571	FARM_C	NO:071	Box_06	H1	Goat	Livestock_Goat	12/6/2018
UG572	FARM_C	NO:072	Box_06	H2	Goat	Livestock_Goat	12/6/2018
UG573	FARM_C	NO:021	Box_06	H3	Goat	Livestock_Goat	11/6/2018
UG574			Box_06	H4			
UG575			Box_06	H5			
UG576			Box_06	H6			
UG577			Box_06	H7			
UG578			Box_06	H8			
UG579			Box_06	H9			
UG580			Box_06	H10			
UG581			Box_06	I1			
UG582			Box_06	I2			
UG583			Box_06	I3			
UG584			Box_06	I4			
UG585			Box_06	I5			
UG586			Box_06	I6			
UG587			Box_06	I7			
UG588			Box_06	I8			
UG589			Box_06	I9			
UG590			Box_06	I10			
UG591			Box_06	J1			
UG592			Box_06	J2			
UG593			Box_06	J3			
UG594			Box_06	J4			
UG595			Box_06	J5			
UG596			Box_06	J6			
UG597			Box_06	J7			
UG598			Box_06	J8			
UG599			Box_06	J9			
UG600			Box_06	J10			

7.1.4.1.2 DNA extraction protocol

PC3 lab DNA extraction from faeces

The following is an outline for DNA extraction from ~555 human, gorilla, cattle and goat faecal samples imported from Uganda. Samples arrived in the Hopkirk on October 1st 2018 under MPI permit number 2018068860.

Preparation and transfer of material Faecal samples in RNA later solution are stored in the walk in fridge in the Hopkirk PC2 (2.60). These will be transported in batches of twenty four into room 2.09 (PC3) inside sterile freezer boxes, previously decontaminated by spraying with 5% SteriGENE Clear and waiting 10 mins. Once inside, they will be placed in the Class II Biological Safety cabinet. After step 1 of methods below, sample box will then be sprayed with 5% SteriGENE Clear, left for 10 minutes and then removed from the Class II Biological Safety cabinet. Samples will be transferred to the fridge (PC3) to keep them cold during processing and returned to Hopkirk PC2 (walk in fridge 2.60) at the end of the day. Once all samples are completed (step 13 of methods below), NAS-containing tubes and box will be wiped with 5% SteriGENE Clear before being removed from the PC3 lab and returned to the Hopkirk PC2 -80 freezer (2.62).

All liquid handling and tube opening (steps 1-12) will take place inside the Class II Biological Safety cabinet. Closed tubes will be carefully transferred outside cabinet in bullet racks for bead beating and centrifugation steps and returned to the cabinet immediately following these processes. All waste generated during sample processing will be disposed of following normal PC3 guidelines – see page 3 of document.

NAS extraction protocol – Zymo Quick-DNA™ Fecal/Soil Microbe Miniprep Kit

1. Add ≤ 150 mg of faecal sample to a ZR BashingBead™ Lysis tube (0.1 & 0.5 mm). Add 750 μ l BashingBead™ Buffer to the tube.
2. Secure in a bead beater fitted with a 2 ml tube holder assembly and process at maximum speed for 3 minutes
3. Centrifuge the ZR BashingBead™ Lysis Tube (0.1 & 0.5 mm) in a microcentrifuge at $\geq 10,000 \times g$ for 1 minute
4. Transfer up to 400 μ l supernatant to a Zymo-Spin™ III-F Filter in a Collection Tube and centrifuge at $8,000 \times g$ for 1 minute
5. Add 1,200 μ l of Genomic Lysis Buffer to the filtrate in the Collection Tube from Step 4
6. Transfer 800 μ l of the mixture from Step 5 to a Zymo-Spin™ IIC Column in a Collection Tube and centrifuge at $10,000 \times g$ for 1 minute
7. Discard the flow through from the Collection Tube and repeat Step 6
8. Add 200 μ l DNA Pre-Wash Buffer to the Zymo-Spin™ IIC Column in a new Collection Tube and centrifuge at $10,000 \times g$ for 1 minute
9. Add 500 μ l g-DNA Wash Buffer to the Zymo-Spin™ IIC Column and centrifuge at $10,000 \times g$ for 1 minute
10. Transfer the Zymo-Spin™ IIC Column to a clean 1.5 ml microcentrifuge tube and add 100 μ l (50 μ l minimum) DNA Elution Buffer directly to the column matrix. Centrifuge at $10,000 \times g$ for 30 seconds to elute the DNA
11. Place a Zymo-Spin™ III-HRC Filter in a clean Collection Tube and add 600 μ l Prep Solution. Centrifuge at $8,000 \times g$ for 3 minutes
12. Transfer the eluted DNA to a prepared Zymo-Spin™ III-HRC Filter in a clean 1.5 ml microcentrifuge tube and centrifuge at exactly $16,000 \times g$ for 3 minutes
13. DNA-containing tubes and box will be wiped with 5% SteriGENE Clear before being removed from the PC3 lab and returned to the Hopkirk PC2

Personal Protective Equipment

- A disposable lab coat shall be worn for all manipulations involving faecal samples.
- Double gloves shall be worn when working in the Class II Biological Safety cabinet; the outermost layer of gloves shall be discarded as Dry Waste prior to exiting the Class II Biological Safety cabinet.
- Disposable overshoes shall be worn for all manipulations involving the use of faecal samples.

Biohazard Waste Disposal

- Before undertaking work each day the autoclaving/disposal requirements should be discussed with the Laboratory Services personnel.
- All dry waste (tissues, filters, used tips etc) used within a Class II cabinet shall be collected in a plastic bag within a container in the Class II cabinet. When full, the top of the bag should be folded over to create a loose seal and sprayed with 5% SteriGENE Clear disinfectant. After 10 minutes, the discard bag should then be removed from the Class II cabinet and placed within an autoclave bag labelled "Biological Hazard" within the closed waste bins provided in each laboratory.
- All liquid waste from the Zymo Quick-DNA™ Fecal/Soil Microbe Miniprep Kit produced within a Class II cabinet shall be collected in a labelled blue-capped Schott bottle. The bottle should be kept in the Class II cabinet. At the end of each day the exterior of the capped bottle shall be sprayed thoroughly with 5% SteriGENE Clear disinfectant. After 10 minutes, the Schott bottle should then be removed from the Class II cabinet and placed within the closed waste bins provided in each laboratory prior to removal from the laboratory for autoclaving. Lab services staff shall be informed of the presence of this waste in the autoclave load.
- General laboratory waste shall be collected in biohazard bags and closed using tape. The exterior of the bags shall be sprayed thoroughly with 5% SteriGENE Clear disinfectant and held in the closed waste bins provided in each laboratory.
- The closed waste bin shall then be taken out of the laboratory on a trolley to await autoclaving; Lab Services personnel shall be informed that waste is available for autoclaving. All waste should be autoclaved as soon as possible after bags/containers are placed in the Restricted Corridor 2.07 – preferably the bags should go straight into the autoclave.
- No sharps or anything that may puncture the bags are to be disposed of in the autoclave bags. Sharps are to be collected in the specialised containers provided and the full containers autoclaved.

Spillage of microorganisms

- Full details of procedures to take if a spillage of microorganisms occurs can be found in the Hopkirk Institute PC3 Containment Manual.

- In every case of a spillage of organisms or infectious materials of any risk group a 'Bacterial/Infectious Material Spillage Report Form' must be completed and handed to a PC3 Manager or the Facility Manager. All report forms shall be retained by the Facility Manager.
- Refer to PC3 Containment Manual Appendix 2B: Personal Safety & the Procedure for Decontaminating Laboratories and Equipment following Accidental Spillage of Hazardous Micro-organisms
- Refer to PC3 Containment Manual Appendix 8: Notice of Procedures for Dealing with Accidental Spillage and Contamination by Pathogenic Organisms
- Refer to PC3 Containment Manual Appendix 13: Bacterial / Infectious Material Spillage Report Form

Spills Outside a Class II Biosafety Cabinet

- In the event of spillage of faecal samples, staff must follow the procedures specified for decontamination.
- Generally the greatest risk from a spill of infectious material is from contamination through aerosol generation. In the PC3 laboratories in the Hopkirk there is continuous air movement and aerosols can be dispersed rapidly. It is therefore important to leave the contaminated areas as quickly and as safely as possible.
- If clothing and footwear, or exposed body areas have possibly been contaminated, measures must be taken to get rid of the bulk of the infectious material before exiting the airlock. A change of clothing is provided in the airlock to each PC3 laboratory.
- Only when you are in a position of safety and the laboratory is contained should steps be taken to decontaminate.
- Do not enter the contaminated area for at least an hour. This allows aerosols to be diluted or removed through continuous air changes and liquid spillages to dry. This will substantially reduce the contamination risk. All contaminated or potential contaminated material must be decontaminated, preferably by autoclaving.
- If a breach in secondary containment has occurred within the PC3 laboratory (such as a break in the outer biohazard bag, but not the inner vessel/bag and there has been no spill of the bacteria) fix the containment problem by placing all containers affected by the breach in a third container/bag and report this to one of the PC3 Laboratory Managers.

Spills Inside a Class II Biosafety Cabinet

- Spills of up to 1 ml treated by wiping or flooding with a suitable disinfectant solution.
- In the event of a larger spill, staff shall ensure the cabinet remains operating and, with gloved hands, lay down absorbent material wetted with disinfectant such as 5% SteriGENE Clear and allow a minimum time of 10 minutes to effect disinfection. Absorbent material shall then be discarded in the biohazard plastic-lined waste bins provided in every laboratory.

Post Extraction Processing

Qubit DNA extractions

MDA following instructions for Genomiphi kit.

https://us.vwr.com/assetsvc/asset/en_US/id/16614366/contents/29013587_instructions.pdf

Qubit amplified DNA

5-10 ug each sample added to DNA stable plate

7.1.4.1.3 Sample metadata

DNASTABLE_PLATE_01	DNASTABLE_PLATE_02	DNASTABLE_PLATE_03	DNASTABLE_PLATE_04	DNASTABLE_PLATE_05	DNASTABLE_PLATE_06
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7.1.4.1.4 Pooled samples metadata

LAB METADATA							LAB METADATA		
Mepi Number	Qubit DNA extraction	Pool_Name	DNA_POOLING_GROUP	ng target	ul required	pooled vol	Mepi Number	ul required	pooled vol
UG001	42.8 UG_DNA_01	GORILLA_WILD_01		20	0.47		UG001	0.47	
UG002	33.8 UG_DNA_01	GORILLA_WILD_01		20	0.59		UG002	0.59	
UG003	35.6 UG_DNA_01	GORILLA_WILD_01		20	0.56		UG003	0.56	
UG004	44.6 UG_DNA_01	GORILLA_WILD_01		20	0.45		UG004	0.45	
UG005	14.5 UG_DNA_01	GORILLA_WILD_01		20	1.38		UG005	1.38	
UG006	12.8 UG_DNA_01	GORILLA_WILD_01		20	1.56		UG006	1.56	
UG007	22.8 UG_DNA_01	GORILLA_WILD_01		20	0.88		UG007	0.88	
UG008	19.7 UG_DNA_01	GORILLA_WILD_01		20	1.02		UG008	1.02	
UG009	17.2 UG_DNA_01	GORILLA_WILD_01		20	1.16		UG009	1.16	
UG010	23.2 UG_DNA_01	GORILLA_WILD_01		20	0.86		UG010	0.86	
UG011	16 UG_DNA_01	GORILLA_WILD_01		20	1.25		UG011	1.25	
UG012	8.24 UG_DNA_01	GORILLA_WILD_01		20	2.43		UG012	2.43	
UG013	39.4 UG_DNA_01	GORILLA_WILD_01		20	0.51		UG013	0.51	
UG014	23.2 UG_DNA_01	GORILLA_WILD_01		20	0.86		UG014	0.86	
UG015	16.9 UG_DNA_01	GORILLA_WILD_01		20	1.18		UG015	1.18	
UG016	13.5 UG_DNA_01	GORILLA_WILD_01		20	1.48		UG016	1.48	
UG017	2.84 UG_DNA_01	GORILLA_WILD_01		20	7.04		UG017	7.04	
UG018	32.6 UG_DNA_01	GORILLA_WILD_01		20	0.61		UG018	0.61	
UG019	10 UG_DNA_01	GORILLA_WILD_01		20	2.00		UG019	2.00	
UG020	20 UG_DNA_01	GORILLA_WILD_01		20	1.00	27.3	UG020	1.00	27.3
UG021	40.4 UG_DNA_02	GORILLA_WILD_02		20	0.50		UG021	0.50	
UG022	56.8 UG_DNA_02	GORILLA_WILD_02		20	0.35		UG022	0.35	
UG023	12.6 UG_DNA_02	GORILLA_WILD_02		20	1.59		UG023	1.59	
UG024	32 UG_DNA_02	GORILLA_WILD_02		20	0.63		UG024	0.63	
UG025	27.6 UG_DNA_02	GORILLA_WILD_02		20	0.72		UG025	0.72	
UG026	7.68 UG_DNA_02	GORILLA_WILD_02		20	2.60		UG026	2.60	
UG027	60 UG_DNA_02	GORILLA_WILD_02		20	0.33		UG027	0.33	
UG028	1.24 UG_DNA_02	GORILLA_WILD_02		20	16.13		UG028	10.00	
UG029	47.8 UG_DNA_02	GORILLA_WILD_02		20	0.42		UG029	0.42	
UG030	10.1 UG_DNA_02	GORILLA_WILD_02		20	1.98		UG030	1.98	
UG031	13.3 UG_DNA_02	GORILLA_WILD_02		20	1.50		UG031	1.50	
UG032	3.38 UG_DNA_02	GORILLA_WILD_02		20	5.92		UG032	5.92	
UG033	7.6 UG_DNA_02	GORILLA_WILD_02		20	2.63		UG033	2.63	
UG034	15.1 UG_DNA_02	GORILLA_WILD_02		20	1.32		UG034	1.32	
UG035	10.1 UG_DNA_02	GORILLA_WILD_02		20	1.98		UG035	1.98	
UG036	4.22 UG_DNA_02	GORILLA_WILD_02		20	4.74		UG036	4.74	
UG037	36.4 UG_DNA_02	GORILLA_WILD_02		20	0.55		UG037	0.55	
UG038	13.2 UG_DNA_02	GORILLA_WILD_02		20	1.52		UG038	1.52	
UG039	15.9 UG_DNA_02	GORILLA_WILD_02		20	1.26		UG039	1.26	
UG040	51 UG_DNA_02	GORILLA_WILD_02		20	0.39	47.1	UG040	0.39	40.9
UG041	12 UG_DNA_03	GORILLA_WILD_03		20	1.67		UG041	1.67	
UG042	11.5 UG_DNA_03	GORILLA_WILD_03		20	1.74		UG042	1.74	
UG043	17.1 UG_DNA_03	GORILLA_WILD_03		20	1.17		UG043	1.17	
UG044	9.22 UG_DNA_03	GORILLA_WILD_03		20	2.17		UG044	2.17	
UG045	13.5 UG_DNA_03	GORILLA_WILD_03		20	1.48		UG045	1.48	
UG046	9.84 UG_DNA_03	GORILLA_WILD_03		20	2.03		UG046	2.03	
UG047	4.87 UG_DNA_03	GORILLA_WILD_03		20	4.11		UG047	4.11	
UG048	9.3 UG_DNA_03	GORILLA_WILD_03		20	2.15		UG048	2.15	
UG049	10.2 UG_DNA_03	GORILLA_WILD_03		20	1.96		UG049	1.96	
UG050	1.96 UG_DNA_03	GORILLA_WILD_03		20	10.20		UG050	10.00	
UG051	1.85 UG_DNA_03	GORILLA_WILD_03		20	10.81		UG051	10.00	
UG052	29.5 UG_DNA_03	GORILLA_WILD_03		20	0.68		UG052	0.68	
UG053	11.1 UG_DNA_03	GORILLA_WILD_03		20	1.80		UG053	1.80	
UG054	17.1 UG_DNA_03	GORILLA_WILD_03		20	1.17		UG054	1.17	
UG055	5.44 UG_DNA_03	GORILLA_WILD_03		20	3.68		UG055	3.68	
UG056	2.12 UG_DNA_03	GORILLA_WILD_03		20	9.43		UG056	9.43	
UG057	16.8 UG_DNA_03	GORILLA_WILD_03		20	1.19		UG057	1.19	
UG058	14.3 UG_DNA_03	GORILLA_WILD_03		20	1.40		UG058	1.40	
UG059	8.23 UG_DNA_03	GORILLA_WILD_03		20	2.43		UG059	2.43	
UG060	10.3 UG_DNA_03	GORILLA_WILD_03		20	1.94	63.2	UG060	1.94	62.2
UG061	25.1 UG_DNA_04	GORILLA_WILD_04		20	0.80		UG061	0.80	
UG062	11.5 UG_DNA_04	GORILLA_WILD_04		20	1.74		UG062	1.74	
UG063	4.45 UG_DNA_04	GORILLA_WILD_04		20	4.49		UG063	4.49	
UG064	14.3 UG_DNA_04	GORILLA_WILD_04		20	1.40		UG064	1.40	
UG065	21.9 UG_DNA_04	GORILLA_WILD_04		20	0.91		UG065	0.91	
UG066	7.14 UG_DNA_04	GORILLA_WILD_04		20	2.80		UG066	2.80	
UG067	6.62 UG_DNA_04	GORILLA_WILD_04		20	3.02		UG067	3.02	
UG068	11 UG_DNA_04	GORILLA_WILD_04		20	1.82		UG068	1.82	
UG069	7.43 UG_DNA_04	GORILLA_WILD_04		20	2.69		UG069	2.69	
UG070	48.8 UG_DNA_04	GORILLA_WILD_04		20	0.41		UG070	0.41	
UG071	4.22 UG_DNA_04	GORILLA_WILD_04		20	4.74		UG071	4.74	
UG072	12.9 UG_DNA_04	GORILLA_WILD_04		20	1.55		UG072	1.55	
UG073	10.7 UG_DNA_04	GORILLA_WILD_04		20	1.87		UG073	1.87	
UG074	34.6 UG_DNA_04	GORILLA_WILD_04		20	0.58		UG074	0.58	
UG075	10.5 UG_DNA_04	GORILLA_WILD_04		20	1.90		UG075	1.90	
UG076	53 UG_DNA_04	GORILLA_WILD_04		20	0.38		UG076	0.38	
UG077	12.9 UG_DNA_04	GORILLA_WILD_04		20	1.55		UG077	1.55	
UG078	8 UG_DNA_04	GORILLA_WILD_04		20	2.50		UG078	2.50	
UG079	10.4 UG_DNA_04	GORILLA_WILD_04		20	1.92		UG079	1.92	
UG080	2.12 UG_DNA_04	GORILLA_WILD_04		20	9.43	46.5	UG080	9.43	46.5
UG081	31.7 UG_DNA_05	GORILLA_WILD_05		20	0.63		UG081	0.63	
UG082	6.49 UG_DNA_05	GORILLA_WILD_05		20	3.08		UG082	3.08	
UG083	20 UG_DNA_05	GORILLA_WILD_05		20	1.00		UG083	1.00	
UG084	25.5 UG_DNA_05	GORILLA_WILD_05		20	0.78		UG084	0.78	
UG085	21.2 UG_DNA_05	GORILLA_WILD_05		20	0.94		UG085	0.94	
UG086	22.1 UG_DNA_05	GORILLA_WILD_05		20	0.90		UG086	0.90	

UG087	15.4	UG_DNA_05	GORILLA_WILD_05	20	1.30		UG087	1.30	
UG088	10.9	UG_DNA_05	GORILLA_WILD_05	20	1.83		UG088	1.83	
UG089	41.3	UG_DNA_05	GORILLA_WILD_05	20	0.48		UG089	0.48	
UG090	26.3	UG_DNA_05	GORILLA_WILD_05	20	0.76		UG090	0.76	
UG091	9.34	UG_DNA_05	GORILLA_WILD_05	20	2.14		UG091	2.14	
UG092	10.9	UG_DNA_05	GORILLA_WILD_05	20	1.83		UG092	1.83	
UG093	14	UG_DNA_05	GORILLA_WILD_05	20	1.43		UG093	1.43	
UG094	0.655	UG_DNA_05	GORILLA_WILD_05	20	30.53		UG094	10.00	
UG095	7.74	UG_DNA_05	GORILLA_WILD_05	20	2.58		UG095	2.58	
UG096	7.28	UG_DNA_05	GORILLA_WILD_05	20	2.75		UG096	2.75	
UG097	4.57	UG_DNA_05	GORILLA_WILD_05	20	4.38		UG097	4.38	
UG098	7.43	UG_DNA_05	GORILLA_WILD_05	20	2.69		UG098	2.69	
UG099	33.6	UG_DNA_05	GORILLA_WILD_05	20	0.60		UG099	0.60	
UG100	3.86	UG_DNA_05	GORILLA_WILD_05	20	5.18	65.8	UG100	5.18	45.3
UG101	14.1	UG_DNA_06	GORILLA_HABITUATED_01	40	2.84		UG101	2.84	
UG102	8.48	UG_DNA_06	GORILLA_HABITUATED_01	40	4.72		UG102	4.72	
UG103	10.8	UG_DNA_06	GORILLA_HABITUATED_01	40	3.70		UG103	3.70	
UG104	16.6	UG_DNA_06	GORILLA_HABITUATED_01	40	2.41		UG104	2.41	
UG105	14.8	UG_DNA_06	GORILLA_HABITUATED_01	40	2.70		UG105	2.70	
UG106	16.7	UG_DNA_06	GORILLA_HABITUATED_01	40	2.40		UG106	2.40	
UG107	30.4	UG_DNA_06	GORILLA_HABITUATED_01	40	1.32		UG107	1.32	
UG108	18.3	UG_DNA_06	GORILLA_HABITUATED_01	40	2.19		UG108	2.19	
UG109	28.8	UG_DNA_06	GORILLA_HABITUATED_01	40	1.39		UG109	1.39	
UG110	31.2	UG_DNA_06	GORILLA_HABITUATED_01	40	1.28		UG110	1.28	
UG111	18	UG_DNA_06	GORILLA_HABITUATED_01	40	2.22		UG111	2.22	
UG112	39.6	UG_DNA_06	GORILLA_HABITUATED_01	40	1.01		UG112	1.01	
UG113	31.2	UG_DNA_06	GORILLA_HABITUATED_01	40	1.28		UG113	1.28	
UG114	6.36	UG_DNA_06	GORILLA_HABITUATED_01	40	6.29		UG114	6.29	
UG115	33.4	UG_DNA_06	GORILLA_HABITUATED_01	40	1.20		UG115	1.20	
UG116	4.52	UG_DNA_06	GORILLA_HABITUATED_01	40	8.85		UG116	8.85	
UG117	40.4	UG_DNA_06	GORILLA_HABITUATED_01	40	0.99		UG117	0.99	
UG118	19.8	UG_DNA_06	GORILLA_HABITUATED_01	40	2.02		UG118	2.02	
UG119	17.9	UG_DNA_06	GORILLA_HABITUATED_01	40	2.23		UG119	2.23	
UG120	10.2	UG_DNA_06	GORILLA_HABITUATED_01	40	3.92	55.0	UG120	3.92	55.0
UG121	34.8	UG_DNA_07	GORILLA_HABITUATED_02	40	1.15		UG121	1.15	
UG122	17.8	UG_DNA_07	GORILLA_HABITUATED_02	40	2.25		UG122	2.25	
UG123	16.9	UG_DNA_07	GORILLA_HABITUATED_02	40	2.37		UG123	2.37	
UG124	53	UG_DNA_07	GORILLA_HABITUATED_02	40	0.75		UG124	0.75	
UG125	18.6	UG_DNA_07	GORILLA_HABITUATED_02	40	2.15		UG125	2.15	
UG126	32.4	UG_DNA_07	GORILLA_HABITUATED_02	40	1.23		UG126	1.23	
UG127	24	UG_DNA_07	GORILLA_HABITUATED_02	40	1.67		UG127	1.67	
UG128	57.4	UG_DNA_07	GORILLA_HABITUATED_02	40	0.70		UG128	0.70	
UG129	41.8	UG_DNA_07	GORILLA_HABITUATED_02	40	0.96		UG129	0.96	
UG130	20.6	UG_DNA_07	GORILLA_HABITUATED_02	40	1.94		UG130	1.94	
UG131	30.6	UG_DNA_07	GORILLA_HABITUATED_02	40	1.31		UG131	1.31	
UG132	24.6	UG_DNA_07	GORILLA_HABITUATED_02	40	1.63		UG132	1.63	
UG133	32.2	UG_DNA_07	GORILLA_HABITUATED_02	40	1.24		UG133	1.24	
UG134	3.18	UG_DNA_07	GORILLA_HABITUATED_02	40	12.58		UG134	10.00	
UG135	46.4	UG_DNA_07	GORILLA_HABITUATED_02	40	0.86		UG135	0.86	
UG136	78.4	UG_DNA_07	GORILLA_HABITUATED_02	40	0.51		UG136	0.51	
UG137	37.2	UG_DNA_07	GORILLA_HABITUATED_02	40	1.08		UG137	1.08	
UG138	77.2	UG_DNA_07	GORILLA_HABITUATED_02	40	0.52		UG138	0.52	
UG139	57	UG_DNA_07	GORILLA_HABITUATED_02	40	0.70		UG139	0.70	
UG140	39.6	UG_DNA_07	GORILLA_HABITUATED_02	40	1.01	36.6	UG140	1.01	34.0
UG141	15.8	UG_DNA_08	GORILLA_HABITUATED_03	40	2.53		UG141	2.53	
UG142	23.6	UG_DNA_08	GORILLA_HABITUATED_03	40	1.69		UG142	1.69	
UG143	9.78	UG_DNA_08	GORILLA_HABITUATED_03	40	4.09		UG143	4.09	
UG144	3.84	UG_DNA_08	GORILLA_HABITUATED_03	40	10.42		UG144	10.00	
UG145	33.2	UG_DNA_08	GORILLA_HABITUATED_03	40	1.20		UG145	1.20	
UG146	17.5	UG_DNA_08	GORILLA_HABITUATED_03	40	2.29		UG146	2.29	
UG147	21	UG_DNA_08	GORILLA_HABITUATED_03	40	1.90		UG147	1.90	
UG148	21.6	UG_DNA_08	GORILLA_HABITUATED_03	40	1.85		UG148	1.85	
UG149	19.5	UG_DNA_08	GORILLA_HABITUATED_03	40	2.05		UG149	2.05	
UG150	37.4	UG_DNA_08	GORILLA_HABITUATED_03	40	1.07		UG150	1.07	
UG151	33	UG_DNA_08	GORILLA_HABITUATED_03	40	1.21		UG151	1.21	
UG152	6.44	UG_DNA_08	GORILLA_HABITUATED_03	40	6.21		UG152	6.21	
UG153	35.2	UG_DNA_08	GORILLA_HABITUATED_03	40	1.14		UG153	1.14	
UG154	4.62	UG_DNA_08	GORILLA_HABITUATED_03	40	8.66		UG154	8.66	
UG155	12.7	UG_DNA_08	GORILLA_HABITUATED_03	40	3.15		UG155	3.15	
UG156	11.2	UG_DNA_08	GORILLA_HABITUATED_03	40	3.57		UG156	3.57	
UG157	38.2	UG_DNA_08	GORILLA_HABITUATED_03	40	1.05		UG157	1.05	
UG158	35	UG_DNA_08	GORILLA_HABITUATED_03	40	1.14		UG158	1.14	
UG159	108	UG_DNA_08	GORILLA_HABITUATED_03	40	0.37		UG159	0.37	
UG160	53.4	UG_DNA_08	GORILLA_HABITUATED_03	40	0.75	56.3	UG160	0.75	55.9
UG161	51.4	UG_DNA_09	GORILLA_HABITUATED_04	40	0.78		UG161	0.78	
UG162	63.4	UG_DNA_09	GORILLA_HABITUATED_04	40	0.63		UG162	0.63	
UG163	10.9	UG_DNA_09	GORILLA_HABITUATED_04	40	3.67		UG163	3.67	
UG164	32.2	UG_DNA_09	GORILLA_HABITUATED_04	40	1.24		UG164	1.24	
UG165	19.1	UG_DNA_09	GORILLA_HABITUATED_04	40	2.09		UG165	2.09	
UG166	49.8	UG_DNA_09	GORILLA_HABITUATED_04	40	0.80		UG166	0.80	
UG167	39	UG_DNA_09	GORILLA_HABITUATED_04	40	1.03		UG167	1.03	
UG168	6.76	UG_DNA_09	GORILLA_HABITUATED_04	40	5.92		UG168	5.92	
UG169	22.4	UG_DNA_09	GORILLA_HABITUATED_04	40	1.79		UG169	1.79	
UG170	116	UG_DNA_09	GORILLA_HABITUATED_04	40	0.34		UG170	0.34	
UG171	29.2	UG_DNA_09	GORILLA_HABITUATED_04	40	1.37		UG171	1.37	
UG172	37	UG_DNA_09	GORILLA_HABITUATED_04	40	1.08		UG172	1.08	
UG173	49.2	UG_DNA_09	GORILLA_HABITUATED_04	40	0.81		UG173	0.81	
UG174	59.6	UG_DNA_09	GORILLA_HABITUATED_04	40	0.67		UG174	0.67	

UG175	8.32	UG_DNA_09	GORILLA_HABITUATED_04	40	4.81		UG175	4.81	
UG176	20.2	UG_DNA_09	GORILLA_HABITUATED_04	40	1.98		UG176	1.98	
UG177	79.4	UG_DNA_09	GORILLA_HABITUATED_04	40	0.50		UG177	0.50	
UG178	38.4	UG_DNA_09	GORILLA_HABITUATED_04	40	1.04		UG178	1.04	
UG179	9.98	UG_DNA_09	GORILLA_HABITUATED_04	40	4.01		UG179	4.01	
UG180	19.3	UG_DNA_09	GORILLA_HABITUATED_04	40	2.07	36.6	UG180	2.07	36.6
UG181	87.4	UG_DNA_10	GORILLA_HABITUATED_05	40	0.46		UG181	0.46	
UG182	29	UG_DNA_10	GORILLA_HABITUATED_05	40	1.38		UG182	1.38	
UG183	53.8	UG_DNA_10	GORILLA_HABITUATED_05	40	0.74		UG183	0.74	
UG184	63.4	UG_DNA_10	GORILLA_HABITUATED_05	40	0.63		UG184	0.63	
UG185	25.8	UG_DNA_10	GORILLA_HABITUATED_05	40	1.55		UG185	1.55	
UG186	54.4	UG_DNA_10	GORILLA_HABITUATED_05	40	0.74		UG186	0.74	
UG187	102	UG_DNA_10	GORILLA_HABITUATED_05	40	0.39		UG187	0.39	
UG188	112	UG_DNA_10	GORILLA_HABITUATED_05	40	0.36		UG188	0.36	
UG189	36	UG_DNA_10	GORILLA_HABITUATED_05	40	1.11		UG189	1.11	
UG190	21	UG_DNA_10	GORILLA_HABITUATED_05	40	1.90		UG190	1.90	
UG191	61.2	UG_DNA_10	GORILLA_HABITUATED_05	40	0.65		UG191	0.65	
UG192	47.8	UG_DNA_10	GORILLA_HABITUATED_05	40	0.84		UG192	0.84	
UG193	70.2	UG_DNA_10	GORILLA_HABITUATED_05	40	0.57		UG193	0.57	
UG194	53	UG_DNA_10	GORILLA_HABITUATED_05	40	0.75		UG194	0.75	
UG195	12.2	UG_DNA_10	GORILLA_HABITUATED_05	40	3.28		UG195	3.28	
UG196	51	UG_DNA_10	GORILLA_HABITUATED_05	40	0.78		UG196	0.78	
UG197	33.8	UG_DNA_10	GORILLA_HABITUATED_05	40	1.18		UG197	1.18	
UG198	25.2	UG_DNA_10	GORILLA_HABITUATED_05	40	1.59		UG198	1.59	
UG199	36.8	UG_DNA_10	GORILLA_HABITUATED_05	40	1.09		UG199	1.09	
UG200	16.1	UG_DNA_10	GORILLA_HABITUATED_05	40	2.48	22.5	UG200	2.48	22.5
UG201	85.4	UG_DNA_11	HUMAN_HOSPITAL_01	100	1.17		UG201	1.17	
UG202	62.2	UG_DNA_11	HUMAN_HOSPITAL_01	100	1.61		UG202	1.61	
UG203	104	UG_DNA_11	HUMAN_HOSPITAL_01	100	0.96		UG203	0.96	
UG204	120	UG_DNA_11	HUMAN_HOSPITAL_01	100	0.83		UG204	0.83	
UG205	118	UG_DNA_11	HUMAN_HOSPITAL_01	100	0.85		UG205	0.85	
UG206	51.2	UG_DNA_11	HUMAN_HOSPITAL_01	100	1.95		UG206	1.95	
UG207	112	UG_DNA_11	HUMAN_HOSPITAL_01	100	0.89		UG207	0.89	
UG208	24	UG_DNA_11	HUMAN_HOSPITAL_01	100	4.17		UG208	4.17	
UG209	14	UG_DNA_11	HUMAN_HOSPITAL_01	100	7.14		UG209	7.14	
UG210	29.2	UG_DNA_11	HUMAN_HOSPITAL_01	100	3.42		UG210	3.42	
UG211	70	UG_DNA_11	HUMAN_HOSPITAL_01	100	1.43		UG211	1.43	
UG212	5.78	UG_DNA_11	HUMAN_HOSPITAL_01	100	17.30		UG212	10.00	
UG213	110	UG_DNA_11	HUMAN_HOSPITAL_01	100	0.91		UG213	0.91	
UG214	118	UG_DNA_11	HUMAN_HOSPITAL_01	100	0.85		UG214	0.85	
UG215	118	UG_DNA_11	HUMAN_HOSPITAL_01	100	0.85		UG215	0.85	
UG216	50	UG_DNA_11	HUMAN_HOSPITAL_01	100	2.00		UG216	2.00	
UG217	102	UG_DNA_11	HUMAN_HOSPITAL_01	100	0.98		UG217	0.98	
UG218	108	UG_DNA_11	HUMAN_HOSPITAL_01	100	0.93		UG218	0.93	
UG219	118	UG_DNA_11	HUMAN_HOSPITAL_01	100	0.85		UG219	0.85	
UG220	83	UG_DNA_11	HUMAN_HOSPITAL_01	100	1.20	50.3	UG220	1.20	43.0
UG221	51.6	UG_DNA_12	HUMAN_HOSPITAL_02	100	1.94		UG221	1.94	
UG222	104	UG_DNA_12	HUMAN_HOSPITAL_02	100	0.96		UG222	0.96	
UG223	99	UG_DNA_12	HUMAN_HOSPITAL_02	100	1.01		UG223	1.01	
UG224	102	UG_DNA_12	HUMAN_HOSPITAL_02	100	0.98		UG224	0.98	
UG225	112	UG_DNA_12	HUMAN_HOSPITAL_02	100	0.89		UG225	0.89	
UG226	91	UG_DNA_12	HUMAN_HOSPITAL_02	100	1.10		UG226	1.10	
UG227	112	UG_DNA_12	HUMAN_HOSPITAL_02	100	0.89		UG227	0.89	
UG228	32.2	UG_DNA_12	HUMAN_HOSPITAL_02	100	3.11		UG228	3.11	
UG229	104	UG_DNA_12	HUMAN_HOSPITAL_02	100	0.96		UG229	0.96	
UG230	36	UG_DNA_12	HUMAN_HOSPITAL_02	100	2.78		UG230	2.78	
UG231	69	UG_DNA_12	HUMAN_HOSPITAL_02	100	1.45		UG231	1.45	
UG232	110	UG_DNA_12	HUMAN_HOSPITAL_02	100	0.91		UG232	0.91	
UG233	47.8	UG_DNA_12	HUMAN_HOSPITAL_02	100	2.09		UG233	2.09	
UG234	104	UG_DNA_12	HUMAN_HOSPITAL_02	100	0.96		UG234	0.96	
UG235	51.8	UG_DNA_12	HUMAN_HOSPITAL_02	100	1.93		UG235	1.93	
UG236	62	UG_DNA_12	HUMAN_HOSPITAL_02	100	1.61		UG236	1.61	
UG237	15.7	UG_DNA_12	HUMAN_HOSPITAL_02	100	6.37		UG237	6.37	
UG238	53.2	UG_DNA_12	HUMAN_HOSPITAL_02	100	1.88		UG238	1.88	
UG239	38.2	UG_DNA_12	HUMAN_HOSPITAL_02	100	2.62		UG239	2.62	
UG240	104	UG_DNA_12	HUMAN_HOSPITAL_02	100	0.96	35.4	UG240	0.96	35.4
UG241	89	UG_DNA_13	HUMAN_HOSPITAL_03	100	1.12		UG241	1.12	
UG242	8.58	UG_DNA_13	HUMAN_HOSPITAL_03	100	11.66		UG242	10.00	
UG243	75.6	UG_DNA_13	HUMAN_HOSPITAL_03	100	1.32		UG243	1.32	
UG244	110	UG_DNA_13	HUMAN_HOSPITAL_03	100	0.91		UG244	0.91	
UG245	118	UG_DNA_13	HUMAN_HOSPITAL_03	100	0.85		UG245	0.85	
UG246	15.2	UG_DNA_13	HUMAN_HOSPITAL_03	100	6.58		UG246	6.58	
UG247	147.5	UG_DNA_13	HUMAN_HOSPITAL_03	100	0.68		UG247	0.68	
UG248	89	UG_DNA_13	HUMAN_HOSPITAL_03	100	1.12		UG248	1.12	
UG249	108	UG_DNA_13	HUMAN_HOSPITAL_03	100	0.93		UG249	0.93	
UG250	81.8	UG_DNA_13	HUMAN_HOSPITAL_03	100	1.22		UG250	1.22	
UG251	112	UG_DNA_13	HUMAN_HOSPITAL_03	100	0.89		UG251	0.89	
UG252	70.8	UG_DNA_13	HUMAN_HOSPITAL_03	100	1.41		UG252	1.41	
UG253	91.6	UG_DNA_13	HUMAN_HOSPITAL_03	100	1.09		UG253	1.09	
UG254	110	UG_DNA_13	HUMAN_HOSPITAL_03	100	0.91		UG254	0.91	
UG255		UG_DNA_13		100			UG255		
UG256	116	UG_DNA_13	HUMAN_HOSPITAL_03	100	0.86		UG256	0.86	
UG257	54.6	UG_DNA_13	HUMAN_HOSPITAL_03	100	1.83		UG257	1.83	
UG258	108	UG_DNA_13	HUMAN_HOSPITAL_03	100	0.93		UG258	0.93	
UG259	118	UG_DNA_13	HUMAN_HOSPITAL_03	100	0.85		UG259	0.85	
UG260	6.68	UG_DNA_13	HUMAN_HOSPITAL_03	100	14.97	50.1	UG260	10.00	43.5
UG261	116	UG_DNA_14	HUMAN_HOSPITAL_04	100	0.86		UG261	0.86	
UG262	120	UG_DNA_14	HUMAN_HOSPITAL_04	100	0.83		UG262	0.83	

UG263	54.8 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.82		UG263	1.82
UG264	104 UG_DNA_14	HUMAN_HOSPITAL_04	100	0.96		UG264	0.96
UG265	92.8 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.08		UG265	1.08
UG266	96.2 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.04		UG266	1.04
UG267	110 UG_DNA_14	HUMAN_HOSPITAL_04	100	0.91		UG267	0.91
UG268	104 UG_DNA_14	HUMAN_HOSPITAL_04	100	0.96		UG268	0.96
UG269	108 UG_DNA_14	HUMAN_HOSPITAL_04	100	0.93		UG269	0.93
UG270	87 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.15		UG270	1.15
UG271	23 UG_DNA_14	HUMAN_HOSPITAL_04	100	4.35		UG271	4.35
UG272	92.8 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.08		UG272	1.08
UG273	96.6 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.04		UG273	1.04
UG274	88.4 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.13		UG274	1.13
UG275	104 UG_DNA_14	HUMAN_HOSPITAL_04	100	0.96		UG275	0.96
UG276	93.8 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.07		UG276	1.07
UG277	100 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.00		UG277	1.00
UG278	108 UG_DNA_14	HUMAN_HOSPITAL_04	100	0.93		UG278	0.93
UG279	81.6 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.23		UG279	1.23
UG280	96.6 UG_DNA_14	HUMAN_HOSPITAL_04	100	1.04	24.4	UG280	1.04 24.4
UG281	33.2 UG_DNA_15	HUMAN_HOSPITAL_05	100	3.01		UG281	3.01
UG282	110 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.91		UG282	0.91
UG283	104 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.96		UG283	0.96
UG284	90.6 UG_DNA_15	HUMAN_HOSPITAL_05	100	1.10		UG284	1.10
UG285	80.6 UG_DNA_15	HUMAN_HOSPITAL_05	100	1.24		UG285	1.24
UG286	110 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.91		UG286	0.91
UG287	112 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.89		UG287	0.89
UG288	102 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.98		UG288	0.98
UG289	102 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.98		UG289	0.98
UG290	100 UG_DNA_15	HUMAN_HOSPITAL_05	100	1.00		UG290	1.00
UG291	112 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.89		UG291	0.89
UG292	27 UG_DNA_15	HUMAN_HOSPITAL_05	100	3.70		UG292	3.70
UG293	75.2 UG_DNA_15	HUMAN_HOSPITAL_05	100	1.33		UG293	1.33
UG294	120 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.83		UG294	0.83
UG295	110 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.91		UG295	0.91
UG296	116 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.86		UG296	0.86
UG297	118 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.85		UG297	0.85
UG298	118 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.85		UG298	0.85
UG299	110 UG_DNA_15	HUMAN_HOSPITAL_05	100	0.91		UG299	0.91
UG300	80.4 UG_DNA_15	HUMAN_HOSPITAL_05	100	1.24	24.4	UG300	1.24 24.4
UG301	82.4 UG_DNA_16	HUMAN_COMMUNITY_01	100	1.21		UG301	1.21
UG302	106 UG_DNA_16	HUMAN_COMMUNITY_01	100	0.94		UG302	0.94
UG303	19 UG_DNA_16	HUMAN_COMMUNITY_01	100	5.26		UG303	5.26
UG304	67.8 UG_DNA_16	HUMAN_COMMUNITY_01	100	1.47		UG304	1.47
UG305	UG_DNA_16		100			UG305	
UG306	32.6 UG_DNA_16	HUMAN_COMMUNITY_01	100	3.07		UG306	3.07
UG307	10.7 UG_DNA_16	HUMAN_COMMUNITY_01	100	9.35		UG307	9.35
UG308	114 UG_DNA_16	HUMAN_COMMUNITY_01	100	0.88		UG308	0.88
UG309	63.6 UG_DNA_16	HUMAN_COMMUNITY_01	100	1.57		UG309	1.57
UG310	58.2 UG_DNA_16	HUMAN_COMMUNITY_01	100	1.72		UG310	1.72
UG311	114 UG_DNA_16	HUMAN_COMMUNITY_01	100	0.88		UG311	0.88
UG312	98 UG_DNA_16	HUMAN_COMMUNITY_01	100	1.02		UG312	1.02
UG313	100 UG_DNA_16	HUMAN_COMMUNITY_01	100	1.00		UG313	1.00
UG314	93.4 UG_DNA_16	HUMAN_COMMUNITY_01	100	1.07		UG314	1.07
UG315	78.2 UG_DNA_16	HUMAN_COMMUNITY_01	100	1.28		UG315	1.28
UG316	104 UG_DNA_16	HUMAN_COMMUNITY_01	100	0.96		UG316	0.96
UG317	93.2 UG_DNA_16	HUMAN_COMMUNITY_01	100	1.07		UG317	1.07
UG318	102 UG_DNA_16	HUMAN_COMMUNITY_01	100	0.98		UG318	0.98
UG319	87 UG_DNA_16	HUMAN_COMMUNITY_01	100	1.15		UG319	1.15
UG320	110 UG_DNA_16	HUMAN_COMMUNITY_01	100	0.91	35.8	UG320	0.91 35.8
UG321	118 UG_DNA_17	HUMAN_COMMUNITY_02	100	0.85		UG321	0.85
UG322	97.6 UG_DNA_17	HUMAN_COMMUNITY_02	100	1.02		UG322	1.02
UG323	97.8 UG_DNA_17	HUMAN_COMMUNITY_02	100	1.02		UG323	1.02
UG324	49.8 UG_DNA_17	HUMAN_COMMUNITY_02	100	2.01		UG324	2.01
UG325	104 UG_DNA_17	HUMAN_COMMUNITY_02	100	0.96		UG325	0.96
UG326	96 UG_DNA_17	HUMAN_COMMUNITY_02	100	1.04		UG326	1.04
UG327	102 UG_DNA_17	HUMAN_COMMUNITY_02	100	0.98		UG327	0.98
UG328	28 UG_DNA_17	HUMAN_COMMUNITY_02	100	3.57		UG328	3.57
UG329	104 UG_DNA_17	HUMAN_COMMUNITY_02	100	0.96		UG329	0.96
UG330	106 UG_DNA_17	HUMAN_COMMUNITY_02	100	0.94		UG330	0.94
UG331	94.2 UG_DNA_17	HUMAN_COMMUNITY_02	100	1.06		UG331	1.06
UG332	45 UG_DNA_17	HUMAN_COMMUNITY_02	100	2.22		UG332	2.22
UG333	73.2 UG_DNA_17	HUMAN_COMMUNITY_02	100	1.37		UG333	1.37
UG334	92 UG_DNA_17	HUMAN_COMMUNITY_02	100	1.09		UG334	1.09
UG335	97.4 UG_DNA_17	HUMAN_COMMUNITY_02	100	1.03		UG335	1.03
UG336	108 UG_DNA_17	HUMAN_COMMUNITY_02	100	0.93		UG336	0.93
UG337	102 UG_DNA_17	HUMAN_COMMUNITY_02	100	0.98		UG337	0.98
UG338	93.2 UG_DNA_17	HUMAN_COMMUNITY_02	100	1.07		UG338	1.07
UG339	104 UG_DNA_17	HUMAN_COMMUNITY_02	100	0.96		UG339	0.96
UG340	102 UG_DNA_17	HUMAN_COMMUNITY_02	100	0.98	25.0	UG340	0.98 25.0
UG341	112 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.89		UG341	0.89
UG342	25 UG_DNA_18	HUMAN_COMMUNITY_03	100	4.00		UG342	4.00
UG343	102 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.98		UG343	0.98
UG344	100 UG_DNA_18	HUMAN_COMMUNITY_03	100	1.00		UG344	1.00
UG345	UG_DNA_18		100			UG345	
UG346	106 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.94		UG346	0.94
UG347	13.5 UG_DNA_18	HUMAN_COMMUNITY_03	100	7.41		UG347	7.41
UG348	114 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.88		UG348	0.88
UG349	130.5 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.77		UG349	0.77
UG350	110 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.91		UG350	0.91

UG351	108 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.93		UG351	0.93	
UG352	120 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.83		UG352	0.83	
UG353	17.1 UG_DNA_18	HUMAN_COMMUNITY_03	100	5.85		UG353	5.85	
UG354	108 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.93		UG354	0.93	
UG355	73.4 UG_DNA_18	HUMAN_COMMUNITY_03	100	1.36		UG355	1.36	
UG356	58.2 UG_DNA_18	HUMAN_COMMUNITY_03	100	1.72		UG356	1.72	
UG357	114 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.88		UG357	0.88	
UG358	55 UG_DNA_18	HUMAN_COMMUNITY_03	100	1.82		UG358	1.82	
UG359	110 UG_DNA_18	HUMAN_COMMUNITY_03	100	0.91		UG359	0.91	
UG360	71.4 UG_DNA_18	HUMAN_COMMUNITY_03	100	1.40	34.4	UG360	1.40	34.4
UG361	110 UG_DNA_19	HUMAN_COMMUNITY_04	100	0.91		UG361	0.91	
UG362	39.6 UG_DNA_19	HUMAN_COMMUNITY_04	100	2.53		UG362	2.53	
UG363	114 UG_DNA_19	HUMAN_COMMUNITY_04	100	0.88		UG363	0.88	
UG364	57.6 UG_DNA_19	HUMAN_COMMUNITY_04	100	1.74		UG364	1.74	
UG365	102 UG_DNA_19	HUMAN_COMMUNITY_04	100	0.98		UG365	0.98	
UG366	102 UG_DNA_19	HUMAN_COMMUNITY_04	100	0.98		UG366	0.98	
UG367	38 UG_DNA_19	HUMAN_COMMUNITY_04	100	2.63		UG367	2.63	
UG368	19.2 UG_DNA_19	HUMAN_COMMUNITY_04	100	5.21		UG368	5.21	
UG369	118 UG_DNA_19	HUMAN_COMMUNITY_04	100	0.85		UG369	0.85	
UG370	112 UG_DNA_19	HUMAN_COMMUNITY_04	100	0.89		UG370	0.89	
UG371	36 UG_DNA_19	HUMAN_COMMUNITY_04	100	2.78		UG371	2.78	
UG372	50.2 UG_DNA_19	HUMAN_COMMUNITY_04	100	1.99		UG372	1.99	
UG373	44 UG_DNA_19	HUMAN_COMMUNITY_04	100	2.27		UG373	2.27	
UG374	49.8 UG_DNA_19	HUMAN_COMMUNITY_04	100	2.01		UG374	2.01	
UG375	112 UG_DNA_19	HUMAN_COMMUNITY_04	100	0.89		UG375	0.89	
UG376	116 UG_DNA_19	HUMAN_COMMUNITY_04	100	0.86		UG376	0.86	
UG377	106 UG_DNA_19	HUMAN_COMMUNITY_04	100	0.94		UG377	0.94	
UG378	48.6 UG_DNA_19	HUMAN_COMMUNITY_04	100	2.06		UG378	2.06	
UG379	82.4 UG_DNA_19	HUMAN_COMMUNITY_04	100	1.21		UG379	1.21	
UG380	9.52 UG_DNA_19	HUMAN_COMMUNITY_04	100	10.50	43.1	UG380	10.00	42.6
UG381	25.2 UG_DNA_20	HUMAN_COMMUNITY_05	100	3.97		UG381	3.97	
UG382	116 UG_DNA_20	HUMAN_COMMUNITY_05	100	0.86		UG382	0.86	
UG383	99.4 UG_DNA_20	HUMAN_COMMUNITY_05	100	1.01		UG383	1.01	
UG384	112 UG_DNA_20	HUMAN_COMMUNITY_05	100	0.89		UG384	0.89	
UG385	114 UG_DNA_20	HUMAN_COMMUNITY_05	100	0.88		UG385	0.88	
UG386	116 UG_DNA_20	HUMAN_COMMUNITY_05	100	0.86		UG386	0.86	
UG387	27 UG_DNA_20	HUMAN_COMMUNITY_05	100	3.70		UG387	3.70	
UG388	118 UG_DNA_20	HUMAN_COMMUNITY_05	100	0.85		UG388	0.85	
UG389	110 UG_DNA_20	HUMAN_COMMUNITY_05	100	0.91		UG389	0.91	
UG390	94.6 UG_DNA_20	HUMAN_COMMUNITY_05	100	1.06		UG390	1.06	
UG391	81.8 UG_DNA_20	HUMAN_COMMUNITY_05	100	1.22		UG391	1.22	
UG392	114 UG_DNA_20	HUMAN_COMMUNITY_05	100	0.88		UG392	0.88	
UG393	39.4 UG_DNA_20	HUMAN_COMMUNITY_05	100	2.54		UG393	2.54	
UG394	49.2 UG_DNA_20	HUMAN_COMMUNITY_05	100	2.03		UG394	2.03	
UG395	87.2 UG_DNA_20	HUMAN_COMMUNITY_05	100	1.15		UG395	1.15	
UG396	59.6 UG_DNA_20	HUMAN_COMMUNITY_05	100	1.68		UG396	1.68	
UG397	50.2 UG_DNA_20	HUMAN_COMMUNITY_05	100	1.99		UG397	1.99	
UG398	224 UG_DNA_20	HUMAN_COMMUNITY_05	100	0.45		UG398	1.30	
UG399	4.78 UG_DNA_20	HUMAN_COMMUNITY_05	100	20.92		UG399	0.40	
UG400	56.2 UG_DNA_20	HUMAN_COMMUNITY_05	100	1.78	49.6	UG400	1.78	30.0
UG401	27.6 UG_DNA_21	LIVESTOCK_COW_01	50	1.81		UG401	1.81	
UG402	18.8 UG_DNA_21	LIVESTOCK_COW_01	50	2.66		UG402	2.66	
UG403	71.4 UG_DNA_21	LIVESTOCK_COW_01	50	0.70		UG403	0.70	
UG404	17.7 UG_DNA_21	LIVESTOCK_COW_01	50	2.82		UG404	2.82	
UG405	40.2 UG_DNA_21	LIVESTOCK_COW_01	50	1.24		UG405	1.24	
UG406	36 UG_DNA_21	LIVESTOCK_COW_01	50	1.39		UG406	1.39	
UG407	65 UG_DNA_21	LIVESTOCK_COW_01	50	0.77		UG407	0.77	
UG408	33 UG_DNA_21	LIVESTOCK_COW_01	50	1.52		UG408	1.52	
UG409	74.8 UG_DNA_21	LIVESTOCK_COW_01	50	0.67		UG409	0.67	
UG410	64.4 UG_DNA_21	LIVESTOCK_COW_01	50	0.78		UG410	0.78	
UG411	67.4 UG_DNA_21	LIVESTOCK_COW_01	50	0.74		UG411	0.74	
UG412	47.6 UG_DNA_21	LIVESTOCK_COW_01	50	1.05		UG412	1.05	
UG413	7.32 UG_DNA_21	LIVESTOCK_COW_01	50	6.83		UG413	6.83	
UG414	26.6 UG_DNA_21	LIVESTOCK_COW_01	50	1.88		UG414	1.88	
UG415	0.114 UG_DNA_21	LIVESTOCK_COW_01	50	438.60		UG415	10.00	
UG416	4.78 UG_DNA_21	LIVESTOCK_COW_01	50	10.46		UG416	10.00	
UG417	12.3 UG_DNA_21	LIVESTOCK_COW_01	50	4.07	478.0	UG417	4.07	48.9
UG418	9.58 UG_DNA_22	LIVESTOCK_COW_02	50	5.22		UG418	5.22	
UG419	12 UG_DNA_22	LIVESTOCK_COW_02	50	4.17		UG419	4.17	
UG420	12.8 UG_DNA_22	LIVESTOCK_COW_02	50	3.91		UG420	3.91	
UG421	20.8 UG_DNA_22	LIVESTOCK_COW_02	50	2.40		UG421	2.40	
UG422	10.8 UG_DNA_22	LIVESTOCK_COW_02	50	4.63		UG422	4.63	
UG423	15.4 UG_DNA_22	LIVESTOCK_COW_02	50	3.25		UG423	3.25	
UG424	16.2 UG_DNA_22	LIVESTOCK_COW_02	50	3.09		UG424	3.09	
UG425	11.1 UG_DNA_22	LIVESTOCK_COW_02	50	4.50		UG425	4.50	
UG426	15.4 UG_DNA_22	LIVESTOCK_COW_02	50	3.25		UG426	3.25	
UG427	6.08 UG_DNA_22	LIVESTOCK_COW_02	50	8.22		UG427	8.22	
UG428	8 UG_DNA_22	LIVESTOCK_COW_02	50	6.25		UG428	6.25	
UG429	13.6 UG_DNA_22	LIVESTOCK_COW_02	50	3.68		UG429	3.68	
UG430	12.5 UG_DNA_22	LIVESTOCK_COW_02	50	4.00		UG430	4.00	
UG431	21 UG_DNA_22	LIVESTOCK_COW_02	50	2.38		UG431	2.38	
UG432	30.6 UG_DNA_22	LIVESTOCK_COW_02	50	1.63		UG432	1.63	
UG433	10.7 UG_DNA_22	LIVESTOCK_COW_02	50	4.67		UG433	4.67	
UG434	11 UG_DNA_22	LIVESTOCK_COW_02	50	4.55	69.8	UG434	4.55	69.8
UG435	13.4 UG_DNA_23	LIVESTOCK_COW_03	50	3.73		UG435	3.73	
UG436	10.2 UG_DNA_23	LIVESTOCK_COW_03	50	4.90		UG436	4.90	
UG437	11 UG_DNA_23	LIVESTOCK_COW_03	50	4.55		UG437	4.55	
UG438	13.8 UG_DNA_23	LIVESTOCK_COW_03	50	3.62		UG438	3.62	

UG439	16.4	UG_DNA_23	LIVESTOCK_COW_03	50	3.05	UG439	3.05
UG440	6.4	UG_DNA_23	LIVESTOCK_COW_03	50	7.81	UG440	7.81
UG441	13.5	UG_DNA_23	LIVESTOCK_COW_03	50	3.70	UG441	3.70
UG442	17.9	UG_DNA_23	LIVESTOCK_COW_03	50	2.79	UG442	2.79
UG443	10.5	UG_DNA_23	LIVESTOCK_COW_03	50	4.76	UG443	4.76
UG444	14	UG_DNA_23	LIVESTOCK_COW_03	50	3.57	UG444	3.57
UG445	11.8	UG_DNA_23	LIVESTOCK_COW_03	50	4.24	UG445	4.24
UG446	11.9	UG_DNA_23	LIVESTOCK_COW_03	50	4.20	UG446	4.20
UG447	9.94	UG_DNA_23	LIVESTOCK_COW_03	50	5.03	UG447	5.03
UG448	5.8	UG_DNA_23	LIVESTOCK_COW_03	50	8.62	UG448	8.62
UG449	8.64	UG_DNA_23	LIVESTOCK_COW_03	50	5.79	UG449	5.79
UG450	18.7	UG_DNA_23	LIVESTOCK_COW_03	50	2.67	UG450	2.67
UG451	19.2	UG_DNA_23	LIVESTOCK_COW_03	50	2.60	UG451	2.60
UG452	25.6	UG_DNA_24	LIVESTOCK_COW_04	50	1.95	UG452	1.95
UG453	10.5	UG_DNA_24	LIVESTOCK_COW_04	50	4.76	UG453	4.76
UG454	12.5	UG_DNA_24	LIVESTOCK_COW_04	50	4.00	UG454	4.00
UG455	14.9	UG_DNA_24	LIVESTOCK_COW_04	50	3.36	UG455	3.36
UG456	14.7	UG_DNA_24	LIVESTOCK_COW_04	50	3.40	UG456	3.40
UG457	24.8	UG_DNA_24	LIVESTOCK_COW_04	50	2.02	UG457	2.02
UG458	10.7	UG_DNA_24	LIVESTOCK_COW_04	50	4.67	UG458	4.67
UG459		UG_DNA_24		50		UG459	
UG460	9.4	UG_DNA_24	LIVESTOCK_COW_04	50	5.32	UG460	5.32
UG461	10.7	UG_DNA_24	LIVESTOCK_COW_04	50	4.67	UG461	4.67
UG462	15	UG_DNA_24	LIVESTOCK_COW_04	50	3.33	UG462	3.33
UG463	21.6	UG_DNA_24	LIVESTOCK_COW_04	50	2.31	UG463	2.31
UG464	22.8	UG_DNA_24	LIVESTOCK_COW_04	50	2.19	UG464	2.19
UG465	22.4	UG_DNA_24	LIVESTOCK_COW_04	50	2.23	UG465	2.23
UG466	16.9	UG_DNA_24	LIVESTOCK_COW_04	50	2.96	UG466	2.96
UG467	36	UG_DNA_24	LIVESTOCK_COW_04	50	1.39	UG467	1.39
UG468	28.8	UG_DNA_24	LIVESTOCK_COW_04	50	1.74	UG468	1.74
UG469	43.6	UG_DNA_25	LIVESTOCK_COW_05	50	1.15	UG469	1.15
UG470	18	UG_DNA_25	LIVESTOCK_COW_05	50	2.78	UG470	2.78
UG471	11.3	UG_DNA_25	LIVESTOCK_COW_05	50	4.42	UG471	4.42
UG472	13.5	UG_DNA_25	LIVESTOCK_COW_05	50	3.70	UG472	3.70
UG473	9.46	UG_DNA_25	LIVESTOCK_COW_05	50	5.29	UG473	5.29
UG474	39.6	UG_DNA_25	LIVESTOCK_COW_05	50	1.26	UG474	1.26
UG475	19.2	UG_DNA_25	LIVESTOCK_COW_05	50	2.60	UG475	2.60
UG476	21.4	UG_DNA_25	LIVESTOCK_COW_05	50	2.34	UG476	2.34
UG477	30.2	UG_DNA_25	LIVESTOCK_COW_05	50	1.66	UG477	1.66
UG478	38.6	UG_DNA_25	LIVESTOCK_COW_05	50	1.30	UG478	1.30
UG479	56.8	UG_DNA_25	LIVESTOCK_COW_05	50	0.88	UG479	0.88
UG480	66.2	UG_DNA_25	LIVESTOCK_COW_05	50	0.76	UG480	0.76
UG481	71.6	UG_DNA_25	LIVESTOCK_COW_05	50	0.70	UG481	0.70
UG482	95	UG_DNA_25	LIVESTOCK_COW_05	50	0.53	UG482	0.53
UG483	11.5	UG_DNA_25	LIVESTOCK_COW_05	50	4.35	UG483	4.35
UG484	9.02	UG_DNA_25	LIVESTOCK_COW_05	50	5.54	UG484	5.54
UG485						UG485	
UG486						UG486	
UG487						UG487	
UG488						UG488	
UG489						UG489	
UG490						UG490	
UG491						UG491	
UG492						UG492	
UG493						UG493	
UG494						UG494	
UG495						UG495	
UG496						UG496	
UG497						UG497	
UG498						UG498	
UG499						UG499	
UG500						UG500	
UG501	24	UG_DNA_26	LIVESTOCK_GOAT_01	100	4.17	UG501	4.17
UG502	66.4	UG_DNA_26	LIVESTOCK_GOAT_01	100	1.51	UG502	1.51
UG503	81	UG_DNA_26	LIVESTOCK_GOAT_01	100	1.23	UG503	1.23
UG504	30	UG_DNA_26	LIVESTOCK_GOAT_01	100	3.33	UG504	3.33
UG505	120	UG_DNA_26	LIVESTOCK_GOAT_01	100	0.83	UG505	0.83
UG506	80	UG_DNA_26	LIVESTOCK_GOAT_01	100	1.25	UG506	1.25
UG507	37.6	UG_DNA_26	LIVESTOCK_GOAT_01	100	2.66	UG507	2.66
UG508	114	UG_DNA_26	LIVESTOCK_GOAT_01	100	0.88	UG508	0.88
UG509	22.8	UG_DNA_26	LIVESTOCK_GOAT_01	100	4.39	UG509	4.39
UG510	13.4	UG_DNA_26	LIVESTOCK_GOAT_01	100	7.46	UG510	7.46
UG511	68.6	UG_DNA_26	LIVESTOCK_GOAT_01	100	1.46	UG511	1.46
UG512	41.6	UG_DNA_26	LIVESTOCK_GOAT_01	100	2.40	UG512	2.40
UG513	36.2	UG_DNA_26	LIVESTOCK_GOAT_01	100	2.76	UG513	2.76
UG514	78	UG_DNA_26	LIVESTOCK_GOAT_01	100	1.28	UG514	1.28
UG515	84.6	UG_DNA_26	LIVESTOCK_GOAT_01	100	1.18	UG515	1.18
UG516	22	UG_DNA_27	LIVESTOCK_GOAT_02	100	4.55	UG516	4.55
UG517	75	UG_DNA_27	LIVESTOCK_GOAT_02	100	1.33	UG517	1.33
UG518	36.2	UG_DNA_27	LIVESTOCK_GOAT_02	100	2.76	UG518	2.76
UG519	43.8	UG_DNA_27	LIVESTOCK_GOAT_02	100	2.28	UG519	2.28
UG520	78.2	UG_DNA_27	LIVESTOCK_GOAT_02	100	1.28	UG520	1.28
UG521	42.8	UG_DNA_27	LIVESTOCK_GOAT_02	100	2.34	UG521	2.34
UG522	96.6	UG_DNA_27	LIVESTOCK_GOAT_02	100	1.04	UG522	1.04
UG523	37.4	UG_DNA_27	LIVESTOCK_GOAT_02	100	2.67	UG523	2.67
UG524	106	UG_DNA_27	LIVESTOCK_GOAT_02	100	0.94	UG524	0.94
UG525	34	UG_DNA_27	LIVESTOCK_GOAT_02	100	2.94	UG525	2.94
UG526	40.4	UG_DNA_27	LIVESTOCK_GOAT_02	100	2.48	UG526	2.48

UG527	82.6 UG_DNA_27	LIVESTOCK_GOAT_02	100	1.21		UG527	1.21	
UG528	97.4 UG_DNA_27	LIVESTOCK_GOAT_02	100	1.03		UG528	1.03	
UG529	96 UG_DNA_27	LIVESTOCK_GOAT_02	100	1.04		UG529	1.04	
UG530	102 UG_DNA_27	LIVESTOCK_GOAT_02	100	0.98	28.9	UG530	0.98	28.9
UG531	102 UG_DNA_28	LIVESTOCK_GOAT_03	100	0.98		UG531	0.98	
UG532	98.8 UG_DNA_28	LIVESTOCK_GOAT_03	100	1.01		UG532	1.01	
UG533	92.6 UG_DNA_28	LIVESTOCK_GOAT_03	100	1.08		UG533	1.08	
UG534	41.4 UG_DNA_28	LIVESTOCK_GOAT_03	100	2.42		UG534	2.42	
UG535	106 UG_DNA_28	LIVESTOCK_GOAT_03	100	0.94		UG535	0.94	
UG536	89.2 UG_DNA_28	LIVESTOCK_GOAT_03	100	1.12		UG536	1.12	
UG537	29.4 UG_DNA_28	LIVESTOCK_GOAT_03	100	3.40		UG537	3.40	
UG538	57 UG_DNA_28	LIVESTOCK_GOAT_03	100	1.75		UG538	1.75	
UG539	51.6 UG_DNA_28	LIVESTOCK_GOAT_03	100	1.94		UG539	1.94	
UG540	26.6 UG_DNA_28	LIVESTOCK_GOAT_03	100	3.76		UG540	3.76	
UG541	45.2 UG_DNA_28	LIVESTOCK_GOAT_03	100	2.21		UG541	2.21	
UG542	64.6 UG_DNA_28	LIVESTOCK_GOAT_03	100	1.55		UG542	1.55	
UG543	32 UG_DNA_28	LIVESTOCK_GOAT_03	100	3.13		UG543	3.13	
UG544	78.6 UG_DNA_28	LIVESTOCK_GOAT_03	100	1.27		UG544	1.27	
UG545	71.6 UG_DNA_28	LIVESTOCK_GOAT_03	100	1.40	28.0	UG545	1.40	28.0
UG546	49.8 UG_DNA_29	LIVESTOCK_GOAT_04	100	2.01		UG546	2.01	
UG547	102 UG_DNA_29	LIVESTOCK_GOAT_04	100	0.98		UG547	0.98	
UG548	73.2 UG_DNA_29	LIVESTOCK_GOAT_04	100	1.37		UG548	1.37	
UG549	41.6 UG_DNA_29	LIVESTOCK_GOAT_04	100	2.40		UG549	2.40	
UG550	83.6 UG_DNA_29	LIVESTOCK_GOAT_04	100	1.20		UG550	1.20	
UG551	70.2 UG_DNA_29	LIVESTOCK_GOAT_04	100	1.42		UG551	1.42	
UG552	80.8 UG_DNA_29	LIVESTOCK_GOAT_04	100	1.24		UG552	1.24	
UG553	52.6 UG_DNA_29	LIVESTOCK_GOAT_04	100	1.90		UG553	1.90	
UG554	50.2 UG_DNA_29	LIVESTOCK_GOAT_04	100	1.99		UG554	1.99	
UG555	3.5 UG_DNA_29	LIVESTOCK_GOAT_04	100	28.57		UG555	10.00	
UG556	41.2 UG_DNA_29	LIVESTOCK_GOAT_04	100	2.43		UG556	2.43	
UG557	23.6 UG_DNA_29	LIVESTOCK_GOAT_04	100	4.24		UG557	4.24	
UG558	22.8 UG_DNA_29	LIVESTOCK_GOAT_04	100	4.39		UG558	4.39	
UG559	47 UG_DNA_29	LIVESTOCK_GOAT_04	100	2.13	56.3	UG559	2.13	37.7
UG560	28.2 UG_DNA_30	LIVESTOCK_GOAT_05	100	3.55		UG560	3.55	
UG561	35 UG_DNA_30	LIVESTOCK_GOAT_05	100	2.86		UG561	2.86	
UG562	45 UG_DNA_30	LIVESTOCK_GOAT_05	100	2.22		UG562	2.22	
UG563	34.4 UG_DNA_30	LIVESTOCK_GOAT_05	100	2.91		UG563	2.91	
UG564	33 UG_DNA_30	LIVESTOCK_GOAT_05	100	3.03		UG564	3.03	
UG565	51 UG_DNA_30	LIVESTOCK_GOAT_05	100	1.96		UG565	1.96	
UG566	92.8 UG_DNA_30	LIVESTOCK_GOAT_05	100	1.08		UG566	1.08	
UG567	104 UG_DNA_30	LIVESTOCK_GOAT_05	100	0.96		UG567	0.96	
UG568	28 UG_DNA_30	LIVESTOCK_GOAT_05	100	3.57		UG568	3.57	
UG569	28.8 UG_DNA_30	LIVESTOCK_GOAT_05	100	3.47		UG569	3.47	
UG570	73.4 UG_DNA_30	LIVESTOCK_GOAT_05	100	1.36		UG570	1.36	
UG571	42.1 UG_DNA_30	LIVESTOCK_GOAT_05	100	2.38		UG571	2.38	
UG572	53 UG_DNA_30	LIVESTOCK_GOAT_05	100	1.89		UG572	1.89	
UG573	98.8 UG_DNA_30	LIVESTOCK_GOAT_05	100	1.01	32.2	UG573	1.01	32.2

7.1.4.1.5 AGRF next-generation sequencing service report



www.agrf.org.au

NEXT-GENERATION SEQUENCING SERVICE REPORT

CAGRF21098330

AGRF BIOINFORMATICS

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AGRF NEXT-GENERATION SEQUENCING

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ABN 63 097 086 292



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Name	Matthew Stevens
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Project Overview

Project code: CAGRF21098330
Type of service: Illumina Sequencing
Project start date: Sunday 12th December, 2021

This document reports the data generation of the Illumina sequencing run and follow up analysis if applicable.

Primary analysis

Image analysis was performed in real time by the NovaSeq Control Software (NCS) v1.7.5 and Real Time Analysis (RTA) v3.4.4, running on the instrument computer. RTA performs real-time base calling on the NovaSeq instrument computer. Then the Illumina bcl2fastq 2.20.0.422 pipeline was used to generate the sequence data. The data generated here meet the AGRF quality standards.

Data Yield

The data yield is as follows:

Table 1:

150bp Paired End - Flowcell ID: H3CGTDSX3

Lane	Sample Name	Paired End	Data Yield(bp)
4	UG_DNA_01	92,875,129	28.05 Gb
	UG_DNA_02	102,970,874	31.10 Gb
	UG_DNA_03	112,971,851	34.12 Gb
	UG_DNA_04	84,796,976	25.61 Gb
	UG_DNA_05	88,168,622	26.63 Gb
	UG_DNA_06	81,283,047	24.55 Gb
	UG_DNA_07	124,797,234	37.69 Gb
	UG_DNA_08	88,269,027	26.66 Gb
	UG_DNA_09	107,005,708	32.32 Gb
	UG_DNA_10	103,829,691	31.36 Gb
	UG_DNA_11	104,497,704	31.56 Gb
	UG_DNA_12	97,494,964	29.44 Gb

Continued on next page

Table 1 – Continued from previous page

Lane	Sample Name	Paired End	Data Yield(bp)
	UG_DNA_13	82,950,421	25.05 Gb
	UG_DNA_14	94,635,612	28.58 Gb
	UG_DNA_15	106,733,109	32.23 Gb
	UG_DNA_16	90,676,347	27.38 Gb
	UG_DNA_17	131,006,284	39.56 Gb
	UG_DNA_18	98,258,585	29.67 Gb
	UG_DNA_19	97,304,704	29.39 Gb
	UG_DNA_20	96,423,246	29.12 Gb
	UG_DNA_21	93,605,306	28.27 Gb
	UG_DNA_22	96,952,961	29.28 Gb
	UG_DNA_23	110,967,531	33.51 Gb
	UG_DNA_24	105,814,994	31.96 Gb
	UG_DNA_25	97,939,765	29.58 Gb
	UG_DNA_26	87,509,730	26.43 Gb
	UG_DNA_27	89,611,086	27.06 Gb
	UG_DNA_28	111,123,374	33.56 Gb
	UG_DNA_29	102,089,609	30.83 Gb
	UG_DNA_30	90,215,447	27.25 Gb
	UG_DNA_31	6,008,379	1.81 Gb
Total		2,978,787,317	899.59Gb

Data Delivery

The data has been transferred and made available to you.

Below is a brief description of the files to expect.

<sample_name>_<flowcell_ID>_<index>_<lane>_<readNum>_fastq.gz - compressed FastQ formatted sequence file containing untrimmed 150 bp reads, where <readNum> specifies the first or second read of the pair.

These files contain the read **sequence output** with the corresponding Illumina **quality scores**. The quality is encoded in symbolic ASCII format in the following way: char (phred-like quality score + 33).

The files have been compressed using gzip and can be uncompressed using gunzip (*nix) or 7-Zip (Windows).



Please review the sequencing files after you have received them. Files will **remain on the server** until the **11th of January, 2022**. After that date they will be removed from the server.

A backup copy will be archived at AGRF until the 22nd of March, 2022. After that date **ONLY** the FASTQ files will be able to be re-created until the 8th of October, 2022. Please note that charges will apply for restoring files to the server.

If you have any questions or require further assistance please do not hesitate to contact us at NextGen@agrif.org.au.

AGRF Data Verification

As part of the general quality assurance AGRF tests the integrity and completeness of the data before it is sent to you.

Your packaged data has checksum information provided by AGRF should you wish to verify that your data is complete and error-free. Verification methods for both Windows and Unix systems are outlined below:

Windows:

The checksum information of the files included has been generated using Exactfile, which is a free third-party tool for Windows:
<http://www.exactfile.com/>.

Included in your directory are two files, "checksums.exf", which contains the MD5 hashes of the original files on AGRF's data server and "TestFiles.exe", an applet created by the Exactfile program to check files against the hashes listed in "checksums.exf".

To test the integrity of your files, you can simply start "TestFiles.exe".

Please be patient as it may take up to several minutes before the file check report appears, because of the size of the fastq files.

Unix:

The checksum information of the files included has been generated using the md5sum program. The calculated checksums of your data files are included in the “checksums.md5” file.

To test the integrity of your files, type the following command while in the directory containing checksums.md5:

```
md5sum -c checksums.md5
```

*Please note: The checksum verification can only be performed on the original data as received from AGRF, before any files are moved or modified. AGRF accepts no responsibility regarding the performance of Exactfile program.

7.1.4.2 Appendices – Chapter 4

7.1.4.2.1 CheckM quality assessment results

Bin Id	Marker lineage	# genomes	# markers	# marker sets	0	1	2	3	4	5+	Completeness	Contamination	Strain heterogeneity
109_sub.hh13	c_Gammaproteobacteria (UID4201)	1164	272	171	0	260	12	0	0	0	100	2.68	25
118_gh06	p_Actinobacteria (UID2112)	31	211	124	0	207	4	0	0	0	100	2.82	0
237.hh15	p_Euryarchaeota (UID3)	148	188	125	0	188	0	0	0	0	100	0	0
3.hc20	c_Gammaproteobacteria (UID4201)	1164	272	171	0	266	6	0	0	0	100	0.75	0
bin.146.gh07	o_Clostridiales (UID1120)	304	247	141	0	240	7	0	0	0	100	4.14	85.71
bin.205.gw05	p_Actinobacteria (UID2112)	31	211	124	0	207	4	0	0	0	100	0.9	0
bin.21.gh08	p_Actinobacteria (UID2112)	31	211	124	0	204	7	0	0	0	100	1.8	0
bin.222.gw03	p_Actinobacteria (UID2112)	31	211	124	0	211	0	0	0	0	100	0	0
bin.25.hh13	p_Euryarchaeota (UID3)	148	188	125	0	184	4	0	0	0	100	2.46	50
bin.261.gw03	o_Clostridiales (UID1212)	172	261	147	0	261	0	0	0	0	100	0	0
bin.296.gh07	k_Bacteria (UID2329)	174	149	89	0	145	4	0	0	0	100	3.18	50
bin.39.hh11	o_Lactobacillales (UID544)	293	475	267	0	441	33	1	0	0	100	3.33	25
bin.99.gp	k_Bacteria (UID2372)	131	177	106	0	172	5	0	0	0	100	2.81	80
77_gh	p_Actinobacteria (UID2112)	31	211	124	1	193	16	1	0	0	99.73	7.35	52.63
bin.326.gh07	f_Enterobacteriaceae (UID5124)	134	1173	336	5	1166	2	0	0	0	99.67	0.1	0
maxbin.341.gh	f_Enterobacteriaceae (UID5124)	134	1173	336	3	1162	8	0	0	0	99.67	0.26	50
123.gw	p_Actinobacteria (UID2112)	31	211	124	3	203	5	0	0	0	99.65	2.74	0
20_sub.gh09	o_Clostridiales (UID1212)	172	261	147	3	258	0	0	0	0	99.55	0	0
172.hh14	k_Bacteria (UID2372)	131	177	106	1	158	17	1	0	0	99.53	16.35	90
175_sub.gh06	p_Actinobacteria (UID2112)	31	211	124	2	208	1	0	0	0	99.46	0.27	100
bin.118.gw04	c_Bacilli (UID285)	586	324	180	1	316	7	0	0	0	99.44	2.59	28.57
bin.221.gw03	c_Bacilli (UID285)	586	324	180	1	319	4	0	0	0	99.44	1.94	25
139_sub.hc18	c_Gammaproteobacteria (UID4201)	1164	272	171	1	268	1	2	0	0	99.42	1.75	42.86
114.hc17	c_Gammaproteobacteria (UID4201)	1164	272	171	1	266	5	0	0	0	99.42	2.37	60
bin.71.gw03	k_Bacteria (UID2495)	2993	147	91	2	145	0	0	0	0	99.39	0	0
222.gh09	o_Clostridiales (UID1212)	172	263	149	1	268	3	1	0	0	99.33	2.35	0
300_sub.gh06	o_Clostridiales (UID1212)	172	263	149	1	261	1	0	0	0	99.33	0.67	0
bin.52.hc16	o_Clostridiales (UID1212)	172	263	149	1	262	0	0	0	0	99.33	0	0
maxbin.039.gh08	o_Clostridiales (UID1212)	172	263	149	1	260	2	0	0	0	99.33	1.34	0
maxbin.056.hh15	k_Bacteria (UID2982)	88	229	147	1	226	2	0	0	0	99.32	1.36	0
160.hc19	o_Clostridiales (UID1120)	304	250	143	1	246	3	0	0	0	99.3	1.17	0
maxbin.016.hc18	f_Spirochaetaceae (UID2535)	33	249	143	1	246	2	0	0	0	99.3	1.05	0
146.hc17	p_Firmicutes (UID1022)	100	295	158	3	286	6	0	0	0	99.25	1.08	0
49.hh15	o_Lactobacillales (UID544)	293	473	265	3	460	10	0	0	0	99.25	2.13	20
52.hc	c_Gammaproteobacteria (UID4201)	1164	272	171	7	262	3	0	0	0	99.22	1.17	100
bin.136.gh06	c_Clostridia (UID1118)	387	223	124	1	221	1	0	0	0	99.19	0.81	0
bin.157.gh10	p_Actinobacteria (UID2112)	31	211	124	1	207	3	0	0	0	99.19	1.12	0
bin.161.gh10	p_Actinobacteria (UID2112)	31	211	124	3	205	3	0	0	0	99.19	1.19	66.67
bin.166.gw02	p_Actinobacteria (UID1118)	387	223	124	1	221	1	0	0	0	99.19	0.81	0
bin.188.gw01	p_Actinobacteria (UID2112)	31	211	124	1	209	1	0	0	0	99.19	0.08	0
bin.215.gw03	p_Actinobacteria (UID2112)	31	211	124	1	207	3	0	0	0	99.19	1.48	0
bin.253.gh	p_Actinobacteria (UID2112)	31	211	124	1	210	0	0	0	0	99.19	0	0
bin.340.gh07	p_Actinobacteria (UID2112)	31	211	124	1	209	1	0	0	0	99.19	0.4	100
bin.586.gw	p_Actinobacteria (UID2112)	31	211	124	1	209	1	0	0	0	99.19	0.27	0
bin.71.gh	p_Actinobacteria (UID2112)	31	211	124	1	210	0	0	0	0	99.19	0	0
maxbin.001.gh09	p_Actinobacteria (UID2112)	31	211	124	1	207	3	0	0	0	99.19	1.34	100
maxbin.034.gw01	k_Bacteria (UID2569)	434	278	186	2	275	1	0	0	0	99.19	0.27	100
maxbin.046_sub.gw05	k_Bacteria (UID2569)	434	278	186	2	274	2	0	0	0	99.19	0.54	0
maxbin.057.gh07	k_Bacteria (UID2569)	434	278	186	2	276	0	0	0	0	99.19	0	0
maxbin.059_sub.gh10	k_Bacteria (UID2569)	434	278	186	2	274	2	0	0	0	99.19	0.54	100
maxbin.056.hh12	f_Moraxellaceae (UID4680)	86	689	365	23	658	8	0	0	0	99.09	1.12	12.5
maxbin.151_sub.hh	f_Moraxellaceae (UID4680)	86	689	365	43	638	8	0	0	0	99.09	1.33	37.5
maxbin.052.gw01	k_Bacteria (UID203)	5449	98	53	6	67	24	1	0	0	98.97	13.55	68.89
30.hc19	o_Lactobacillales (UID374)	471	350	191	2	348	0	0	0	0	98.95	0	0
bin.3.hc16	f_Spirochaetaceae (UID2535)	33	249	143	3	245	1	0	0	0	98.95	0.7	100
maxbin.032.hh12	o_Lactobacillales (UID374)	471	350	191	2	347	1	0	0	0	98.95	0.26	100
bin.44.ca	f_Enterobacteriaceae (UID5162)	88	1207	328	7	1190	10	0	0	0	98.92	1.34	40
bin.63.gh	k_Bacteria (UID2569)	434	278	186	2	275	1	0	0	0	98.92	0.54	0
bin.201.gw01	k_Bacteria (UID2329)	174	149	89	1	146	2	0	0	0	98.88	1.69	50
bin.202.hh	k_Bacteria (UID2329)	174	149	89	1	145	3	0	0	0	98.88	3.37	0
bin.28.gw	k_Bacteria (UID2329)	174	149	89	1	146	2	0	0	0	98.88	2.25	0
bin.56.gw02	p_Actinobacteria (UID2112)	31	211	124	3	207	1	0	0	0	98.87	0.81	0
108_sub.gh09	p_Actinobacteria (UID2112)	31	211	124	3	202	6	0	0	0	98.79	3.23	83.33
218_sub.gw04	p_Actinobacteria (UID2112)	31	211	124	2	191	17	1	0	0	98.79	7.57	40
bin.98_sub.gw05	o_Clostridiales (UID1226)	155	278	158	2	267	9	0	0	0	98.73	3.04	0
bin.3.hh15	p_Firmicutes (UID1022)	100	295	158	5	272	18	0	0	0	98.71	6.79	61.11
61.hc	g_Lactobacillus (UID377)	91	430	154	4	413	13	0	0	0	98.7	3.22	84.62
204.gh09	k_Bacteria (UID2569)	434	278	186	3	273	2	0	0	0	98.66	0.38	50
bin.177.hc20	o_Clostridiales (UID1212)	172	263	149	2	261	0	0	0	0	98.66	0	0
bin.179.gw	o_Clostridiales (UID1212)	172	263	149	3	259	1	0	0	0	98.66	0.17	100
maxbin.065_sub.gw02	k_Bacteria (UID2569)	434	278	186	3	274	1	0	0	0	98.66	0.27	0
maxbin.079.gw03	k_Bacteria (UID2569)	434	278	186	3	275	0	0	0	0	98.66	0	0
bin.103_sub.gw04	f_Spirochaetaceae (UID2535)	33	249	143	2	239	8	0	0	0	98.6	3.54	0
bin.143.gh06	f_Spirochaetaceae (UID2535)	33	249	143	2	244	3	0	0	0	98.6	2.1	0
bin.307.gh07	f_Spirochaetaceae (UID2535)	33	249	143	3	244	2	0	0	0	98.6	0.74	0
maxbin.036.gw	f_Spirochaetaceae (UID2535)	33	249	143	2	244	3	0	0	0	98.6	1.57	0
maxbin.095.gw05	f_Spirochaetaceae (UID2535)	33	249	143	2	238	9	0	0	0	98.6	3.82	0
67_sub.hc19	g_Lactobacillus (UID377)	91	430	154	23	398	9	0	0	0	98.54	2.12	77.78
138.gp29	p_Bacteroidetes (UID3605)	314	350	208	5	304	5	0	0	0	98.46	2.4	60
204.hh13	o_Lactobacillales (UID374)	471	350	191	3	345	2	0	0	0	98.43	0.34	50
bin.22.gh10	p_Actinobacteria (UID2112)	31	211	124	7	199	4	1	0	0	98.43	3.43	57.14
maxbin.029.hc16	o_Lactobacillales (UID374)	471	350	191	3	344	3	0	0	0	98.43	0.47	100
maxbin.097_sub.gw01	o_Clostridiales (UID1226)	155	278	158	3	262	13	0	0	0	98.42	3.97	23.08
7_sub.hh14	c_Spirochaetia (UID2496)	172	215	125	2	199	13	1	0	0	98.4	6.9	100
141_sub.gh09	k_Bacteria (UID2569)	434	278	186	3	266	8	1	0	0	98.39	4.23	63.64
163.gw04	k_Bacteria (UID2569)	434	278	186	3	264	10	1	0	0	98.39	3.51	7.69
98.gw01	c_Clostridia (UID1118)	387	223	124	3	209	11	0	0	0	98.39	5.72	90.91
bin.263.gh09	p_Euryarchaeota (UID3)	148	187	124	3	181	3	0	0	0	98.39	2.42	100
bin.88.gw05	p_Euryarchaeota (UID3)	148	187	124	3	173	11	0	0	0	98.39	1.53	27.27
bin.97.gh	p_Actinobacteria (UID2112)	31	211	124	2	207	1	1	0	0	98.39	1.21	25
bin.52.hc17	g_Lactobacillus (UID377)	91	430	154	3	427	0	0	0	0	98.38	0	0
13_sub.gw04	p_Euryarchaeota (UID3)	148	188	125	3	176	9	0	0	0	98.34	6.8	100
59.gp28	f_Enterobacteriaceae (UID5162)	88	1207	328	10	1165	32	0	0	0	98.34	2.87	87.5
maxbin.101.hh	o_Lactobacillales (UID374)	471	350	191	4	335	11	0	0	0	98.3	3.66	45.45
bin.2_sub.gh07	k_Bacteria (UID203)	5449	103	57	1	75	27	0	0	0	98.25	7.18	40.74
bin.45.gw01	p_Actinobacteria (UID2112)	31	211	124	4	203	4	0	0	0	98.25	2.62	25
maxbin.353_sub.hc	k_Bacteria (UID203)	5449	103	57	2	74	23	2	2	2	98.25	8.85	82.93
bin.179.gw02	f_Lachnospiraceae (UID1286)	420	57	207	8	406	6	0	0	0	98.23	2.19	100
160.hc16	c_Gammaproteobacteria (UID4201)	1164	271	170	4	253	8	6	0	0	98.2	6.11	38.46
214.hc19	o_Selenomonadales (UID1024)	64	334	167	3	323	7	1	0	0	98.2	3.01	100
bin.77.hc16	o_Lactobacillales (UID544)	293	473	265	7	457	9	0	0	0	98.18	1.64	77.78
bin.252.gw04	f_Lachnospiraceae (UID1286)	57	420	207	9	404	7	0					

maxbin.327.gw	o_Clostridiales (UID1212)	172	263	149	6	252	5	0	0	0	98.04	2.85	20
142.gw05	p_Proteobacteria (UID3887)	1487	256	160	4	247	5	0	0	0	98.02	2.1	20
35.gw09	p_Proteobacteria (UID3887)	1487	256	160	4	246	5	1	0	0	98.02	3.54	12.5
bin.208.gw03	p_Proteobacteria (UID3887)	1487	256	160	4	251	1	0	0	0	98.02	0.62	0
bin.73.gw01	p_Proteobacteria (UID3887)	1487	256	160	4	249	2	1	0	0	98.02	1.91	40
bin.257_sub.gw05	k_Bacteria (UID2569)	434	278	186	5	270	3	0	0	0	98.01	1.08	0
maxbin.020_sub.gw10	k_Bacteria (UID2569)	434	278	186	5	252	20	1	0	0	98.01	4.52	0
maxbin.026.gw08	o_Lactobacillales (UID355)	490	334	183	6	322	6	0	0	0	98	2.46	100
284.gw04	o_Clostridiales (UID1212)	172	263	149	3	255	5	0	0	0	97.99	1.69	60
bin.154.gw	o_Clostridiales (UID1212)	172	263	149	3	253	7	0	0	0	97.99	4.7	28.57
maxbin.013.hc19	o_Clostridiales (UID1212)	172	263	149	4	245	13	1	0	0	97.99	6.15	31.25
bin.35.gw10	c_Clostridia (UID1118)	387	223	124	3	217	3	0	0	0	97.98	0.97	0
bin.172.gw09	o_Selenomonadales (UID1024)	64	334	167	18	309	7	0	0	0	97.97	2.25	42.86
211.gw	o_Clostridiales (UID1212)	172	261	147	3	257	1	0	0	0	97.96	0.34	0
bin.158.hc17	k_Bacteria (UID2982)	88	229	147	3	226	0	0	0	0	97.96	0	0
191.gw28	p_Bacteroidetes (UID2605)	350	314	208	6	290	18	0	0	0	97.92	5.9	77.78
195.gw10	f_Spirochaetaceae (UID2535)	33	249	143	3	244	2	0	0	0	97.9	1.05	50
205_sub.gw06	f_Spirochaetaceae (UID2535)	33	249	143	3	238	8	0	0	0	97.9	4.24	0
28.gw08	f_Spirochaetaceae (UID2535)	33	249	143	3	245	1	0	0	0	97.9	0.7	0
55.gw10	f_Spirochaetaceae (UID2535)	33	249	143	3	241	5	0	0	0	97.9	1.98	20
bin.163_sub.gw01	f_Spirochaetaceae (UID2535)	33	249	143	4	241	4	0	0	0	97.9	1.79	0
bin.290.gw07	f_Spirochaetaceae (UID2535)	33	249	143	3	244	2	0	0	0	97.9	1.05	0
bin.40.cw21	f_Spirochaetaceae (UID2535)	249	33	143	2	241	3	0	0	0	97.9	1.63	0
148.ca25	k_Bacteria (UID2569)	434	278	186	4	273	1	0	0	0	97.85	0.54	0
284_sub.gw10	k_Bacteria (UID2569)	434	278	186	5	269	4	0	0	0	97.85	1.45	75
bin.245.gw03	k_Bacteria (UID2569)	434	278	186	4	273	1	0	0	0	97.85	0.54	0
bin.40.gw01	k_Bacteria (UID2569)	434	278	186	4	271	3	0	0	0	97.85	0.82	100
maxbin.042_sub.gw01	k_Bacteria (UID2569)	434	278	186	4	272	2	0	0	0	97.85	1.08	100
bin.22.gw02	o_Clostridiales (UID1212)	172	263	149	7	254	2	0	0	0	97.82	0.89	50
maxbin.017.gw27	f_Enterobacteriaceae (UID5162)	88	1207	328	18	1154	35	0	0	0	97.81	3.47	94.29
maxbin.070.hc18	o_Clostridiales (UID1212)	172	263	149	7	255	1	0	0	0	97.8	0.34	0
288_sub.gw03	k_Bacteria (UID2329)	174	149	89	2	142	5	0	0	0	97.75	3.42	0
bin.13.gw07	k_Bacteria (UID2329)	174	149	89	2	147	0	0	0	0	97.75	0	0
bin.151_sub.hh11	k_Bacteria (UID2329)	174	149	89	3	141	5	0	0	0	97.75	4.49	0
bin.227.gw02	k_Bacteria (UID2329)	174	149	89	2	145	2	0	0	0	97.75	2.25	100
bin.50.gw06	k_Bacteria (UID2329)	174	149	89	2	146	1	0	0	0	97.75	1.12	100
bin.53.gw03	k_Bacteria (UID2329)	174	149	89	2	147	0	0	0	0	97.75	0	0
maxbin.083.gw05	k_Bacteria (UID2329)	174	149	89	2	146	1	0	0	0	97.75	1.12	100
maxbin.082_sub.hc18	c_Epsilonproteobacteria (UID3065)	111	445	271	12	430	3	0	0	0	97.72	0.49	66.67
bin.32.hc20	o_Lactobacillales (UID544)	293	473	265	36	423	14	0	0	0	97.71	3.3	57.14
bin.179.gw10	f_Lachnospiraceae (UID1256)	33	333	171	4	321	8	0	0	0	97.66	2.83	0
maxbin.021.hh15	c_Gammaproteobacteria (UID4201)	1164	272	171	4	267	0	0	0	0	97.66	0.29	100
157.gw	c_Gammaproteobacteria (UID4201)	1164	271	170	4	263	4	0	0	0	97.65	1.26	50
63.gw	k_Bacteria (UID2565)	2921	142	87	3	139	0	0	0	0	97.63	0	0
bin.115.gw04	o_Lactobacillales (UID355)	490	334	183	6	324	4	0	0	0	97.63	1.09	75
285.hh	p_Euryarchaeota (UID3)	148	188	125	3	180	3	0	0	2	97.6	3.08	0
301.gw07	p_Actinobacteria (UID2112)	31	211	124	6	200	5	0	0	0	97.6	1.75	40
36_sub.hc	o_Bacteroidales (UID2621)	198	427	260	38	377	12	0	0	0	97.6	3.56	58.33
123_sub.gw06	p_Euryarchaeota (UID3)	148	187	124	4	177	6	0	0	0	97.58	4.09	33.33
25.gw27	k_Bacteria (UID2569)	434	278	186	5	268	5	0	0	0	97.58	2.15	0
98.gw03	c_Clostridia (UID1118)	387	223	124	3	205	15	0	0	0	97.58	8.09	80
bin.10.gw08	p_Euryarchaeota (UID3)	148	187	124	4	179	4	0	0	0	97.58	1.77	50
bin.138.gw04	p_Euryarchaeota (UID3)	148	187	124	4	182	1	0	0	0	97.58	0.81	100
bin.17.gw01	p_Actinobacteria (UID2112)	31	211	124	5	206	0	0	0	0	97.58	0	0
bin.200.hh	f_Veillonellaceae (UID1032)	33	423	214	12	404	7	0	0	0	97.58	0.86	42.86
bin.24.gw02	p_Euryarchaeota (UID3)	148	187	124	4	183	0	0	0	0	97.58	0	0
bin.244.gw07	c_Clostridia (UID1118)	387	223	124	4	217	2	0	0	0	97.58	1.21	50
bin.269.gw07	p_Euryarchaeota (UID3)	148	187	124	4	182	1	0	0	0	97.58	0.81	100
bin.368.gw	p_Actinobacteria (UID2112)	31	211	124	3	204	4	0	0	0	97.58	1.68	75
bin.428.gw	c_Clostridia (UID1118)	387	223	124	3	219	1	0	0	0	97.58	0.81	0
bin.51.gw29	p_Actinobacteria (UID2112)	31	211	124	3	206	2	0	0	0	97.58	0.67	50
bin.82.gw02	k_Bacteria (UID2569)	434	278	186	5	271	2	0	0	0	97.58	0.81	100
bin.97.gw10	p_Euryarchaeota (UID3)	148	187	124	4	180	3	0	0	0	97.58	1.67	0
maxbin.039.gw03	p_Euryarchaeota (UID3)	148	187	124	4	168	14	1	0	0	97.58	2.89	5.88
bin.105.hh15	f_Spirochaetaceae (UID2535)	33	249	143	5	244	0	0	0	0	97.55	0	0
bin.156.hh15	c_Epsilonproteobacteria (UID3066)	110	450	273	10	424	16	0	0	0	97.55	3.64	87.5
maxbin.086.gw	o_Lactobacillales (UID355)	490	334	183	5	322	7	0	0	0	97.54	2.64	85.71
bin.281.gw03	f_Lachnospiraceae (UID1255)	90	354	174	5	342	7	0	0	0	97.51	2.41	71.43
275_sub.gw01	o_Clostridiales (UID1212)	172	263	149	7	256	2	0	0	0	97.5	0.4	0
bin.161.gw03	o_Bacteroidales (UID2621)	198	427	260	7	415	5	0	0	0	97.5	1.03	20
bin.458_sub.gw	f_Lachnospiraceae (UID1286)	57	420	207	9	394	17	0	0	0	97.49	2.42	0
maxbin.038.hc20	o_Lactobacillales (UID374)	471	350	191	8	340	2	0	0	0	97.49	0.28	100
208.gw30	f_Enterobacteriaceae (UID5162)	88	1207	328	21	1167	18	1	0	0	97.48	1.18	23.81
280_sub.gw03	k_Bacteria (UID2569)	434	278	186	6	263	9	0	0	0	97.47	3.76	0
bin.227.gw	p_Firmicutes (UID1022)	100	295	158	32	261	2	0	0	0	97.47	0.95	50
bin.71.gw08	k_Bacteria (UID2569)	434	278	186	6	270	2	0	0	0	97.47	0.54	0
237_sub.gw	c_Clostridia (UID1118)	387	223	124	8	189	25	1	0	0	97.45	16.33	85.71
308_sub.gw07	c_Clostridia (UID1118)	387	223	124	6	213	4	0	0	0	97.45	1.96	50
bin.40.gw02	p_Actinobacteria (UID2112)	31	211	124	5	205	1	0	0	0	97.45	0.81	100
bin.273.gw	p_Actinobacteria (UID2112)	31	211	124	4	200	7	0	0	0	97.42	4.01	14.29
16.gw02	p_Proteobacteria (UID3887)	1487	256	160	5	249	1	1	0	0	97.4	1.88	0
303.gw	p_Proteobacteria (UID3887)	1487	256	160	5	244	6	1	0	0	97.4	3.59	0
maxbin.072_sub.gw06	f_Lachnospiraceae (UID1286)	57	420	207	11	402	7	0	0	0	97.38	1.36	71.43
171.hh11	o_Bacteroidales (UID2617)	213	406	265	10	382	14	0	0	0	97.36	4.11	0
bin.63.hh11	c_Epsilonproteobacteria (UID3065)	111	445	271	10	422	12	1	0	0	97.36	2.95	60
maxbin.391.gw	c_Gammaproteobacteria (UID4201)	1164	271	170	5	263	3	0	0	0	97.35	0.23	0
bin.173.gw	p_Actinobacteria (UID2112)	31	211	124	5	205	1	0	0	0	97.34	0.2	0
bin.228.gw05	c_Clostridia (UID1118)	387	223	124	6	214	3	0	0	0	97.33	2.02	33.33
240.hc19	o_Clostridiales (UID1212)	172	263	149	4	257	2	0	0	0	97.32	0.4	0
35.hh15	o_Clostridiales (UID1212)	172	263	149	4	258	1	0	0	0	97.32	0.22	100
bin.125.gw09	o_Clostridiales (UID1212)	172	263	149	7	255	1	0	0	0	97.32	0.67	100
bin.245.gw07	o_Clostridiales (UID1212)	172	263	149	7	255	1	0	0	0	97.32	0.22	100
bin.254.hh15	o_Clostridiales (UID1212)	172	263	149	5	258	0	0	0	0	97.32	0	0
bin.33_sub.gw27	o_Clostridiales (UID1212)	172	263	149	7	246	9	1	0	0	97.32	5.7	16.67
bin.357.gw07	o_Clostridiales (UID1212)	172	263	149	7	255	4	0	0	0	97.32	1.12	100
bin.44.hc16	f_Enterobacteriaceae (UID5124)	134	1173	336	26	1112	34	1	0	0	97.32	3.25	89.19
bin.85.hh12	o_Clostridiales (UID1212)	172	263	149	5	256	2	0	0	0	97.32	1.34	50
maxbin.035.hh12	o_Clostridiales (UID1212)	172	263	149	14	245	4	0	0	0	97.32	1.17	0
maxbin.147.gw	o_Clostridiales (UID1212)	172	263	149	5	256	2	0	0	0	97.32	1.34	0
70.gw05	k_Bacteria (UID2569)	434	278	186	5	269	4	0	0	0	97.31	1.39	100
bin.152.gw07	k_Bacteria (UID2569)	434	278	186	5	271	2	0	0	0	97.31	0.54	100
bin.203.gw04	p_Euryarchaeota (UID3)	148	187	124	5	182	0	0					

40.g909	f_Spirochaetaceae (UID2535)	33	249	143	4	244	1	0	0	0	97.2	0.7	0
bin.144.gw01	f_Spirochaetaceae (UID2535)	33	249	143	4	244	1	0	0	0	97.2	0.7	0
bin.263_sub.gw03	f_Spirochaetaceae (UID2535)	33	249	143	5	239	5	0	0	0	97.2	1.63	20
bin.265.g907	f_Spirochaetaceae (UID2535)	33	249	143	4	243	2	0	0	0	97.2	1.05	100
bin.43.gw05	f_Spirochaetaceae (UID2535)	33	249	143	4	244	1	0	0	0	97.2	0.7	0
bin.669.g9	f_Spirochaetaceae (UID2535)	33	249	143	4	244	1	0	0	0	97.2	0.7	0
bin.98.gw26	f_Spirochaetaceae (UID2535)	33	249	143	33	214	2	0	0	0	97.2	1.4	100
bin.39.g906	k_Bacteria (UID2329)	174	149	89	3	143	3	0	0	0	97.19	2.25	66.67
93.gw02	c_Clostridia (UID1118)	367	223	124	4	207	12	0	0	0	97.18	5.31	83.33
bin.67.g908	p_Euryarchaeota (UID3)	148	187	124	4	182	1	0	0	0	97.18	0.81	100
maxbin.059_sub.g9	k_Bacteria (UID2569)	434	278	186	9	265	4	0	0	0	97.18	1.08	25
148_sub.g906	o_Clostridiales (UID1120)	304	247	141	4	242	1	0	0	0	97.16	0.24	100
305.gw04	o_Clostridiales (UID1120)	304	247	141	4	237	6	0	0	0	97.16	1.3	33.33
73.gw05	o_Clostridiales (UID1120)	304	247	141	4	239	4	0	0	0	97.16	1.77	25
bin.280.g9	o_Clostridiales (UID1120)	304	247	141	5	239	3	0	0	0	97.16	1.65	66.67
bin.46.g907	o_Clostridiales (UID1120)	304	247	141	4	241	2	0	0	0	97.16	0.47	100
bin.496.gw	o_Clostridiales (UID1120)	304	247	141	5	239	3	0	0	0	97.16	2.13	33.33
bin.106.gw01	o_Clostridiales (UID1212)	172	263	149	8	252	3	0	0	0	97.15	1.57	66.67
bin.197.gw	k_Bacteria (UID2372)	131	176	105	3	173	0	0	0	0	97.14	0	0
bin.231.gw03	k_Bacteria (UID2372)	131	176	105	3	168	5	0	0	0	97.14	1.94	40
118_sub.hh11	f_Spirochaetaceae (UID2535)	33	249	143	5	241	3	0	0	0	97.13	2.1	33.33
bin.223.gw03	o_Clostridiales (UID1212)	172	263	149	9	250	4	0	0	0	97.13	0.69	75
bin.589_sub.g9	o_Clostridiales (UID1226)	145	188	125	6	169	10	0	0	0	97.13	1.48	75
maxbin.004.ca21	p_Bacteroidetes (UID2605)	350	314	208	25	274	15	0	0	0	97.13	3.15	73.33
234_sub.hh13	o_Selenomonadales (UID1024)	64	334	167	8	318	8	0	0	0	97.09	2.74	25
bin.143.hc17	o_Clostridiales (UID1212)	172	263	149	6	255	2	0	0	0	97.09	0.39	100
bin.418.g9	o_Selenomonadales (UID1024)	64	334	167	27	301	6	0	0	0	97.09	2.02	50
28.hc19	p_Euryarchaeota (UID3)	148	188	125	6	174	8	0	0	0	97.07	6	87.5
bin.269.gw02	p_Euryarchaeota (UID3)	148	188	125	12	261	5	0	0	0	97.07	2.11	20
33.gw04	c_Clostridia (UID1118)	367	223	124	6	206	11	0	0	0	97.04	4.47	45.45
bin.108.gw	k_Bacteria (UID2569)	434	278	186	8	269	1	0	0	0	97.04	0.54	0
bin.197.gw03	k_Bacteria (UID2569)	434	278	186	6	269	3	0	0	0	97.04	0.54	33.33
bin.203.g906	k_Bacteria (UID2569)	434	278	186	6	268	4	0	0	0	97.04	2.15	100
maxbin.011_sub.g908	k_Bacteria (UID2569)	434	278	186	6	266	6	0	0	0	97.04	1.43	16.67
196_sub.g910	f_Lachnospiraceae (UID1286)	57	420	207	12	396	12	0	0	0	97.02	2.88	83.33
bin.164.gw02	p_Euryarchaeota (UID3)	148	188	125	9	169	10	0	0	0	96.99	6.5	90
maxbin.363_sub.hc	o_Lactobacillales (UID355)	490	334	183	7	325	2	0	0	0	96.99	0.46	100
110.hh14	o_Bacteroidales (UID2617)	213	406	265	11	394	1	0	0	0	96.98	0.13	100
bin.402.gw	o_Clostridiales (UID1212)	172	263	149	5	257	1	0	0	0	96.98	0.67	0
bin.6.g908	p_Actinobacteria (UID2112)	31	211	124	6	202	3	0	0	0	96.98	2.42	33.33
maxbin.055.g907	o_Clostridiales (UID1212)	172	263	149	5	258	0	0	0	0	96.98	0	0
bin.136.hh12	f_Spirochaetaceae (UID2535)	33	249	143	7	239	3	0	0	0	96.97	0.47	66.67
bin.43.hh11	f_Spirochaetaceae (UID2535)	33	249	143	6	241	2	0	0	0	96.97	1.05	50
bin.196.gw02	k_Bacteria (UID2569)	434	278	186	7	268	3	0	0	0	96.94	0.59	0
bin.219.g906	k_Bacteria (UID2569)	434	278	186	8	268	2	0	0	0	96.94	0.54	0
maxbin.018_sub.gw04	k_Bacteria (UID2569)	434	278	186	8	261	9	0	0	0	96.94	3.23	0
bin.244.g9	p_Actinobacteria (UID2112)	31	211	124	6	186	17	2	0	0	96.93	4.33	30.43
maxbin.044_sub.g908	o_Clostridiales (UID1212)	172	263	149	9	250	4	0	0	0	96.92	0.64	75
bin.220.g906	p_Actinobacteria (UID2112)	31	211	124	6	196	8	0	1	0	96.91	7	28.57
57.gw26	o_Bacteroidales (UID2617)	213	406	265	29	375	2	0	0	0	96.89	0.5	0
bin.116.hh13	o_Lactobacillales (UID544)	293	473	265	11	452	10	0	0	0	96.89	1.77	80
maxbin.011.gw30	o_Clostridiales (UID1212)	172	263	149	16	245	2	0	0	0	96.88	0.69	0
bin.111.gw27	c_Epsilonproteobacteria (UID3065)	111	445	271	9	411	25	0	0	0	96.86	5.76	76
166_sub.hh	o_Clostridiales (UID1212)	172	263	149	15	222	26	0	0	0	96.85	7.23	76.92
bin.118.hc20	f_Spirochaetaceae (UID2535)	33	249	143	6	242	1	0	0	0	96.85	0.04	0
bin.208.hc18	f_Spirochaetaceae (UID2535)	33	249	143	6	242	1	0	0	0	96.85	0.7	100
bin.3_sub.g908	f_Spirochaetaceae (UID2535)	33	249	143	6	241	2	0	0	0	96.85	1.4	0
maxbin.299.gw	f_Spirochaetaceae (UID2535)	33	249	143	6	243	0	0	0	0	96.85	0	0
173_sub.gw05	o_Clostridiales (UID1212)	172	263	149	9	254	0	0	0	0	96.83	0	0
bin.24.g910	o_Clostridiales (UID1212)	172	263	149	8	254	1	0	0	0	96.83	0.17	0
323_sub.g9	k_Bacteria (UID2329)	174	149	89	4	142	3	0	0	0	96.82	2.41	33.33
bin.33.gw01	k_Bacteria (UID2329)	174	149	89	4	143	2	0	0	0	96.82	1.28	50
maxbin.032.hc19	f_Enterobacteriaceae (UID5162)	88	1207	328	35	1148	24	0	0	0	96.82	1.47	79.17
14.gw28	c_Spirochaetia (UID2496)	72	215	125	5	206	4	0	0	0	96.8	1.73	75
bin.122.hc20	p_Euryarchaeota (UID3)	148	188	125	4	180	4	0	0	0	96.8	2.8	100
bin.145.hh11	p_Euryarchaeota (UID3)	148	188	125	4	179	5	0	0	0	96.8	4	100
maxbin.004.gw29	p_Bacteroidetes (UID2605)	350	314	208	13	292	9	0	0	0	96.79	1.69	11.11
173.g910	c_Clostridia (UID1118)	367	223	124	4	206	13	0	0	0	96.77	6.04	53.85
183_sub.g910	c_Clostridia (UID1118)	367	223	124	6	210	5	0	0	0	96.77	2.29	100
84_sub.g907	p_Actinobacteria (UID2112)	31	211	124	4	195	10	2	0	0	96.77	5.83	31.25
bin.149.g909	k_Bacteria (UID2569)	434	278	186	7	269	2	0	0	0	96.77	0.81	50
bin.201.gw03	p_Actinobacteria (UID2112)	31	211	124	4	201	6	0	0	0	96.77	1.61	16.67
bin.208.g909	p_Actinobacteria (UID2112)	31	211	124	10	191	10	0	0	0	96.77	4.84	0
bin.214.g906	k_Bacteria (UID2569)	434	278	186	6	270	2	0	0	0	96.77	1.08	100
bin.253.gw	c_Clostridia (UID1118)	367	223	124	5	213	5	0	0	0	96.77	1.95	80
bin.256.gw01	p_Euryarchaeota (UID3)	148	187	124	5	181	1	0	0	0	96.77	0.81	100
bin.266.gw02	p_Euryarchaeota (UID3)	148	187	124	7	178	2	0	0	0	96.77	1.21	50
bin.31.g910	p_Actinobacteria (UID2112)	31	211	124	7	201	3	0	0	0	96.77	1.48	100
bin.334.g9	p_Actinobacteria (UID2112)	31	211	124	7	203	1	0	0	0	96.77	0.27	0
bin.4.gw01	p_Euryarchaeota (UID3)	148	187	124	5	180	2	0	0	0	96.77	1.61	50
bin.422.g9	p_Euryarchaeota (UID3)	148	187	124	5	182	0	0	0	0	96.77	0	0
bin.491.g9	p_Actinobacteria (UID2112)	31	211	124	7	204	0	0	0	0	96.77	0	0
bin.505.gw	p_Euryarchaeota (UID3)	148	187	124	5	181	1	0	0	0	96.77	0.81	100
maxbin.168_sub.g9	p_Proteobacteria (UID3887)	1487	256	160	6	242	8	0	0	0	96.77	3.12	25
maxbin.009.hh12	c_Gammaproteobacteria (UID4201)	1164	272	171	15	250	7	0	0	0	96.75	0.91	0
bin.363.g9	o_Clostridiales (UID1212)	172	263	149	12	248	3	0	0	0	96.74	0.69	66.67
bin.391.gw	c_Deltaproteobacteria (UID3218)	61	284	169	8	274	2	0	0	0	96.74	1.18	50
bin.495.g9	c_Deltaproteobacteria (UID3218)	61	284	169	8	274	2	0	0	0	96.74	1.18	0
maxbin.024_sub.g906	p_Euryarchaeota (UID3)	148	188	125	5	180	3	0	0	0	96.74	1.76	100
bin.186_sub.gw02	k_Bacteria (UID203)	5449	103	57	4	84	13	2	0	0	96.73	4.31	5.26
bin.47.hc16	c_Gammaproteobacteria (UID4201)	1164	272	171	18	253	1	0	0	0	96.72	0.58	100
bin.109_sub.gw02	p_Actinobacteria (UID2112)	31	211	124	7	199	4	1	0	0	96.71	3.03	42.86
maxbin.223.gw	k_Bacteria (UID2495)	2993	147	91	29	115	3	0	0	0	96.7	2.75	0
maxbin.069_sub.gw01	k_Bacteria (UID2372)	131	176	105	4	167	5	0	0	0	96.67	3.27	80
bin.35.hc10	o_Lactobacillales (UID543)	471	294	164	12	443	16	0	0	0	96.65	4.66	43.75
123_sub.gw01	o_Clostridiales (UID1212)	172	263	149	8	250	2	1	1	1	96.64	4.25	9.38
50.g908	c_Clostridia (UID1118)	367	223	124	7	211	5	0	0	0	96.64	2.36	60
70.hc19	f_Verrucomicrobia (UID1032)	33	423	214	16	378	28	1	0	0	96.64	7.59	90.32
92.hh11	o_Clostridiales (UID1212)	172	263	149	6	248	9	0	0	0	96.64	2.87	77.78
bin.165.g910	o_Clostridiales (UID1212)	172	263	149	9	254	0	0	0	0	96.64	0	0
bin.625.g9	o_Clostridiales (UID1212)	172	263	149	6	254	3	0	0	0	96.64	2.01	100
bin.89.gw	o_Bacteroidales (UID2716)												

5.hc19	k_Bacteria (UID2982)	88	229	147	5	210	12	2	0	0	96.6	7.24	100
bin.152_sub.gw05	k_Bacteria (UID2329)	174	149	89	4	143	2	0	0	0	96.58	2.25	100
bin.77.gw01	p_Euryarchaeota (UID3)	148	187	124	7	172	8	0	0	0	96.58	4.87	87.5
bin.21.hh13	k_Bacteria (UID2495)	2993	143	89	4	139	0	0	0	0	96.56	0	0
bin.279_sub.gw	k_Bacteria (UID203)	5449	104	58	2	85	17	0	0	0	96.55	6.9	35.29
bin.89_sub.hh15	k_Bacteria (UID203)	5449	104	58	2	82	20	0	0	0	96.55	6.37	70
bin.170.hh13	o_Clostridiales (UID1212)	172	263	149	15	238	10	0	0	0	96.54	2.5	40
bin.295.hh	o_Clostridiales (UID1212)	172	263	149	9	251	3	0	0	0	96.53	0.73	100
bin.247_gh07	f_Lachnospiraceae (UID1286)	57	420	207	12	387	11	0	0	0	96.52	2.87	63.64
bin.119_gh10	k_Bacteria (UID2569)	434	278	186	7	268	3	0	0	0	96.51	1.34	100
bin.31_gh08	k_Bacteria (UID2569)	434	278	186	8	267	3	0	0	0	96.51	1.08	66.67
maxbin.005_sub.gw05	k_Bacteria (UID2569)	434	278	186	7	263	8	0	0	0	96.51	3.76	50
maxbin.055_sub.gw	k_Bacteria (UID2569)	434	278	186	8	268	2	0	0	0	96.51	1.08	0
100.gw02	f_Spirochaetaceae (UID2535)	33	249	143	5	243	1	0	0	0	96.5	0.7	0
bin.31.hh13	o_Clostridiales (UID1120)	304	250	143	7	243	0	0	0	0	96.5	0	0
bin.113_gh27	f_Lachnospiraceae (UID1256)	333	333	171	7	319	7	0	0	0	96.49	3.07	42.86
155_gh10	k_Bacteria (UID2565)	2921	142	87	4	137	1	0	0	0	96.48	1.15	100
225_gh08	k_Bacteria (UID2565)	2921	142	87	4	137	1	0	0	0	96.48	1.15	0
239.gw01	k_Bacteria (UID2565)	2921	142	87	4	138	0	0	0	0	96.48	0	0
255.gw05	k_Bacteria (UID2565)	2921	142	87	4	138	0	0	0	0	96.48	0	0
267_gh09	k_Bacteria (UID2565)	2921	142	87	4	138	0	0	0	0	96.48	0	0
273_gh	k_Bacteria (UID2565)	2921	142	87	4	138	0	0	0	0	96.48	0	0
296.gw02	k_Bacteria (UID2565)	2921	142	87	4	138	0	0	0	0	96.48	0	0
91.gw04	k_Bacteria (UID2565)	2921	142	87	4	138	0	0	0	0	96.48	0	0
bin.65.hc20	o_Clostridiales (UID1212)	172	263	149	6	253	4	0	0	0	96.48	1.79	50
bin.61.gw01	f_Spirochaetaceae (UID2535)	33	249	143	11	236	2	0	0	0	96.46	0.82	50
maxbin.027_sub.gh07	k_Bacteria (UID2569)	434	278	186	10	262	6	0	0	0	96.45	3.23	50
maxbin.200.gw	o_Clostridiales (UID1120)	304	247	141	11	234	2	0	0	0	96.45	0.59	50
12_gh	o_Clostridiales (UID1212)	172	263	149	6	255	1	1	0	0	96.42	0.89	25
188.gw	o_Clostridiales (UID1212)	172	263	149	6	254	2	0	0	1	96.42	2.35	0
maxbin.141_gh	o_Clostridiales (UID1212)	172	263	149	9	253	1	0	0	0	96.42	0.67	100
maxbin.342_sub.gw	o_Clostridiales (UID1212)	172	263	149	11	250	2	0	0	0	96.4	0.34	0
bin.152_gh09	p_Actinobacteria (UID2112)	31	211	124	6	195	10	0	0	0	96.37	3.35	40
bin.23.hh14	o_Clostridiales (UID1212)	172	261	147	8	245	7	1	0	0	96.37	6.12	50
bin.266_gh09	p_Euryarchaeota (UID3)	148	187	124	5	173	9	0	0	0	96.37	5.4	88.89
bin.31.gw	p_Actinobacteria (UID2112)	31	211	124	11	195	5	0	0	0	96.37	4.03	20
bin.246.hc17	o_Lactobacillales (UID544)	293	473	265	15	456	2	0	0	0	96.35	0.19	100
bin.181_gh07	o_Clostridiales (UID1212)	172	263	149	14	245	4	0	0	0	96.33	1.34	0
180.gw04	o_Clostridiales (UID1212)	172	263	149	6	250	7	0	0	0	96.31	3.69	100
bin.100.hc19	o_Clostridiales (UID1212)	172	263	149	6	254	3	0	0	0	96.31	1.68	100
bin.211_gh06	p_Euryarchaeota (UID3)	148	187	124	6	177	4	0	0	0	96.31	2.48	50
bin.375.gw	o_Clostridiales (UID1212)	172	263	149	7	254	0	0	0	0	96.31	0.67	0
bin.200_sub.gw03	k_Bacteria (UID2372)	131	177	106	7	165	5	0	0	0	96.29	1.31	20
bin.10.hc18	o_Clostridiales (UID1212)	172	263	149	13	244	6	0	0	0	96.28	2.13	83.33
bin.201_sub.gw02	f_Lachnospiraceae (UID1255)	90	354	174	17	330	7	0	0	0	96.26	2.38	71.43
126.gw03	k_Bacteria (UID2569)	434	278	186	11	265	2	0	0	0	96.25	1.08	50
0_sub.hc18	c_Gammaproteobacteria (UID4201)	1164	271	170	9	226	32	4	0	0	96.24	17.24	72.73
68.gw28	k_Bacteria (UID2569)	434	278	186	9	268	1	0	0	0	96.24	0.54	0
bin.1.gw05	p_Actinobacteria (UID2112)	31	211	124	11	198	2	0	0	0	96.24	1.61	50
bin.230_gh08	p_Actinobacteria (UID2112)	31	211	124	6	202	3	0	0	0	96.24	1.48	100
bin.33.gw28	k_Bacteria (UID2569)	434	278	186	17	259	2	0	0	0	96.24	0.54	0
bin.25.hc16	o_Clostridiales (UID1212)	172	263	149	8	251	4	0	0	0	96.2	1.03	100
bin.265_sub.gw02	o_Clostridiales (UID1212)	172	263	149	8	253	2	0	0	0	96.2	0.89	100
bin.305.gw03	k_Bacteria (UID2372)	131	176	105	5	168	3	0	0	0	96.19	1.75	66.67
maxbin.047_gh08	k_Bacteria (UID2372)	131	176	105	4	166	0	0	0	0	96.19	4.6	83.33
bin.116.gw01	p_Actinobacteria (UID2112)	31	211	124	7	201	9	0	0	0	96.17	1.32	100
217_gh09	k_Bacteria (UID2569)	434	278	186	10	263	5	0	0	0	96.15	1.29	20
303_gh	f_Spirochaetaceae (UID2535)	33	249	143	7	242	0	0	0	0	96.15	0	0
bin.143.hh11	f_Spirochaetaceae (UID2535)	33	249	143	7	239	3	0	0	0	96.15	2.1	100
bin.235_gh10	f_Lachnospiraceae (UID1255)	90	354	174	22	329	3	0	0	0	96.15	0.65	0
bin.275.gw04	f_Spirochaetaceae (UID2535)	33	249	143	7	241	1	0	0	0	96.15	0.35	100
bin.63_sub.hc18	f_Spirochaetaceae (UID2535)	33	249	143	7	238	4	0	0	0	96.15	1.44	100
bin.96.gw05	f_Spirochaetaceae (UID2535)	33	249	143	7	240	2	0	0	0	96.15	0.93	100
maxbin.146.gw03	f_Spirochaetaceae (UID2535)	33	249	143	7	238	4	0	0	0	96.15	2.1	25
201_sub.gw27	o_Clostridiales (UID1212)	172	263	149	8	240	14	1	0	0	96.12	7.55	82.35
247.hh14	o_Selenomonadales (UID1024)	64	334	167	15	307	12	0	0	0	96.11	3.41	41.67
bin.556_gh	f_Lachnospiraceae (UID1255)	90	354	174	10	341	3	0	0	0	96.11	1.44	66.67
204_sub.gw03	o_Clostridiales (UID1120)	304	247	141	6	236	5	0	0	0	96.1	2.2	60
bin.136.gw05	c_Clostridia (UID1119)	287	224	124	23	202	2	0	0	0	96.1	1.08	100
bin.3_gh10	k_Bacteria (UID2329)	174	149	89	4	145	0	0	0	0	96.07	0	0
bin.104_sub.gw30	c_Gammaproteobacteria (UID4201)	1164	272	171	39	216	17	0	0	0	96.05	6.38	88.24
bin.357_sub.gw	o_Clostridiales (UID1212)	172	263	149	17	241	5	0	0	0	96.02	2.85	0
bin.29.gw	k_Bacteria (UID2328)	3167	126	75	3	122	1	0	0	0	96	1.33	0
bin.570_gh	o_Clostridiales (UID1226)	155	278	158	7	269	2	0	0	0	95.99	0.84	50
10.hc16	o_Clostridiales (UID1212)	172	263	149	7	230	25	1	0	0	95.97	11.44	96.43
166_gh07	k_Bacteria (UID2569)	434	278	186	8	268	2	0	0	0	95.97	1.08	0
214.gw02	k_Bacteria (UID2569)	434	278	186	8	263	7	0	0	0	95.97	3.49	28.57
244.hh12	o_Clostridiales (UID1212)	172	263	149	6	251	6	0	0	0	95.97	2.35	100
bin.103.gw30	p_Actinobacteria (UID2112)	31	211	124	7	201	3	0	0	0	95.97	0.94	33.33
bin.159.gw05	o_Clostridiales (UID1212)	172	263	149	6	255	2	0	0	0	95.97	0.67	0
bin.202.hh14	o_Clostridiales (UID1375)	50	332	124	23	308	1	0	0	0	95.97	0.16	100
bin.206.gw04	p_Actinobacteria (UID2112)	31	211	124	5	205	1	0	0	0	95.97	0.08	0
bin.213_gh10	p_Euryarchaeota (UID3)	148	187	124	6	181	0	0	0	0	95.97	0	0
bin.335.hh	o_Clostridiales (UID1212)	172	263	149	8	242	13	0	0	0	95.97	5.66	92.31
bin.35_gh09	p_Euryarchaeota (UID3)	148	187	124	6	181	0	0	0	0	95.97	0	0
bin.403.hc	o_Clostridiales (UID1212)	172	263	149	10	251	2	0	0	0	95.97	0.81	100
bin.42.hc19	o_Clostridiales (UID1212)	172	263	149	8	253	2	0	0	0	95.97	1.34	100
bin.427_sub.gw	p_Actinobacteria (UID2112)	31	211	124	8	201	2	0	0	0	95.97	0.52	0
bin.55.hh15	o_Clostridiales (UID1375)	50	332	124	23	309	0	0	0	0	95.97	0	0
bin.592.gw	p_Actinobacteria (UID2112)	31	211	124	6	205	0	0	0	0	95.97	0	0
bin.68.gw03	o_Clostridiales (UID1212)	172	263	149	6	252	5	0	0	0	95.97	1.57	40
maxbin.023_gh10	k_Bacteria (UID2569)	434	278	186	8	266	4	0	0	0	95.97	2.15	50
bin.227.gw04	p_Bacteroidetes (UID2605)	350	316	210	9	304	3	0	0	0	95.95	1.19	100
bin.54_gh06	o_Lactobacillales (UID355)	490	334	183	12	314	8	0	0	0	95.95	3.1	62.5
bin.81.ca22	p_Bacteroidetes (UID2605)	350	316	210	9	306	1	0	0	0	95.95	0.48	0
bin.89_sub.gh09	p_Bacteroidetes (UID2605)	350	316	210	9	305	2	0	0	0	95.95	0.63	100
bin.61_gh09	o_Clostridiales (UID1120)	304	247	141	8	237	2	0	0	0	95.92	1.42	100
129.gw27	p_Bacteroidetes (UID2605)	350	314	208	9	300	5	0	0	0	95.91	1.71	60
bin.149_gh	o_Bacteroidales (UID2621)	198	427	260	13	414	0	0	0	0	95.9	0	0
bin.179_gh09	f_Lachnospiraceae (UID1286)	57	420	207	29	389	1	1	0	0	95.89	0.31	25
129_sub.hh12	c_Gammaproteobacteria (UID4201)	1164	271	170	9	244	16	2	0	0	95.88	7	81.82
92.gw04	o_Selenomonadales (UID1024)	64	334	167	32	291	11	0	0	0</			

bin.191.gp06	f_Spirochaetaceae (UID2535)	33	249	143	6	242	1	0	0	0	95.8	0.7	0
bin.67_sub.hh13	f_Spirochaetaceae (UID2535)	33	249	143	6	233	10	0	0	0	95.8	3.87	10
maxbin.159.gp	f_Spirochaetaceae (UID2535)	33	249	143	6	239	2	0	0	0	95.8	0.93	100
bin.537.gp	p_Actinobacteria (UID2112)	31	211	124	9	200	2	0	0	0	95.79	1.08	100
bin.18.gp27	k_Bacteria (UID2372)	131	177	106	13	163	1	0	0	0	95.78	0.09	0
bin.195.hc20	o_Bacteroidales (UID2654)	163	486	266	25	455	5	1	0	0	95.76	2.01	50
bin.29.gp02	o_Clostridiales (UID1212)	172	263	149	7	253	3	0	0	0	95.75	1.01	33.33
maxbin.261.gw	o_Clostridiales (UID1212)	172	263	149	9	251	3	0	0	0	95.75	0.5	0
288_sub.gw	o_Clostridiales (UID1120)	304	247	141	8	236	3	0	0	0	95.74	1.13	66.67
53.gp07	o_Clostridiales (UID1120)	304	247	141	7	237	3	0	0	0	95.74	1.77	66.67
60.gp10	o_Clostridiales (UID1120)	304	247	141	6	239	2	0	0	0	95.74	0.26	50
bin.197.gp08	o_Clostridiales (UID1120)	304	247	141	6	241	0	0	0	0	95.74	0	0
bin.200.gp08	o_Clostridiales (UID1120)	304	247	141	7	239	1	0	0	0	95.74	0.71	100
maxbin.269_sub.gp	o_Clostridiales (UID1120)	304	247	141	12	232	3	0	0	0	95.74	0.33	66.67
153_sub.hc20	f_Spirochaetaceae (UID2535)	33	249	143	8	239	2	0	0	0	95.73	1.4	0
47.hc19	o_Clostridiales (UID1212)	172	263	149	11	252	0	0	0	0	95.73	0	0
bin.172.hh15	f_Mycoplasmataceae (UID2414)	89	228	130	15	212	1	0	0	0	95.73	0.38	0
bin.95.gp26	f_Lachnospiraceae (UID1255)	90	354	174	39	312	3	0	0	0	95.71	1.29	66.67
maxbin.064.gp06	k_Bacteria (UID2372)	131	176	105	5	167	4	0	0	0	95.71	3.17	75
148.hc19	k_Bacteria (UID2565)	2921	152	93	5	145	2	0	0	0	95.7	2.15	100
bin.157.gp05	p_Euryarchaeota (UID3)	148	187	124	16	169	2	0	0	0	95.69	1.61	100
maxbin.151.gp06	k_Bacteria (UID2329)	174	149	89	5	142	2	0	0	0	95.69	1.24	25
bin.194.gp	o_Clostridiales (UID1212)	263	149	89	4	218	15	0	0	0	95.68	5.73	93.33
bin.100.gp01	o_Clostridiales (UID1212)	172	257	149	9	244	4	0	0	0	95.64	1.81	50
bin.92_sub.gp07	o_Clostridiales (UID1212)	172	257	149	7	239	10	1	0	0	95.64	3.47	53.85
285.gp01	o_Clostridiales (UID1120)	304	247	141	29	217	1	0	0	0	95.59	0.24	100
bin.295.gw	o_Bacteroidales (UID2621)	198	427	260	15	409	3	0	0	0	95.58	0.96	100
bin.149_sub.gp08	f_Spirochaetaceae (UID2535)	33	249	143	7	238	4	0	0	0	95.57	1.79	0
275_sub.gp	p_Firmicutes (UID1022)	100	295	158	14	205	15	1	0	0	95.56	6.27	77.78
bin.191.gp	o_Clostridiales (UID1212)	172	263	149	40	222	1	0	0	0	95.53	0.22	100
bin.207_sub.gp03	o_Clostridiales (UID1212)	172	263	149	9	254	0	0	0	0	95.53	0	0
maxbin.063.hh11	o_Clostridiales (UID1212)	172	263	149	10	238	15	0	0	0	95.53	5.93	26.67
bin.140.gp06	p_Proteobacteria (UID3887)	1487	256	160	25	229	2	0	0	0	95.52	1.25	0
bin.427.hc	p_Bacteroidetes (UID2605)	350	314	208	35	271	8	0	0	0	95.52	3.04	62.5
54_sub.hc19	k_Bacteria (UID2329)	174	149	89	4	144	1	0	0	0	95.51	0.05	100
bin.191.gp08	k_Bacteria (UID2329)	174	149	89	4	141	1	0	0	0	95.51	2.92	25
bin.304.gp07	k_Bacteria (UID2329)	174	149	89	5	138	5	1	0	0	95.51	5.27	62.5
bin.339.gp07	k_Bacteria (UID2329)	174	149	89	4	143	2	0	0	0	95.51	2.25	50
bin.93.gp	k_Bacteria (UID2329)	174	149	89	4	142	3	0	0	0	95.51	3.37	33.33
108.hh14	p_Firmicutes (UID1022)	100	295	158	28	240	26	1	0	0	95.49	10.8	65.52
bin.99.gp02	p_Bacteroidetes (UID2605)	350	316	210	10	304	2	0	0	0	95.48	0.71	50
194.hc20	o_Clostridiales (UID1212)	172	263	149	9	241	13	0	0	0	95.47	6.72	100
241_sub.gp01	f_Spirochaetaceae (UID2535)	33	249	143	8	229	12	0	0	0	95.45	6.99	50
bin.66.gp05	p_Actinobacteria (UID2112)	31	211	124	11	198	2	0	0	0	95.45	1.08	100
maxbin.082.hh13	k_Bacteria (UID2565)	2921	152	93	9	142	1	0	0	0	95.45	1.08	100
21.gp06	o_Clostridiales (UID1212)	172	263	149	13	249	1	0	0	0	95.44	0.67	0
221.hc20	k_Bacteria (UID2495)	2993	143	89	6	137	0	0	0	0	95.44	0	0
bin.105.hc19	k_Bacteria (UID2495)	2993	143	89	5	138	0	0	0	0	95.44	0	0
95.gp05	k_Bacteria (UID2569)	434	278	186	9	266	3	0	0	0	95.43	1.61	33.33
bin.106.gp05	p_Actinobacteria (UID2112)	31	211	124	8	202	1	0	0	0	95.43	0.81	0
bin.280_sub.gp01	k_Bacteria (UID2569)	434	278	186	9	267	2	0	0	0	95.43	0.72	100
bin.478.gw	k_Bacteria (UID2569)	434	278	186	11	263	4	0	0	0	95.43	1.12	75
30_sub.gp04	k_Bacteria (UID2372)	131	177	106	12	155	10	0	0	0	95.42	5.18	20
206_sub.hh12	o_Clostridiales (UID1212)	172	263	149	10	241	11	1	0	0	95.41	6.98	100
bin.50_sub.gp	o_Clostridiales (UID1120)	304	247	141	8	239	10	0	0	0	95.39	1.6	100
bin.80.hh13	o_Clostridiales (UID1212)	172	263	149	10	246	7	0	0	0	95.39	3.21	100
333_sub.hc	o_Lactobacillales (UID374)	471	350	191	12	323	15	0	0	0	95.38	4.77	86.67
bin.192.hc20	f_Bifidobacteriaceae (UID1462)	65	476	217	16	443	16	1	0	0	95.36	4.55	42.11
bin.164.gp10	k_Bacteria (UID2569)	434	278	186	10	267	1	0	0	0	95.34	0.54	100
304_sub.gp03	c_Clostridia (UID1118)	387	223	124	8	203	12	0	0	0	95.3	5.17	33.33
bin.172.gp08	o_Clostridiales (UID1212)	172	263	149	7	253	3	0	0	0	95.3	1.34	0
bin.213.gp	o_Clostridiales (UID1212)	172	263	149	9	254	0	0	0	0	95.3	0	0
bin.351.hg	o_Clostridiales (UID1212)	172	263	149	10	247	6	0	0	0	95.3	0.69	16.67
maxbin.432.hh	o_Clostridiales (UID1212)	172	263	149	11	242	10	0	0	0	95.3	3.92	30
bin.262_sub.gp04	o_Clostridiales (UID1212)	172	263	149	8	250	5	0	0	0	95.28	1.29	40
16.hc19	o_Clostridiales (UID1120)	304	250	143	12	231	7	0	0	0	95.27	3.61	28.57
316.hc	k_Bacteria (UID2982)	88	230	148	7	220	3	0	0	0	95.27	1.69	0
maxbin.064.hc18	k_Bacteria (UID2982)	88	230	148	7	220	3	0	0	0	95.27	1.69	0
170_sub.gp	o_Clostridiales (UID1212)	172	263	149	14	232	17	0	0	0	95.26	3.57	52.94
189_sub.hh13	c_Gammaproteobacteria (UID4201)	1164	271	170	10	219	41	1	0	0	95.26	16.38	70.45
bin.284.gp09	p_Actinobacteria (UID2112)	31	211	124	10	191	9	1	0	0	95.25	4.19	25
bin.12_sub.gp08	k_Bacteria (UID2372)	131	176	105	6	160	10	0	0	0	95.24	5.22	40
maxbin.048.gp01	f_Lachnospiraceae (UID1286)	57	420	207	16	395	9	0	0	0	95.23	3.26	88.89
bin.123.hc20	f_Spirochaetaceae (UID2535)	33	249	143	10	232	7	0	0	0	95.22	3.22	85.71
bin.73.hc22	f_Enterobacteriaceae (UID5162)	88	1207	328	42	1152	13	0	0	0	95.22	0.98	30.77
bin.41.hc20	o_Clostridiales (UID1212)	172	260	146	10	246	4	0	0	0	95.21	2.17	75
bin.128.gw	c_Deltaproteobacteria (UID3218)	61	284	169	10	272	2	0	0	0	95.2	0.26	0
69.gp29	o_Clostridiales (UID1212)	172	263	149	11	237	14	1	0	0	95.19	8.05	70.59
bin.265.gp09	o_Clostridiales (UID1212)	172	263	149	13	247	3	0	0	0	95.19	1.57	66.67
bin.202.gp07	p_Actinobacteria (UID2112)	31	211	124	10	186	14	1	0	0	95.18	4.22	23.53
bin.55.hc	o_Selenomonadales (UID1024)	64	334	167	21	308	5	0	0	0	95.18	1.54	80
maxbin.067.hh13	o_Clostridiales (UID1212)	172	263	149	16	242	5	0	0	0	95.18	2.35	20
169.hc17	k_Bacteria (UID2569)	434	278	186	10	247	21	0	0	0	95.16	9.18	80.95
bin.169.gp05	p_Euryarchaeota (UID3)	148	187	124	7	180	0	0	0	0	95.16	0	0
bin.199.gp06	k_Bacteria (UID2569)	434	278	186	11	264	3	0	0	0	95.16	1.61	33.33
bin.28.gp08	k_Bacteria (UID2569)	434	278	186	12	263	3	0	0	0	95.16	1.61	33.33
bin.311.gp07	c_Clostridia (UID1118)	387	223	124	8	205	10	0	0	0	95.16	4.08	80
bin.116_sub.gp06	f_Lachnospiraceae (UID1286)	57	420	207	17	396	5	0	0	0	95.15	1.32	40
bin.232.gp10	o_Clostridiales (UID1226)	155	278	158	21	254	3	0	0	0	95.15	1.48	0
bin.304.hg	c_Epsilonproteobacteria (UID3065)	111	445	271	21	406	18	0	0	0	95.14	3.91	88.89
bin.416.gw	o_Clostridiales (UID1212)	172	263	149	8	250	5	0	0	0	95.13	2.24	60
bin.525.gw	k_Bacteria (UID2329)	174	149	89	7	141	1	0	0	0	95.13	0.56	0
maxbin.049.gp	o_Clostridiales (UID1212)	172	263	149	11	251	1	0	0	0	95.13	0.67	100
bin.228.gp09	k_Bacteria (UID2569)	434	278	186	12	266	0	0	0	0	95.11	0	0
bin.97.gp01	o_Bacteroidales (UID2657)	160	492	269	23	467	2	0	0	0	95.11	0.37	0
bin.92.hh	o_Clostridiales (UID1120)	304	250	143	11	239	0	0	0	0	95.1	0	0
bin.214.hc18	f_Verrucomicrobiota (UID1032)	33	423	214	20	398	5	0	0	0	95.09	0.97	80
63.gp05	o_Clostridiales (UID1212)	172	263	149	9	254	0	0	0	0	95.08	0	0
bin.193.gp02	o_Clostridiales (UID1212)	172	263	149	8	255	0	0	0	0	95.08	0	0
277.hc	c_Spirochaetia (UID2496)	72	215	125	10	178	27	0	0	0	95.07	11.9	92.59
bin.8.gp08	k_Bacteria (UID2569)	434	278	186	12	262	4	0	0	0	95.07		

25.gi08	o_Clostridiales (UID1212)	172	263	149	13	242	4	4	0	0	95.02	3.64	12.5
bin.143.hh14	k_Bacteria (UID2329)	174	149	89	6	143	0	0	0	0	95.02	0	0
bin.225.hh	f_Verrucomicrobiales (UID1032)	33	423	214	23	391	9	0	0	0	95.02	2.77	77.78
bin.179.hc19	o_Lactobacillales (UID543)	294	469	262	20	434	15	0	0	0	95.01	3.31	6.67
bin.103.gi28	c_Clostridia (UID1118)	387	223	124	8	213	2	0	0	0	95	0.83	50
bin.110.gi10	p_Actinobacteria (UID2112)	31	211	124	18	186	6	1	0	0	95	3.04	22.22
bin.117.gw01	p_Bacteroidetes (UID2605)	350	316	210	11	303	2	0	0	0	95	0.71	50
bin.153.gw05	p_Bacteroidetes (UID2605)	350	316	210	11	302	3	0	0	0	95	1.43	100
bin.306.gw03	p_Bacteroidetes (UID2605)	350	316	210	11	302	3	0	0	0	95	1.19	100
bin.114.gw	o_Lactobacillales (UID355)	490	334	153	13	318	3	0	0	0	94.99	0.87	100
bin.185_sub.gw04	f_Lachnospiraceae (UID1286)	57	420	207	16	381	21	2	0	0	94.99	3.64	14.81
bin.274.gi09	f_Lachnospiraceae (UID1286)	57	420	207	17	396	7	0	0	0	94.99	2.15	42.86
bin.289.gi09	o_Clostridiales (UID1212)	172	257	149	10	239	8	0	0	0	94.97	2.68	12.5
bin.330.gw	p_Actinobacteria (UID2112)	31	211	124	9	200	2	0	0	0	94.96	0.92	0
219_sub.gw01	f_Lachnospiraceae (UID1286)	57	420	207	25	369	26	0	0	0	94.95	3.54	7.69
bin.15.gi07	k_Bacteria (UID2329)	174	149	89	5	142	2	0	0	0	94.94	2.25	100
bin.281.gi10	k_Bacteria (UID2329)	174	149	89	5	139	5	0	0	0	94.94	5.06	80
bin.75.gi09	f_Lachnospiraceae (UID1286)	57	420	207	19	395	6	0	0	0	94.94	1.27	100
bin.85.gi27	f_Spirochaetaceae (UID2535)	33	249	143	12	219	18	0	0	0	94.94	5.35	94.44
maxbin.133.hh15	k_Bacteria (UID2982)	88	230	148	8	219	3	0	0	0	94.93	1.69	0
202_sub.gi06	o_Clostridiales (UID1120)	304	250	143	23	216	11	0	0	0	94.92	5.83	36.36
bin.69.gw02	k_Bacteria (UID2372)	131	176	105	8	161	7	0	0	0	94.92	4.22	28.57
128.gw	k_Bacteria (UID2569)	434	278	186	10	266	4	0	0	0	94.89	1.08	0
139_sub.gw03	p_Actinobacteria (UID2112)	31	211	124	17	172	22	0	0	0	94.89	12.06	63.64
bin.104_sub.gw02	k_Bacteria (UID2569)	434	278	186	10	266	2	0	0	0	94.89	0.1	100
bin.139.gw01	k_Bacteria (UID2569)	434	278	186	10	265	3	0	0	0	94.89	1.34	33.33
bin.311.gw	p_Actinobacteria (UID2112)	31	211	124	10	198	3	0	0	0	94.89	0.81	100
maxbin.058.gi06	k_Bacteria (UID2569)	434	278	186	11	267	0	0	0	0	94.89	0	0
maxbin.070.gi08	p_Actinobacteria (UID2112)	211	211	124	11	196	4	0	0	0	94.89	2.15	100
42.gw05	o_Burkholderiales (UID4000)	193	427	214	17	407	3	0	0	0	94.86	1	0
maxbin.193.gw	o_Burkholderiales (UID4000)	193	427	214	17	407	3	0	0	0	94.86	1	0
maxbin.236.gi	o_Burkholderiales (UID4000)	193	427	214	17	407	3	0	0	0	94.86	1	0
bin.127_sub.gw03	o_Clostridiales (UID1212)	172	263	149	19	239	5	0	0	0	94.85	2.15	0
124_sub.gi28	p_Bacteroidetes (UID2605)	350	314	208	35	268	11	0	0	0	94.84	3.77	54.55
bin.638.hh	k_Bacteria (UID203)	5449	104	58	3	86	15	0	0	0	94.83	2.35	20
bin.126.gi06	c_Gammaproteobacteria (UID4201)	1164	270	171	21	245	4	0	0	0	94.82	0.58	0
bin.251.hh	k_Bacteria (UID2565)	2921	152	93	14	131	7	0	0	0	94.82	0.91	42.86
bin.209.gi	c_Deltaproteobacteria (UID3218)	61	284	169	25	254	5	0	0	0	94.81	2.06	60
bin.282.ca	p_Bacteroidetes (UID2605)	350	316	210	24	288	4	0	0	0	94.81	0.98	50
bin.63.gw05	o_Clostridiales (UID1212)	172	263	149	12	247	4	0	0	0	94.8	0.08	0
111.hc19	o_Clostridiales (UID1212)	172	263	149	15	240	8	0	0	0	94.77	2.59	75
269.hc	f_Spirochaetaceae (UID2535)	33	249	143	13	227	9	0	0	0	94.76	2.87	77.78
maxbin.065.gi09	k_Bacteria (UID2372)	131	176	105	6	161	9	0	0	0	94.76	5.65	55.56
bin.70.ca25	o_Bacteroidales (UID2617)	213	406	265	17	387	2	0	0	0	94.72	0.75	0
29.hc17	f_Verrucomicrobiales (UID1032)	33	423	214	26	354	41	1	1	0	94.71	11.82	72
182_sub.hc16	o_Clostridiales (UID1212)	172	263	149	29	230	4	0	0	0	94.68	2.35	75
bin.127.gw	o_Clostridiales (UID1120)	304	247	141	18	226	3	0	0	0	94.68	1.77	66.67
maxbin.142.hh11	c_Epsilonproteobacteria (UID3066)	110	450	273	18	426	6	0	0	0	94.68	1.34	83.33
130_sub.hc	k_Bacteria (UID203)	5449	104	58	4	61	36	2	1	0	94.67	51.41	95.83
69.hh12	o_Clostridiales (UID1212)	172	263	149	20	231	12	0	0	0	94.67	3	66.67
bin.11.gw04	c_Deltaproteobacteria (UID3218)	61	284	169	12	270	1	0	1	0	94.67	2.37	14.29
bin.78.gi	c_Deltaproteobacteria (UID3218)	61	284	169	10	271	3	0	0	0	94.67	1.48	100
236.gw03	c_Deltaproteobacteria (UID3218)	61	284	169	13	270	0	0	1	0	94.64	1.78	16.67
bin.153.gw02	o_Clostridiales (UID1120)	304	247	141	26	219	2	0	0	0	94.64	0.85	50
206_sub.gi	c_Clostridia (UID1118)	387	223	124	17	153	52	1	0	0	94.63	29.44	63.64
bin.519.gi	o_Clostridiales (UID1212)	172	263	149	8	254	1	0	0	0	94.63	0.34	100
0_sub.gw	c_Clostridia (UID1118)	387	223	124	9	204	10	0	0	0	94.62	5.17	100
324_sub.gi	k_Bacteria (UID2569)	434	278	186	12	264	2	0	0	0	94.62	1.08	50
bin.152.gw04	c_Clostridia (UID1118)	387	223	124	11	202	10	0	0	0	94.62	5.38	60
bin.241_sub.gw04	k_Bacteria (UID2569)	434	278	186	12	264	2	0	0	0	94.62	1.08	100
223_sub.hh14	o_Clostridiales (UID1212)	172	263	149	26	225	12	0	0	0	94.61	5.03	16.67
bin.57.gw05	k_Bacteria (UID2372)	131	176	105	7	167	2	0	0	0	94.6	0.79	50
bin.74.gi28	p_Actinobacteria (UID2112)	31	211	124	17	188	6	0	0	0	94.59	2.06	50
215.gw05	o_Clostridiales (UID1120)	304	250	143	10	231	9	0	0	0	94.58	4.69	55.56
bin.179.hh15	f_Spirochaetaceae (UID2535)	33	249	143	11	237	1	0	0	0	94.58	0.08	0
bin.289.gw	o_Bacteroidales (UID2657)	160	492	269	26	462	4	0	0	0	94.58	1.12	0
bin.336.gi07	o_Lactobacillales (UID355)	490	334	183	19	309	6	0	0	0	94.58	2.32	83.33
196.hc17	p_Firmicutes (UID1022)	100	295	158	29	249	17	0	0	0	94.57	6.05	58.82
97_sub.gi	k_Bacteria (UID2569)	434	278	186	12	251	14	1	0	0	94.57	5.93	23.53
bin.106.gi28	o_Bacteroidales (UID2617)	213	406	265	41	363	2	0	0	0	94.57	0.57	100
bin.125.gw	k_Bacteria (UID2329)	174	149	89	6	140	3	0	0	0	94.57	3.37	66.67
bin.181.gw05	k_Bacteria (UID2329)	174	149	89	6	140	3	0	0	0	94.57	2.81	66.67
maxbin.277.hh	k_Bacteria (UID2982)	88	229	147	9	203	17	0	0	0	94.56	7.97	82.35
bin.182.hh12	k_Bacteria (UID2328)	3167	126	75	5	121	0	0	0	0	94.55	0	0
bin.228.gw04	f_Lachnospiraceae (UID1255)	90	354	174	12	338	4	0	0	0	94.54	1.45	0
bin.133.gi28	p_Bacteroidetes (UID2605)	350	316	210	16	292	8	0	0	0	94.52	2.54	100
bin.48.gi08	p_Bacteroidetes (UID2605)	350	316	210	13	301	2	0	0	0	94.52	0.95	100
maxbin.038.gi08	f_Lachnospiraceae (UID1286)	57	420	207	19	396	5	0	0	0	94.52	1.59	0
maxbin.056_sub.gw	p_Bacteroidetes (UID2605)	350	316	210	13	296	6	1	0	0	94.52	3.17	88.89
bin.111.hh15	k_Bacteria (UID2495)	2993	147	91	5	142	0	0	0	0	94.51	0	0
bin.61.hh	k_Bacteria (UID2495)	2993	147	91	5	141	1	0	0	0	94.51	1.1	100
229.gi26	f_Enterobacteriaceae (UID5162)	88	1207	328	52	1101	54	0	0	0	94.5	5.38	83.33
maxbin.175.gw02	o_Clostridiales (UID1120)	304	247	141	12	223	12	0	0	0	94.5	5.58	25
bin.273.gw04	o_Clostridiales (UID1212)	172	263	149	13	249	1	0	0	0	94.46	0.67	0
maxbin.040.gi10	o_Clostridiales (UID1212)	172	263	149	14	247	2	0	0	0	94.46	0.5	100
130.hc19	o_Clostridiales (UID1212)	172	263	149	30	225	8	0	0	0	94.45	3.81	50
bin.140.gw03	p_Actinobacteria (UID2112)	31	211	124	11	199	1	0	0	0	94.44	0.27	100
maxbin.051_sub.gi08	c_Clostridia (UID1118)	387	223	124	10	198	14	1	0	0	94.42	6.69	41.18
bin.121.gi09	o_Clostridiales (UID1212)	172	263	149	10	253	0	0	0	0	94.41	0	0
bin.144.gi	o_Clostridiales (UID1212)	172	257	149	13	238	6	0	0	0	94.41	3.13	100
bin.78.gi10	p_Bacteroidetes (UID2605)	350	316	210	20	292	4	0	0	0	94.41	1.67	50
bin.99.hh15	o_Clostridiales (UID1212)	172	263	149	13	250	0	0	0	0	94.41	0	0
0_sub.hh12	p_Euryarchaeota (UID3)	148	188	125	8	169	11	0	0	0	94.4	7.52	72.73
bin.46.hc	p_Euryarchaeota (UID3)	148	188	125	30	155	3	0	0	0	94.4	0.18	0
30_sub.gw02	k_Bacteria (UID2329)	174	149	89	5	140	4	0	0	0	94.38	4.49	50
bin.160.hh15	p_Proteobacteria (UID3887)	1487	256	160	28	224	4	0	0	0	94.38	1.77	100
bin.258.gi	k_Bacteria (UID2329)	174	149	89	5	139	5	0	0	0	94.38	5.62	40
bin.308_sub.gi07	k_Bacteria (UID2329)	174	149	89	6	139	4	0	0	0	94.38	2.36	0
bin.82.gi07	k_Bacteria (UID2329)	174	149	89	5	143	1	0	0	0	94.38	1.12	0
214.hh15	o_Clostridiales (UID1212)	172	263	149	16	238	9	0	0	0	94.36	3.91	88.89
maxbin.142.gi07	o_Clostridiales (UID1212)	172	263	149	20	238	4	1	0	0			

maxbin.012.gh06	k_Bacteria (UID2569)	434	278	186	11	264	3	0	0	0	94.35	1.18	33.33
bin.149.gw01	k_Bacteria (UID2372)	131	177	106	8	168	1	0	0	0	94.34	0.13	0
127.gh10	o_Clostridiales (UID1212)	172	261	147	14	246	1	0	0	0	94.33	0.34	100
bin.72.gh10	o_Clostridiales (UID1120)	304	247	141	16	229	2	0	0	0	94.33	1.06	50
199_sub.gw04	p_Actinobacteria (UID2112)	31	211	124	12	189	10	0	0	0	94.31	3.61	30
bin.273.gw02	k_Bacteria (UID2372)	131	176	105	7	167	2	0	0	0	94.29	1.27	50
bin.54.gw04	o_Clostridiales (UID1212)	172	263	149	15	248	0	0	0	0	94.29	0	0
bin.135_sub.gh09	o_Clostridiales (UID1226)	155	278	158	11	249	18	0	0	0	94.28	5.16	11.11
bin.39.hh12	o_Clostridiales (UID1212)	172	263	149	20	234	9	0	0	0	94.26	4.64	44.44
bin.310.gh	k_Bacteria (UID2569)	434	278	186	13	265	0	0	0	0	94.25	0	0
181.hh13	f_Spirochaetaceae (UID2535)	33	249	143	10	234	5	0	0	0	94.23	1.84	100
218.hc20	o_Clostridiales (UID1212)	172	263	149	18	223	22	0	0	0	94.22	9.9	81.82
maxbin.001.gv30	p_Bacteroidetes (UID2605)	350	314	208	22	280	12	0	0	0	94.2	2.61	41.67
191.gh06	k_Bacteria (UID2565)	2921	142	87	6	136	0	0	0	0	94.19	0	0
36.gw03	k_Bacteria (UID2565)	2921	142	87	6	136	0	0	0	0	94.19	0	0
bin.629.hh	o_Clostridia (UID1118)	387	223	124	11	207	1	4	0	0	94.19	2.42	0
156.gw04	o_Clostridiales (UID1212)	172	263	149	12	251	0	0	0	0	94.18	0	0
66_sub.gw04	o_Bacteroidales (UID2617)	213	406	265	20	369	17	0	0	0	94.18	4.72	23.53
bin.105.gw02	o_Bacteroidales (UID2657)	160	492	269	29	452	11	0	0	0	94.18	1.03	54.55
255.hh	c_Spirochaetia (UID2496)	72	215	125	12	179	23	1	0	0	94.17	11.95	73.08
bin.154.gh08	c_Clostridia (UID1118)	387	223	124	9	206	8	0	0	0	94.15	4.91	50
176.gw01	k_Bacteria (UID2496)	2963	147	91	9	136	2	0	0	0	94.14	1.65	50
72.hh12	f_Veillonellaceae (UID1032)	33	423	214	20	389	12	0	0	0	94.14	3.22	16.67
bin.283.hc17	o_Clostridiales (UID1212)	172	263	149	22	239	2	0	0	0	94.14	0.89	50
bin.147_sub.gh09	o_Clostridiales (UID1212)	172	263	149	28	225	10	0	0	0	94.13	4.26	10
bin.71.gw	o_Clostridiales (UID1212)	172	263	149	14	247	2	0	0	0	94.13	0.45	50
205_sub.gw	o_Clostridiales (UID1212)	172	263	149	14	233	15	1	0	0	94.12	3.08	11.11
bin.11.gv26	c_Epsilonproteobacteria (UID3065)	111	445	271	25	408	12	0	0	0	94.1	2.55	50
49_sub.gh06	o_Bacteroidales (UID2657)	223	387	223	10	208	9	4	0	0	94.09	3.76	28.57
bin.269.gw04	k_Bacteria (UID2569)	434	278	186	12	265	1	0	0	0	94.09	0.54	100
bin.53.gv	k_Bacteria (UID2569)	434	278	186	22	252	4	0	0	0	94.09	1.34	0
bin.64.hh11	c_Gammaproteobacteria (UID4201)	1164	271	170	12	254	5	0	0	0	94.08	1.54	40
bin.272.gw	f_Spirochaetaceae (UID2535)	33	249	143	25	222	2	0	0	0	94.06	1.4	50
maxbin.029_sub.hc20	f_Spirochaetaceae (UID2535)	33	249	143	9	240	0	0	0	0	94.06	0	0
maxbin.291_sub.gw	o_Clostridiales (UID1120)	304	247	141	22	222	3	0	0	0	94.06	0.53	0
bin.184.gv07	p_Bacteroidetes (UID2605)	316	310	15	16	296	3	0	0	0	94.05	0.97	100
bin.2.gv06	p_Bacteroidetes (UID2605)	350	316	210	14	301	1	0	0	0	94.05	0.16	100
226_sub.hc	o_Clostridiales (UID1120)	304	247	141	38	201	8	0	0	0	94.04	3.9	87.5
bin.543.hc	f_Bifidobacteriaceae (UID1462)	65	476	217	44	410	22	0	0	0	94.03	4.27	31.82
bin.254.gw01	o_Clostridiales (UID1212)	172	263	149	13	249	1	0	0	0	94.02	0.67	100
bin.190.gh09	p_Actinobacteria (UID2112)	31	211	124	22	185	4	0	0	0	94	1.75	50
bin.229.gh10	o_Bacteroidetes (UID2657)	160	492	269	28	454	10	0	0	0	93.99	0.82	20
bin.62.gv09	o_Bacteroidales (UID2657)	160	492	269	27	463	2	0	0	0	93.99	0.74	0
maxbin.159.gw	o_Clostridiales (UID1226)	155	278	158	24	249	4	1	0	0	93.99	3.38	42.86
bin.85.hh	f_Spirochaetaceae (UID2535)	33	249	143	13	227	9	0	0	0	93.97	4.2	55.56
93_sub.hc20	o_Clostridiales (UID1212)	172	263	149	14	245	4	0	0	0	93.96	1.34	0
bin.124.gw01	o_Clostridiales (UID1212)	172	263	149	13	247	3	0	0	0	93.96	0.27	33.33
bin.218_sub.gh10	o_Clostridiales (UID1212)	172	263	149	20	241	2	0	0	0	93.96	0.67	0
bin.224.gv09	o_Clostridiales (UID1212)	172	263	149	9	252	2	0	0	0	93.96	0.56	100
bin.464.gw	o_Clostridiales (UID1212)	172	263	149	16	247	0	0	0	0	93.96	0	0
bin.19.gw	p_Actinobacteria (UID2112)	31	211	124	9	193	9	0	0	0	93.95	3.03	33.33
bin.6.gw04	p_Actinobacteria (UID2112)	31	211	124	15	187	9	0	0	0	93.95	2.53	33.33
bin.98.gh	k_Bacteria (UID2372)	131	177	106	17	160	0	0	0	0	93.95	0	0
bin.13.gw01	f_Lachnospiraceae (UID1286)	57	420	207	21	393	6	0	0	0	93.94	1.76	16.67
bin.126.hh15	k_Bacteria (UID2962)	88	230	148	9	216	5	0	0	0	93.92	3.04	60
105.hc18	k_Bacteria (UID2962)	88	230	148	11	211	8	0	0	0	93.89	3.72	25
213.hc19	k_Bacteria (UID2372)	131	177	106	11	158	8	0	0	0	93.87	4.8	87.5
26_sub.gv08	o_Bacteroidales (UID2617)	213	406	265	22	375	9	0	0	0	93.87	2.53	11.11
bin.93.gw04	o_Burkholderiales (UID4000)	193	427	214	21	401	5	0	0	0	93.86	1.17	40
bin.152.gv	o_Bacteroidales (UID2657)	160	492	269	27	464	1	0	0	0	93.85	0.37	0
bin.67.hc17	c_Epsilonproteobacteria (UID3065)	111	445	271	25	391	29	0	0	0	93.85	6.04	82.76
bin.178.hh13	p_Actinobacteria (UID2112)	31	211	124	10	193	8	0	0	0	93.84	4.19	87.5
maxbin.018.gv03	k_Bacteria (UID2569)	434	278	186	13	261	4	0	0	0	93.82	1.45	50
maxbin.041.gv08	k_Bacteria (UID2569)	434	278	186	14	261	3	0	0	0	93.82	1.61	66.67
bin.236.gw04	k_Bacteria (UID2372)	131	176	105	7	164	5	0	0	0	93.81	4.13	60
maxbin.063.gv	p_Bacteroidetes (UID2605)	350	316	210	14	297	5	0	0	0	93.81	1.59	60
bin.136.hh	o_Gammaproteobacteria (UID4201)	293	473	265	27	434	12	0	0	0	93.8	1.54	58.33
26.hh14	c_Gammaproteobacteria (UID4201)	1164	271	170	13	240	15	3	0	0	93.79	8.12	62.5
bin.133.gw04	p_Actinobacteria (UID2112)	31	211	124	15	186	8	2	0	0	93.78	8.45	42.86
maxbin.146.gw	c_Deltaproteobacteria (UID3218)	61	284	169	14	268	1	0	0	1	93.78	3.55	25
maxbin.223_sub.gv	k_Bacteria (UID2569)	434	278	186	30	237	11	0	0	0	93.78	3.6	27.27
bin.70.gw	p_Actinobacteria (UID2112)	31	211	124	10	199	2	0	0	0	93.75	1.21	50
bin.29.gv08	o_Clostridiales (UID1212)	172	263	149	10	252	1	0	0	0	93.74	0.34	0
bin.425.gv	o_Clostridiales (UID1212)	172	263	149	15	248	0	0	0	0	93.74	0	0
maxbin.086.gw02	o_Clostridiales (UID1212)	172	263	149	11	252	0	0	0	0	93.74	0	0
bin.15_sub.hh12	o_Lactobacillales (UID544)	293	475	267	56	403	15	1	0	0	93.72	3.73	44.44
bin.39.gw01	o_Clostridiales (UID1212)	172	263	149	14	247	2	0	0	0	93.72	0.45	0
maxbin.073_sub.hh14	p_Euryarchaeota (UID3)	148	188	125	19	158	11	0	0	0	93.72	7.47	81.82
bin.78.hh11	f_Enterobacteriaceae (UID5162)	88	1207	328	69	1074	64	0	0	0	93.7	5.46	90.62
bin.8.gw04	f_Prevotella (UID2724)	55	567	296	32	513	20	2	0	0	93.69	4.93	30.77
bin.137.gv10	p_Euryarchaeota (UID3)	148	187	124	13	166	8	0	0	0	93.68	3.39	100
bin.3_sub.gv05	f_Lachnospiraceae (UID1286)	57	420	207	48	365	7	0	0	0	93.68	1.2	28.57
bin.42_sub.gv06	f_Lachnospiraceae (UID1255)	90	354	174	24	320	10	0	0	0	93.68	2.23	50
bin.271.gw04	p_Proteobacteria (UID3887)	1487	256	160	12	242	2	0	0	0	93.65	1.25	0
73.hc	f_Lachnospiraceae (UID1255)	90	354	174	23	311	20	0	0	0	93.64	4.84	60
bin.315.gv	o_Clostridiales (UID1226)	155	278	158	19	250	9	0	0	0	93.64	3.31	55.56
bin.632.hh	k_Bacteria (UID2982)	88	230	148	16	207	7	0	0	0	93.64	2.36	42.86
bin.96.hc17	f_Bifidobacteriaceae (UID1462)	65	476	217	39	420	16	1	0	0	93.64	5.3	42.11
bin.36.gv05	o_Clostridiales (UID1212)	172	263	149	13	246	3	1	0	0	93.62	2.07	33.33
maxbin.054.hc18	f_Enterobacteriaceae (UID5124)	134	1173	336	64	1050	59	0	0	0	93.61	5.49	74.58
235_sub.hc17	o_Clostridiales (UID1212)	172	260	146	18	214	28	0	0	0	93.59	13.06	85.71
maxbin.291.gv	p_Actinobacteria (UID2112)	31	211	124	20	167	24	0	0	0	93.59	8.36	91.67
bin.149.hc17	o_Bacteroidales (UID2657)	160	492	269	38	416	37	0	1	0	93.58	9.44	62.79
bin.91.hh14	o_Clostridiales (UID1212)	172	263	149	14	243	6	0	0	0	93.57	2.09	100
bin.250.gw04	o_Clostridiales (UID1212)	172	263	149	28	229	6	0	0	0	93.56	2.35	100
65.gv03	c_Clostridia (UID1118)	387	223	124	11	209	3	0	0	0	93.55	0.94	66.67
bin.146.gw01	p_Actinobacteria (UID2112)	31	211	124	13	191	7	0	0	0	93.55	4.26	28.57
bin.199.gv	k_Bacteria (UID2569)	434	278	186	14	259	5	0	0	0	93.55	2.06	80
bin.23.gv10	p_Actinobacteria (UID2112)	31	211	124	14	196	1	0	0	0	93.55	0.81	0
bin.236.gv	k_Bacteria (UID2569)	434	278	186	19	254	5	0	0	0	93.55	2.42	80
bin.26.hh	o_Clostridiales (UID												

bin.194.hc	k_Bacteria (UID2329)	174	149	89	8	133	8	0	0	0	93.45	7.42	87.5
bin.461.hh	o_Clostridiales (UID1212)	172	263	149	23	235	5	0	0	0	93.43	2.4	20
211.gp29	c_Epsilonproteobacteria (UID3065)	111	445	271	33	394	18	0	0	0	93.42	3.14	61.11
298.gw03	c_Clostridia (UID1118)	387	223	124	13	205	5	0	0	0	93.41	2.9	60
bin.127.gw01	c_Clostridia (UID1118)	387	223	124	11	208	4	0	0	0	93.41	2.22	50
bin.138.gw05	o_Clostridiales (UID1212)	172	263	149	16	245	2	0	0	0	93.4	1.34	0
bin.96.gw06	k_Bacteria (UID2372)	131	177	106	9	165	3	0	0	0	93.4	1.55	66.67
bin.427_sub.gw	f_Lachnospiraceae (UID1286)	57	420	207	23	387	10	0	0	0	93.39	2.56	10
maxbin.079.gw	f_Lachnospiraceae (UID1286)	57	420	207	24	383	13	0	0	0	93.35	3.75	76.92
maxbin.017.hc17	o_Lactobacillales (UID574)	471	350	191	22	322	6	0	0	0	93.34	2.4	50
bin.324.gw	o_Clostridiales (UID1212)	172	263	149	19	235	9	0	0	0	93.33	2.93	0
bin.528.hc	k_Bacteria (UID2328)	3167	126	75	5	120	1	0	0	0	93.33	1.33	100
maxbin.035.gw07	k_Bacteria (UID2372)	131	176	105	7	165	4	0	0	0	93.33	1.41	25
maxbin.027_sub.gw29	p_Bacteroidetes (UID2605)	350	314	208	35	261	18	0	0	0	93.32	5.69	77.78
109_sub.hh15	o_Clostridiales (UID1212)	172	263	149	12	215	33	2	1	0	93.29	18.45	97.78
62.hh15	o_Clostridiales (UID1212)	172	263	149	11	245	7	0	0	0	93.29	4.03	42.86
bin.219.gw07	o_Clostridiales (UID1212)	172	263	149	18	242	3	0	0	0	93.29	0.75	66.67
bin.42.gw08	o_Clostridiales (UID1212)	172	263	149	10	248	5	0	0	0	93.29	1.09	80
bin.52.gw	o_Clostridiales (UID1212)	172	263	149	11	244	8	0	0	0	93.29	4.14	75
bin.60.hc20	o_Clostridiales (UID1212)	172	263	149	17	246	0	0	0	0	93.29	0	0
maxbin.285.gw	o_Clostridiales (UID1212)	172	263	149	11	250	2	0	0	0	93.29	1.01	50
bin.108.gp26	k_Bacteria (UID2569)	434	278	186	18	247	13	0	0	0	93.28	4.05	46.15
bin.22.gp26	k_Bacteria (UID2569)	434	278	186	14	263	1	0	0	0	93.28	15.64	0
232_sub.hh13	k_Bacteria (UID2329)	174	149	89	6	136	5	2	0	0	93.26	4.53	0
bin.184.gw08	k_Bacteria (UID2329)	174	149	89	6	136	7	0	0	0	93.26	5.43	100
bin.644.gw	o_Clostridiales (UID1120)	304	247	141	16	230	1	0	0	0	93.26	0.35	0
94.gp28	k_Bacteria (UID2982)	88	230	148	10	217	3	0	0	0	93.24	1.69	0
bin.292.gw03	p_Actinobacteria (UID2112)	31	211	124	15	194	2	0	0	0	93.23	0.92	100
bin.125.hc17	p_Euryarchaeota (UID3)	148	188	125	11	170	7	0	0	0	93.2	3.57	50
maxbin.182.hc	k_Bacteria (UID2495)	2993	143	89	8	131	4	0	0	0	93.19	2.42	100
bin.211.gw10	g_Prevotella (UID2724)	55	567	296	33	493	40	1	0	0	93.18	7.55	51.16
bin.26.hh13	o_Bacteroidales (UID2657)	160	492	269	38	441	13	0	0	0	93.18	3.3	53.85
bin.298_sub.gw10	o_Clostridiales (UID1226)	155	278	158	39	235	4	0	0	0	93.18	0.63	0
bin.456.gw	o_Bacteroidales (UID2657)	160	492	269	31	457	4	0	0	0	93.18	1.19	50
bin.95_sub.gw10	c_Clostridia (UID1118)	387	223	124	16	204	3	0	0	0	93.18	1.64	66.67
bin.2.hh13	o_Clostridiales (UID1212)	172	263	149	12	246	5	0	0	0	93.16	2.57	60
bin.278_sub.gw10	g_Prevotella (UID2724)	55	567	296	57	496	12	2	0	0	93.16	3.56	44.44
bin.6_sub.gw	f_Lachnospiraceae (UID1286)	57	420	207	35	356	25	4	0	0	93.16	6.2	35.14
175.gw01	p_Euryarchaeota (UID3)	148	188	125	11	166	11	0	0	0	93.14	8.04	100
bin.62.gw01	p_Firmicutes (UID1022)	100	295	158	19	271	5	0	0	0	93.14	2.17	60
bin.51.gw	p_Actinobacteria (UID2112)	31	211	124	13	175	23	0	0	0	93.13	9.98	91.3
bin.168.hc17	f_Spirochaetaceae (UID2635)	33	249	143	12	231	6	0	0	0	93.12	3.13	33.33
bin.241.gw	o_Clostridiales (UID1212)	172	263	149	22	238	3	0	0	0	93.12	1.24	33.33
bin.127_sub.gw04	o_Clostridiales (UID1212)	172	263	149	28	222	13	0	0	0	93.11	5.68	46.15
189_sub.gw09	f_Lachnospiraceae (UID1255)	90	354	174	32	300	22	0	0	0	93.11	1.81	18.18
bin.149_sub.gw02	o_Clostridiales (UID1226)	155	278	158	22	250	6	0	0	0	93.09	2.64	66.67
maxbin.207.gw	c_Deltaproteobacteria (UID3218)	61	284	169	27	227	30	0	0	0	93.09	10.25	80
bin.176.hh14	f_Mycoplasmataceae (UID2414)	89	228	130	17	209	2	0	0	0	93.08	0.42	50
bin.299.gw03	f_Lachnospiraceae (UID1286)	57	420	207	23	392	5	0	0	0	93.07	1.59	0
bin.48.gw05	o_Clostridiales (UID1212)	172	263	149	27	233	3	0	0	0	93.06	0.73	100
maxbin.114.hh	p_Proteobacteria (UID3887)	1487	256	160	16	217	23	0	0	0	93.06	4.92	21.74
maxbin.132.gw07	o_Clostridiales (UID1226)	155	278	158	27	248	3	0	0	0	93.04	1.9	33.33
172.hh15	o_Clostridiales (UID1212)	172	261	147	16	233	12	0	0	0	93.03	4.95	83.33
maxbin.219.gw07	o_Burkholderiales (UID4000)	193	427	214	24	398	5	0	0	0	93.03	1.62	20
35.hh12	o_Bacteroidales (UID2617)	213	406	265	23	374	9	0	0	0	93.02	2.29	77.78
bin.585.hc	c_Betaproteobacteria (UID3971)	223	425	211	25	396	3	0	0	1	93.02	4.09	9.68
76_sub.gw07	f_Spirochaetaceae (UID2535)	33	249	143	14	226	9	0	0	0	93.01	3.73	22.22
bin.664.gw	f_Spirochaetaceae (UID2535)	33	249	143	11	234	4	0	0	0	93.01	2.33	100
bin.30.gw	f_Lachnospiraceae (UID1255)	90	354	174	21	327	6	0	0	0	92.98	2.35	66.67
maxbin.100_sub.gw03	k_Bacteria (UID203)	5449	103	57	4	83	16	0	0	0	92.98	7.02	50
29.hc20	o_Selenomonadales (UID1024)	64	334	167	34	268	12	0	0	0	92.95	4.59	66.67
bin.161.hh12	o_Clostridiales (UID1212)	172	263	149	13	240	10	0	0	0	92.95	2.79	30
50.gw	f_Enterobacteriaceae (UID5162)	88	1207	328	70	1097	39	1	0	0	92.93	4.69	76.19
221.gw02	k_Bacteria (UID2372)	131	177	106	11	163	3	0	0	0	92.92	0.65	66.67
89_sub.gw05	o_Bacteroidales (UID2617)	213	406	265	27	370	9	0	0	0	92.92	2.22	22.22
bin.211.hh	k_Bacteria (UID2982)	88	230	148	11	213	6	0	0	0	92.91	3.08	33.33
bin.33.gw	p_Actinobacteria (UID2112)	31	211	124	16	193	2	0	0	0	92.91	1.08	100
maxbin.100.gw09	o_Clostridiales (UID1120)	304	247	141	15	227	5	0	0	0	92.91	2.6	80
14_sub.hh13	k_Bacteria (UID2495)	2993	143	89	9	131	3	0	0	0	92.88	1.26	100
bin.128_sub.gw29	o_Clostridiales (UID1212)	172	263	149	36	222	5	0	0	0	92.87	2.82	20
bin.159.gw	f_Spirochaetaceae (UID2535)	33	249	143	37	211	1	0	0	0	92.86	0.7	0
bin.515.gw	o_Clostridiales (UID1226)	155	278	158	16	256	6	0	0	0	92.86	3.16	66.67
bin.47.gw	o_Clostridiales (UID1212)	172	263	149	43	214	6	0	0	0	92.84	2.74	16.67
228.gw04	o_Clostridiales (UID1212)	172	261	147	19	237	5	0	0	0	92.83	2.61	20
bin.64_sub.gw02	g_Prevotella (UID2724)	55	567	296	71	480	16	0	0	0	92.83	3.63	50
maxbin.265.gw	f_Lachnospiraceae (UID1255)	90	354	174	25	316	13	0	0	0	92.82	1.8	23.08
bin.124_sub.hc20	o_Bacteroidales (UID2657)	160	492	269	54	434	4	0	0	0	92.81	0.48	25
bin.164.gw06	k_Bacteria (UID2329)	174	149	89	11	135	3	0	0	0	92.81	2.81	100
158_sub.gw02	o_Bacteroidales (UID2617)	213	406	265	50	345	11	0	0	0	92.78	3.71	27.27
bin.531.go	f_Bifidobacteriaceae (UID1458)	77	464	220	24	439	1	0	0	0	92.76	0.09	0
maxbin.017.go30	f_Bifidobacteriaceae (UID1458)	77	464	220	24	438	2	0	0	0	92.76	0.24	0
bin.112.gw08	k_Bacteria (UID2569)	434	278	186	15	258	5	0	0	0	92.74	1.99	60
bin.167.gw	p_Actinobacteria (UID2112)	31	211	124	14	192	5	0	0	0	92.74	2.8	60
bin.216.hh15	c_Clostridia (UID1118)	387	223	124	14	207	2	0	0	0	92.74	1.61	0
bin.301_sub.gw07	p_Actinobacteria (UID2112)	31	211	124	19	185	7	0	0	0	92.74	4.03	85.71
110_sub.gw08	o_Clostridiales (UID1120)	304	247	141	13	231	3	0	0	0	92.73	1.3	66.67
135_sub.hc18	o_Clostridiales (UID1212)	172	261	147	15	237	9	0	0	0	92.72	3.97	100
190.gp28	o_Clostridiales (UID1212)	172	263	149	15	239	9	0	0	0	92.72	3.19	77.78
11.hc18	k_Bacteria (UID2329)	174	149	89	7	142	0	0	0	0	92.7	0	0
bin.56.gw09	c_Deltaproteobacteria (UID3218)	61	284	169	17	264	2	0	1	0	92.7	2.43	25
maxbin.208.gw	f_Lachnospiraceae (UID1255)	90	354	174	26	322	6	0	0	0	92.7	2.7	16.67
159.gw08	p_Proteobacteria (UID3887)	1487	256	160	27	223	6	0	0	0	92.66	2.81	16.67
bin.200.hc20	f_Spirochaetaceae (UID2535)	33	249	143	12	227	10	0	0	0	92.66	3.54	70
bin.539.hc	o_Lactobacillales (UID543)	294	469	262	34	415	19	1	0	0	92.65	4.99	4.55
169.hh13	f_Comamonadaceae (UID4119)	693	323	40	640	13	0	0	0	0	92.62	15.38	0
184_sub.hh14	o_Clostridiales (UID1212)	172	263	149	13	237	13	0	0	0	92.62	5.13	84.62
59.ca25	p_Bacteroidetes (UID2605)	350	316	210	17	290	9	0	0	0	92.62	3.1	11.11
81_sub.gw05	o_Clostridiales (UID1212)	172	263	149	15	235	13	0	0	0	92.62	6.54	30.77
107.hc20	o_Clostridiales (UID1212)	172	263	149	23	223	17	0	0	0	92.6	9.01	100
bin.38.hh15	f_Lachnospiraceae (UID1286)	57	420	207	38	373	7	2	0	0	92.		

140.jh13	o__Bacteroidales (UID2657)	160	492	269	44	432	16	0	0	0	0	92.49	3.8	37.5
250.sub.gw05	c__Clostridia (UID1118)	387	223	124	12	204	7	0	0	0	0	92.47	3.23	71.43
bin.220.gw	k__Bacteria (UID2569)	434	278	186	16	261	1	0	0	0	0	92.47	0.18	100
bin.344.sub.gw07	p__Actinobacteria (UID2112)	31	211	124	15	190	6	0	0	0	0	92.47	3.54	50
124.sub.gw09	p__Bacteroidetes (UID2605)	350	316	210	19	278	18	1	0	0	0	92.46	8.1	57.14
bin.184.gw05	k__Bacteria (UID2372)	131	177	106	10	163	4	0	0	0	0	92.45	2.49	0
bin.67.gw08	k__Bacteria (UID2372)	131	177	106	11	162	4	0	0	0	0	92.45	1.17	75
maxbin.107.sub.gw09	p__Actinobacteria (UID2112)	31	211	124	23	178	10	0	0	0	0	92.45	5.17	10
bin.54.gw07	c__Deitaproteobacteria (UID3218)	61	284	169	34	234	16	0	0	0	0	92.43	5.27	68.75
bin.108.gw03	g__Prevotellia (UID2724)	55	567	296	32	516	18	1	0	0	0	92.42	4.96	33.33
336.sub.gw	k__Bacteria (UID2569)	434	278	186	39	228	8	3	0	0	0	92.41	4.86	0
bin.215.hc20	p__Actinobacteria (UID2112)	31	211	124	31	171	9	0	0	0	0	92.41	5.03	55.56
bin.88.sub.gw08	o__Clostridiales (UID1226)	155	278	158	27	237	14	0	0	0	0	92.41	4.17	7.14
220.jh13	k__Bacteria (UID2495)	2993	147	91	22	123	2	0	0	0	0	92.4	1.1	0
bin.211.gw09	o__Clostridiales (UID1226)	155	278	158	43	232	3	0	0	0	0	92.4	1.39	33.33
bin.234.sub.gw07	f__Lachnospiraceae (UID1286)	420	57	207	52	355	13	0	0	0	0	92.4	2.16	30.77
bin.61.gw04	o__Clostridiales (UID1212)	172	263	149	13	247	3	0	0	0	0	92.39	1.51	0
maxbin.139.sub.gw05	f__Lachnospiraceae (UID1255)	90	354	174	30	283	41	0	0	0	0	92.39	9.63	58.54
bin.52.gw04	k__Bacteria (UID2372)	131	176	105	8	157	11	0	0	0	0	92.38	4.86	0
bin.294.gw03	k__Bacteria (UID2372)	131	177	106	12	164	1	0	0	0	0	92.37	0.47	100
bin.145.gw05	p__Bacteroidetes (UID2605)	350	314	208	31	282	1	0	0	0	0	92.36	0.48	0
bin.220.gw	p__Actinobacteria (UID2112)	31	211	124	14	191	6	0	0	0	0	92.36	3.49	83.33
bin.177.gw07	o__Clostridiales (UID1212)	263	172	149	30	229	3	1	0	0	0	92.34	2.15	33.33
bin.81.gw02	o__Clostridiales (UID1212)	172	263	149	24	232	7	0	0	0	0	92.34	3.91	71.43
bin.14.gw03	f__Lachnospiraceae (UID1286)	57	420	207	27	388	5	0	0	0	0	92.33	1.55	40
maxbin.035.gw06	p__Firmicutes (UID1022)	100	295	158	20	265	10	0	0	0	0	92.33	2.96	90
237.sub.hc	k__Bacteria (UID2495)	2993	147	91	7	130	9	1	0	0	0	92.31	9.54	91.67
bin.195.sub.gw03	c__Clostridia (UID1118)	387	223	124	18	187	17	1	0	0	0	92.31	8.74	45
bin.336.ca	k__Bacteria (UID2372)	131	176	105	15	150	12	0	0	0	0	92.29	7.36	38.46
bin.146.gw06	o__Clostridiales (UID1212)	172	263	149	18	242	3	0	0	0	0	92.28	0.62	33.33
bin.55.hh11	o__Clostridiales (UID1212)	172	263	149	15	238	10	0	0	0	0	92.28	3.59	80
bin.627.gw	k__Bacteria (UID203)	5449	103	57	6	81	16	0	0	0	0	92.28	4.86	31.25
bin.45.gw09	o__Clostridiales (UID1226)	155	278	158	15	259	4	0	0	0	0	92.25	1.41	75
bin.164.gw	o__Clostridiales (UID1212)	172	263	149	21	242	0	0	0	0	0	92.24	0	0
maxbin.092.sub.gw07	o__Clostridiales (UID1212)	172	263	149	29	224	10	0	0	0	0	92.24	5	70
102.gw27	o__Clostridiales (UID1212)	263	172	149	14	237	11	1	0	0	0	92.23	5.93	92.86
bin.256.gw	o__Clostridiales (UID1226)	155	278	158	24	251	3	0	0	0	0	92.23	1.9	33.33
176.sub.gw04	p__Bacteroidetes (UID2605)	350	316	210	20	280	15	1	0	0	0	92.22	6.43	72.22
bin.56.gw26	f__Lachnospiraceae (UID1255)	90	354	174	54	292	8	0	0	0	0	92.22	2.87	50
22.gw02	c__Clostridia (UID1118)	387	223	124	13	205	5	0	0	0	0	92.2	2.57	80
bin.88.gw01	c__Clostridia (UID1118)	387	223	124	17	205	1	0	0	0	0	92.2	0.27	0
bin.84.gw03	p__Actinobacteria (UID2112)	31	211	124	11	189	11	0	0	0	0	92.2	3.24	45.45
bin.172.gw	p__Actinobacteria (UID2112)	31	211	124	20	182	9	0	0	0	0	92.19	5.49	77.78
bin.298.gw09	p__Actinobacteria (UID2112)	31	211	124	20	180	10	1	0	0	0	92.19	2.8	23.08
bin.191.gw10	o__Clostridiales (UID1212)	172	263	149	19	241	3	0	0	0	0	92.18	1.07	66.67
bin.580.gw	p__Bacteroidetes (UID2605)	350	316	210	40	274	2	0	0	0	0	92.17	0.95	0
bin.242.gw02	o__Clostridiales (UID1212)	172	263	149	24	238	1	0	0	0	0	92.16	0.67	0
bin.187.sub.gw05	o__Clostridiales (UID1120)	304	247	141	22	219	6	0	0	0	0	92.14	1.25	66.67
bin.58.sub.hc18	o__Clostridiales (UID1212)	172	263	149	38	219	6	0	0	0	0	92.14	2.6	66.67
bin.89.hc19	p__Actinobacteria (UID2112)	31	211	124	17	170	14	0	0	0	0	92.14	6.68	42.86
186.sub.gw10	k__Bacteria (UID2329)	174	149	89	7	135	7	0	0	0	0	92.13	5.22	57.14
75.hh15	k__Bacteria (UID2329)	174	149	89	7	136	6	0	0	0	0	92.13	3.03	83.33
bin.150.gw	k__Bacteria (UID2329)	174	149	89	7	134	8	0	0	0	0	92.13	7.58	37.5
bin.159.gw06	k__Bacteria (UID2329)	174	149	89	7	138	4	0	0	0	0	92.13	4.49	25
bin.5.hh15	k__Bacteria (UID2329)	174	149	89	11	136	2	0	0	0	0	92.13	2.25	50
bin.93.gw06	k__Bacteria (UID2329)	174	149	89	7	140	2	0	0	0	0	92.13	1.28	0
bin.240.sub.gw10	f__Lachnospiraceae (UID1255)	90	354	174	26	323	5	0	0	0	0	92.09	1.38	80
bin.190.gw	o__Clostridiales (UID1212)	172	263	149	43	213	7	0	0	0	0	92.08	3.36	0
bin.576.hh	f__Spirochaetaceae (UID2535)	33	249	143	15	227	7	0	0	0	0	92.07	3.05	100
bin.584.gw	o__Clostridiales (UID1226)	155	278	158	18	259	1	0	0	0	0	92.07	0.32	100
maxbin.023.sub.gw02	c__Clostridia (UID1118)	387	223	124	13	208	2	0	0	0	0	92.07	1.61	100
bin.55.hc17	o__Bacteroidales (UID2654)	465	163	265	38	449	4	0	0	0	0	92.03	1.02	0
102.jh14	o__Clostridiales (UID1212)	172	263	149	20	225	18	0	0	0	0	92.02	3.94	33.33
bin.607.hh	o__Clostridiales (UID1212)	172	263	149	16	244	3	0	0	0	0	92	2.01	66.67
178.gw27	p__Bacteroidetes (UID2605)	350	314	208	19	264	31	0	0	0	0	91.99	9.88	80.65
199.gw03	o__Clostridiales (UID1212)	172	263	149	16	244	3	0	0	0	0	91.98	0.75	66.67
237.hc20	o__Bacteroidales (UID2617)	123	406	265	26	336	44	0	0	0	0	91.98	11.57	72.73
bin.141.sub.hc17	o__Bacteroidales (UID2716)	92	487	270	67	413	7	0	0	0	0	91.98	2.22	14.29
295.gw04	c__Deitaproteobacteria (UID3218)	61	284	169	19	258	7	0	0	0	0	91.97	2.4	28.57
bin.215.gw	o__Clostridiales (UID1120)	304	247	141	19	226	2	0	0	0	0	91.96	1.06	50
bin.290.gw	f__Spirochaetaceae (UID2535)	33	249	143	13	235	1	0	0	0	0	91.96	0.7	100
maxbin.042.hh12	f__Enterobacteriaceae (UID5124)	134	1173	336	83	1017	73	0	0	0	0	91.96	5.62	79.45
218.gw	o__Clostridiales (UID1212)	172	263	149	24	235	4	0	0	0	0	91.95	2.07	0
76.sub.hh	o__Clostridiales (UID1212)	172	263	149	16	221	26	0	0	0	0	91.95	10.66	88.46
maxbin.019.gw10	o__Clostridiales (UID1120)	304	247	141	15	232	0	0	0	0	0	91.95	0	0
maxbin.288.sub.gw	o__Clostridiales (UID1212)	172	263	149	25	237	1	0	0	0	0	91.95	0.67	0
137.jh12	c__Clostridia (UID1118)	387	223	124	12	211	0	0	0	0	0	91.94	0	0
bin.103.gw03	c__Clostridia (UID1118)	387	223	124	11	211	1	0	0	0	0	91.94	0.81	0
bin.185.gw07	c__Clostridia (UID1118)	387	223	124	13	207	3	0	0	0	0	91.94	1.75	66.67
bin.258.gw02	k__Bacteria (UID2569)	434	278	186	18	256	4	0	0	0	0	91.94	1.88	100
bin.44.gw	p__Actinobacteria (UID2112)	31	211	124	15	191	4	1	0	0	0	91.94	3.36	57.14
bin.84.gw05	k__Bacteria (UID2569)	434	278	186	18	256	4	0	0	0	0	91.94	1.72	100
maxbin.175.hh	c__Clostridia (UID1118)	387	223	124	12	209	2	0	0	0	0	91.94	1.08	0
27.gw10	o__Clostridiales (UID1212)	172	263	149	18	239	6	0	0	0	0	91.93	1.41	33.33
139.hc17	f__Enterobacteriaceae (UID5162)	88	1207	328	90	1066	50	1	0	0	0	91.92	5.92	88.68
10.gw	p__Bacteroidetes (UID2605)	350	314	208	21	270	23	0	0	0	0	91.91	9.21	86.96
bin.64.sub.gw	o__Bacteroidales (UID2657)	160	492	269	37	442	13	0	0	0	0	91.9	3.35	7.69
bin.98.sub.gw06	c__Clostridia (UID1118)	387	223	124	20	200	3	0	0	0	0	91.9	2.42	66.67
bin.606.hc	o__Clostridiales (UID1212)	172	263	149	20	228	10	5	0	0	0	91.89	4.09	20
bin.137.sub.hh13	k__Bacteria (UID2328)	3167	126	75	10	112	4	0	0	0	0	91.88	4.12	75
bin.161.gw06	p__Euryarchaeota (UID3)	148	187	124	12	175	0	0	0	0	0	91.87	0	0
maxbin.027.sub.gw05	p__Firmicutes (UID1022)	100	295	158	18	262	15	0	0	0	0	91.86	6.82	60
46.hc17	o__Clostridiales (UID1212)	172	261	147	14	240	7	0	0	0	0	91.84	2.89	85.71
bin.132.sub.gw03	o__Clostridiales (UID1226)	155	278	158	34	239	5	0	0	0	0	91.84	1.64	80
bin.195.jh12	o__Clostridiales (UID1375)	332	50	332	124	32	289	11	0	0	0	91.84	1.18	

maxbin.077.gw03	o__Clostridiales (UID1212)	172	263	149	14	249	0	0	0	0	91.72	0	0
bin.58.hh12	o__Clostridiales (UID1120)	304	250	143	18	229	3	0	0	0	91.7	1.28	66.67
bin.88.gw	o__Clostridiales (UID1212)	172	263	149	19	238	6	0	0	0	91.7	1.92	83.33
bin.70.gw04	k__Bacteria (UID2372)	131	177	106	14	157	6	0	0	0	91.68	2.73	33.33
51_sub.gw08	p__Bacteroidetes (UID2605)	350	316	210	22	288	6	0	0	0	91.67	2.54	83.33
bin.211_sub.hh15	o__Clostridiales (UID1212)	172	263	149	30	222	11	0	0	0	91.67	4.41	100
bin.217.gw09	k__Bacteria (UID2569)	434	278	186	17	259	2	0	0	0	91.67	1.08	0
bin.189_sub.gw04	o__Bacteroidales (UID2657)	160	492	269	51	436	5	0	0	0	91.64	0.4	40
bin.575.gw	f__Lachnospiraceae (UID1286)	57	420	207	53	363	4	0	0	0	91.64	1.52	40
bin.154_sub.gw	o__Bacteroidales (UID2657)	160	492	269	29	460	3	0	0	0	91.62	0.42	33.33
bin.202.gw06	f__Lachnospiraceae (UID1286)	57	420	207	33	382	5	0	0	0	91.62	1.59	0
bin.212.gw09	f__Lachnospiraceae (UID1286)	57	420	207	38	377	5	0	0	0	91.62	1.59	0
bin.231.gw05	f__Lachnospiraceae (UID1286)	57	420	207	38	377	5	0	0	0	91.62	1.59	0
maxbin.049.gw10	f__Lachnospiraceae (UID1286)	57	420	207	38	377	5	0	0	0	91.62	1.59	0
189_sub.hh15	o__Clostridiales (UID1212)	172	263	149	22	227	13	1	0	0	91.61	6.68	50
200.hh12	o__Clostridiales (UID1212)	172	263	149	34	216	13	0	0	0	91.6	5.2	61.54
77.hc18	o__Clostridiales (UID1120)	304	250	143	19	220	9	2	0	0	91.6	6.01	20
bin.72.gw	p__Bacteroidetes (UID2605)	350	314	208	19	295	0	0	0	0	91.59	0	0
bin.225.gw02	p__Actinobacteria (UID2112)	31	211	124	16	181	14	0	0	0	91.58	6.68	50
bin.291_sub.gw	c__Clostridia (UID1118)	387	223	124	34	171	18	0	0	0	91.56	9.54	72.22
bin.294.ca	o__Actinomycetales (UID1812)	229	457	227	34	415	8	0	0	0	91.56	1.51	50
bin.207.hc18	o__Clostridiales (UID1212)	172	263	149	19	234	10	0	0	0	91.55	3.22	40
bin.340.gw	o__Bacteroidales (UID2657)	160	492	269	41	447	4	0	0	0	91.53	1.3	50
bin.496.hc	o__Clostridiales (UID1212)	172	263	149	27	224	12	0	0	0	91.55	4.22	66.67
bin.217.gw03	o__Bacteroidales (UID2657)	160	492	269	41	445	6	0	0	0	91.52	1.49	50
134.hc19	o__Clostridiales (UID1212)	172	263	149	16	209	36	2	0	0	91.51	17.23	92.86
bin.126.gw04	k__Bacteria (UID2372)	131	177	106	12	164	1	0	0	0	91.51	0.13	0
bin.265.gw10	k__Bacteria (UID2372)	131	177	106	12	161	4	0	0	0	91.51	2.02	25
maxbin.065.hh15	k__Bacteria (UID2495)	2993	143	89	9	130	4	0	0	0	91.51	3.47	100
245.gw01	o__Clostridiales (UID1120)	304	247	141	14	232	1	0	0	0	91.49	0.71	100
maxbin.112.gw	o__Clostridiales (UID1120)	304	247	141	13	223	11	0	0	0	91.49	4.26	18.18
187_sub.gw02	k__Bacteria (UID2569)	434	278	186	27	235	16	0	0	0	91.48	5.43	31.25
bin.86.gw01	f__Lachnospiraceae (UID1255)	90	354	174	50	300	4	0	0	0	91.48	1.63	0
bin.143_sub.hc20	o__Clostridiales (UID1212)	172	263	149	23	232	8	0	0	0	91.46	3.66	37.5
bin.20.gw27	o__Clostridiales (UID1226)	155	278	158	23	255	0	0	0	0	91.46	0	0
bin.40.gw04	f__Lachnospiraceae (UID1286)	57	420	207	38	375	7	0	0	0	91.46	1.88	28.57
bin.238.gw08	o__Burkholderiales (UID4000)	193	427	214	32	387	8	0	0	0	91.45	2.57	12.5
bin.267_sub.gw09	f__Lachnospiraceae (UID1255)	90	354	174	43	301	10	0	0	0	91.45	4.31	70
269_sub.gw09	o__Clostridiales (UID1212)	172	263	149	20	238	5	0	0	0	91.44	2.68	0
bin.141_sub.gw05	o__Bacteroidales (UID2716)	92	487	270	53	421	12	1	0	0	91.44	3.37	13.33
bin.64.hc	o__Bacteroidales (UID2657)	160	492	269	57	426	8	1	0	0	91.44	2.47	45.45
maxbin.048_sub.gw06	o__Clostridiales (UID1212)	172	263	149	20	238	4	1	0	0	91.44	4.2	42.86
bin.257.hh15	k__Bacteria (UID2372)	131	176	105	11	159	6	0	0	0	91.43	4.76	100
38.hc17	o__Selenomonadales (UID1024)	64	334	167	40	282	12	0	0	0	91.41	3.3	66.67
63.hc20	k__Bacteria (UID2495)	2993	142	88	9	131	2	0	0	0	91.41	1.24	0
bin.180.hh	k__Bacteria (UID2565)	2921	152	93	10	140	2	0	0	0	91.4	0.6	50
maxbin.087.gw07	k__Bacteria (UID2495)	2993	142	88	27	109	6	0	0	0	91.38	2.58	83.33
bin.21.hh11	f__Lachnospiraceae (UID1255)	90	354	174	19	324	11	0	0	0	91.38	4.43	72.73
bin.247.gw02	k__Bacteria (UID2329)	174	149	89	14	133	2	0	0	0	91.36	2.25	0
maxbin.086.hh13	o__Clostridiales (UID1120)	304	250	143	19	222	8	1	0	0	91.35	4.62	63.64
bin.119.gw09	o__Clostridiales (UID1212)	172	263	149	42	214	6	1	0	0	91.34	3.24	22.22
maxbin.048.gw04	o__Clostridiales (UID1212)	172	263	149	19	241	3	0	0	0	91.33	0.94	100
180_sub.hc	k__Bacteria (UID2329)	174	149	89	10	131	8	0	0	0	91.3	4.92	0
maxbin.119.gw01	f__Lachnospiraceae (UID1286)	57	420	207	27	360	30	3	0	0	91.3	4.38	12.82
maxbin.020_sub.hh14	c__Gammaproteobacteria (UID4201)	1164	272	171	35	237	0	0	0	0	91.29	0	0
bin.223.hh15	o__Clostridiales (UID1212)	172	263	149	24	233	6	0	0	0	91.28	3.24	83.33
bin.31.gw	o__Clostridiales (UID1212)	172	263	149	25	238	0	0	0	0	91.28	0	0
bin.360.gw	o__Clostridiales (UID1212)	172	263	149	16	247	0	0	0	0	91.28	0	0
maxbin.129_sub.gw	f__Lachnospiraceae (UID1286)	57	420	207	50	344	26	0	0	0	91.28	4.96	19.23
bin.22.hc16	c__Epsilonproteobacteria (UID3065)	111	445	271	31	405	9	0	0	0	91.27	2.05	33.33
bin.433.gw	f__Spirochaetaceae (UID2535)	33	249	143	18	230	1	0	0	0	91.26	0.7	0
maxbin.029.gw06	c__Clostridia (UID1118)	387	223	124	15	204	4	0	0	0	91.26	2.82	75
145.hc19	o__Clostridiales (UID1212)	172	263	149	21	231	11	0	0	0	91.25	4.05	90.91
156.hc16	o__Bacteroidales (UID2617)	213	406	265	27	362	17	0	0	0	91.25	4.28	82.35
bin.193.gw05	o__Clostridiales (UID1212)	172	263	149	17	246	0	0	0	0	91.25	0	0
bin.59.hh15	o__Clostridiales (UID1120)	304	250	143	18	231	1	0	0	0	91.24	0.7	0
maxbin.218_sub.gw	o__Clostridiales (UID1226)	155	278	158	24	229	25	0	0	0	91.24	4.52	84
bin.214.gw03	k__Bacteria (UID203)	5449	104	58	6	85	13	0	0	0	91.22	4.86	7.69
bin.69.hh15	k__Bacteria (UID2982)	88	230	148	15	208	7	0	0	0	91.22	2.18	28.57
147.gw04	c__Clostridia (UID1118)	387	223	124	14	200	9	0	0	0	91.2	5.78	77.78
52.hh15	g__Prevotella (UID2722)	64	532	281	48	460	24	0	0	0	91.2	5.08	70.83
bin.70.gw28	p__Bacteroidetes (UID2605)	350	314	208	22	285	7	0	0	0	91.19	2.4	85.71
bin.123_sub.gw01	o__Clostridiales (UID1212)	172	263	149	23	233	6	1	0	0	91.18	3.13	55.56
bin.323.gw	o__Bacteroidales (UID2657)	160	492	269	36	453	3	0	0	0	91.16	0.87	66.67
bin.62.gw26	o__Clostridiales (UID1212)	172	263	149	16	239	7	1	0	0	91.16	4.98	70
bin.174.hh14	f__Spirochaetaceae (UID2535)	33	249	143	19	222	8	0	0	0	91.14	2.95	100
bin.101_sub.gw02	o__Clostridiales (UID1120)	304	247	141	36	208	3	0	0	0	91.13	2.13	0
bin.15.gw09	c__Clostridia (UID1118)	387	223	124	16	206	1	0	0	0	91.13	0.27	0
bin.153.gw01	c__Clostridia (UID1118)	387	223	124	15	205	3	0	0	0	91.13	1.08	100
bin.185.ca	k__Bacteria (UID2569)	434	278	186	24	246	8	0	0	0	91.13	3.49	50
110.hc16	o__Bacteroidales (UID2657)	160	492	269	68	411	13	0	0	0	91.08	2.67	53.85
bin.120.gw08	p__Actinobacteria (UID2112)	31	211	124	17	194	0	0	0	0	91.06	0	0
bin.387.gw	o__Bacteroidales (UID2716)	92	487	270	37	450	0	0	0	0	91.06	0	0
12.gw03	c__Deltaproteobacteria (UID3218)	61	284	169	28	251	5	0	0	0	91.05	2.56	60
bin.454.gw	p__Bacteroidetes (UID2605)	350	316	210	24	289	3	0	0	0	91.03	0.74	0
bin.125.gw29	k__Bacteria (UID2982)	88	229	147	28	199	2	0	0	0	91.02	0.91	50
bin.39.gw02	f__Lachnospiraceae (UID1286)	57	420	207	36	373	11	0	0	0	91.01	2.26	45.45
bin.43.gw06	k__Bacteria (UID2329)	174	149	89	10	133	6	0	0	0	91.01	5.17	50
158_sub.gw10	p__Bacteroidetes (UID2605)	350	316	210	38	265	12	1	0	0	90.99	4.15	73.33
bin.11.ca21	k__Bacteria (UID2982)	88	230	148	15	213	2	0	0	0	90.99	0.71	0
maxbin.116.hc20	f__Enterobacteriaceae (UID5162)	88	1207	328	85	1014	108	0	0	0	90.99	8.34	76.85
bin.50.hc20	k__Bacteria (UID2372)	131	176	105	24	149	3	0	0	0	90.95	2.38	33.33
90.hh15	o__Clostridiales (UID1212)	172	263	149	16	242	5	0	0	0	90.94	1.05	60
5.hh11	o__Clostridiales (UID1212)	172	261	147	29	227	5	0	0	0	90.93	2.38	80
bin.39.hc	o__Bacteroidales (UID2617)	213	406	265	35	369	2	0	0	0	90.93	0.5	50
79.gw29	o__Clostridiales (UID1212)	172	263	149	21	238	4	0	0	0	90.92	1.29	0
bin.400.gw	o__Clostridiales (UID1212)	172	263	149	21	240	2	0	0	0	90.92	0.36	50
256.hh14	o__Clostridiales (UID1212)	172	263	149	18	226	18	1	0	0	90.9	6.77	66.67
58.hh14	o__Bacteroidales (UID2657)	160	492	269	42	435	14	0	0	1	90.89	4.58	2.86
bin.153.gw	k__Bacteria (UID2982)	88	229	147	39	186	4	0	0				

maxbin.040.hh14	f_Enterobacteriaceae (UID5124)	134	1173	336	89	1010	71	3	0	0	90.79	5.4	78.75
maxbin.057.gh	k_Bacteria (UID2372)	131	176	105	12	159	5	0	0	0	90.79	2.41	40
maxbin.087.hh11	f_Lachnospiraceae (UID1286)	57	420	207	54	343	23	0	0	0	90.79	6.08	26.08
bin.18.gh10	o_Clostridiales (UID1120)	304	247	141	20	225	2	0	0	0	90.78	1.42	100
bin.264.gh	o_Clostridiales (UID1212)	172	263	149	23	236	4	0	0	0	90.76	2.01	25
bin.79.gw28	p_Euryarchaeota (UID54)	90	234	153	41	190	3	0	0	0	90.76	1.96	0
bin.77_sub.gh09	o_Clostridiales (UID1212)	172	263	149	22	239	2	0	0	0	90.75	0.5	50
78.gw04	c_Clostridia (UID1118)	387	223	124	15	204	4	0	0	0	90.73	2.82	75
bin.22.gw01	c_Clostridia (UID1118)	387	223	124	15	205	3	0	0	0	90.73	1.88	66.67
bin.205_sub.gw02	o_Clostridiales (UID1226)	155	278	158	33	241	4	0	0	0	90.72	2.53	0
bin.385.gw	f_Lachnospiraceae (UID1256)	33	333	171	25	303	4	0	1	0	90.72	4.09	50
bin.5.hc18	o_Clostridiales (UID1212)	172	263	149	31	224	8	0	0	0	90.7	1.26	62.5
210_sub.gh10	o_Bacteroidales (UID2617)	213	406	265	31	367	8	0	0	0	90.66	2.26	12.5
bin.356.gw	f_Lachnospiraceae (UID1286)	57	420	207	31	382	7	0	0	0	90.65	2.56	28.57
82.hh12	f_Verrucomicrobiota (UID1032)	33	423	214	51	338	34	0	0	0	90.62	9.29	85.29
203.gw01	c_Deltaproteobacteria (UID3218)	61	284	169	35	240	8	0	1	0	90.61	4.24	21.43
178_sub.hc18	c_Epsilonproteobacteria (UID3066)	110	450	273	36	395	19	0	0	0	90.6	3.19	31.58
bin.182.gh09	o_Clostridiales (UID1212)	172	263	149	20	239	4	0	0	0	90.6	1.73	50
bin.39.hh15	o_Clostridiales (UID1212)	172	263	149	18	235	9	1	0	0	90.6	5.82	83.33
242.gh08	c_Clostridia (UID1118)	387	223	124	15	204	4	0	0	0	90.59	2.69	75
bin.13.gw04	k_Bacteria (UID2569)	434	278	186	21	254	3	0	0	0	90.59	1.34	100
112.hc18	o_Clostridiales (UID1212)	172	263	149	28	226	9	0	0	0	90.58	5.26	88.89
bin.1.hc19	c_Gammaproteobacteria (UID4201)	1164	272	171	21	246	5	0	0	0	90.58	2.92	0
maxbin.024_sub.gh07	k_Bacteria (UID2372)	131	177	106	13	154	9	1	0	0	90.57	1.79	0
bin.452.gw	f_Spirochaetaceae (UID2535)	33	249	143	19	230	0	0	0	0	90.56	0	0
maxbin.006_sub.gh07	p_Bacteroidetes (UID2605)	350	316	210	22	283	11	0	0	0	90.56	4.05	81.82
bin.12.gw03	f_Lachnospiraceae (UID1286)	57	420	207	35	378	7	0	0	0	90.53	1.51	28.57
bin.237.gw03	f_Lachnospiraceae (UID1286)	57	420	207	51	361	8	0	0	0	90.5	1.71	25
bin.463.hh	o_Clostridiales (UID1212)	172	263	149	36	218	9	0	0	0	90.49	2.3	33.33
28.hh	o_Clostridiales (UID1212)	172	263	149	20	221	21	1	0	0	90.47	8.39	87.5
249.gw01	c_Clostridia (UID1118)	387	223	124	17	196	10	0	0	0	90.46	5.31	90
maxbin.017.gh09	c_Clostridia (UID1118)	387	223	124	14	202	7	0	0	0	90.46	4.26	100
bin.21.gw29	k_Bacteria (UID2329)	174	149	89	9	140	0	0	0	0	90.45	0	0
bin.29.gw04	f_Lachnospiraceae (UID1255)	90	354	174	38	312	4	0	0	0	90.45	1.44	0
bin.93_sub.gw02	k_Bacteria (UID2329)	174	149	89	12	133	4	0	0	0	90.45	3.37	25
bin.44.gw06	o_Clostridiales (UID1212)	172	263	149	23	238	2	0	0	0	90.43	0.67	0
bin.240.gh	o_Burkholderiales (UID4000)	193	412	208	32	375	5	0	0	0	90.42	1.43	20
maxbin.185_sub.hh	p_Proteobacteria (UID3887)	1487	256	160	30	217	9	0	0	0	90.42	4.48	77.78
maxbin.068.gw06	p_Actinobacteria (UID2112)	31	211	124	16	185	10	0	0	0	90.41	7.12	80
bin.106.hh11	k_Bacteria (UID2495)	2993	143	89	10	130	3	0	0	0	90.38	3.37	100
bin.160.gh10	o_Clostridiales (UID1212)	172	263	149	21	228	12	2	0	0	90.38	2.46	11.11
bin.169.gw06	p_Actinobacteria (UID2112)	31	211	124	25	177	0	0	0	0	90.37	0	2
bin.14.gw29	k_Bacteria (UID2982)	88	229	147	31	197	1	0	0	0	90.34	0.68	0
198.gw06	c_Clostridia (UID1118)	387	223	124	17	200	6	0	0	0	90.32	3.29	83.33
bin.13.gw30	k_Bacteria (UID2982)	88	229	147	17	212	0	0	0	0	90.31	0	0
bin.80.gh10	p_Euryarchaeota (UID3)	148	188	125	14	162	12	0	0	0	90.28	8.8	91.67
bin.134.gw06	o_Clostridiales (UID1212)	172	263	149	17	244	2	0	0	0	90.27	0.5	50
bin.201.gh09	o_Clostridiales (UID1212)	172	263	149	17	245	1	0	0	0	90.27	0.34	0
bin.227.gw05	o_Clostridiales (UID1212)	172	263	149	17	245	1	0	0	0	90.27	0.02	100
bin.254.gw03	o_Clostridiales (UID1212)	172	263	149	17	245	1	0	0	0	90.27	0.67	0
bin.262.gw02	o_Clostridiales (UID1212)	172	263	149	23	238	2	0	0	0	90.27	0.56	100
bin.56_sub.hh11	o_Clostridiales (UID1212)	172	263	149	23	233	7	0	0	0	90.27	3.64	71.43
165.hc	c_Clostridia (UID1118)	387	223	124	35	179	9	0	0	0	90.26	4.45	66.67
bin.495.gw	o_Bacteroidales (UID2617)	213	406	265	50	347	9	0	0	0	90.25	2.26	44.44
bin.9.gw29	o_Clostridiales (UID1212)	172	263	149	33	226	4	0	0	0	90.24	1.24	50
maxbin.393.gw	p_Proteobacteria (UID3887)	1487	256	160	23	222	11	0	0	0	90.24	2.19	9.09
131_sub.gw08	o_Clostridiales (UID1212)	172	263	149	19	241	3	0	0	0	90.23	0.42	66.67
bin.596.gw	o_Clostridiales (UID1212)	172	257	149	24	223	10	0	0	0	90.23	3.55	60
bin.199_sub.gw04	o_Bacteroidales (UID2716)	92	487	270	50	410	27	0	0	0	90.22	4.01	55.56
bin.83.gw30	k_Bacteria (UID2569)	434	278	186	26	243	9	0	0	0	90.22	2.55	22.22
bin.168.gh10	f_Spirochaetaceae (UID2535)	33	249	143	20	225	4	0	0	0	90.21	2.27	25
267_sub.hh	o_Bacteroidales (UID2617)	213	406	265	35	311	56	4	0	0	90.19	19.26	88.24
150_sub.hc18	k_Bacteria (UID203)	5449	103	57	11	86	23	3	0	0	90.18	28.79	84.38
191.hh13	k_Bacteria (UID2982)	88	230	148	16	206	7	1	0	0	90.17	4.3	10
maxbin.062_sub.gw	o_Bacteroidales (UID2617)	213	406	265	59	333	14	0	0	0	90.14	2.61	42.86
120.ca22	p_Bacteroidetes (UID2605)	350	314	208	28	263	23	0	0	0	90.13	7.11	73.91
bin.211.hh11	o_Clostridiales (UID1212)	172	263	149	18	245	0	0	0	0	90.13	0	0
bin.5.gw08	p_Bacteroidetes (UID2605)	350	316	210	42	271	3	0	0	0	90.12	0.43	66.67
bin.349_sub.gh	k_Bacteria (UID2495)	2993	147	91	10	135	2	0	0	0	90.11	1.16	50
maxbin.015.hh15	k_Bacteria (UID2495)	2993	147	91	9	137	1	0	0	0	90.11	0.1	100
bin.276.gw02	o_Bacteroidales (UID2617)	213	406	265	38	358	10	0	0	0	90.09	2.4	50
bin.78.gw02	k_Bacteria (UID2372)	131	177	106	13	158	5	1	0	0	90.09	2.16	25
158.gw05	o_Clostridiales (UID1120)	304	247	141	20	217	10	0	0	0	90.07	5.44	60
bin.455.hh	k_Bacteria (UID2329)	174	149	89	10	139	0	0	0	0	90.07	0	0
bin.7.gw09	k_Bacteria (UID2329)	174	149	89	10	135	4	0	0	0	90.07	2.86	75
bin.127.gh10	k_Bacteria (UID2569)	434	278	186	21	251	6	0	0	0	90.05	2.2	50
bin.285_sub.gw	o_Clostridiales (UID1226)	155	278	158	52	222	4	0	0	0	90.05	1.6	25
maxbin.039.gw01	k_Bacteria (UID2569)	434	278	186	21	251	6	0	0	0	90.05	0.99	50
maxbin.025.gw08	p_Firmicutes (UID1022)	100	295	158	41	232	22	0	0	0	90.04	8.04	95.45
281_sub.gw03	o_Clostridiales (UID1212)	172	263	149	43	218	2	0	0	0	90.03	1.34	0
79.gw03	o_Bacteroidales (UID2617)	213	406	265	36	355	15	0	0	0	90.01	2.8	6.67
bin.33.gw29	o_Bacteroidales (UID2716)	92	487	270	34	439	13	1	0	0	90	3.32	50
bin.424.gw	p_Bacteroidetes (UID2605)	350	316	210	29	285	2	0	0	0	90	0.95	100
bin.9.gh	k_Bacteria (UID2328)	3167	126	75	33	92	1	0	0	0	90	1.33	0
208_sub.hc18	o_Clostridiales (UID1212)	172	263	149	20	223	20	0	0	0	89.98	9.22	100
45.gw27	p_Bacteroidetes (UID2605)	350	314	208	22	263	28	1	0	0	89.98	10.32	83.87
bin.193.gw03	o_Clostridiales (UID1226)	155	278	158	23	251	4	0	0	0	89.98	2.53	75
bin.241.gh	o_Clostridiales (UID1212)	172	263	149	48	212	3	0	0	0	89.98	1.68	0
bin.293.gw03	o_Clostridiales (UID1226)	155	278	158	24	246	8	0	0	0	89.98	3.22	87.5
249_sub.hc17	f_Lachnospiraceae (UID1286)	57	420	207	58	346	14	2	0	0	89.97	5.23	60
92.gh10	p_Actinobacteria (UID2112)	31	211	124	34	171	6	0	0	0	89.95	3.58	33.33
14.gw08	p_Actinobacteria (UID2112)	31	211	124	18	187	6	0	0	0	89.94	3.9	50
bin.331_sub.gw	f_Lachnospiraceae (UID1255)	90	354	174	49	299	6	0	0	0	89.94	2.41	50
maxbin.391.gh	o_Clostridiales (UID1212)	172	263	149	19	243	1	0	0	0	89.93	0.13	0
201.hc20	o_Clostridiales (UID1212)	172	261	147	20	236	5	0	0	0	89.92	3.4	80
bin.206.gh10	p_Bacteroidetes (UID2605)	350	314	208	32	276	6	0	0	0	89.9	1.52	0
bin.68.gw09	c_Deltaproteobacteria (UID3218)	61	284	169	25	257	2	0	0	0	89.9	0.62	50
114_sub.gw	k_Bacteria (UID2329)	174	149	89	10	132	6	1	0	0	89.89	5.99	22.22
35_sub.hc19	o_Clostridiales (UID1212)	172	263	149	36	215	12	0	0	0	89.89	5.84	83.33
bin.131_sub.gw08	o_Bacteroidales (UID2657)	160	492	269	68	415	8	1	0	0	89.89	2.65	36.36
bin.229.gw03	k_Bacteria (UID2329)												

59_sub.hc16	o_Bacteroidales (UID2617)	213	406	265	56	340	10	0	0	0	0	89.82	2.58	70
bin.230_sub.gp09	o_Clostridiales (UID1212)	172	263	149	32	229	2	0	0	0	0	89.82	0.81	50
bin.124.gw02	k_Bacteria (UID2495)	2993	147	91	13	129	5	0	0	0	0	89.81	3.95	60
bin.205_sub.gv	p_Actinobacteria (UID2112)	31	211	124	19	188	4	0	0	0	0	89.78	1.96	100
bin.199.hh14	o_Clostridiales (UID1212)	172	263	149	21	233	9	0	0	0	0	89.77	4.98	88.89
bin.260_sub.hc17	o_Clostridiales (UID1212)	172	263	149	29	219	15	0	0	0	0	89.75	5.78	40
bin.27.hc17	k_Bacteria (UID1453)	901	171	117	13	156	2	0	0	0	0	89.74	1.28	50
98.gp08	f_Spirochaetaceae (UID2535)	33	249	143	35	209	5	0	0	0	0	89.72	0.86	40
bin.173.gw01	p_Actinobacteria (UID2112)	31	211	124	14	186	11	0	0	0	0	89.72	5.89	63.64
bin.25.gw05	p_Actinobacteria (UID2112)	31	211	124	17	189	5	0	0	0	0	89.72	2.61	100
183_sub.hh13	o_Clostridiales (UID1212)	172	263	149	22	231	10	0	0	0	0	89.68	5.12	100
63.gw04	k_Bacteria (UID2495)	2993	147	91	14	130	3	0	0	0	0	89.68	1.75	0
maxbin.032_sub.gp07	o_Clostridiales (UID1212)	172	263	149	23	235	5	0	0	0	0	89.67	2.35	0
98.hh15	f_Enterobacteriaceae (UID5162)	88	1207	328	98	1027	80	1	1	0	0	89.66	6.54	76.4
bin.44.gp	k_Bacteria (UID203)	5449	102	58	6	80	16	0	0	0	0	89.66	8.62	56.25
bin.17.ca	o_Lactobacillales (UID544)	293	475	267	42	417	16	0	0	0	0	89.65	1.63	50
44_sub.gp07	f_Spirochaetaceae (UID2535)	33	249	143	23	224	2	0	0	0	0	89.64	1.4	0
bin.129.gp06	k_Bacteria (UID2569)	434	278	186	30	244	4	0	0	0	0	89.61	1.88	100
bin.189.gw02	o_Clostridiales (UID1212)	172	263	149	18	244	1	0	0	0	0	89.6	0.34	0
bin.292.gp09	c_Clostridia (UID1118)	387	223	124	23	186	14	0	0	0	0	89.6	8.49	78.57
bin.593.gv	o_Clostridiales (UID1212)	172	263	149	18	245	0	0	0	0	0	89.6	0	0
104.hh14	f_Lachnospiraceae (UID1286)	57	420	207	52	346	22	0	0	0	0	89.57	6.28	50
6.gp10	k_Bacteria (UID2495)	2993	147	91	10	136	1	0	0	0	0	89.56	0.37	0
maxbin.125.gv	f_Lachnospiraceae (UID1286)	57	420	207	51	358	11	0	0	0	0	89.56	2.41	36.36
maxbin.457.gp	k_Bacteria (UID2495)	2993	147	91	10	137	0	0	0	0	0	89.56	0	0
39.gw03	o_Clostridiales (UID1212)	172	263	149	23	236	4	0	0	0	0	89.55	0.94	0
bin.55.gw05	c_Deltaproteobacteria (UID3218)	61	284	169	26	251	7	0	0	0	0	89.54	2.79	28.57
bin.429.hh	k_Bacteria (UID2565)	2921	152	93	18	131	3	0	0	0	0	89.53	2.51	33.33
bin.186_sub.gp08	c_Clostridia (UID1118)	387	223	124	16	205	2	0	0	0	0	89.52	0.81	0
bin.142.gp28	p_Bacteroidetes (UID2605)	350	314	208	23	283	7	1	0	0	0	89.5	3.85	50
bin.195.gw02	o_Clostridiales (UID1120)	304	247	141	28	219	0	0	0	0	0	89.5	0	0
bin.339.gv	o_Clostridiales (UID1212)	172	263	149	34	221	8	0	0	0	0	89.49	4.7	87.5
bin.560.gv	o_Clostridiales (UID1226)	155	278	158	60	215	3	0	0	0	0	89.48	1.42	0
maxbin.024_sub.gp09	p_Firmicutes (UID1022)	100	295	158	31	250	14	0	0	0	0	89.48	5.05	78.57
bin.344.hh	o_Clostridiales (UID1212)	172	263	149	25	235	3	0	0	0	0	89.47	1.23	100
222_sub.gw01	k_Bacteria (UID2569)	434	278	186	33	238	7	0	0	0	0	89.45	2.87	0
56.hh12	c_Epsilonproteobacteria (UID3065)	111	445	271	48	390	7	0	0	0	0	89.45	1.97	57.14
bin.263_sub.gw01	k_Bacteria (UID2329)	174	149	89	18	127	4	0	0	0	0	89.44	3.18	75
bin.15_sub.gw	o_Clostridiales (UID1212)	172	263	149	17	238	8	0	0	0	0	89.43	1.69	75
27.hh13	f_Veillonellaceae (UID1032)	33	423	214	43	373	7	0	0	0	0	89.41	1.13	0
bin.326.gp	k_Bacteria (UID2982)	88	229	147	46	181	2	0	0	0	0	89.41	1.02	50
maxbin.202_sub.hh	c_Clostridia (UID1118)	387	223	124	24	182	16	1	0	0	0	89.41	5.88	47.27
102.gp09	o_Clostridiales (UID1212)	172	263	149	25	231	7	0	0	0	0	89.39	3.75	28.57
maxbin.178_sub.hh15	p_Proteobacteria (UID3887)	1487	256	160	20	221	14	1	0	0	0	89.38	3.4	17.65
bin.20.gp	o_Clostridiales (UID1212)	172	263	149	25	234	4	0	0	0	0	89.37	0.89	25
bin.279.gp	k_Bacteria (UID2372)	131	176	105	31	134	9	2	0	0	0	89.37	8.21	46.67
maxbin.064.gw01	o_Clostridiales (UID1212)	172	263	149	20	242	1	0	0	0	0	89.37	0.67	100
102_sub.gv	p_Firmicutes (UID1022)	100	295	158	43	208	38	6	0	0	0	89.35	15.52	80.36
bin.260.gp10	o_Clostridiales (UID1212)	172	263	149	26	236	1	0	0	0	0	89.35	0.17	100
bin.332.gp07	o_Clostridiales (UID1212)	172	263	149	23	239	1	0	0	0	0	89.35	0.17	100
bin.83.gp09	f_Lachnospiraceae (UID1286)	57	420	207	48	369	3	0	0	0	0	89.34	0.63	0
bin.101.hh14	k_Bacteria (UID2329)	174	149	89	13	134	2	0	0	0	0	89.33	2.25	50
bin.187.hh14	k_Bacteria (UID2982)	88	230	148	19	200	9	2	0	0	0	89.33	7.3	53.33
bin.572.gv	p_Euryarchaeota (UID3)	148	187	124	19	168	0	0	0	0	0	89.33	0	0
bin.57.hh	c_Clostridia (UID1118)	387	223	124	17	203	3	0	0	0	0	89.31	2.42	0
maxbin.047.gp09	k_Bacteria (UID2569)	434	278	186	25	249	4	0	0	0	0	89.3	1.16	75
193.hc17	o_Bacteroidales (UID2657)	160	492	269	49	435	8	0	0	0	0	89.28	2.17	12.5
135.ca23	o_Clostridiales (UID1212)	172	263	149	20	212	29	2	0	0	0	89.27	15.97	85.71
bin.166_sub.gp09	c_Clostridia (UID1118)	387	223	124	19	203	1	0	0	0	0	89.25	0.4	100
bin.174_sub.gw02	f_Lachnospiraceae (UID1286)	57	420	207	63	347	10	0	0	0	0	89.24	2	50
bin.34_sub.gp08	p_Bacteroidetes (UID2605)	350	316	210	37	266	13	0	0	0	0	89.24	2.68	69.23
bin.192.gv	f_Lachnospiraceae (UID1286)	57	420	207	33	380	7	0	0	0	0	89.23	1.07	57.14
bin.42.ca21	p_Euryarchaeota (UID54)	90	234	153	19	210	5	0	0	0	0	89.22	2.61	100
3.hc	p_Bacteroidetes (UID2605)	350	316	210	27	275	13	1	0	0	0	89.21	4.29	68.75
maxbin.004.gp06	p_Bacteroidetes (UID2605)	350	316	210	26	287	3	0	0	0	0	89.21	1.19	33.33
bin.108.hc18	k_Bacteria (UID2982)	88	230	148	20	202	8	0	0	0	0	89.19	3.54	25
bin.88.gp	k_Bacteria (UID2982)	88	230	148	18	206	5	1	0	0	0	89.19	4.73	62.5
242.gp07	k_Bacteria (UID2982)	88	230	148	19	203	8	0	0	0	0	89.15	3.79	75
bin.6.gp26	o_Bacteroidales (UID2657)	160	492	269	65	420	7	0	0	0	0	89.14	2.09	42.86
maxbin.109.gp06	o_Clostridiales (UID1212)	172	263	149	22	239	2	0	0	0	0	89.13	1.01	100
bin.280_sub.gv	k_Bacteria (UID2329)	174	149	89	40	103	5	1	0	0	0	89.11	7.87	37.5
bin.58.gp08	p_Actinobacteria (UID2112)	31	211	124	16	187	7	1	0	0	0	89.11	2.99	60
maxbin.032.gw04	c_Clostridia (UID1118)	387	223	124	19	193	11	0	0	0	0	89.05	6.79	63.64
bin.156.gp08	k_Bacteria (UID2329)	174	149	89	11	136	2	0	0	0	0	89.04	2.25	0
bin.309_sub.gp07	f_Lachnospiraceae (UID1255)	354	90	354	174	53	290	11	0	0	0	89.04	3.52	72.73
bin.25_sub.hh11	o_Clostridiales (UID1212)	172	263	149	45	201	17	0	0	0	0	89.03	7.13	64.71
bin.104.hh13	c_Clostridia (UID1118)	387	223	124	18	203	2	0	0	0	0	89.02	1.01	50
bin.244_sub.gw03	k_Bacteria (UID2495)	2993	147	91	12	132	3	0	0	0	0	89.01	2.75	66.67
bin.38.ca21	k_Bacteria (UID2982)	88	229	147	32	192	5	0	0	0	0	89	1.48	60
147.gp09	c_Clostridia (UID1118)	387	223	124	17	198	8	0	0	0	0	88.98	3.97	75
bin.265_sub.gp06	c_Clostridia (UID1118)	387	223	124	18	197	8	0	0	0	0	88.98	4.17	62.5
maxbin.004.gw05	p_Bacteroidetes (UID2605)	350	316	210	28	272	16	0	0	0	0	88.97	3.22	50
maxbin.006.gp08	p_Bacteroidetes (UID2605)	350	316	210	28	277	10	1	0	0	0	88.97	4.52	46.15
bin.10_sub.gw02	f_Lachnospiraceae (UID1295)	33	543	238	73	439	29	2	0	0	0	88.96	7.17	60
184_sub.gw02	k_Archaea (UID2)	207	149	107	16	111	20	2	0	0	0	88.94	12.52	88.46
bin.271_sub.gp10	p_Bacteroidetes (UID2605)	350	316	210	45	247	23	1	0	0	0	88.94	8.62	53.85
maxbin.051_sub.gp10	o_Clostridiales (UID1212)	172	263	149	22	238	3	0	0	0	0	88.93	1.34	0
maxbin.200_sub.gp	f_Spirochaetaceae (UID2535)	33	249	143	22	218	9	0	0	0	0	88.93	4.9	55.56
227_sub.gp10	p_Bacteroidetes (UID2605)	350	316	210	26	270	18	0	0	0	0	88.89	5.87	83.33
85_sub.hh14	k_Bacteria (UID1453)	901	171	117	14	144	13	0	0	0	0	88.89	6.38	53.85
bin.135.hc16	k_Bacteria (UID1453)	901	171	117	14	154	3	0	0	0	0	88.89	1.28	0
bin.173.gw04	p_Bacteroidetes (UID2605)	350	316	210	45	263	8	0	0	0	0	88.89	2.46	75
bin.224.gp07	o_Bacteroidales (UID2716)	92	487	270	49	426	12	0	0	0	0	88.89	1.96	58.33
maxbin.023_sub.gp07	k_Bacteria (UID2569)	434	278	186	27	240	11	0	0	0	0	88.87	2.26	9.09
maxbin.047.gp06	o_Clostridiales (UID1212)	172	263	149	24	224	15	0	0	0	0	88.87	3.02	13.33
287.hp	o_Clostridiales (UID1212)	172	263	149	23	238	2	0						

maxbin.032.gh	o__Clostridiales (UID1120)	304	247	141	21	219	7	0	0	0	88.71	1.74	28.57
bin.237.gw05	o__Clostridiales (UID1120)	304	247	141	28	217	2	0	0	0	88.68	0.95	50
221.hh14	o__Bacteroidetes (UID2617)	213	406	265	59	331	16	0	0	0	88.67	4.59	62.5
200.gh10	k__Bacteria (UID2329)	174	149	89	12	136	1	0	0	0	88.65	0.56	0
360_sub.gh	o__Clostridiales (UID1212)	172	263	149	30	228	5	0	0	0	88.65	0.76	20
bin.39_sub.gh09	k__Bacteria (UID2329)	174	149	89	12	135	2	0	0	0	88.65	0.66	100
maxbin.324.gw	k__Bacteria (UID2329)	174	149	89	12	137	0	0	0	0	88.65	0	0
maxbin.354.gh	k__Bacteria (UID2329)	174	149	89	12	137	0	0	0	0	88.65	0	0
215_sub.hc	k__Bacteria (UID2329)	174	149	89	32	115	1	1	0	0	88.59	2.25	25
bin.655.gh	o__Clostridiales (UID1212)	172	263	149	20	240	3	0	0	0	88.59	1.17	100
bin.38_sub.gh09	c__Clostridia (UID1118)	387	223	124	19	191	13	0	0	0	88.58	6.21	30.77
bin.236.gh09	k__Bacteria (UID2372)	131	176	105	20	152	3	1	0	0	88.57	4.76	50
78.gw28	o__Clostridiales (UID1212)	172	263	149	34	224	5	0	0	0	88.56	1.9	60
bin.315.gh07	o__Clostridiales (UID1212)	172	263	149	28	234	1	0	0	0	88.53	0.34	100
bin.233_sub.gh06	o__Clostridiales (UID1212)	172	263	149	28	233	2	0	0	0	88.52	1.34	100
231.hc	o__Clostridiales (UID1212)	172	263	149	28	215	18	2	0	0	88.51	8.45	91.67
bin.199.hc18	o__Bacteroidales (UID2617)	213	406	265	35	368	3	0	0	0	88.49	0.69	66.67
bin.255.gw02	k__Bacteria (UID2495)	2993	142	88	39	101	2	0	0	0	88.49	1.7	50
bin.14.gh	k__Bacteria (UID2982)	88	230	148	23	202	4	1	0	0	88.48	2.73	0
bin.183_sub.gw02	p__Actinobacteria (UID2112)	31	211	124	26	170	11	4	0	0	88.44	4.38	26.09
140.hh14	o__Bacteroidales (UID2617)	213	406	265	44	320	41	1	0	0	88.43	10.83	88.64
109.hc17	k__Bacteria (UID2329)	174	149	89	15	134	0	0	0	0	88.42	0	0
bin.30_sub.hc18	o__Clostridiales (UID1212)	263	149	89	41	217	5	0	0	0	88.41	2.48	100
maxbin.019_sub.gw28	p__Euryarchaeota (UID3)	148	188	125	19	164	5	0	0	0	88.4	3.6	60
bin.600.hh	k__Bacteria (UID2329)	174	149	89	23	124	2	0	0	0	88.39	0.61	100
273.hc	o__Clostridiales (UID1212)	172	263	149	37	211	15	0	0	0	88.37	4.45	66.67
bin.58_sub.gw01	o__Clostridiales (UID1212)	172	263	149	24	219	20	0	0	0	88.37	2.08	10
maxbin.019.gw03	c__Clostridia (UID1118)	387	223	124	22	197	4	0	0	0	88.37	2.42	75
bin.126.gw	f__Lachnospiraceae (UID1298)	57	420	207	52	358	10	0	0	0	88.36	3.24	60
335_sub.hc	o__Clostridiales (UID1212)	172	263	149	28	200	34	1	0	0	88.35	11.32	59.46
bin.160_sub.hh12	o__Clostridiales (UID1212)	172	261	147	24	231	6	0	0	0	88.32	3.29	50
bin.165.gw03	p__Actinobacteria (UID2112)	31	211	124	31	177	3	0	0	0	88.31	2.42	100
bin.16.gw03	o__Clostridiales (UID1212)	172	263	149	30	214	18	1	0	0	88.3	3.62	19.05
254_sub.hh15	o__Clostridiales (UID1226)	155	278	158	26	232	19	1	0	0	88.29	7.81	59.09
bin.571.hc	o__Clostridiales (UID1212)	172	263	149	32	216	15	0	0	0	88.29	2.87	6.67
bin.208_sub.gw	p__Actinobacteria (UID2112)	31	211	124	25	177	8	0	0	0	88.28	4.68	90.91
bin.520.gw	o__Bacteroidales (UID2657)	160	492	269	54	435	3	0	0	0	88.28	0.93	33.33
bin.90.gw01	p__Bacteroidetes (UID2605)	350	316	210	31	276	9	0	0	0	88.28	3.13	100
bin.82.gw	o__Clostridiales (UID1212)	172	263	149	36	217	8	1	1	0	88.27	1.87	5.88
bin.278.hc17	o__Clostridiales (UID1212)	172	263	149	24	226	12	1	0	0	88.26	5.99	53.33
maxbin.123.gh	o__Clostridiales (UID1212)	172	263	149	22	234	7	0	0	0	88.26	3.24	0
20_sub.gh06	f__Lachnospiraceae (UID1298)	57	420	207	74	291	55	0	0	0	88.25	17.79	72.73
bin.79.gw07	f__Lachnospiraceae (UID1255)	90	354	174	32	314	8	0	0	0	88.24	4.31	62.5
bin.374.hh	o__Clostridiales (UID1212)	172	263	149	29	223	11	0	0	0	88.21	4.98	90.91
bin.294.gh10	o__Clostridiales (UID1212)	172	263	149	23	239	1	0	0	0	88.2	0.67	100
bin.114.gw05	f__Lachnospiraceae (UID1255)	90	354	174	35	314	5	0	0	0	88.19	2.06	20
bin.264.gh10	c__Clostridia (UID1118)	387	223	124	20	197	6	0	0	0	88.17	3.3	66.67
maxbin.008.gw01	p__Bacteroidetes (UID2605)	350	316	210	32	278	6	0	0	0	88.17	2.38	83.33
bin.10.gw09	k__Bacteria (UID2982)	88	230	148	22	204	3	1	0	0	88.15	2.39	16.67
bin.215.gw02	o__Clostridiales (UID1226)	155	278	158	28	239	11	0	0	0	88.15	3.72	100
97_sub.gw05	f__Spirochaetaceae (UID2535)	33	249	143	41	203	5	0	0	0	88.13	2.68	0
maxbin.026.gw02	p__Firmicutes (UID1022)	100	295	158	33	253	9	0	0	0	88.12	3.11	77.78
164.ca24	k__Bacteria (UID2982)	88	229	147	27	180	18	4	0	0	88.1	10.27	76.67
bin.1.gh	o__Clostridiales (UID1212)	172	263	149	50	207	6	0	0	0	88.1	3.13	0
bin.253_sub.gw05	o__Bacteroidetes (UID2657)	160	492	269	74	411	6	1	0	0	88.1	2.08	0
bin.67.gw02	o__Clostridiales (UID1212)	172	257	149	26	224	7	0	0	0	88.1	2.57	57.14
bin.98.hc17	c__Epsilonproteobacteria (UID3066)	110	450	273	49	394	7	0	0	0	88.1	1.62	42.86
70_sub.gw01	o__Clostridiales (UID1120)	304	247	141	21	214	12	0	0	0	88.06	6.26	83.33
bin.276.gh	f__Lachnospiraceae (UID1256)	33	333	171	37	287	8	1	0	0	88.05	4	81.82
maxbin.186_sub.gw03	f__Lachnospiraceae (UID1255)	90	354	174	50	291	13	0	0	0	88.04	6.32	23.08
209_sub.gh	f__Lachnospiraceae (UID1255)	90	354	174	31	306	15	2	0	0	87.99	5.48	47.62
bin.136.hc18	o__Clostridiales (UID1212)	172	263	149	26	224	10	1	0	0	87.98	6.94	61.54
111_sub.gw29	p__Bacteroidetes (UID2605)	350	314	208	45	247	22	0	0	0	87.94	5.56	40.91
bin.213_sub.gw02	k__Bacteria (UID2329)	174	149	89	12	136	1	0	0	0	87.92	1.12	0
bin.47.ca25	o__Clostridiales (UID1212)	172	263	149	20	229	14	0	0	0	87.92	6.66	85.71
bin.509.gw	k__Bacteria (UID2329)	174	149	89	14	133	2	0	0	0	87.92	2.25	0
bin.7.ca22	o__Clostridiales (UID1212)	172	263	149	22	233	8	0	0	0	87.92	2.84	62.5
bin.97.hh11	o__Clostridiales (UID1226)	155	278	158	32	230	15	1	0	0	87.92	7.18	38.89
bin.277_sub.gw	k__Bacteria (UID2495)	2993	147	91	12	134	1	0	0	0	87.91	0.37	100
bin.65.gh08	k__Bacteria (UID2495)	2993	147	91	12	134	1	0	0	0	87.91	0.1	0
maxbin.018.gw28	k__Bacteria (UID2495)	2993	147	91	11	132	4	0	0	0	87.91	3.36	50
bin.104.gw28	k__Bacteria (UID2982)	88	229	147	36	189	4	0	0	0	87.9	2.04	25
274.hh15	o__Bacteroidales (UID2617)	213	406	265	45	311	49	1	0	0	87.89	13.87	84.62
bin.142.ca	p__Bacteroidetes (UID2605)	350	315	209	53	233	29	0	0	0	87.88	10.33	58.62
maxbin.327.ca	c__Epsilonproteobacteria (UID3065)	111	445	271	49	384	12	0	0	0	87.88	3.57	75
222.gw02	o__Clostridiales (UID1212)	172	261	147	27	230	4	0	0	0	87.87	1.27	25
5_sub.hc16	o__Clostridiales (UID1212)	172	263	149	24	208	30	1	0	0	87.86	13.63	93.94
bin.6.hh12	o__Clostridiales (UID1212)	172	263	149	33	228	2	0	0	0	87.86	0.84	100
maxbin.022.hh11	o__Clostridiales (UID1120)	304	250	143	24	217	9	0	0	0	87.86	4.6	88.89
maxbin.265_sub.gw	o__Clostridiales (UID1226)	155	278	158	36	222	19	1	0	0	87.85	7.77	36.36
bin.145.hh14	k__Bacteria (UID2982)	88	230	148	20	206	4	0	0	0	87.84	2.06	50
bin.41.gw01	o__Clostridiales (UID1212)	172	263	149	41	222	0	0	0	0	87.84	0	0
bin.353.gw	o__Clostridiales (UID1226)	155	278	158	28	238	12	0	0	0	87.82	2.83	66.67
bin.48.gw30	o__Clostridiales (UID1212)	172	263	149	50	210	3	0	0	0	87.81	0.75	66.67
maxbin.073.hh15	k__Bacteria (UID2982)	88	230	148	22	193	15	0	0	0	87.81	8.2	86.67
bin.218.gh09	k__Bacteria (UID2982)	88	230	148	21	207	2	0	0	0	87.8	0.71	0
bin.128.gw04	o__Clostridiales (UID1226)	155	278	158	45	226	7	0	0	0	87.79	3.69	0
bin.86.gw04	o__Clostridiales (UID1212)	172	263	149	31	222	10	0	0	0	87.79	3.36	30
maxbin.005.gw03	p__Bacteroidetes (UID2605)	350	316	210	31	267	18	0	0	0	87.78	6.03	77.78
bin.15.gh06	o__Clostridiales (UID1120)	304	247	141	20	226	1	0	0	0	87.77	0.35	0
110_sub.gh10	o__Clostridiales (UID1212)	172	257	149	32	216	9	0	0	0	87.76	3.51	22.22
bin.532.go	o__Bacteroidales (UID2657)	160	492	269	92	394	6	0	0	0	87.74	1.28	33.33
116_sub.gw01	p__Bacteroidetes (UID2605)	350	316	210	30	274	12	0	0	0	87.7	4.29	50
bin.173_sub.gh07	o__Clostridiales (UID1120)	304	247	141	23	223	1	0	0	0	87.7	0.71	100
maxbin.025.hc20	g__Prevotella (UID2724)	55	567	296	84	462	21	0	0	0	87.7	4.89	38.1
118_sub.gh	k__Bacteria (UID2569)	434	278	186	35	233	10	0	0	0	87.67	3.53	40
bin.145.hc20	o__Clostridiales (UID1212)	172	263	149	36	225	2	0	0	0	87.65	0.81	50
bin.203.gw03	k__Bacteria (UID2329)	174	149	89	12	134	3	0	0	0	87.64	3.37	33.33
79.gh09	c__Clostridia (UID1118)	387	223	124	21	197	5	0	0	0	87.63	2.76	60
bin.65.gw01	k__Bacteria (UID2372)	131	17										

73.gw02	o__Clostridiales (UID1212)	172	263	149	22	234	7	0	0	0	87.47	3.08	71.43
maxbin.133.gw	f__Lachnospiraceae (UID1255)	90	354	174	46	286	22	0	0	0	87.47	4.88	36.36
maxbin.187.gw07	o__Clostridiales (UID1120)	304	247	141	40	204	3	0	0	0	87.47	1.54	33.33
bin.155.gw10	p__Bacteroidetes (UID2605)	350	316	210	34	279	3	0	0	0	87.46	1.19	100
bin.225_sub.gw07	c__Clostridia (UID1118)	387	223	124	26	184	13	0	0	0	87.45	5.34	76.92
bin.97.gw30	p__Bacteroidetes (UID2605)	350	314	208	34	265	15	0	0	0	87.45	5.93	46.67
bin.188.hc	k__Bacteria (UID2495)	2993	142	88	13	127	2	0	0	0	87.43	2.27	50
bin.184.hc20	c__Gammaproteobacteria (UID4201)	1164	271	170	39	226	6	0	0	0	87.42	2.55	100
bin.198.gw	k__Bacteria (UID2329)	174	149	89	15	132	2	0	0	0	87.42	1.69	50
80.gw07	p__Actinobacteria (UID2112)	31	211	124	27	181	3	0	0	0	87.41	1.69	33.33
maxbin.028.hc16	f__Bifidobacteriaceae (UID1458)	77	464	220	56	342	64	2	0	0	87.41	15.12	87.14
maxbin.051_sub.gw07	k__Bacteria (UID2495)	2993	142	88	14	116	12	0	0	0	87.37	3.12	50
bin.90.hh11	o__Clostridiales (UID1212)	172	263	149	41	218	4	0	0	0	87.36	1.03	0
maxbin.062_sub.gw04	o__Clostridiales (UID1212)	172	263	149	24	235	4	0	0	0	87.36	2.01	75
49_sub.gw07	o__Clostridiales (UID1226)	155	278	158	30	239	9	0	0	0	87.32	2.93	44.44
maxbin.144.hc16	c__Epsilonproteobacteria (UID3066)	110	450	273	50	384	16	0	0	0	87.32	3.91	81.25
bin.108.gw07	k__Bacteria (UID2569)	434	278	186	30	244	4	0	0	0	87.31	0.9	75
bin.14.hh13	c__Clostridia (UID1118)	387	223	124	23	199	1	0	0	0	87.27	0.81	0
bin.201.gw04	k__Bacteria (UID203)	5449	100	55	10	73	17	0	0	0	87.27	5.21	47.06
104.hh13	k__Bacteria (UID2982)	88	229	147	25	201	3	0	0	0	87.26	1.16	33.33
90.gw09	o__Clostridiales (UID1212)	172	263	149	23	234	6	0	0	0	87.25	3.24	66.67
maxbin.281.gw	o__Clostridiales (UID1226)	155	278	158	28	235	15	0	0	0	87.24	5.14	80
156.hc17	o__Bacteroidetes (UID2617)	406	215	406	40	329	36	1	0	0	87.23	8.45	76.92
148_sub.hc16	g__Prevotella (UID2722)	64	532	281	84	430	18	0	0	0	87.22	4.61	66.67
158_sub.gw08	p__Bacteroidetes (UID2605)	350	314	208	45	266	3	0	0	0	87.21	0.96	33.33
294.gw01	p__Actinobacteria (UID2112)	31	211	124	22	178	11	0	0	0	87.18	4.12	63.64
266_sub.hh	o__Clostridiales (UID1212)	172	263	149	34	223	5	1	0	0	87.17	2.52	50
bin.185.hh12	k__Bacteria (UID2982)	88	230	148	21	204	5	0	0	0	87.16	2.1	20
bin.194.hh12	p__Actinobacteria (UID2112)	211	211	124	23	174	14	0	0	0	87.15	8.45	76.92
bin.97_sub.hh14	k__Bacteria (UID2372)	131	176	105	18	157	1	0	0	0	87.14	0.48	100
53.hc16	o__Clostridiales (UID1212)	172	263	149	28	229	6	0	0	0	87.13	3.24	66.67
bin.1.gw04	k__Bacteria (UID2982)	88	230	148	22	204	4	0	0	0	87.12	1.58	75
maxbin.020.gw01	p__Firmicutes (UID1022)	100	295	158	35	253	7	0	0	0	87.11	3.96	71.43
bin.110.gw09	c__Clostridia (UID1118)	387	223	124	23	197	3	0	0	0	87.1	1.69	100
bin.221.gw02	c__Clostridia (UID1118)	387	223	124	20	195	8	0	0	0	87.1	4.04	75
bin.28.gw04	k__Bacteria (UID2329)	174	149	89	13	132	2	0	0	0	87.08	3.48	75
bin.475.hh	k__Bacteria (UID2329)	174	149	89	12	134	3	0	0	0	87.08	2.81	66.67
maxbin.267.gw	f__Lachnospiraceae (UID1256)	33	333	171	38	273	22	0	0	0	87.08	7.4	50
bin.136.gw09	o__Clostridiales (UID1212)	172	263	149	27	230	6	0	0	0	87.07	3.24	16.67
191.hc16	k__Bacteria (UID2329)	174	149	89	18	130	1	0	0	0	87.04	0.05	0
bin.93_sub.hc19	f__Leuconostocaceae (UID486)	29	443	178	53	372	18	0	0	0	87.04	4.18	66.67
maxbin.101_sub.gw	o__Clostridiales (UID1212)	172	263	149	32	221	10	0	0	0	87.04	4.72	20
bin.248.gw08	p__Actinobacteria (UID2112)	31	211	124	28	173	10	0	0	0	87	2.34	10
bin.248.hc17	o__Clostridiales (UID1212)	172	263	149	42	214	7	0	0	0	87	4.36	28.57
131.hh	k__Bacteria (UID2495)	2993	147	91	28	112	6	1	0	0	86.98	6.96	100
maxbin.248_sub.hc	c__Clostridia (UID1118)	387	223	124	43	169	11	0	0	0	86.98	5.72	63.64
maxbin.317.gw	o__Clostridiales (UID1120)	304	247	141	37	207	3	0	0	0	86.97	1.42	66.67
bin.187.hh11	o__Clostridiales (UID1212)	172	263	149	28	234	1	0	0	0	86.94	0.13	0
maxbin.564.gw	p__Euryarchaeota (UID3)	148	187	124	19	156	11	1	0	0	86.94	2.28	21.43
maxbin.044_sub.gw07	p__Bacteroidetes (UID2605)	350	316	210	57	243	16	0	0	0	86.92	5.36	50
bin.19.gw06	o__Clostridiales (UID1212)	172	263	149	26	237	0	0	0	0	86.91	0	0
bin.97.gw03	o__Clostridiales (UID1120)	304	247	141	36	209	2	0	0	0	86.89	0.71	50
bin.111_sub.gw01	k__Bacteria (UID2982)	88	230	148	41	186	2	1	0	0	86.88	1.73	20
bin.164_sub.hc20	o__Clostridiales (UID1212)	172	263	149	34	226	3	0	0	0	86.88	2.01	66.67
maxbin.127.gw07	f__Lachnospiraceae (UID1255)	354	354	174	51	284	9	0	0	0	86.88	3.02	11.11
bin.5.gw03	k__Bacteria (UID2495)	2993	142	88	14	122	6	0	0	0	86.86	2.54	100
bin.166.gw10	k__Bacteria (UID2982)	88	230	148	24	202	4	0	0	0	86.85	0.97	50
128_sub.gw07	p__Bacteroidetes (UID2605)	350	316	210	33	279	4	0	0	0	86.83	0.82	50
bin.176_sub.hh	o__Clostridiales (UID1212)	172	263	149	46	197	20	0	0	0	86.8	9.9	55
bin.512.hc	c__Epsilonproteobacteria (UID3065)	111	445	271	50	380	15	0	0	0	86.8	3.38	80
maxbin.110_sub.gw	p__Actinobacteria (UID2112)	31	211	124	25	179	7	0	0	0	86.8	3.64	57.14
bin.115.gw10	k__Bacteria (UID2982)	88	230	148	24	201	4	1	0	0	86.79	3.07	14.29
bin.133.hh12	k__Bacteria (UID2329)	174	149	89	16	133	0	0	0	0	86.78	0	0
bin.148.gw10	k__Bacteria (UID2329)	174	149	89	18	127	3	1	0	0	86.74	3.86	33.33
bin.89.gw28	k__Bacteria (UID2982)	88	229	147	24	201	4	0	0	0	86.73	1.74	75
bin.210_sub.gw04	o__Clostridiales (UID1226)	155	278	158	42	227	9	0	0	0	86.71	3.04	11.11
bin.46.gw26	k__Bacteria (UID2982)	88	230	148	24	202	4	0	0	0	86.71	1.72	25
maxbin.044_sub.gw	k__Bacteria (UID2495)	2993	142	88	27	97	17	1	0	0	86.71	10.14	60
bin.105_sub.gw10	o__Clostridiales (UID1212)	172	263	149	46	212	3	0	0	0	86.7	1.12	66.67
maxbin.097.gw05	c__Clostridia (UID1118)	387	223	124	21	191	11	0	0	0	86.69	5.48	36.36
bin.118.hc19	o__Lactobacillales (UID544)	293	473	265	59	394	20	0	0	0	86.68	3.11	65
bin.191.gw02	o__Clostridiales (UID1212)	172	263	149	43	210	9	1	0	0	86.67	4.85	16.67
bin.92.gw09	p__Bacteroidetes (UID2605)	350	316	210	53	244	19	0	0	0	86.67	6.51	68.42
bin.12_sub.gw04	o__Clostridiales (UID1120)	304	247	141	25	220	2	0	0	0	86.64	0.35	0
maxbin.122.gw01	o__Clostridiales (UID1212)	172	263	149	29	233	1	0	0	0	86.61	0.67	0
bin.233.gw10	o__Clostridiales (UID1212)	172	263	149	45	215	3	0	0	0	86.6	1.34	0
161.gw04	o__Clostridiales (UID1212)	172	263	149	28	233	2	0	0	0	86.59	0.45	100
308.gw03	p__Actinobacteria (UID2112)	31	211	124	29	176	6	0	0	0	86.59	2.67	83.33
194.gw05	o__Clostridiales (UID1212)	172	263	149	26	234	3	0	0	0	86.58	1.01	0
maxbin.010_sub.gw02	o__Clostridiales (UID1212)	172	263	149	28	231	4	0	0	0	86.56	1.85	75
bin.399.hh	k__Bacteria (UID2328)	3167	126	75	12	107	7	0	0	0	86.55	7.45	85.71
296_sub.gw	k__Bacteria (UID2372)	131	177	106	24	152	1	0	0	0	86.54	0.13	0
bin.18.gw30	o__Clostridiales (UID1120)	304	247	141	40	203	4	0	0	0	86.52	1.62	50
bin.284.hc17	k__Bacteria (UID2495)	2993	143	89	13	125	5	0	0	0	86.52	3.54	60
bin.637.gw	k__Bacteria (UID2329)	174	149	89	16	131	2	0	0	0	86.52	2.25	0
bin.430.gw	o__Bacteroidetes (UID2621)	198	427	260	56	367	4	0	0	0	86.5	1.09	50
maxbin.093.gw07	o__Clostridiales (UID1212)	172	263	149	33	228	2	0	0	0	86.49	1.01	50
289.gw08	o__Clostridiales (UID1120)	304	247	141	41	204	2	0	0	0	86.48	1.42	50
maxbin.225.gw	o__Clostridiales (UID1226)	155	278	158	31	238	9	1	0	0	86.45	4.11	100
maxbin.005_sub.hh15	c__Gammaproteobacteria (UID4201)	1164	271	170	43	211	17	0	0	0	86.44	3.59	17.65
71_sub.gw03	p__Bacteroidetes (UID2605)	350	316	210	33	274	9	0	0	0	86.43	3.49	88.89
bin.238_sub.gw	p__Actinobacteria (UID2112)	31	211	124	42	154	15	0	0	0	86.42	7.23	86.67
302_sub.gw	o__Clostridiales (UID1212)	172	263	149	41	215	7	0	0	0	86.41	2.13	71.43
bin.125.hh12	f__Lachnospiraceae (UID1255)	90	354	174	42	287	24	1	0	0	86.4	8.48	66.67
bin.176_sub.gw02	f__Lachnospiraceae (UID1255)	354	354	174	66	279	9	0	0	0	86.36	3.4	55.56
bin.72.gw08	o__Clostridiales (UID1120)	304	250	143	30	217	3	0	0	0	86.36	1.13	33.33
bin.153.gw04	o__Clostridiales (UID1120)	304	247	141	37	198	10	2	0	0	86.35	2.19	6.25
204.hc16	o__Clostridiales (UID1212)	172	263	149	29	195	37	2	0	0	86.34	14.32	65.12
170.hc	o__Clostridiales (UID1120)	304	250	143	29	201	19	1	0	0	86.33	11.11	81.82
bin.162.hc	o__Clostr												

179_sub.gh07	o_Bacteroidales (UID2657)	160	492	269	86	396	10	0	0	0	86.23	2.5	30
201_sub.gh10	c_Clostridia (UID1118)	387	223	124	23	193	7	0	0	0	86.22	3.9	85.71
293_sub.gw01	c_Clostridia (UID1118)	387	223	124	22	199	2	0	0	0	86.22	1.61	0
bin.126_sub.gw05	p_Bacteroidetes (UID2605)	350	316	210	46	266	4	0	0	0	86.22	0.89	50
bin.70.gw27	k_Bacteria (UID2982)	88	229	147	50	170	9	0	0	0	86.22	3.7	88.89
bin.107.hh12	k_Bacteria (UID2372)	131	177	106	23	148	6	0	0	0	86.21	4.09	100
bin.93.gh08	f_Lachnospiraceae (UID1255)	90	354	174	62	280	12	0	0	0	86.21	3.05	58.33
14.gw03	p_Actinobacteria (UID2112)	31	211	124	27	171	13	0	0	0	86.19	6.52	53.85
bin.278_sub.gw03	k_Bacteria (UID2372)	131	176	105	21	147	7	1	0	0	86.19	7.71	50
maxbin.121.gh07	o_Clostridiales (UID1212)	172	263	149	27	235	1	0	0	0	86.19	0.13	100
bin.267.gw03	k_Bacteria (UID2329)	174	149	89	16	131	2	0	0	0	86.14	1.24	0
bin.6_sub.gh06	p_Bacteroidetes (UID2605)	350	316	210	59	241	16	0	0	0	86.14	4.48	56.25
bin.163_sub.gh09	p_Actinobacteria (UID2112)	31	211	124	28	170	13	0	0	0	86.13	6.91	46.15
bin.137_sub.gh06	p_Bacteroidetes (UID2605)	350	316	210	36	277	3	0	0	0	86.11	1.19	66.67
bin.74.ca24	k_Bacteria (UID2982)	88	230	148	26	201	3	0	0	0	86.09	1.38	0
234_sub.hh	k_Bacteria (UID1453)	901	171	117	23	143	4	1	0	0	86.04	3.92	28.57
214.hh11	k_Bacteria (UID2329)	174	149	89	20	129	0	0	0	0	86.01	0	0
maxbin.244_sub.hc	k_Bacteria (UID2982)	88	230	148	24	187	17	2	0	0	85.98	8.06	43.48
maxbin.213.gw02	o_Clostridiales (UID1226)	155	278	158	31	240	7	0	0	0	85.96	2.05	85.71
bin.247.gw01	k_Bacteria (UID2982)	88	230	148	27	197	6	0	0	0	85.94	2.76	50
bin.236.gh10	p_Bacteroidetes (UID2605)	350	316	210	39	268	9	0	0	0	85.92	3.28	44.44
bin.122.gh08	o_Clostridiales (UID1212)	172	263	149	28	225	10	0	0	0	85.91	5.22	80
bin.256.gw	p_Bacteroidetes (UID2605)	350	316	210	54	259	3	0	0	0	85.91	1.19	66.67
bin.18.hc18	k_Bacteria (UID1453)	901	171	117	22	134	15	0	0	0	85.9	4.74	46.67
165_sub.gh07	k_Bacteria (UID203)	5449	104	58	11	70	22	1	0	0	85.89	10.74	64
bin.624.gh	c_Clostridia (UID1118)	387	223	124	26	191	6	0	0	0	85.89	3.09	66.67
bin.84.gh08	p_Euryarchaeota (UID3)	148	188	125	22	156	10	0	0	0	85.88	6.53	70
maxbin.260.gh07	k_Bacteria (UID2329)	174	149	89	19	127	3	0	0	0	85.86	1.4	33.33
bin.81.gw01	k_Bacteria (UID2569)	434	278	186	43	233	2	0	0	0	85.85	0.81	0
bin.267.hc	k_Bacteria (UID2565)	2921	152	93	17	131	4	0	0	0	85.83	2.21	100
bin.76.hc16	o_Clostridiales (UID1120)	304	250	143	31	209	10	0	0	0	85.82	5.36	20
bin.21.gw03	p_Euryarchaeota (UID3)	148	187	124	28	157	2	0	0	0	85.8	1.08	50
210.hc20	o_Clostridiales (UID1120)	304	250	143	28	204	17	1	0	0	85.78	5.46	45
bin.157.gh06	k_Bacteria (UID2982)	88	230	148	27	200	2	1	0	0	85.78	1.72	0
maxbin.099_sub.gh06	k_Bacteria (UID2329)	172	263	149	33	207	23	0	0	0	85.76	9.21	82.61
bin.184.gw04	p_Actinobacteria (UID2112)	31	211	124	25	171	15	0	0	0	85.75	1.25	66.67
bin.281_sub.hc17	f_Lachnospiraceae (UID1255)	90	354	174	40	294	19	1	0	0	85.71	6.22	36.36
15.hc19	o_Clostridiales (UID1212)	172	263	149	47	213	3	0	0	0	85.7	1.68	0
96.gh	k_Bacteria (UID2982)	88	230	148	28	196	6	0	0	0	85.69	3.07	33.33
bin.164_sub.gh07	o_Clostridiales (UID1212)	172	263	149	33	222	8	0	0	0	85.67	2.52	75
bin.178.gh07	o_Clostridiales (UID1212)	172	263	149	37	223	3	0	0	0	85.66	1.57	0
6.hc20	o_Bacteroidetes (UID2657)	160	492	269	77	408	7	0	0	0	85.63	1.67	57.14
262.gw01	o_Clostridiales (UID1212)	172	263	149	32	200	31	0	0	0	85.62	13.57	70.97
bin.41.gh	c_Clostridia (UID1118)	387	223	124	33	188	2	0	0	0	85.62	1.01	50
bin.49.hh13	o_Clostridiales (UID1212)	172	263	149	29	233	1	0	0	0	85.61	0.13	0
bin.6.hc19	f_Lachnospiraceae (UID1255)	90	354	174	65	279	10	0	0	0	85.6	3.21	80
bin.80.gw30	k_Bacteria (UID2982)	88	229	147	46	168	15	0	0	0	85.59	8.39	80
bin.598.hh	k_Bacteria (UID2328)	3167	126	75	20	99	7	0	0	0	85.58	2.59	0
bin.269.hh	o_Clostridiales (UID1120)	304	250	143	31	206	13	0	0	0	85.54	5.36	46.15
bin.6.gw05	p_Bacteroidetes (UID2605)	350	316	210	50	258	8	0	0	0	85.54	2.78	75
bin.234.gw03	p_Actinobacteria (UID2112)	31	211	124	42	166	3	0	0	0	85.53	1.19	66.67
bin.35_sub.ca21	o_Bacteroidales (UID2657)	160	492	269	93	379	19	1	0	0	85.53	4.4	31.82
maxbin.117.gh	f_Lachnospiraceae (UID1255)	90	354	174	62	281	11	0	0	0	85.53	4.66	63.64
235.hh15	o_Clostridiales (UID1212)	172	263	149	43	214	6	0	0	0	85.51	3.13	16.67
44.gw01	o_Clostridiales (UID1212)	172	261	147	53	202	6	0	0	0	85.51	2.21	16.67
98.hc20	o_Selenomonadales (UID1024)	64	334	167	47	276	11	0	0	0	85.48	4.12	54.55
bin.573.gw	k_Bacteria (UID2569)	434	278	186	31	242	5	0	0	0	85.48	1.45	100
bin.368.hh	k_Bacteria (UID1453)	901	171	117	18	145	8	0	0	0	85.47	6.41	25
bin.105.hh12	o_Clostridiales (UID1226)	155	278	158	34	229	15	0	0	0	85.46	5.16	80
bin.55.gh07	p_Euryarchaeota (UID3)	148	187	124	52	122	13	0	0	0	85.46	8.2	92.31
234.hc20	o_Clostridiales (UID1212)	172	263	149	31	221	11	0	0	0	85.45	5.31	27.27
306_sub.gh10	o_Clostridiales (UID1212)	172	263	149	29	222	11	1	0	0	85.44	7.61	43.48
85.gw02	o_Lactobacillales (UID543)	294	472	265	63	387	22	0	0	0	85.43	5.19	68.18
bin.173.gw02	k_Bacteria (UID2982)	88	230	148	27	201	2	0	0	0	85.43	0.71	0
bin.111.hc17	o_Clostridiales (UID1120)	304	250	143	27	215	8	0	0	0	85.41	3.75	75
bin.187.hc20	k_Bacteria (UID2329)	174	149	89	14	134	1	0	0	0	85.39	1.12	0
bin.423_sub.gh	k_Bacteria (UID2329)	174	149	89	26	119	4	0	0	0	85.39	3.75	75
maxbin.382.hc	p_Bacteroidetes (UID2605)	350	316	210	50	250	10	6	0	0	85.39	3.92	7.14
211.gh09	o_Clostridiales (UID1226)	155	278	158	33	233	12	0	0	0	85.35	4.91	91.67
bin.73.hh12	k_Bacteria (UID1453)	901	171	117	30	139	2	0	0	0	85.35	1.71	0
bin.184.hh11	k_Bacteria (UID1453)	901	171	117	32	137	2	0	0	0	85.29	1.28	50
bin.11.gw	k_Bacteria (UID2372)	131	176	105	20	152	4	0	0	0	85.24	2.46	75
109_sub.gh06	o_Clostridiales (UID1212)	172	263	149	25	235	3	0	0	0	85.23	1.34	33.33
17_sub.gh08	c_Deltaproteobacteria (UID3218)	61	284	169	45	229	10	0	0	0	85.22	1.36	60
12.hc19	f_Lachnospiraceae (UID1255)	90	354	174	40	295	19	0	0	0	85.2	5.46	47.37
bin.390.gh	o_Clostridiales (UID1212)	172	263	149	34	229	0	0	0	0	85.19	0	0
54.gh06	o_Burkholderiales (UID4000)	193	427	214	57	360	10	0	0	0	85.18	1.86	10
19_sub.gw02	p_Bacteroidetes (UID2605)	350	316	210	60	245	11	0	0	0	85.16	2.61	81.82
bin.107.gh09	p_Bacteroidetes (UID2605)	350	316	210	41	272	3	0	0	0	85.16	0.79	33.33
maxbin.044.gh	k_Bacteria (UID2569)	434	278	186	34	238	6	0	0	0	85.16	1.56	100
bin.183.hh11	k_Bacteria (UID2982)	88	230	148	27	200	3	0	0	0	85.14	0.93	0
maxbin.011.gh06	c_Clostridia (UID1118)	387	223	124	26	190	7	0	0	0	85.14	3.9	85.71
bin.145_sub.gw03	k_Bacteria (UID2372)	131	176	105	33	134	8	1	0	0	85.11	6.67	36.36
bin.155.gw04	o_Clostridiales (UID1120)	304	247	141	30	215	2	0	0	0	85.11	1.06	100
bin.3_sub.gh07	k_Bacteria (UID203)	5449	104	58	18	73	13	0	0	0	85.11	3.98	0
bin.112.gh06	k_Bacteria (UID2982)	88	230	148	25	201	4	0	0	0	85.1	1.72	75
bin.601.gw	c_Clostridia (UID1085)	35	420	196	56	357	7	0	0	0	85.1	1.4	57.14
132.gw30	p_Bacteroidetes (UID2605)	350	314	208	56	246	12	0	0	0	85.06	3.19	25
maxbin.011.go	o_Clostridiales (UID1212)	172	263	149	31	226	6	0	0	0	85.02	2.74	66.67
50_sub.gw	p_Actinobacteria (UID2112)	31	211	124	33	163	14	1	0	0	85.01	7.15	76.47
bin.204_sub.gh09	o_Clostridiales (UID1212)	172	263	149	35	226	2	0	0	0	85.01	0.67	0
maxbin.075_sub.gw02	c_Clostridia (UID1118)	387	223	124	24	183	16	0	0	0	85.01	6.76	62.5
12.hc17	c_Clostridia (UID1118)	387	223	124	47	169	7	0	0	0	85	3.49	14.29
79.gw02	o_Clostridiales (UID1120)	304	247	141	26	207	13	1	0	0	84.99	6.44	87.5
maxbin.037.gh08	o_Clostridiales (UID1212)	172	263	149	32	231	0	0	0	0	84.97	0	0
290.gh08	o_Clostridiales (UID1212)	172	263	149	26	235	2	0	0	0	84.9	0.08	50
bin.165.gw05	p_Bacteroidetes (UID2605)	350	316	210	50	259	7	0	0	0	84.88	2.5	85.71
bin.125_sub.hh13	f_Bifidobacteriaceae (UID1462)	65	476	217	92	376	8	0	0	0	84.86	2.2	50
25.hc16	c_Spirochaetia (UID2496)	72	215	125	27	186	2	0	0	0	84.85	0.43	50
bin.38.hc	o_Clostridiales (UID1212)	172	263	149	50	205	8	0	0	0	84.8	3.91	75
bin.408.hc	o_Clostridiales (UID1212)	172	263	149									

bin.511_sub.gw	o_Clostridiales (UID1226)	155	278	158	65	194	19	0	0	0	84.68	8.02	68.42
bin.100_sub.gw08	c_Clostridia (UID1118)	387	223	124	30	175	17	1	0	0	84.65	9.84	50
bin.42.ca22	k_Bacteria (UID2569)	434	278	186	35	229	14	0	0	0	84.61	4.74	57.14
bin.18.hh14	g_Prevotella (UID2724)	55	567	296	75	475	16	1	0	0	84.58	3.1	36.84
bin.222.hh15	k_Bacteria (UID2329)	174	149	89	22	127	0	0	0	0	84.57	0	0
maxbin.022.gw07	p_Firmicutes (UID1022)	100	295	158	45	240	10	0	0	0	84.55	3.34	80
bin.156.hc18	k_Bacteria (UID2565)	2921	152	93	23	129	0	0	0	0	84.54	0	0
bin.104.gw04	o_Clostridiales (UID1212)	172	261	147	56	202	3	0	0	0	84.52	0.57	66.67
bin.359.gj	p_Euryarchaeota (UID3)	148	187	124	45	140	2	0	0	0	84.5	1.21	100
bin.49.ca25	o_Bacteroidales (UID2657)	160	492	269	90	390	12	0	0	0	84.49	3.45	83.33
170_sub.hh	o_Clostridiales (UID1212)	172	263	149	31	217	15	0	0	0	84.45	5.4	60
281_sub.gw06	o_Clostridiales (UID1120)	304	247	141	25	213	9	0	0	0	84.4	4.67	88.89
292.gw01	p_Actinobacteria (UID2112)	31	211	124	50	152	9	0	0	0	84.39	5.02	44.44
bin.338.hh	p_Euryarchaeota (UID3)	148	188	125	29	152	7	0	0	0	84.37	3.76	85.71
bin.81_sub.hh15	o_Clostridiales (UID1212)	172	263	149	40	220	3	0	0	0	84.31	0.62	66.67
228_sub.hh12	p_Proteobacteria (UID3887)	256	160	42	206	8	0	0	0	0	84.3	4.06	25
bin.229.gw08	k_Bacteria (UID2372)	131	176	105	27	145	3	1	0	0	84.29	4.29	33.33
bin.569.gw	o_Clostridiales (UID1226)	155	278	158	53	220	5	0	0	0	84.29	1.59	80
201_sub.gw	o_Clostridiales (UID1212)	172	263	149	33	226	4	0	0	0	84.28	1.4	25
bin.216.gw08	k_Bacteria (UID2982)	88	230	148	28	199	3	0	0	0	84.28	1.38	0
bin.87_sub.gw01	o_Clostridiales (UID1212)	172	263	149	52	208	3	0	0	0	84.28	0.67	0
maxbin.174_sub.hh	o_Clostridiales (UID1212)	172	263	149	47	208	8	0	0	0	84.27	4.25	62.5
bin.86_sub.gw07	o_Clostridiales (UID1212)	172	263	149	38	203	19	0	0	0	84.26	4.51	0
193.hh	g_Prevotella (UID2722)	64	532	281	81	439	12	0	0	0	84.24	2.56	83.33
bin.170.hc	o_Clostridiales (UID1212)	172	263	149	41	212	10	0	0	0	84.24	4.05	80
maxbin.312_sub.gj	o_Clostridiales (UID1212)	172	263	149	42	221	0	0	0	0	84.23	0	0
37_sub.gw03	o_Clostridiales (UID1120)	304	247	141	25	213	7	2	0	0	84.22	6.5	61.54
bin.124.gj	p_Bacteroidetes (UID2605)	350	316	210	45	270	1	0	0	0	84.21	0.48	100
bin.125.gw04	p_Bacteroidetes (UID2605)	316	210	210	274	2	0	0	0	0	84.21	0.57	100
maxbin.060.gw30	k_Bacteria (UID2495)	2993	147	91	26	114	7	0	0	0	84.18	4.6	85.71
160_sub.gw	c_Epsilonproteobacteria (UID3065)	111	445	271	64	346	33	2	0	0	84.17	7.93	71.79
bin.145.gj	k_Bacteria (UID2982)	88	230	148	36	186	8	0	0	0	84.16	4.42	50
bin.168.gw08	p_Euryarchaeota (UID3)	148	187	124	32	155	0	0	0	0	84.15	0	0
203.gw08	o_Clostridiales (UID1226)	155	278	158	39	230	9	0	0	0	84.14	3.68	44.44
bin.42_sub.hc20	o_Clostridiales (UID1212)	172	263	149	55	205	3	0	0	0	84.14	1.51	100
bin.266.gw	f_Lachnospiraceae (UID1256)	33	171	44	6	287	2	0	0	0	84.13	1.17	0
bin.383.hc	c_Clostridia (UID1118)	387	223	124	37	184	2	0	0	0	84.11	0.97	50
bin.33.gw03	k_Bacteria (UID2982)	88	230	148	30	195	5	0	0	0	84.08	2.73	0
bin.348.gw	k_Bacteria (UID2982)	88	230	148	29	199	2	0	0	0	84.08	0.71	0
129_sub.gw08	f_Lachnospiraceae (UID1255)	90	354	174	69	277	8	0	0	0	84.07	2.32	12.5
166.gj	p_Actinobacteria (UID2112)	31	211	124	37	173	1	0	0	0	84.06	0.81	0
bin.176.hh11	g_Prevotella (UID2722)	64	532	281	109	406	4	0	0	0	84.05	3.21	58.82
bin.264.gw07	c_Clostridia (UID1118)	387	223	124	29	190	4	0	0	0	84.01	2.69	50
bin.184.gw03	k_Bacteria (UID2328)	3167	126	75	26	96	4	0	0	0	84	4	25
bin.350.gw07	c_Gammaproteobacteria (UID4201)	1164	270	171	45	213	6	6	0	0	84	3.27	8.33
bin.448.hh	k_Bacteria (UID2328)	3167	126	75	25	93	8	0	0	0	84	5.6	37.5
105.gw27	k_Bacteria (UID2569)	434	278	186	47	223	6	2	0	0	83.96	3.85	16.67
bin.205.hh	o_Clostridiales (UID1212)	172	263	149	47	208	8	0	0	0	83.95	2.85	50
311.gw07	o_Bacteroidales (UID2617)	213	406	265	63	323	19	1	0	0	83.93	4.28	18.18
bin.246_sub.gw01	o_Clostridiales (UID1212)	172	263	149	46	217	0	0	0	0	83.93	0	0
288_sub.gj10	f_Lachnospiraceae (UID1255)	90	354	174	74	272	8	0	0	0	83.9	3.07	12.5
bin.240.gw07	o_Clostridiales (UID1212)	172	263	149	32	228	3	0	0	0	83.89	1.03	66.67
bin.39_sub.gw04	p_Bacteroidetes (UID2605)	350	316	210	60	229	27	0	0	0	83.88	5.61	55.56
259_sub.gj10	o_Clostridiales (UID1120)	304	247	141	32	206	9	0	0	0	83.87	4.02	77.78
195_sub.hc17	k_Bacteria (UID1453)	901	171	117	36	130	5	0	0	0	83.86	2.71	60
bin.177_sub.gj	k_Bacteria (UID2329)	174	149	89	18	130	1	14	0	0	83.85	0.05	100
maxbin.265_sub.gw07	p_Euryarchaeota (UID3)	148	187	124	30	152	5	0	0	0	83.82	1.15	0
bin.591.hh	k_Bacteria (UID2372)	131	176	105	22	146	8	0	0	0	83.81	3.27	25
bin.99.gw01	p_Bacteroidetes (UID2605)	350	316	210	72	240	4	0	0	0	83.8	1.59	50
43_sub.hh12	k_Bacteria (UID1453)	901	171	117	20	149	2	0	0	0	83.76	0.95	0
bin.200_sub.gw09	p_Bacteroidetes (UID2605)	350	316	210	46	262	8	0	0	0	83.76	3.57	12.5
bin.426.gj	p_Actinobacteria (UID1454)	732	206	120	26	180	0	0	0	0	83.75	0	0
bin.58_sub.gw06	o_Clostridiales (UID1212)	172	263	149	40	201	22	0	0	0	83.75	3.24	4.55
bin.176_sub.gw	o_Clostridiales (UID1212)	172	263	149	33	201	29	0	0	0	83.74	9.71	89.66
bin.259.gj	p_Actinobacteria (UID2112)	31	211	124	47	147	17	0	0	0	83.73	5.25	29.41
293_sub.gw06	o_Clostridiales (UID1212)	172	263	149	32	217	14	0	0	0	83.65	7.05	78.57
bin.94.hh14	p_Proteobacteria (UID3887)	1487	256	160	34	207	15	0	0	0	83.63	5.9	66.67
maxbin.094.gw	c_Clostridia (UID1118)	387	223	124	28	186	9	0	0	0	83.6	3.78	77.78
228_sub.gj	c_Epsilonproteobacteria (UID3065)	111	445	271	65	349	31	0	0	0	83.58	6.87	74.19
maxbin.314_sub.gw	k_Bacteria (UID2569)	434	278	186	41	229	8	0	0	0	83.55	2.8	0
182_sub.gw03	p_Firmicutes (UID1022)	100	295	158	43	223	28	1	0	0	83.5	10.08	83.87
bin.15.gw08	o_Clostridiales (UID1212)	172	257	149	33	211	12	1	0	0	83.5	4.69	6.67
203.hh15	o_Clostridiales (UID1212)	172	263	149	49	205	9	0	0	0	83.48	4.25	33.33
290_sub.gw07	o_Clostridiales (UID1212)	172	263	149	33	213	17	0	0	0	83.48	7.39	41.18
bin.80.gw07	o_Clostridiales (UID1212)	172	257	149	34	201	22	0	0	0	83.48	1.78	0
bin.4_sub.gw03	o_Clostridiales (UID1212)	172	263	149	38	208	17	0	0	0	83.45	5.07	17.65
bin.94.gw26	k_Bacteria (UID2495)	2993	147	91	17	129	1	0	0	0	83.45	1.1	0
137_sub.hc16	k_Bacteria (UID1453)	901	171	117	37	128	5	1	0	0	83.41	4.27	12.5
maxbin.074.gw02	o_Clostridiales (UID1212)	172	261	147	42	217	2	0	0	0	83.36	0.91	100
22.ca	o_Bacteroidales (UID2657)	160	492	269	71	407	13	1	0	0	83.31	3.89	81.25
151_sub.hh15	o_Clostridiales (UID1212)	172	263	149	39	212	12	0	0	0	83.3	4.73	91.67
18.gj	c_Epsilonproteobacteria (UID3066)	110	450	273	65	377	8	0	0	0	83.27	1.89	12.5
bin.360.hc	o_Bacteroidales (UID2617)	213	406	265	55	349	2	0	0	0	83.27	0.5	0
maxbin.015.gw07	c_Clostridia (UID1118)	387	223	124	28	187	8	0	0	0	83.27	5.38	87.5
bin.155.hh12	k_Bacteria (UID2495)	2993	147	91	18	126	3	0	0	0	83.22	2.3	100
bin.215.gj	o_Clostridiales (UID1212)	172	257	149	33	216	8	0	0	0	83.22	3.36	25
bin.414.gj	o_Clostridiales (UID1120)	304	250	143	35	208	7	0	0	0	83.22	3.73	71.43
bin.61.gw03	o_Clostridiales (UID1212)	172	257	149	31	223	3	0	0	0	83.22	1.06	66.67
85.hc17	c_Sporobactria (UID2496)	72	215	125	26	179	10	0	0	0	83.2	3.64	90
229.hh13	f_Enterobacteriaceae (UID5124)	134	1173	336	165	951	53	3	1	0	83.17	6.22	92.65
bin.140.gw07	k_Bacteria (UID2329)	174	149	89	15	130	4	0	0	0	83.15	4.49	25
56_sub.gw02	p_Actinobacteria (UID2112)	31	211	124	28	164	19	0	0	0	83.13	11.12	94.74
bin.213.gw07	o_Clostridiales (UID1212)	172	263	149	33	226	4	0	0	0	83.11	0.56	75
145_sub.gw02	p_Firmicutes (UID1022)	100	295	158	48	228	19	0	0	0	83.07	6.98	68.42
maxbin.493.gw	f_Enterobacteriaceae (UID5124)	134	1173	336	135	978	58	2	0	0	83.07	3.9	62.5
bin.191.gw01	p_Actinobacteria (UID2112)	31	211	124	32	172	7	0	0	0	83.06	3.79	71.43
bin.45.gw04	f_Lachnospiraceae (UID1286)	57	420	207	77	332	10	1	0	0	83.06	2.98	53.85
178.gw02	o_Clostridiales (UID1212)	172	263	149	36	222	5	0	0	0	83.03	2.1	60
bin.133.hc18	o_Clostridiales (UID1212)	172	263	149	33	227	3	0	0	0	82.98	1.34	33.33
bin.114_sub.hh15	p_Bacteroidetes (UID2605)	350	316	210	56	241	19	0	0	0	82.97	6.9	57.89
bin.291_sub.gw09	p_Actinobacteria												

bin.40.go	p_Euryarchaeota (UID3)	148	188	125	66	113	9	0	0	0	82.67	6.4	44.44
maxbin.075.hh11	k_Bacteria (UID1453)	901	171	117	24	142	5	0	0	0	82.62	4.27	0
bin.161_sub.hh11	o_Clostridiales (UID1212)	172	263	149	39	215	9	0	0	0	82.55	4.36	77.78
bin.233.gw02	o_Clostridiales (UID1212)	172	263	149	38	221	4	0	0	0	82.55	1.96	25
maxbin.016_sub.gw	o_Clostridiales (UID1212)	172	263	149	44	205	14	0	0	0	82.54	2.26	42.86
bin.213.gw09	o_Clostridiales (UID1212)	172	263	149	44	210	9	0	0	0	82.53	4.25	11.11
bin.179.hh12	o_Clostridiales (UID1212)	172	263	149	33	229	1	0	0	0	82.47	0.13	0
23.gw08	o_Bacteroidales (UID2617)	213	406	265	72	329	5	0	0	0	82.45	1.13	40
bin.455.gw	o_Clostridiales (UID1120)	304	250	143	42	208	11	0	0	0	82.43	0	0
bin.140.hc19	o_Clostridiales (UID1212)	172	263	149	49	205	9	0	0	0	82.38	4.92	88.89
108_sub.gw07	p_Actinobacteria (UID2112)	31	211	124	31	167	13	0	0	0	82.35	5.05	76.92
bin.121.hh11	o_Clostridiales (UID1212)	172	263	149	47	203	13	0	0	0	82.34	3.14	15.38
bin.242_sub.gw03	p_Actinobacteria (UID2112)	31	211	124	33	167	11	0	0	0	82.34	4.95	90.91
63.gw02	p_Actinobacteria (UID1454)	732	206	120	26	177	3	0	0	0	82.33	0.99	66.67
81.gw06	o_Lactobacillales (UID543)	294	472	265	71	386	15	0	0	0	82.3	3.25	80
bin.520_sub.gw	p_Actinobacteria (UID2112)	172	263	149	54	202	7	0	0	0	82.3	0.84	85.71
bin.153.hh11	o_Clostridiales (UID1212)	172	263	149	42	204	17	0	0	0	82.27	8.17	88.24
bin.163.hc19	o_Bacteroidales (UID2617)	213	406	265	60	345	1	0	0	0	82.26	0.38	0
bin.260_sub.gw09	c_Clostridia (UID1118)	387	223	124	29	193	1	0	0	0	82.26	0.81	0
bin.132.gw05	o_Clostridiales (UID1212)	172	263	149	40	210	13	0	0	0	82.24	7.11	76.92
54_sub.hh13	o_Bacteroidales (UID2657)	160	492	269	99	364	26	3	0	0	82.17	5.34	80
bin.564.gw	o_Clostridiales (UID1212)	172	263	149	42	218	3	0	0	0	82.15	2.01	33.33
bin.63.gw27	k_Bacteria (UID2329)	211	124	124	30	170	11	0	0	0	82.12	4.79	9.09
bin.162.gw08	k_Bacteria (UID2329)	174	149	89	20	124	5	0	0	0	82.1	1.51	20
bin.262.gw	p_Euryarchaeota (UID54)	90	234	153	54	171	9	0	0	0	82.1	4.58	88.89
51.hc18	k_Bacteria (UID2982)	88	229	147	37	183	9	0	0	0	82.08	4.39	22.22
bin.226.gw04	o_Clostridiales (UID1120)	172	263	149	51	208	4	0	0	0	82.06	1.57	0
112_sub.gw27	o_Clostridiales (UID1120)	304	250	143	31	195	21	3	0	0	82.04	9.33	66.67
bin.275.hc17	k_Bacteria (UID2329)	149	149	89	21	127	1	0	0	0	82.02	1.12	0
164.ca25	o_Selenomonadales (UID1024)	64	334	167	54	237	41	2	0	0	82.01	13.53	82.98
196_sub.gw	o_Clostridiales (UID1212)	172	263	149	51	207	5	0	0	0	81.97	2.68	20
181.gw03	o_Lactobacillales (UID543)	294	472	265	70	376	26	0	0	0	81.96	5.69	73.08
maxbin.042.gw07	p_Actinobacteria (UID2112)	31	211	124	34	165	12	0	0	0	81.94	7.6	100
bin.148.gw02	o_Clostridiales (UID1212)	172	263	149	36	227	0	0	0	0	81.88	0	0
maxbin.170.hh11	k_Bacteria (UID2495)	2993	147	91	18	128	1	0	0	0	81.87	1.1	100
90.hh12	k_Bacteria (UID2565)	2921	152	83	25	124	1	0	0	0	81.84	6.1	0
maxbin.056_sub.gw02	o_Clostridiales (UID1212)	172	263	149	65	191	7	0	0	0	81.81	3.36	28.57
bin.192.hh15	o_Clostridiales (UID1212)	172	263	149	38	220	5	0	0	0	81.76	0.77	40
maxbin.197.hh15	k_Bacteria (UID2495)	2993	143	89	19	118	6	0	0	0	81.73	5.24	33.33
bin.95.gw01	k_Bacteria (UID2329)	174	149	89	40	106	3	0	0	0	81.69	2.62	100
300_sub.hh	c_Clostridia (UID1118)	387	223	124	50	166	7	0	0	0	81.68	3.9	42.86
bin.171.gw06	p_Actinobacteria (UID2112)	31	211	124	40	166	2	0	0	0	81.67	1.08	50
54.gw05	o_Clostridiales (UID1212)	172	263	149	32	229	2	0	0	0	81.66	0.28	0
86.gw01	k_Bacteria (UID2569)	434	278	186	57	217	4	0	0	0	81.64	0.93	25
bin.192.gw05	o_Clostridiales (UID1212)	172	263	149	42	216	5	0	0	0	81.57	1.29	0
18_sub.hc20	k_Bacteria (UID1453)	901	171	117	30	135	6	0	0	0	81.53	4.37	50
bin.84.hh	c_Clostridia (UID1118)	387	223	124	57	154	12	0	0	0	81.53	6.45	58.33
maxbin.006.go30	p_Euryarchaeota (UID3)	148	188	125	44	136	8	0	0	0	81.52	6.4	37.5
bin.62.ca	o_Bacteroidales (UID2617)	213	406	265	61	338	7	0	0	0	81.51	1.18	14.29
maxbin.206.hh	k_Bacteria (UID2495)	2993	143	89	17	118	8	0	0	0	81.46	7.37	87.5
maxbin.089.go	k_Bacteria (UID2495)	2993	147	91	25	114	8	0	0	0	81.44	1.8	87.5
maxbin.142_sub.gw	o_Clostridiales (UID1212)	172	263	149	38	224	1	0	0	0	81.43	0.67	0
bin.145_sub.gw	p_Euryarchaeota (UID3)	148	188	125	27	144	17	0	0	0	81.41	7.28	52.94
3.gw10	o_Clostridiales (UID1226)	155	278	158	41	232	5	0	0	0	81.38	1.85	40
bin.294.hc	k_Bacteria (UID2982)	88	230	148	35	187	8	0	0	0	81.36	3.79	50
bin.41_sub.gw28	f_Spirochaetaceae (UID2535)	249	249	143	65	174	10	0	0	0	81.34	4.9	20
115_sub.gw06	p_Bacteroidetes (UID2605)	350	316	210	75	225	15	1	0	0	81.33	3.17	61.11
bin.171.hc20	k_Bacteria (UID2372)	131	177	106	38	135	4	0	0	0	81.29	2.2	100
bin.242.gw09	p_Actinobacteria (UID2112)	31	211	124	55	142	14	0	0	0	81.26	6.96	85.71
bin.283.gw	f_Spirochaetaceae (UID2535)	33	249	143	41	204	4	0	0	0	81.24	2.45	25
154.hh15	o_Clostridiales (UID1212)	172	263	149	58	197	8	0	0	0	81.23	3.37	50
155.gw03	o_Clostridiales (UID1212)	172	263	149	35	228	0	0	0	0	81.21	0	0
bin.177.gw06	o_Clostridiales (UID1212)	172	263	149	33	227	3	0	0	0	81.21	0.56	100
bin.59.go30	o_Clostridiales (UID1212)	172	263	149	33	221	9	0	0	0	81.21	3.98	77.78
bin.249.gw	f_Lachnospiraceae (UID1256)	33	333	171	52	280	1	0	0	0	81.2	0.58	0
bin.302.gw09	p_Actinobacteria (UID2112)	31	211	124	39	166	6	0	0	0	81.18	4.44	66.67
bin.80.gw	p_Euryarchaeota (UID3)	148	187	124	42	144	1	0	0	0	81.15	0.4	100
bin.167_sub.gw09	o_Clostridiales (UID1212)	172	263	149	45	201	16	1	0	0	81.09	6.34	42.11
maxbin.024.gw04	p_Actinobacteria (UID1022)	295	158	40	234	13	0	0	0	0	81.09	5.24	100
maxbin.120.hc	k_Bacteria (UID2982)	88	229	147	50	168	11	0	0	0	81.09	5.82	100
bin.480.gw	k_Bacteria (UID2982)	88	230	148	38	190	2	0	0	0	81.08	0.37	50
bin.332.gw	c_Clostridia (UID1118)	387	223	124	31	191	1	0	0	0	81.05	0.81	0
bin.284.gw10	k_Bacteria (UID203)	5449	104	58	11	73	20	0	0	0	81.03	5.64	30
bin.60_sub.hh12	k_Bacteria (UID2372)	131	176	105	44	130	2	0	0	0	81.02	1.9	50
bin.87.gw03	o_Clostridiales (UID1212)	172	263	149	39	221	3	0	0	0	81.02	1.51	66.67
maxbin.173_sub.gw	o_Bacteroidales (UID2657)	160	492	269	103	384	5	0	0	0	81.01	1.49	0
bin.416_sub.gw	o_Bacteroidales (UID2716)	92	487	270	85	398	4	0	0	0	81	0.46	75
bin.353.hc	c_Clostridia (UID1118)	387	223	124	40	173	9	1	0	0	80.94	5.11	16.67
bin.469.hc	f_Lachnospiraceae (UID1286)	57	420	207	83	299	37	1	0	0	80.92	7.08	35
maxbin.009.go	o_Clostridiales (UID1212)	172	263	149	37	211	15	0	0	0	80.91	6.53	66.67
bin.176.hc17	o_Clostridiales (UID1212)	172	263	149	49	204	10	0	0	0	80.88	2.99	60
maxbin.076.gw06	p_Actinobacteria (UID2112)	211	211	124	31	163	17	0	0	0	80.85	7.73	76.47
198.ca23	p_Bacteroidetes (UID2605)	350	314	208	64	226	24	0	0	0	80.76	7.55	79.17
bin.57.gw26	k_Bacteria (UID2569)	434	278	186	56	214	8	0	0	0	80.75	2.96	12.5
bin.77.gw03	o_Clostridiales (UID1120)	304	247	141	38	208	1	0	0	0	80.73	0.07	100
65_sub.gw	c_Clostridia (UID1118)	387	223	124	35	181	7	0	0	0	80.71	3.7	85.71
103.hc18	k_Bacteria (UID2329)	174	149	89	21	126	2	0	0	0	80.7	0.61	50
bin.347.gw	o_Bacteroidales (UID2617)	213	406	265	83	319	4	0	0	0	80.69	1.13	75
240_sub.gw01	o_Clostridiales (UID1226)	155	278	158	50	219	9	0	0	0	80.65	4.17	44.44
292_sub.gw	o_Clostridiales (UID1212)	172	263	149	36	224	2	1	0	0	80.65	2.01	0
45.gw	o_Campylobacteriales (UID3068)	106	477	284	81	335	60	1	0	0	80.61	13.53	69.84
bin.106.hc20	k_Bacteria (UID2982)	88	230	148	37	184	9	0	0	0	80.61	1.83	0
bin.137.hh	o_Clostridiales (UID1212)	172	263	149	58	202	3	0	0	0	80.61	1.34	33.33
bin.179.ca	k_Bacteria (UID2982)	88	230	148	37	190	3	0	0	0	80.59	1.38	33.33
bin.218.gw	p_Firmicutes (UID240)	1316	179	104	52	125	2	0	0	0	80.59	1.28	0
bin.360.gw	o_Clostridiales (UID1212)	172	263	149	64	195	4	0	0	0	80.54	2.35	25
maxbin.082.hh	k_Bacteria (UID2982)	88	230	148	36	185	8	1	0	0	80.54	5.24	45.45
maxbin.334.gw	o_Clostridiales (UID1212)	172	263	149	42	219	2	0	0	0	80.54	1.01	0
207.gw06	p_Actinobacteria (UID2112)	31	211	124	35	162	14	0	0	0	80.4	7.75	85.71
bin.67_sub.hc16	o_Clostridiales (UID1212)	172	263	149	42	203	18	0	0	0	80.4	8.41	83.33
62_sub.gw07	o_Clostridiales (UID1120)	304	247										

254_sub.hh	c__Clostridia (UID1118)	387	223	124	32	161	28	1	1	0	80.11	18.18	89.19
maxbin.022.go	p__Euryarchaeota (UID3)	148	188	125	41	135	12	0	0	0	80.1	2.29	58.33
bin.144.gn08	o__Bacteroidetes (UID2857)	160	492	269	94	377	20	1	0	0	80.09	4.85	17.39
maxbin.148.gw	o__Clostridiales (UID1212)	172	263	149	38	212	13	0	0	0	80.09	5.79	76.92
7_sub.gw	o__Campylobacteriales (UID3068)	106	477	284	81	339	52	5	0	0	80.06	12.67	73.13
bin.109.gw05	k__Bacteria (UID2329)	174	149	89	23	121	5	0	0	0	80.06	4.49	20
bin.151.hh13	o__Clostridiales (UID1212)	172	263	149	36	217	10	0	0	0	80.03	2.89	80
12.hh14	o__Clostridiales (UID1212)	172	263	149	47	196	19	1	0	0	80.02	10.51	63.64
bin.103.gw29	p__Actinobacteria (UID1454)	732	206	120	28	176	2	0	0	0	80	0.92	0
bin.22.gn06	k__Bacteria (UID2328)	3167	126	75	29	96	1	0	0	0	80	1.33	100
bin.147_sub.gn08	o__Clostridiales (UID1212)	172	263	149	56	203	4	0	0	0	79.97	2.35	50
111_sub.gw04	p__Actinobacteria (UID2112)	31	211	124	40	171	0	0	0	0	79.88	0	0
bin.72.gn06	o__Clostridiales (UID1212)	172	263	149	60	200	3	0	0	0	79.88	0.71	0
maxbin.637_sub.hc	k__Bacteria (UID2495)	2993	147	91	46	96	5	0	0	0	79.88	3.43	20
172_sub.gw05	o__Clostridiales (UID1212)	172	263	149	38	210	15	0	0	0	79.87	5.79	80
bin.97_sub.gn06	o__Clostridiales (UID1212)	261	261	147	73	187	1	0	0	0	79.85	0.68	100
maxbin.053.ca24	k__Bacteria (UID2495)	2993	147	91	25	119	3	0	0	0	79.8	0.75	66.67
bin.81.go30	p__Actinobacteria (UID1454)	732	206	120	30	172	4	0	0	0	79.79	2.17	75
89_sub.hc18	o__Clostridiales (UID1226)	155	278	158	56	183	35	4	0	0	79.76	16.4	91.49
94_sub.hh13	c__Epsilonproteobacteria (UID3066)	110	450	273	82	341	27	0	0	0	79.75	6.3	85.19
bin.245_sub.gw02	p__Actinobacteria (UID2112)	31	211	124	46	151	14	0	0	0	79.67	5.52	21.43
83.gw01	p__Actinobacteria (UID2112)	31	211	124	50	158	3	0	0	0	79.66	1.48	0
bin.180_sub.gw01	o__Clostridiales (UID1212)	172	263	149	49	204	10	0	0	0	79.63	1.48	20
bin.51.gn07	o__Bacteroidales (UID2657)	160	492	269	108	383	1	0	0	0	79.59	0.37	100
bin.86.gw02	k__Bacteria (UID2982)	88	230	148	38	191	1	0	0	0	79.59	0.03	0
bin.285.gn09	o__Clostridiales (UID1212)	172	263	149	67	191	5	0	0	0	79.58	2.35	20
bin.149.hh14	k__Bacteria (UID2495)	2993	147	91	30	113	4	0	0	0	79.56	3.3	50
bin.62.hc16	p__Bacteroidetes (UID2605)	350	316	210	54	251	10	1	0	0	79.55	3.81	23.08
bin.209_sub.gw	p__Bacteroidetes (UID2605)	316	316	210	80	232	3	1	0	0	79.54	1.19	100
maxbin.137_sub.hc18	k__Bacteria (UID2982)	88	230	148	42	180	7	1	0	0	79.54	5.1	20
bin.257.gn10	o__Clostridiales (UID1212)	172	263	149	40	222	1	0	0	0	79.53	0.17	0
maxbin.060_sub.hh14	o__Clostridiales (UID1212)	172	263	149	44	202	17	0	0	0	79.52	8.28	94.12
bin.446.hc	k__Bacteria (UID1453)	901	171	117	51	119	1	0	0	0	79.51	0.85	0
130.gw04	o__Bacteroidales (UID2617)	213	406	265	103	297	6	0	0	0	79.48	1.76	16.67
60.hc20	k__Bacteria (UID2982)	88	229	147	38	185	6	0	0	0	79.36	3.44	33.33
99.hc16	k__Bacteria (UID2982)	88	230	148	41	175	14	0	0	0	79.33	3.76	21.43
155.hh15	o__Clostridiales (UID1212)	172	263	149	60	199	4	0	0	0	79.3	1.4	75
bin.96.gn09	k__Bacteria (UID2982)	88	230	148	37	179	14	0	0	0	79.28	5.37	50
bin.75.ca	p__Euryarchaeota (UID54)	90	234	153	66	159	9	0	0	0	79.27	4.96	66.67
bin.219.gn	o__Clostridiales (UID1212)	172	263	149	48	191	24	0	0	0	79.23	9.68	87.5
bin.148.gn09	o__Clostridiales (UID1212)	172	263	149	43	219	1	0	0	0	79.19	0.22	100
maxbin.252_sub.gw02	f__Spirochaetaceae (UID2535)	33	248	133	68	176	5	0	0	0	79.18	1.86	0
75_sub.gw03	k__Bacteria (UID2372)	172	107	106	31	141	5	0	0	0	79.11	2.73	20
bin.406.hc	c__Clostridia (UID1118)	387	223	124	40	176	7	0	0	0	79.1	3.3	71.43
18_sub.gw27	o__Clostridiales (UID1120)	304	247	141	38	180	28	1	0	0	79.08	13.27	74.19
283.gw01	c__Deltaproteobacteria (UID3218)	61	284	169	60	216	8	0	0	0	79.06	1.58	12.5
bin.367.gw	o__Bacteroidales (UID2617)	213	406	265	66	332	8	0	0	0	79.06	2.39	75
147.hh14	o__Clostridiales (UID1212)	172	263	149	45	201	15	2	0	0	79.05	4.81	42.86
bin.29.gn07	k__Bacteria (UID2372)	172	176	105	32	139	5	0	0	0	79.05	4.13	60
bin.85_sub.gw02	k__Bacteria (UID2329)	174	149	89	25	120	4	0	0	0	79.05	3.48	0
bin.112.gn09	f__Lachnospiraceae (UID1255)	90	354	174	78	269	7	0	0	0	79.04	2.13	42.86
bin.253_sub.gn07	f__Lachnospiraceae (UID1286)	57	420	207	104	294	22	0	0	0	79.02	3.63	36.36
bin.392.gw	k__Bacteria (UID2495)	2993	142	88	53	87	2	0	0	0	79.01	1.7	50
maxbin.090.gw	c__Clostridia (UID1118)	387	223	124	49	168	6	0	0	0	78.97	3.43	16.67
60_sub.hh12	o__Clostridiales (UID1212)	172	263	148	48	185	30	0	0	0	78.91	12.82	66.67
bin.125.hh	p__Bacteroidetes (UID2605)	316	210	56	255	5	0	0	0	0	78.88	1.68	60
bin.57.gn07	o__Clostridiales (UID1212)	172	263	149	41	218	4	0	0	0	78.86	1.17	0
maxbin.058.go26	p__Actinobacteria (UID1454)	732	206	120	32	167	7	0	0	0	78.83	3.14	28.57
87_sub.hh14	f__Spirochaetaceae (UID2535)	33	249	143	41	195	12	1	0	0	78.76	5.19	46.67
bin.67.hc	k__Bacteria (UID2372)	131	176	105	29	142	5	0	0	0	78.73	3.17	80
107_sub.hc	f__Pasteurellaceae (UID4932)	83	767	440	140	439	169	18	1	0	78.68	28.14	83.84
maxbin.007.hc	f__Bifidobacteriaceae (UID1458)	77	464	220	83	356	25	0	0	0	78.65	3.5	40
15.gw02	c__Clostridia (UID1118)	387	223	124	42	175	6	0	0	0	78.63	3.9	100
maxbin.038_sub.gw08	k__Bacteria (UID2495)	2993	143	89	24	115	4	0	0	0	78.63	1.39	100
maxbin.141_sub.gw04	p__Actinobacteria (UID2112)	31	211	124	54	150	7	0	0	0	78.63	3.61	0
137_sub.gw	o__Clostridiales (UID1120)	304	247	141	35	191	20	1	0	0	78.61	10.22	78.26
bin.184_sub.gn	p__Bacteroidetes (UID2605)	350	316	210	86	226	4	0	0	0	78.57	1.23	75
bin.123_sub.gn09	p__Euryarchaeota (UID3)	148	188	125	41	133	14	0	0	0	78.52	9.11	92.86
bin.290.gn	o__Clostridiales (UID1212)	172	263	149	59	203	1	0	0	0	78.52	0.67	0
bin.195_sub.hc18	o__Clostridiales (UID1226)	155	278	158	64	201	12	1	0	0	78.5	7.28	60
36_sub.hh15	c__Clostridia (UID1118)	387	223	124	35	182	6	0	0	0	78.47	2.77	33.33
bin.466_sub.hh	o__Clostridiales (UID1212)	172	263	149	58	194	11	0	0	0	78.42	4.61	72.73
bin.594_sub.gw	o__Clostridiales (UID1212)	172	263	149	45	218	0	0	0	0	78.41	0	0
maxbin.238_sub.gw01	o__Selenomonadales (UID1024)	64	334	167	92	231	11	0	0	0	78.41	4.61	18.18
bin.2.ca21	o__Clostridiales (UID1212)	172	263	149	47	195	21	0	0	0	78.37	9.37	80.95
bin.277.gw03	o__Clostridiales (UID1212)	172	263	149	42	216	5	0	0	0	78.36	1.2	80
bin.294.gn	k__Bacteria (UID2372)	131	177	106	33	136	8	0	0	0	78.36	5	37.5
bin.39.gw	p__Actinobacteria (UID2112)	31	211	124	34	155	21	1	0	0	78.36	8.2	66.67
maxbin.098_sub.gn	o__Clostridiales (UID1212)	172	263	149	66	184	13	0	0	0	78.36	7.49	76.92
293_sub.gn07	p__Bacteroidetes (UID2605)	350	316	210	80	230	6	0	0	0	78.31	2.06	33.33
34.gn06	o__Clostridiales (UID1212)	172	263	149	62	194	7	0	0	0	78.31	2.59	28.57
220_sub.gw28	o__Clostridiales (UID1120)	304	247	141	39	181	25	2	0	0	78.3	11.88	64.52
bin.65_sub.hc16	o__Bacteroidales (UID2716)	92	487	270	113	338	37	1	0	0	78.3	7.81	70
34.ca25	p__Euryarchaeota (UID54)	90	234	153	39	186	8	1	0	0	78.27	3.36	45.45
maxbin.171_sub.gn	c__Clostridia (UID1118)	387	223	124	41	178	3	1	0	0	78.23	2.9	50
110_sub.gw29	o__Clostridiales (UID1120)	304	247	141	41	180	26	0	0	0	78.22	12.9	65.38
193.go26	o__Bacteroidales (UID2617)	213	406	265	100	297	8	1	0	0	78.21	3.04	9.09
363.gn	p__Actinobacteria (UID1454)	732	206	120	34	166	6	0	0	0	78.19	4.17	83.33
bin.369.gn	k__Bacteria (UID2565)	2921	142	67	33	98	10	1	0	0	78.19	8.99	53.85
bin.271_sub.gn07	p__Euryarchaeota (UID3)	148	188	125	37	138	13	0	0	0	78.17	8.27	92.31
bin.219_sub.hc	k__Bacteria (UID1453)	901	171	117	40	122	9	0	0	0	78.14	6.32	33.33
bin.404.gn	o__Clostridiales (UID1212)	172	263	149	59	203	1	0	0	0	78.12	0.67	0
bin.59.go28	p__Actinobacteria (UID1454)	732	206	120	35	154	15	2	0	0	78.08	3.34	4.76
bin.90.gn09	k__Bacteria (UID2982)	88	230	148	39	175	16	0	0	0	78.01	6.1	31.25
218_sub.gw26	c__Clostridia (UID1118)	387	223	124	40	170	12	1	0	0	77.99	4.47	60
273.hh	c__Clostridia (UID1118)	387	223	124	44	174	5	0	0	0	77.97	3.43	60
bin.115.gw01	f__Lachnospiraceae (UID1286)	57	420	207	115	300	5	0	0	0	77.97	0.75	0
bin.13.hc17	o__Clostridiales (UID1212)	172	263	149	67	195	1	0	0	0	77.96	0.67	0
137.hc	o__Clostridiales (UID1212)	172	261	147	48	208	5	0	0	0	77.93	2.72	60
maxbin.071.gn	k__Bacteria (UID203)	5449	103	57	14	74	15	0					

49_sub.hc16	p_Euryarchaeota (UID3)	148	188	125	36	132	20	0	0	0	77.69	9.4	50
bin.43.gn08	o_Clostridiales (UID1212)	172	263	149	47	213	3	0	0	0	77.68	0.9	33.33
bin.19_sub.hc18	o_Clostridiales (UID1212)	172	263	149	59	187	12	5	0	0	77.59	1.78	7.41
bin.179_sub.hh13	o_Clostridiales (UID1212)	172	263	149	51	198	13	1	0	0	77.57	6.66	43.75
bin.40.gw03	o_Clostridiales (UID1226)	155	278	158	57	209	12	0	0	0	77.57	2.32	16.67
86.ca23	k_Bacteria (UID2569)	434	278	186	54	221	3	0	0	0	77.51	0.99	33.33
bin.101.hc	o_Rhodospirillales (UID3754)	63	336	201	72	258	6	0	0	0	77.47	1.79	50
maxbin.132_sub.gn06	k_Bacteria (UID2329)	174	149	89	36	97	15	1	0	0	77.46	11.13	61.11
bin.131.gw01	o_Clostridiales (UID1226)	155	278	158	56	218	4	0	0	0	77.38	1.79	0
22.hc20	k_Bacteria (UID2495)	2993	147	91	28	117	2	0	0	0	77.37	1.2	0
bin.2_sub.ca25	o_Bacteroidales (UID2657)	160	492	269	118	352	22	0	0	0	77.26	1.95	13.64
bin.79.hc18	o_Rhodospirillales (UID3754)	63	336	201	53	278	5	0	0	0	77.24	1.45	60
87_sub.gw05	c_Clostridia (UID1118)	387	223	124	40	176	7	0	0	0	77.19	3.63	0
173_sub.gn	p_Actinobacteria (UID2112)	31	211	124	39	153	18	1	0	0	77.08	10.85	90.48
maxbin.054.gw04	p_Firmicutes (UID1022)	100	295	158	63	223	9	0	0	0	77.08	4.22	55.56
bin.10.hc16	k_Bacteria (UID2328)	3167	126	75	31	95	0	0	0	0	77.03	0	0
bin.56.gn06	k_Bacteria (UID2982)	88	230	148	38	188	4	0	0	0	77.03	1.82	50
161.gn06	o_Clostridiales (UID1212)	172	263	149	58	202	3	0	0	0	77.02	2.01	0
155_sub.gn06	o_Clostridiales (UID1212)	172	263	149	53	197	13	0	0	0	77.01	3.04	0
91_sub.gn08	k_Bacteria (UID2982)	88	230	148	42	171	16	1	0	0	77	8.2	52.63
bin.545.gw	c_Clostridia (UID1118)	387	223	124	41	180	2	0	0	0	76.98	1.21	50
maxbin.116_sub.gw	o_Clostridiales (UID1212)	172	261	147	67	191	3	0	0	0	76.98	0.68	0
bin.215.hc17	o_Clostridiales (UID1212)	172	263	149	59	200	9	1	0	0	76.9	2.01	50
maxbin.052.hh12	p_Bacteroidetes (UID2605)	350	316	210	69	185	60	2	0	0	76.9	21.54	78.79
bin.239.gw	c_Deltaproteobacteria (UID3216)	83	247	155	41	202	4	0	0	0	76.88	2.26	0
bin.477.gn	p_Firmicutes (UID1022)	100	295	158	66	227	2	0	0	0	76.85	1.27	50
bin.484.gn	o_Clostridiales (UID1212)	172	263	149	47	210	6	0	0	0	76.85	1.34	16.67
38.gw02	o_Clostridiales (UID1212)	172	263	149	55	206	1	1	0	0	76.84	1.01	0
maxbin.007.hc19	c_Gammaproteobacteria (UID4201)	1164	271	170	80	151	9	0	0	0	76.84	4.45	41.67
bin.149.hh15	o_Bacteroidales (UID2617)	213	406	265	93	305	8	0	0	0	76.79	1.98	62.5
bin.160.hc19	o_Clostridiales (UID1212)	172	263	149	58	203	2	0	0	0	76.78	1.01	0
maxbin.106_sub.gw04	o_Clostridiales (UID1212)	172	263	149	53	208	2	0	0	0	76.73	1.01	50
260.gw05	f_Enterobacteriaceae (UID5124)	134	1173	336	211	925	36	1	0	0	76.72	2.87	51.28
bin.186_sub.hh	o_Clostridiales (UID1212)	172	263	149	64	183	15	1	0	0	76.7	4.19	0
bin.105.hc20	f_Lachnospiraceae (UID1255)	90	354	174	78	259	17	0	0	0	76.61	4.01	76.47
maxbin.356_sub.gn	o_Bacteroidales (UID2617)	213	406	265	90	310	16	0	0	0	76.6	3.92	60
bin.261_sub.gw04	k_Bacteria (UID2372)	131	177	106	40	127	10	0	0	0	76.57	6.37	30
maxbin.184.go	o_Clostridiales (UID1212)	172	263	149	57	194	12	0	0	0	76.55	5.73	66.67
234.go	c_Deltaproteobacteria (UID3216)	83	247	155	46	197	4	0	0	0	76.53	0.88	25
bin.105.gn08	o_Clostridiales (UID1212)	172	263	149	53	204	6	0	0	0	76.51	2.39	50
104.hc18	c_Clostridia (UID1118)	387	223	124	52	166	5	0	0	0	76.5	2.85	40
119.hc19	f_Verruillaceae (UID1032)	33	423	214	91	321	11	0	0	0	76.48	1.92	27.27
7.hc19	f_Pasteurellaceae (UID4932)	83	767	440	170	530	65	2	0	0	76.43	9.8	63.66
80.gw01	o_Clostridiales (UID1212)	172	261	147	60	201	0	0	0	0	76.43	0	0
bin.135.gn06	k_Bacteria (UID2982)	88	230	148	45	173	12	0	0	0	76.41	5.11	58.33
133_sub.gw02	p_Actinobacteria (UID2112)	31	211	124	41	157	13	0	0	0	76.4	4.38	84.62
maxbin.033.gw	p_Firmicutes (UID1022)	100	295	158	80	201	14	0	0	0	76.39	5.21	42.86
bin.159_sub.hh	k_Bacteria (UID1453)	901	171	117	43	110	17	1	0	0	76.38	7.48	45
bin.128_sub.gn	p_Bacteroidetes (UID2605)	316	316	210	74	234	8	0	0	0	76.37	2.04	75
bin.184.hc	o_Clostridiales (UID1212)	172	263	149	73	182	8	0	0	0	76.37	3.08	87.5
maxbin.039.gw04	p_Actinobacteria (UID2112)	31	211	124	41	160	10	0	0	0	76.32	6.12	90
335.hh	o_Bacteroidales (UID2617)	213	406	265	81	270	48	7	0	0	76.26	17.79	73.91
354_sub.gw	p_Actinobacteria (UID2112)	31	211	124	43	146	22	0	0	0	76.22	11.12	63.64
bin.134_sub.hh14	o_Clostridiales (UID1212)	172	263	149	46	209	7	1	0	0	76.22	2.96	50
45_sub.gw03	o_Clostridiales (UID1212)	172	263	148	62	195	5	1	0	0	76.17	2.03	0
bin.128.gw01	k_Bacteria (UID1452)	904	163	110	124	8	0	0	0	0	76.16	5.4	50
29_sub.gn06	p_Firmicutes (UID1022)	100	295	158	74	210	9	2	0	0	76.15	6.1	53.33
93_sub.gw03	k_Bacteria (UID2329)	174	149	89	29	115	5	0	0	0	76.14	4.09	20
bin.13.gw05	k_Bacteria (UID2982)	88	230	148	42	180	8	0	0	0	76.13	4.56	62.5
147_sub.hc18	k_Bacteria (UID2495)	2993	143	89	56	85	2	0	0	0	76.1	2.25	100
77_sub.hh13	k_Bacteria (UID2565)	2921	152	93	28	124	0	0	0	0	76.09	0	0
bin.80.ca24	p_Euryarchaeota (UID54)	234	90	153	42	188	4	0	0	0	76.08	1.85	0
222_sub.gn07	o_Clostridiales (UID1212)	172	263	149	67	194	2	0	0	0	75.93	0.78	0
bin.5.hh	o_Clostridiales (UID1212)	172	263	149	73	187	3	0	0	0	75.87	1.68	33.33
109.gn07	k_Bacteria (UID2565)	2921	142	87	23	119	0	0	0	0	75.86	0	0
223_sub.hh13	o_Clostridiales (UID1212)	172	263	149	67	185	10	1	0	0	75.83	2.74	23.08
bin.16.ca21	k_Bacteria (UID2569)	434	278	186	58	200	20	0	0	0	75.82	5.03	70
maxbin.222_sub.hc	o_Clostridiales (UID1212)	172	263	149	55	189	18	1	0	0	75.73	5.9	42.86
bin.250.gn07	k_Bacteria (UID2982)	88	230	148	48	167	15	0	0	0	75.68	4.15	40
bin.37.gw03	o_Clostridiales (UID1212)	172	263	149	63	198	2	0	0	0	75.65	1.34	0
78.gn06	o_Clostridiales (UID1226)	155	278	158	57	217	4	0	0	0	75.62	1.96	50
maxbin.245.gn	p_Euryarchaeota (UID3)	148	187	124	57	126	4	0	0	0	75.62	1.29	25
maxbin.028_sub.gw04	p_Actinobacteria (UID2112)	31	211	124	60	139	12	0	0	0	75.6	7.26	100
maxbin.130.gw04	k_Bacteria (UID2982)	88	230	148	47	170	13	0	0	0	75.52	5.5	38.46
bin.388.gn	p_Actinobacteria (UID2112)	31	211	124	62	144	5	0	0	0	75.51	2.1	20
bin.130.hh14	o_Rhodospirillales (UID3754)	63	336	201	58	265	13	0	0	0	75.5	3.17	84.62
bin.258.hh15	o_Clostridiales (UID1212)	172	263	149	55	202	6	0	0	0	75.5	2.47	16.67
bin.129.hh12	p_Actinobacteria (UID2112)	31	211	124	58	140	13	0	0	0	75.48	1.98	38.46
maxbin.152.hc17	c_Clostridia (UID1118)	387	223	124	66	150	7	0	0	0	75.44	3.05	28.57
bin.152.gn06	p_Actinobacteria (UID2112)	31	211	124	58	140	12	1	0	0	75.41	3.48	6.67
112.gn10	k_Bacteria (UID2982)	88	230	148	45	175	10	0	0	0	75.38	3.91	40
bin.523.gn	c_Clostridia (UID1118)	387	223	124	47	176	0	0	0	0	75.27	0	0
8_sub.gw03	p_Bacteroidetes (UID2605)	350	316	210	89	191	34	2	0	0	75.23	10.76	85
143_sub.gw04	o_Clostridiales (UID1212)	172	263	149	65	193	5	0	0	0	75.2	3.02	0
75.gn09	o_Clostridiales (UID1120)	304	247	141	43	192	11	1	0	0	75.17	4.04	50
bin.57.gn08	o_Clostridiales (UID1212)	172	263	149	74	186	3	0	0	0	75.17	1.23	0
103_sub.gw27	k_Bacteria (UID2372)	131	177	106	36	129	12	0	0	0	75.14	2.22	0
bin.260_sub.gw02	k_Bacteria (UID2569)	434	278	186	57	220	1	0	0	0	75.09	0.27	100
97.hh13	k_Bacteria (UID1453)	901	171	117	46	124	1	0	0	0	75.03	0.09	100
bin.100.hc16	o_Rhodospirillales (UID3754)	63	336	201	61	268	7	0	0	0	75.03	1.57	42.86
190_sub.gn09	k_Bacteria (UID2329)	174	149	89	32	113	4	0	0	0	74.98	3.37	0
207_sub.gw	k_Bacteria (UID2982)	88	230	148	49	165	16	0	0	0	74.98	5.56	43.75
2.hc16	o_Bacteroidales (UID2617)	213	406	265	92	303	9	2	0	0	74.93	1.76	26.67
bin.92.gw03	o_Clostridiales (UID1212)	172	263	149	55	208	0	0	0	0	74.87	0	0
bin.273.gn07	p_Bacteroidetes (UID2605)	316	316	210	71	238	7	0	0	0	74.81	2.54	71.43
138_sub.gw02	o_Clostridiales (UID1212)	172	263	149	51	209	3	0	0	0	74.73	0.56	0
bin.489_sub.gn	o_Clostridiales (UID1212)	172	263	149	79	179	5	0	0	0	74.73	2.01	0
198.hh12	o_Clostridiales (UID1212)	172	263	149	55	205	3	0	0	0	74.71	0.92	0
bin.46.go	o_Clostridiales (UID1120)	304	250	143	64	175	11	0	0	0	74.7	3.69	81.82
bin.70_sub.hh11	o_Bacteroidales (UID2617)	213	406	265	95	298	13	0	0	0	74.69	4.09	84.62
bin.164_sub.gn08	c_Clostridia (UID1118)	387	223	124	52	1							

maxbin.196_sub.gw01	p_Actinobacteria (UID2112)	31	211	124	52	146	13	0	0	0	74.03	7.19	38.46
maxbin.091.g027	p_Actinobacteria (UID1454)	732	206	120	40	162	4	0	0	0	74	2.01	25
bin.178_sub.gv	o_Clostridiales (UID1120)	250	143	50	198	2	0	0	0	0	73.99	1.05	0
bin.131.gw04	o_Clostridiales (UID1212)	172	263	149	57	203	3	0	0	0	73.96	2.01	33.33
bin.160.gw03	k_Bacteria (UID2982)	88	230	148	46	171	13	0	0	0	73.96	6.25	46.15
bin.183_sub.hh14	k_Bacteria (UID1453)	901	171	117	39	132	0	0	0	0	73.93	0	0
maxbin.033_sub.gw04	p_Bacteroidetes (UID2605)	350	316	210	85	208	22	1	0	0	73.93	5.39	20
4.ca24	c_Clostridia (UID1085)	35	420	196	95	304	21	0	0	0	73.92	6.64	66.67
bin.85_sub.hh14	c_Epsilonproteobacteria (UID3066)	110	450	273	96	307	47	0	0	0	73.92	9.81	91.49
bin.553.gv	p_Euryarchaeota (UID3)	148	187	124	63	124	0	0	0	0	73.91	0	0
maxbin.048_sub.hh11	o_Clostridiales (UID1212)	172	263	149	86	163	14	0	0	0	73.88	6.31	85.71
11_sub.gh10	c_Epsilonproteobacteria (UID3065)	111	445	271	105	328	12	0	0	0	73.86	2.72	25
bin.147_sub.gv	o_Clostridiales (UID1212)	172	263	149	58	204	1	0	0	0	73.83	0.11	100
maxbin.081_sub.gh07	o_Clostridiales (UID1212)	172	263	149	59	198	6	0	0	0	73.83	3.69	0
maxbin.504.hc	c_Deltaproteobacteria (UID3216)	83	247	155	55	188	4	0	0	0	73.82	1.77	0
bin.101_sub.g028	o_Bacteroidales (UID2657)	160	492	269	142	347	3	0	0	0	73.81	0.68	33.33
maxbin.014.ca23	p_Bacteroidetes (UID2605)	350	316	210	89	213	14	0	0	0	73.81	4.02	42.86
bin.164_sub.g0	p_Euryarchaeota (UID3)	148	188	125	77	101	8	2	0	0	73.78	8	64.29
bin.43.hh15	k_Bacteria (UID1453)	901	171	117	47	117	7	0	0	0	73.78	3.76	71.43
maxbin.007.gv08	o_Clostridiales (UID1120)	304	247	141	51	185	11	0	0	0	73.76	5.15	90.91
153.g027	o_Bacteroidales (UID2617)	213	406	265	105	282	19	0	0	0	73.73	4.76	15.79
85_sub.gh06	k_Bacteria (UID203)	5449	98	53	26	53	17	2	0	0	73.66	11.23	96.52
maxbin.012_sub.gw03	o_Clostridiales (UID1212)	172	263	149	58	198	9	0	0	0	73.65	3.44	55.56
bin.184.hc17	p_Euryarchaeota (UID3)	148	187	124	43	143	1	0	0	0	73.61	0.81	0
bin.79.gh10	p_Actinobacteria (UID2112)	31	211	124	52	152	7	0	0	0	73.58	4.17	28.57
maxbin.059_sub.gw03	p_Euryarchaeota (UID3)	148	188	125	45	138	5	0	0	0	73.58	3.24	80
279_sub.gw01	k_Bacteria (UID2982)	88	230	148	49	169	11	1	0	0	73.53	4.52	57.14
bin.147.g0	o_Bacteroidales (UID2718)	92	487	270	105	373	9	0	0	0	73.52	2.84	22.22
maxbin.035.gv	c_Epsilonproteobacteria (UID3065)	111	445	271	100	325	20	0	0	0	73.48	5.74	70
247.gw04	p_Actinobacteria (UID2112)	31	211	124	50	152	9	0	0	0	73.43	3.86	55.56
bin.82.hh14	f_Lachnospiraceae (UID1286)	57	420	207	97	305	18	0	0	0	73.42	3.54	72.22
bin.25_sub.gh09	p_Actinobacteria (UID2112)	31	211	124	63	133	11	4	0	0	73.34	5.46	13.04
bin.580.hh	p_Proteobacteria (UID3887)	1487	256	160	73	181	2	0	0	0	73.33	0.75	0
bin.46.hc20	o_Clostridiales (UID1212)	172	263	149	77	180	6	0	0	0	73.28	2.24	16.67
bin.126.gh07	o_Clostridiales (UID1212)	172	261	147	65	191	5	0	0	0	73.25	2.21	0
maxbin.184.gw02	k_Bacteria (UID2229)	174	149	89	49	98	2	0	0	0	73.19	2.25	0
bin.27.gv09	o_Clostridiales (UID1212)	172	263	149	61	200	2	0	0	0	73.15	1.34	0
32.gw02	o_Campylobacteriales (UID3068)	106	477	284	113	327	36	1	0	0	73.12	8.34	74.36
bin.54.hc19	o_Clostridiales (UID1212)	172	263	149	57	205	1	0	0	0	73.11	0.34	0
bin.6_sub.g030	p_Actinobacteria (UID2112)	31	211	124	71	125	14	1	0	0	73.11	3.58	5.88
bin.105.hh	o_Clostridiales (UID1212)	172	263	149	72	190	1	0	0	0	73.06	0.02	0
21.hc18	k_Bacteria (UID2486)	2993	147	81	37	106	4	0	0	0	72.99	9.4	0
bin.139.gv06	o_Clostridiales (UID1212)	172	263	149	54	187	19	3	0	0	72.99	4.09	10.71
bin.351_sub.hc	o_Clostridiales (UID1212)	172	263	149	71	184	8	0	0	0	72.94	4.59	87.5
bin.140.gw02	k_Bacteria (UID2982)	88	230	148	49	167	13	1	0	0	72.77	5.87	43.75
bin.427_sub.hh	o_Clostridiales (UID1212)	172	263	149	59	189	15	0	0	0	72.71	2.12	33.33
158.ca25	p_Proteobacteria (UID3887)	1487	256	160	52	193	10	1	0	0	72.55	3.65	38.46
245_sub.gh09	o_Clostridiales (UID1212)	172	263	149	67	170	26	0	0	0	72.55	9.44	57.69
bin.260.hh	k_Bacteria (UID2272)	131	176	105	37	129	9	1	0	0	72.54	5.67	58.33
bin.103.gw01	o_Clostridiales (UID1212)	172	263	149	60	201	2	0	0	0	72.48	1.34	0
maxbin.104_sub.gw02	o_Clostridiales (UID1212)	172	263	149	52	211	0	0	0	0	72.48	0	0
maxbin.137.gh10	o_Clostridiales (UID1212)	172	263	149	50	211	2	0	0	0	72.48	1.01	0
86_sub.hh12	o_Rhodospirillales (UID3754)	63	336	201	83	223	29	1	0	0	72.43	7.54	50
bin.24.gw03	p_Actinobacteria (UID2112)	31	211	124	52	154	5	0	0	0	72.41	3.49	40
298_sub.gh08	p_Actinobacteria (UID2112)	31	211	124	51	145	14	1	0	0	72.33	6.1	35.29
bin.39.g026	k_Bacteria (UID203)	5449	104	58	21	60	17	6	0	0	72.28	13.61	71.43
maxbin.385.hc	c_Clostridia (UID1118)	387	223	124	66	148	9	0	0	0	72.26	3.55	88.89
62.hc20	k_Bacteria (UID1453)	901	171	117	42	122	7	0	0	0	72.24	4.8	14.29
28.gw04	o_Clostridiales (UID1226)	155	278	158	69	204	5	0	0	0	72.21	1.81	60
55_sub.g030	p_Bacteroidetes (UID2605)	350	314	208	107	196	10	1	0	0	72.18	4.5	15.38
bin.193.hh14	o_Clostridiales (UID1226)	155	278	158	73	205	0	0	0	0	72.15	0	0
bin.27_sub.g027	p_Euryarchaeota (UID3)	148	188	125	62	119	7	0	0	0	72.14	2.85	0
86.g029	c_Clostridia (UID1118)	387	223	124	69	150	3	1	0	0	72.13	3.63	16.67
bin.198.g0	o_Bacteroidales (UID2657)	160	492	269	158	311	22	1	0	0	72.11	5.64	40
bin.123_sub.gw02	o_Clostridiales (UID1212)	172	263	149	66	195	2	0	0	0	72.1	0.69	100
bin.235_sub.gh	p_Bacteroidetes (UID2605)	350	316	210	85	229	2	0	0	0	72.06	0.95	50
bin.89_sub.gh08	p_Actinobacteria (UID2112)	31	211	124	47	133	31	0	0	0	72.04	12.08	64.52
maxbin.008.gw04	o_Clostridiales (UID1120)	304	247	141	56	188	3	0	0	0	72.04	1.42	66.67
43_sub.hh13	o_Clostridiales (UID1212)	172	263	149	78	171	14	0	0	0	72.02	5.67	28.57
bin.34_sub.gw04	p_Actinobacteria (UID2112)	31	211	124	62	143	6	0	0	0	71.97	3.52	50
maxbin.010.hc18	f_Bifidobacteriaceae (UID1458)	77	464	220	121	307	35	1	0	0	71.92	5.89	18.42
84.gw05	k_Bacteria (UID2329)	174	149	89	36	113	0	0	0	0	71.9	0	0
bin.181.hc	p_Actinobacteria (UID2112)	31	211	124	57	150	4	0	0	0	71.78	1.97	25
51.hh12	o_Clostridiales (UID1212)	172	263	149	60	197	6	0	0	0	71.68	2.46	100
maxbin.117.gv	o_Clostridiales (UID1212)	172	263	149	54	205	4	0	0	0	71.64	0.27	50
bin.223.gw01	o_Clostridiales (UID1212)	172	263	149	55	204	4	0	0	0	71.59	0.79	75
82.hh11	o_Clostridiales (UID1120)	304	250	143	63	181	6	0	0	0	71.58	2.14	33.33
bin.149.gw05	p_Actinobacteria (UID2112)	31	211	124	49	154	8	0	0	0	71.58	1.04	25
226_sub.gv	k_Bacteria (UID2495)	2993	147	91	35	103	9	0	0	0	71.55	3.79	11.11
maxbin.010.gv	p_Bacteroidetes (UID2605)	350	316	210	75	230	11	0	0	0	71.51	3.49	63.64
bin.388.gv	o_Clostridiales (UID1212)	172	263	149	68	193	2	0	0	0	71.48	1.34	0
bin.156_sub.gv	c_Clostridia (UID1119)	387	223	124	54	164	5	0	0	0	71.44	1.55	40
19_sub.gh	k_Bacteria (UID2982)	88	230	148	51	164	15	0	0	0	71.42	5.23	60
bin.280.gh10	p_Actinobacteria (UID2112)	31	211	124	57	149	5	0	0	0	71.42	2.02	80
201.hh13	k_Bacteria (UID2569)	434	278	186	78	197	3	0	0	0	71.37	1.12	0
128.gh09	o_Burkholderiales (UID4000)	193	427	214	128	293	6	0	0	0	71.31	1.22	16.67
bin.60.g027	o_Clostridiales (UID1212)	172	263	149	59	203	1	0	0	0	71.2	0.67	100
bin.76.gw05	k_Bacteria (UID1452)	924	163	110	40	117	6	0	0	0	71.16	4.85	33.33
bin.68.hc	o_Clostridiales (UID1212)	172	263	149	79	182	2	0	0	0	71.15	1.34	50
bin.151.gw02	o_Clostridiales (UID1212)	172	263	149	66	194	3	0	0	0	71.14	1.36	33.33
maxbin.155.gh07	o_Clostridiales (UID1212)	172	263	149	56	196	11	0	0	0	71.14	3.38	0
bin.209.hh14	o_Clostridiales (UID1212)	172	263	149	67	191	5	0	0	0	71.1	2.04	100
bin.80.gw04	p_Actinobacteria (UID2112)	31	211	124	50	158	3	0	0	0	71.04	1.13	0
maxbin.051.gw03	p_Actinobacteria (UID2112)	31	211	124	51	155	5	0	0	0	71	2.2	100
bin.455.hc	o_Clostridiales (UID1212)	172	257	149	59	185	13	0	0	0	70.92	2.85	38.46
bin.342.gh07	k_Bacteria (UID2982)	88	230	148	56	165	9	0	0	0	70.8	3.76	44.44
bin.166.hc18	o_Clostridiales (UID1212)	172	263	149	78	184	1	0	0	0	70.77	0.67	100
bin.57.hc17	o_Rhodospirillales (UID3754)	63	336	201	99	234	3	0	0	0	70.76	0.79	0
maxbin.061_sub.gw02	p_Actinobacteria (UID2112)	31	211	124	61	148	2	0	0	0	70.64	1.21	100
302_sub.gw03	p_Actinobacteria (UID2112)	31	211	124	50	152	9	0	0	0	70.58	3.93	

bin.293_sub.gh	c__Clostridia (UD1118)	387	223	124	52	170	1	0	0	0	69.96	0.81	100
maxbin.143.gh	o__Clostridiales (UD1212)	172	263	149	57	197	9	0	0	0	69.8	1.27	44.44
58.gh	o__Rhodospirillales (UD3754)	63	336	201	82	245	9	0	0	0	69.73	1.92	22.22
bin.223_sub.go	c__Clostridia (UD1085)	35	420	196	114	277	28	1	0	0	69.53	5.51	77.42
bin.111_gh10	k__Bacteria (UD2372)	131	176	105	46	126	4	0	0	0	69.52	3.33	75
bin.196.ca	f__Lachnospiraceae (UD1286)	57	420	207	104	298	18	0	0	0	69.41	4.21	61.11
bin.11_sub.hh14	o__Clostridiales (UD1212)	172	263	149	60	198	5	0	0	0	69.38	1.92	40
bin.26_sub.hh11	g__Prevotella (UD2724)	55	567	296	169	391	7	0	0	0	69.36	0.87	57.14
maxbin.198_sub.hc20	k__Bacteria (UD2495)	2993	143	89	34	107	2	0	0	0	69.33	1.69	100
188.hh13	o__Lactobacillales (UD375)	177	350	163	105	233	11	1	0	0	69.3	1.97	0
268.gw05	o__Clostridiales (UD1120)	304	250	143	64	183	3	0	0	0	69.28	1.05	0
maxbin.063_sub.hh15	p__Bacteroidetes (UD2605)	350	316	210	120	177	19	0	0	0	69.26	7.86	47.37
maxbin.109_sub.gh08	o__Clostridiales (UD1212)	172	263	149	74	180	9	0	0	0	69.25	4.36	0
42.go28	o__Clostridiales (UD1212)	172	263	149	62	189	12	0	0	0	69.22	5	58.33
bin.224_sub.gw02	o__Clostridiales (UD1212)	172	263	149	79	169	15	0	0	0	69.21	3.54	6.67
bin.44.hc18	o__Clostridiales (UD1120)	250	304	143	58	177	15	0	0	0	69.21	4.45	6.67
234_sub.hh14	k__Bacteria (UD2495)	2993	147	91	47	98	2	0	0	0	69.14	2.2	0
bin.136.gw03	o__Clostridiales (UD1212)	172	263	149	61	202	0	0	0	0	69.13	0	0
bin.32.hh14	o__Clostridiales (UD1212)	172	263	149	81	178	4	0	0	0	69.05	2.24	50
maxbin.066.gw	p__Actinobacteria (UD2112)	31	211	124	51	158	2	0	0	0	68.92	0.54	50
bin.7_sub.go	k__Bacteria (UD2495)	2993	147	91	47	90	10	0	0	0	68.84	4.72	90
292.gh06	c__Epsilonproteobacteria (UD3065)	111	445	271	125	311	9	0	0	0	68.81	1.72	44.44
bin.57.ca23	p__Euryarchaeota (UD154)	234	149	89	51	93	5	0	0	0	68.76	1.51	100
221.gh10	o__Clostridiales (UD1212)	172	263	149	71	183	8	1	0	0	68.74	4.58	27.27
bin.217.gw04	o__Clostridiales (UD1212)	172	263	149	88	167	8	0	0	0	68.74	2.42	0
164.hc20	o__Clostridiales (UD1212)	172	263	149	65	183	15	0	0	0	68.4	4.69	0
171_sub.gh09	p__Euryarchaeota (UD3)	148	187	124	66	119	2	0	0	0	68.37	1.61	50
bin.196.gw04	k__Bacteria (UD2982)	88	230	148	62	159	9	0	0	0	68.25	3.21	44.44
29_sub.gw	o__Clostridiales (UD1226)	172	263	149	68	183	2	0	0	0	68.19	2.85	20
bin.213.hh	o__Clostridiales (UD1212)	172	263	149	75	180	8	0	0	0	68.12	2.76	75
61.hc17	k__Bacteria (UD2982)	88	230	148	77	150	3	0	0	0	68.11	2.03	66.67
bin.468.gh	c__Clostridia (UD1118)	387	223	124	55	162	6	0	0	0	68.01	2.89	66.67
138_sub.gh10	p__Euryarchaeota (UD3)	148	187	124	73	113	1	0	0	0	67.91	0.4	100
202_sub.gw	p__Actinobacteria (UD2112)	31	211	124	54	151	6	0	0	0	67.88	2.97	83.33
4.gh	p__Euryarchaeota (UD3)	148	187	124	52	125	10	0	0	0	67.84	4.9	40
bin.95.gw05	o__Clostridiales (UD1212)	172	263	149	68	183	2	0	0	0	67.79	1.34	0
maxbin.130_sub.gw	o__Clostridiales (UD1212)	172	263	149	75	185	3	0	0	0	67.79	2.01	0
bin.530.gw	o__Clostridiales (UD1120)	304	250	143	82	167	1	0	0	0	67.53	0.35	0
bin.358.hc	k__Bacteria (UD2328)	3167	126	75	56	68	2	0	0	0	67.51	2.67	50
bin.505.gh	k__Bacteria (UD2329)	174	149	89	36	112	1	0	0	0	67.42	1.12	0
bin.461.go	o__Bacteroidales (UD2617)	213	406	265	128	267	10	1	0	0	67.17	3.25	69.23
bin.518_sub.gh07	o__Clostridiales (UD1226)	155	278	158	89	176	13	0	0	0	67.13	3.55	15.38
bin.26.hh13	o__Rhodospirillales (UD3754)	63	336	201	98	228	10	0	0	0	67.13	2.21	60
226.gh08	o__Clostridiales (UD1226)	155	278	158	91	183	4	0	0	0	67.12	1.58	0
bin.219_gh10	o__Clostridiales (UD1212)	172	263	149	71	192	0	0	0	0	67.11	0	0
bin.197.gw05	k__Bacteria (UD2982)	88	230	148	60	161	9	0	0	0	67.04	2.56	44.44
110.ca23	p__Proteobacteria (UD3887)	1487	256	160	66	178	12	0	0	0	66.96	5.21	41.67
bin.609.hh	k__Bacteria (UD2982)	88	230	148	80	144	5	1	0	0	66.85	4.39	12.5
334_sub.gw	c__Spirochaetia (UD2496)	72	215	125	59	137	17	1	0	1	66.79	7.14	50
maxbin.028_sub.hh	o__Clostridiales (UD1212)	172	263	149	66	181	16	0	0	0	66.78	5.26	31.25
bin.489.hh	o__Clostridiales (UD1212)	172	263	149	82	178	3	0	0	0	66.66	1.17	100
bin.13.hh14	k__Bacteria (UD2565)	2921	152	93	59	89	4	0	0	0	66.64	2.75	50
49.gh	c__Spirochaetia (UD2496)	72	215	125	64	138	12	1	0	0	66.57	4.77	73.33
bin.118_gh09	o__Bacteroidales (UD2657)	160	492	269	145	346	1	0	0	0	66.55	0.37	0
bin.155.gh	o__Bacteroidales (UD2657)	160	492	269	145	347	0	0	0	0	66.55	0	0
bin.54.gw	o__Bacteroidales (UD2657)	160	492	269	146	346	0	0	0	0	66.53	0	0
bin.51.hh14	p__Actinobacteria (UD2112)	31	211	124	87	122	2	0	0	0	66.49	1.61	0
maxbin.155_sub.gh	k__Bacteria (UD2329)	174	149	89	33	115	1	0	0	0	66.48	0.56	0
bin.276.gw03	c__Epsilonproteobacteria (UD3065)	111	445	271	132	301	12	0	0	0	66.47	2.46	50
150.hh15	o__Clostridiales (UD1212)	172	263	149	89	172	2	0	0	0	66.2	0.34	50
bin.21_sub.hh14	k__Bacteria (UD203)	5449	104	58	30	54	20	0	0	0	66.15	7.35	90
maxbin.011_sub.gh	o__Clostridiales (UD1120)	304	247	141	71	167	9	0	0	0	66.11	3.62	44.44
bin.104.gw	o__Clostridiales (UD1212)	172	263	149	76	185	2	0	0	0	65.99	1.34	0
bin.1_sub.hh15	g__Prevotella (UD2722)	64	532	281	185	339	8	0	0	0	65.99	1.93	75
122.gh10	p__Euryarchaeota (UD3)	148	187	124	58	121	8	0	0	0	65.9	3.62	50
298_sub.gw	p__Bacteroidetes (UD2605)	350	316	210	112	193	10	1	0	0	65.89	4.84	76.92
61_sub.gw01	o__Clostridiales (UD1212)	172	263	149	79	181	3	0	0	0	65.87	0.75	33.33
bin.167.gw02	c__Epsilonproteobacteria (UD3065)	111	445	271	138	296	11	0	0	0	65.85	1.98	72.73
bin.110.gh	f__Lachnospiraceae (UD1255)	90	354	174	130	208	16	0	0	0	65.81	4.41	56.25
bin.265_sub.gh	k__Bacteria (UD2372)	131	177	106	62	114	1	0	0	0	65.74	0.47	100
73.gh08	p__Actinobacteria (UD2112)	31	211	124	71	136	4	0	0	0	65.69	1.96	0
bin.275.hh	o__Clostridiales (UD1212)	172	263	149	92	167	4	0	0	0	65.65	2.01	25
maxbin.120.gw04	o__Clostridiales (UD1212)	172	263	149	65	197	1	0	0	0	65.64	0.67	0
maxbin.038.gh09	p__Actinobacteria (UD2112)	31	211	124	58	148	5	0	0	0	65.56	2.8	100
51.hh14	c__Clostridia (UD1118)	387	223	124	81	133	9	0	0	0	65.5	4.74	11.11
maxbin.222_sub.gw01	p__Actinobacteria (UD2112)	31	211	124	79	128	4	0	0	0	65.42	3.23	25
50_sub.gw03	o__Campylobacteriales (UD3068)	106	477	284	156	303	18	0	0	0	65.36	3.4	77.78
maxbin.051_sub.gw02	k__Bacteria (UD2495)	2993	143	89	52	90	1	0	0	0	65.35	1.12	0
144_sub.gw	o__Clostridiales (UD1212)	172	263	149	80	179	4	0	0	0	65.3	1.45	25
19.go28	o__Clostridiales (UD1212)	172	263	149	80	177	6	0	0	0	65.23	2.93	16.67
75_sub.hh12	g__Prevotella (UD2722)	64	532	281	189	332	11	0	0	0	65.23	2.24	45.45
bin.98.hh12	o__Clostridiales (UD1212)	172	263	149	72	196	5	0	0	0	65.22	0.32	20
132.hc19	k__Bacteria (UD1453)	901	171	117	55	112	4	0	0	0	65.21	2.74	25
252_sub.hh	k__Bacteria (UD2329)	174	149	89	40	94	15	0	0	0	65.18	3.66	6.67
140.ca23	o__Bacteroidales (UD2617)	213	406	265	139	246	21	0	0	0	65.01	5.16	52.38
bin.271_gh09	p__Actinobacteria (UD2112)	31	211	124	66	142	3	0	0	0	64.95	1.29	66.67
maxbin.076.gh	o__Clostridiales (UD1212)	172	263	149	83	173	7	0	0	0	64.93	3.75	0
bin.261.hh	o__Bacteroidales (UD2657)	160	492	268	172	320	0	0	0	0	64.89	0	0
187.hc17	k__Bacteria (UD2495)	2993	147	91	83	92	2	0	0	0	64.85	1.65	50
bin.33.hh13	o__Clostridiales (UD1212)	172	263	149	82	178	3	0	0	0	64.81	0.42	0
35_sub.go30	p__Bacteroidetes (UD2605)	350	314	208	109	184	20	1	0	0	64.78	8.06	47.83
bin.163.gw	k__Bacteria (UD2569)	434	278	186	85	191	2	0	0	0	64.78	1.08	100
bin.190.hh	o__Clostridiales (UD1212)	172	263	149	71	191	1	0	0	0	64.72	0.67	0
bin.117.gw05	o__Selenomonadales (UD1024)	64	334	167	81	236	17	0	0	0	64.65	2.55	47.06
bin.272_sub.gh06	k__Bacteria (UD1452)	924	163	110	45	111	7	0	0	0	64.61	1.85	66.67
bin.69.gw05	o__Clostridiales (UD1212)	172	263	149	97	156	10	0	0	0	64.55	2.3	0
174_sub.gh08	k__Bacteria (UD2982)	88	230	148	72	149	8	1	0	0	64.51	5.41	54.55
253.hc17	o__Bacteroidales (UD2617)	213	406	265	140	254	12	0	0	0	64.48	1.74	0
bin.75_sub.ca23	f__Lachnospiraceae (UD1286)	57	420	207	143	252	25	0	0	0	64.45	6.57	72
bin.541.gw	c__Gammaproteobacteria (UD4201)	1164	270	171	88	182	0	0	0	0	64.41	0	0
bin.11.gw01	p__Actinobacteria (UD2112)												

bin.202.g09	c_Epsilonproteobacteria (UID3065)	111	445	271	143	298	4	0	0	0	63.92	0.88	50
maxbin.013_sub.g010	k_Bacteria (UID1452)	924	163	110	49	110	4	0	0	0	63.91	2.83	75
191.ca23	p_Bacteroidetes (UID2605)	350	314	208	100	209	5	0	0	0	63.8	1.16	0
bin.121_sub.gw03	o_Bacteroidales (UID2617)	213	406	265	125	276	5	0	0	0	63.77	1.51	20
bin.124.g010	o_Clostridiales (UID1212)	172	263	149	80	182	1	0	0	0	63.76	0.67	0
bin.136.g01	o_Clostridiales (UID1212)	172	263	149	86	174	3	0	0	0	63.74	0.45	100
bin.51.ca23	c_Clostridia (UID1085)	35	420	196	144	261	15	0	0	0	63.73	3.77	60
maxbin.159_sub.g07	o_Clostridiales (UID1120)	304	247	141	95	136	16	0	0	0	63.7	3.55	62.5
bin.70_sub.gw03	p_Actinobacteria (UID2112)	31	211	124	69	129	11	2	0	0	63.64	1.92	11.76
24_sub.gw	o_Clostridiales (UID1212)	172	263	149	82	103	60	16	1	1	63.59	38.49	92.74
59.hh15	c_Spirochaetia (UID2496)	72	215	125	57	154	4	0	0	0	63.47	0.9	75
bin.194.hc17	p_Bacteroidetes (UID2605)	350	316	210	98	206	12	0	0	0	63.47	4.05	33.33
bin.116.g07	p_Actinobacteria (UID2112)	31	211	124	71	136	4	0	0	0	63.37	2.53	100
161_sub.g010	p_Actinobacteria (UID2112)	31	211	124	63	139	9	0	0	0	63.15	4.78	44.44
bin.129.g07	o_Bacteroidales (UID2617)	213	406	265	124	279	3	0	0	0	63.11	0.75	0
53.g030	p_Euryarchaeota (UID3)	148	158	125	91	94	2	1	0	0	63.06	3.2	0
maxbin.176_sub.gw03	c_Gammaproteobacteria (UID4201)	1164	270	171	97	167	6	0	0	0	63.06	1.83	0
bin.6.gw01	o_Clostridiales (UID1212)	172	263	149	84	177	2	0	0	0	62.91	1.01	0
bin.186_sub.g09	o_Clostridiales (UID1212)	172	263	149	104	158	1	0	0	0	62.87	0.67	0
maxbin.043_sub.hc20	p_Bacteroidetes (UID2605)	350	316	210	106	191	19	0	0	0	62.83	5.82	63.16
maxbin.085_sub.g08	k_Bacteria (UID1453)	901	171	117	49	110	12	0	0	0	62.82	5.7	16.67
maxbin.188.hc	o_Rhodospirillales (UID3754)	63	336	201	103	217	16	0	0	0	62.81	5.05	68.75
116.g010	c_Deltaproteobacteria (UID3218)	61	284	169	114	163	7	0	0	0	62.79	2.9	42.86
bin.307.hh	c_Gammaproteobacteria (UID4201)	1164	271	170	89	178	4	0	0	0	62.76	1.37	75
bin.492_sub.g01	o_Clostridiales (UID1212)	172	263	149	80	178	5	0	0	0	62.74	2.29	40
bin.194.g08	k_Bacteria (UID1452)	924	163	110	48	109	5	1	0	0	62.73	4.75	37.5
5_sub.hc20	o_Clostridiales (UID1212)	172	263	149	95	161	7	0	0	0	62.67	2.41	28.57
maxbin.269_sub.g0	p_Bacteroidetes (UID2605)	350	316	210	126	186	4	0	0	0	62.4	1.44	50
bin.268.gw03	o_Clostridiales (UID1212)	172	263	149	42	176	5	0	0	0	62.23	2.91	40
maxbin.094_sub.gw05	k_Bacteria (UID2329)	174	149	89	40	97	11	1	0	0	62.2	8.75	57.14
bin.509_sub.g0	k_Bacteria (UID2569)	434	278	186	110	157	11	0	0	0	62.13	4.05	63.64
bin.33.g06	o_Bacteroidales (UID2617)	213	406	265	130	273	3	0	0	0	62.08	0.75	0
maxbin.015_sub.g09	k_Bacteria (UID1453)	901	171	117	52	113	6	0	0	0	61.92	3.78	50
298_sub.g01	o_Clostridiales (UID1212)	172	263	149	103	151	9	0	0	0	61.91	2.89	22.22
bin.75.gw02	k_Bacteria (UID2329)	174	149	89	39	108	2	0	0	0	61.8	2.25	0
bin.219_sub.g0	k_Bacteria (UID203)	5449	104	58	49	54	1	0	0	0	61.77	1.72	100
bin.522.gw	k_Bacteria (UID2329)	174	149	89	41	107	1	0	0	0	61.75	0.16	0
maxbin.223.g08	c_Epsilonproteobacteria (UID3066)	110	450	273	159	272	19	0	0	0	61.7	3.59	42.11
15.hc20	c_Deltaproteobacteria (UID3216)	83	247	155	81	160	6	0	0	0	61.64	1.51	0
bin.65.g029	o_Clostridiales (UID1212)	172	263	149	83	180	0	0	0	0	61.63	0	0
maxbin.089_sub.gw03	k_Bacteria (UID1453)	901	171	117	52	115	4	0	0	0	61.59	2.21	75
38_sub.g07	c_Epsilonproteobacteria (UID3065)	111	445	171	263	111	0	0	0	0	61.49	3.13	27.27
maxbin.007_sub.hc17	g_Prevotella (UID2722)	64	532	261	195	223	14	0	0	0	61.48	3.42	28.57
maxbin.152.g026	c_Clostridia (UID1118)	387	223	124	87	120	16	0	0	0	61.45	6.8	50
86_sub.hc18	k_Bacteria (UID203)	5449	103	58	27	59	15	2	0	0	61.44	8.78	57.14
bin.24.hc19	o_Bacteroidales (UID2617)	213	406	265	142	260	4	0	0	0	61.44	1.13	25
bin.199.g01	o_Clostridiales (UID1120)	304	250	143	88	161	1	0	0	0	61.4	0.7	0
253.g010	o_Clostridiales (UID1120)	304	249	142	88	156	5	0	0	0	61.38	1.08	0
maxbin.050.g028	o_Bacteroidales (UID2716)	487	170	270	170	298	19	0	0	0	61.36	2.98	26.32
237.hh13	c_Spirochaetia (UID2496)	72	215	125	71	139	5	0	0	0	61.3	1.72	0
53.ca25	o_Actinomycetales (UID1812)	229	457	227	180	269	8	0	0	0	61.17	2.03	25
126.hh12	o_Clostridiales (UID1120)	304	250	143	82	163	5	0	0	0	61.09	1.54	20
bin.602.hc	o_Clostridiales (UID1212)	172	263	149	92	167	4	0	0	0	61.07	0.64	75
216_sub.gw05	p_Actinobacteria (UID2112)	31	211	124	69	134	8	0	0	0	60.71	4.42	92.31
maxbin.046.hh12	c_Epsilonproteobacteria (UID3066)	110	450	273	170	256	23	1	0	0	60.67	5.13	37.5
51.gw02	p_Actinobacteria (UID2112)	31	211	124	69	132	9	1	0	0	60.66	6.62	33.33
bin.9.g028	o_Clostridiales (UID1212)	172	263	149	83	179	1	0	0	0	60.63	0.34	100
276.g010	c_Deltaproteobacteria (UID3216)	83	247	155	92	151	4	0	0	0	60.6	1.94	0
bin.137_sub.g09	p_Actinobacteria (UID2112)	31	211	124	81	116	14	0	0	0	60.59	6.27	35.71
197.hh13	k_Bacteria (UID2329)	174	149	89	50	97	2	0	0	0	60.58	1.69	0
51.gw05	o_Clostridiales (UID1226)	155	278	158	113	164	1	0	0	0	60.45	0.32	0
200_sub.hh11	k_Bacteria (UID1453)	901	171	117	69	96	6	0	0	0	60.39	4.56	16.67
312_sub.gw03	o_Bacteroidales (UID2617)	213	406	265	163	236	7	0	0	0	60.16	0.74	28.57
250.gw03	k_Bacteria (UID2982)	88	230	148	86	140	3	1	0	0	60.09	2.39	0
bin.233_sub.gw03	p_Actinobacteria (UID2112)	31	211	124	83	126	2	0	0	0	60.08	0.47	50
maxbin.030.gw01	k_Bacteria (UID1453)	901	171	117	53	116	2	0	0	0	59.97	0.93	50
maxbin.033.g010	k_Bacteria (UID1453)	901	171	117	53	115	3	0	0	0	59.97	1.71	66.67
maxbin.113_sub.gw03	c_Clostridia (UID1118)	387	223	124	69	101	3	0	0	0	59.95	1.81	66.67
maxbin.039_sub.g07	k_Bacteria (UID1452)	924	161	108	50	108	3	0	0	0	59.88	1.94	66.67
bin.57_sub.gw01	p_Firmicutes (UID1022)	100	295	158	118	176	1	0	0	0	59.85	0.63	0
bin.101.gw	p_Actinobacteria (UID2112)	31	211	124	64	146	1	0	0	0	59.77	0.27	0
bin.341.ca	o_Clostridiales (UID1212)	172	263	149	92	170	1	0	0	0	59.76	0.67	0
bin.437.g01	o_Clostridiales (UID1212)	172	263	149	86	175	2	0	0	0	59.67	1.01	50
bin.197.g06	k_Bacteria (UID1453)	901	171	117	54	115	2	0	0	0	59.54	1.28	50
265.g01	o_Clostridiales (UID1212)	172	263	149	104	153	6	0	0	0	59.42	1.61	16.67
bin.51.gw03	k_Bacteria (UID1452)	924	161	108	55	103	3	0	0	0	59.33	2.78	33.33
maxbin.195_sub.hc19	p_Actinobacteria (UID2112)	31	211	124	83	113	15	0	0	0	59.29	5.19	33.33
bin.138.hh11	g_Prevotella (UID2722)	64	532	281	202	327	3	0	0	0	59.16	0.83	33.33
160.ca21	p_Proteobacteria (UID3887)	1487	256	160	84	160	11	1	0	0	59.1	2.78	35.71
bin.270.gw02	k_Bacteria (UID1453)	901	171	117	56	114	1	0	0	0	59.02	0.85	0
bin.64.g01	k_Bacteria (UID1453)	901	171	117	55	115	1	0	0	0	58.9	0.08	100
167.g08	o_Clostridiales (UID1120)	304	250	143	86	162	2	0	0	0	58.87	0.87	0
bin.201_sub.g06	c_Clostridia (UID1118)	387	223	124	72	150	1	0	0	0	58.87	0.81	100
bin.55.g06	k_Bacteria (UID2329)	174	149	89	44	105	0	0	0	0	58.83	0	0
bin.19.hh14	g_Prevotella (UID2724)	55	567	296	237	316	14	0	0	0	58.81	3.02	78.57
291.gw01	o_Clostridiales (UID1120)	304	249	142	100	144	5	0	0	0	58.77	1.76	0
maxbin.009_sub.gw04	k_Bacteria (UID1452)	924	163	110	58	101	3	1	0	0	58.69	3.28	33.33
318_sub.ca	k_Bacteria (UID2982)	88	230	148	85	136	9	0	0	0	58.65	3.14	55.56
bin.204.hc18	k_Bacteria (UID1452)	924	151	101	60	88	3	0	0	0	58.6	2.09	33.33
bin.207.gw	k_Bacteria (UID2569)	434	278	186	93	183	2	0	0	0	58.49	0.54	0
7.hc17	k_Bacteria (UID1452)	924	161	108	58	103	0	0	0	0	58.32	0	0
bin.249.g07	p_Actinobacteria (UID2112)	31	211	124	98	112	1	0	0	0	58.19	0.12	0
bin.517_sub.hh	o_Clostridiales (UID1212)	172	263	149	97	149	16	1	0	0	57.83	3.14	15.79
bin.363.g01	k_Bacteria (UID2329)	174	149	89	54	91	4	0	0	0	57.8	3.93	0
bin.504_sub.gw	p_Actinobacteria (UID2112)	31	211	124	85	121	5	0	0	0	57.76	2.55	100
bin.308.gw03	c_Clostridia (UID1118)	387	223	124	88	134	1	0	0	0	57.56	0.81	100
maxbin.181_sub.hh	o_Rhodospirillales (UID3754)	63	336	201	121	176	39	0	0	0	57.47	10.93	79.49
bin.122_sub.hc	p_Proteobacteria (UID3887)	1487	255	158	110	143	2	0	0	0	57.44	1.27	50
bin.235.g09	k_Bacteria (UID2569)	434	278	186	96	180	2	0	0	0	57.42	0.54	0
221.hc16	k_Bacteria (UID2495)	2993	147	91	57	87	3	0	0	0	57.35	2.3	100
bin.199_sub.gw03	k_Bacteria (UID1452)	924	163	110</									

maxbin.014_sub_gh07	k_Bacteria (UID1452)	924	163	110	58	98	7	0	0	0	56.52	5.56	28.57
bin.50_sub.ca25	c_Clostridia (UID1085)	35	420	196	180	231	9	0	0	0	56.41	3.42	33.33
maxbin.100_sub_gh08	k_Bacteria (UID2329)	174	149	89	55	98	6	0	0	0	56.03	5.67	66.67
bin.43_sub.gw02	p_Actinobacteria (UID2112)	31	211	124	94	113	4	0	0	0	55.96	1.94	25
72_gh06	o_Clostridiales (UID1212)	172	263	149	94	162	7	0	0	0	55.91	1.82	0
259.hh15	p_Bacteroidetes (UID2605)	350	316	210	144	168	4	0	0	0	55.87	1.14	50
bin.272_sub_gh10	c_Clostridia (UID1118)	387	223	124	77	142	4	0	0	0	55.85	3.23	25
maxbin.043_gh07	c_Clostridia (UID1118)	387	223	124	86	134	3	0	0	0	55.71	2.42	100
286.gw04	c_Betaproteobacteria (UID3971)	223	425	211	167	236	22	0	0	0	55.68	4.26	72.73
maxbin.121_sub.gw03	o_Clostridiales (UID1212)	172	263	149	119	135	8	1	0	0	55.59	2.81	9.09
bin.217_gw02	k_Bacteria (UID1452)	924	163	110	59	101	3	0	0	0	55.51	2.73	0
31.gw02	c_Betaproteobacteria (UID3971)	223	425	211	162	228	35	0	0	0	55.5	6.88	71.43
maxbin.152_sub_gh07	p_Euryarchaeota (UID3)	148	187	124	98	86	3	0	0	0	55.35	1.61	100
38_gh09	o_Lactobacillales (UID355)	490	334	183	143	189	2	0	0	0	55.11	0.41	0
253_gh08	o_Lactobacillales (UID543)	284	472	265	206	262	4	0	0	0	55.06	1.32	25
maxbin.183.gw	o_Clostridiales (UID1120)	304	249	142	89	157	3	0	0	0	54.93	0.7	0
bin.163.hc20	k_Bacteria (UID2569)	2921	152	93	72	78	2	0	0	0	54.85	2.15	0
bin.100.gw	k_Bacteria (UID2372)	131	177	106	63	114	0	0	0	0	54.81	0	0
198.ca22	c_Epsilonproteobacteria (UID3065)	111	445	271	201	238	6	0	0	0	54.72	1.55	50
47.hh15	k_Bacteria (UID2329)	174	149	89	73	74	2	0	0	0	54.69	2.25	50
bin.62.g029	o_Clostridiales (UID1212)	172	263	149	96	164	3	0	0	0	54.68	0.75	66.67
bin.590.gw	o_Bacteroidales (UID2617)	213	406	265	157	249	0	0	0	0	54.65	0	0
bin.86.gw	k_Bacteria (UID1453)	901	171	117	62	109	0	0	0	0	54.62	0	0
bin.2.hh12	g_Prevotella (UID2721)	65	530	280	211	308	11	0	0	0	54.61	1.27	72.73
bin.123.g029	o_Clostridiales (UID1212)	172	263	149	112	151	0	0	0	0	54.59	0	0
232_sub.hh11	o_Clostridiales (UID1212)	172	263	149	111	144	8	0	0	0	54.3	3.53	62.5
maxbin.048_sub_gh	k_Bacteria (UID2495)	2993	143	89	69	71	3	0	0	0	54.04	2.31	33.33
293.gw04	k_Bacteria (UID2569)	434	278	186	116	153	9	0	0	0	53.85	2.5	11.11
maxbin.133.ca24	p_Proteobacteria (UID3887)	256	160	92	154	9	1	0	0	0	53.85	2.6	16.67
151_sub.hc20	k_Bacteria (UID2372)	131	177	106	65	107	5	0	0	0	53.84	1.7	20
bin.506_sub_gh	k_Bacteria (UID2329)	174	149	89	49	95	5	0	0	0	53.56	3.37	40
206_gh06	c_Betaproteobacteria (UID3971)	223	425	211	168	238	19	0	0	0	53.52	2.87	73.68
160_sub.hh13	f_Spirochaetaceae (UID2535)	33	249	143	89	158	2	0	0	0	53.44	0.39	100
134_sub.hh14	o_Rhodospirillales (UID3754)	63	336	201	140	179	17	0	0	0	53.36	5.32	35.29
bin.54_gh08	o_Bacteroidales (UID2716)	92	487	270	210	275	2	0	0	0	53.2	0.74	50
maxbin.114_gh09	o_Clostridiales (UID1120)	304	249	142	99	146	4	0	0	0	53.17	1.41	25
maxbin.190_gh08	c_Epsilonproteobacteria (UID3065)	111	445	271	185	255	5	0	0	0	53.13	1.16	60
bin.263_gh07	p_Actinobacteria (UID2112)	31	211	124	88	120	3	0	0	0	53.09	2.42	66.67
maxbin.013_sub_gh	k_Bacteria (UID1452)	924	163	110	59	100	4	0	0	0	53.08	3.64	0
bin.60_sub.gw02	c_Bacilli (UID256)	765	274	150	128	138	8	0	0	0	53.03	3.22	12.5
132_sub_gh08	c_Betaproteobacteria (UID3971)	223	425	211	179	228	18	0	0	0	52.94	3.98	77.78
bin.157_gh	o_Clostridiales (UID1212)	172	263	149	113	149	1	0	0	0	52.94	0.67	0
bin.4.hh15	p_Actinobacteria (UID2112)	31	211	124	98	101	12	0	0	0	52.93	8.74	100
bin.327.gw	k_Bacteria (UID2329)	174	149	89	60	88	1	0	0	0	52.81	1.12	0
bin.196_gh10	o_Clostridiales (UID1120)	304	250	143	108	142	0	0	0	0	52.6	0	0
bin.23.g030	o_Clostridiales (UID1212)	172	263	149	102	161	0	0	0	0	52.57	0	0
bin.667_gh	o_Clostridiales (UID1212)	172	263	149	128	134	1	0	0	0	52.52	0.22	100
bin.196.hh13	g_Prevotella (UID2722)	64	532	281	235	294	3	0	0	0	52.36	0.89	66.67
maxbin.003_sub.g027	p_Bacteroidetes (UID2605)	350	314	208	125	173	16	0	0	0	52.34	3.61	87.5
bin.449_sub_gh	o_Clostridiales (UID1212)	172	263	149	111	140	12	0	0	0	52.32	4.38	25
bin.510_sub_gh	k_Bacteria (UID2329)	174	149	89	53	95	1	0	0	0	52.25	1.12	0
85_sub.hh13	o_Clostridiales (UID1212)	172	263	149	110	146	7	0	0	0	52.19	2.23	100
maxbin.039.g0	o_Clostridiales (UID1212)	172	263	149	114	143	6	0	0	0	52.18	2.03	50
bin.26_gh	o_Clostridiales (UID1212)	172	263	149	96	167	0	0	0	0	52.1	0	0
maxbin.021.ca21	o_Selenomonadales (UID1024)	64	334	167	141	173	18	2	0	0	52.08	7.2	87.5
bin.62_sub.hc20	g_Prevotella (UID2722)	64	532	281	252	273	7	0	0	0	51.95	0.42	57.14
maxbin.194_sub.gw02	o_Clostridiales (UID1120)	304	249	142	105	134	10	0	0	0	51.94	4.93	0
bin.200.ca	k_Bacteria (UID2569)	434	278	186	126	143	8	1	0	0	51.69	4.05	72.73
175.ca	p_Actinobacteria (UID1454)	732	206	120	85	106	15	0	0	0	51.33	6.25	66.67
290_sub.gw02	c_Epsilonproteobacteria (UID3066)	110	450	273	195	237	18	0	0	0	51.31	3.17	50
bin.489_gh	p_Actinobacteria (UID2112)	31	211	124	99	109	2	1	0	0	51.24	1.21	60
6_sub_gh07	c_Betaproteobacteria (UID3971)	223	425	211	176	226	23	0	0	0	51.23	4.09	60.67
bin.41.hh12	g_Prevotella (UID2722)	64	532	281	247	279	6	0	0	0	51.08	1.03	66.67
214.gw01	c_Epsilonproteobacteria (UID3066)	110	450	273	213	218	18	1	0	0	51.07	3.43	9.52
249.hh12	c_Alphaproteobacteria (UID3305)	564	349	230	141	171	35	2	0	0	51.03	9.98	65.85
bin.159.hh12	p_Actinobacteria (UID2112)	31	211	124	102	108	1	0	0	0	50.91	0.81	100
maxbin.034_sub.go	o_Bacteroidales (UID2657)	160	492	269	222	256	14	0	0	0	50.91	3.1	71.43
97.gw02	c_Deltaproteobacteria (UID3216)	83	247	155	106	138	3	0	0	0	50.87	1.29	0
56_sub.hc	o_Actinomycetales (UID1530)	622	254	150	102	130	20	1	1	0	50.83	5.1	31.03
141.ca23	p_Euryarchaeota (UID3)	148	187	124	77	99	11	0	0	0	50.75	2.76	9.09
179.gw03	o_Clostridiales (UID1226)	155	278	158	113	160	4	1	0	0	50.6	3.18	42.86
maxbin.189_sub_gh	k_Bacteria (UID2329)	174	149	89	57	77	15	0	0	0	50.56	3.53	0
bin.93_gh09	k_Bacteria (UID1452)	924	163	110	67	94	2	0	0	0	50.51	1.82	50
93_sub.hh12	c_Clostridia (UID1118)	387	223	124	101	118	4	0	0	0	50.5	1.01	25
58.g029	k_Bacteria (UID2565)	2921	142	67	62	76	4	0	0	0	50.42	2.43	25
bin.318.hc	o_Clostridiales (UID1212)	172	263	149	112	150	1	0	0	0	50.14	0.13	0

7.1.4.2.2 Completeness and contamination of MAGs after quality control

Figure 7.1: Completeness and contamination of MAGs after quality control

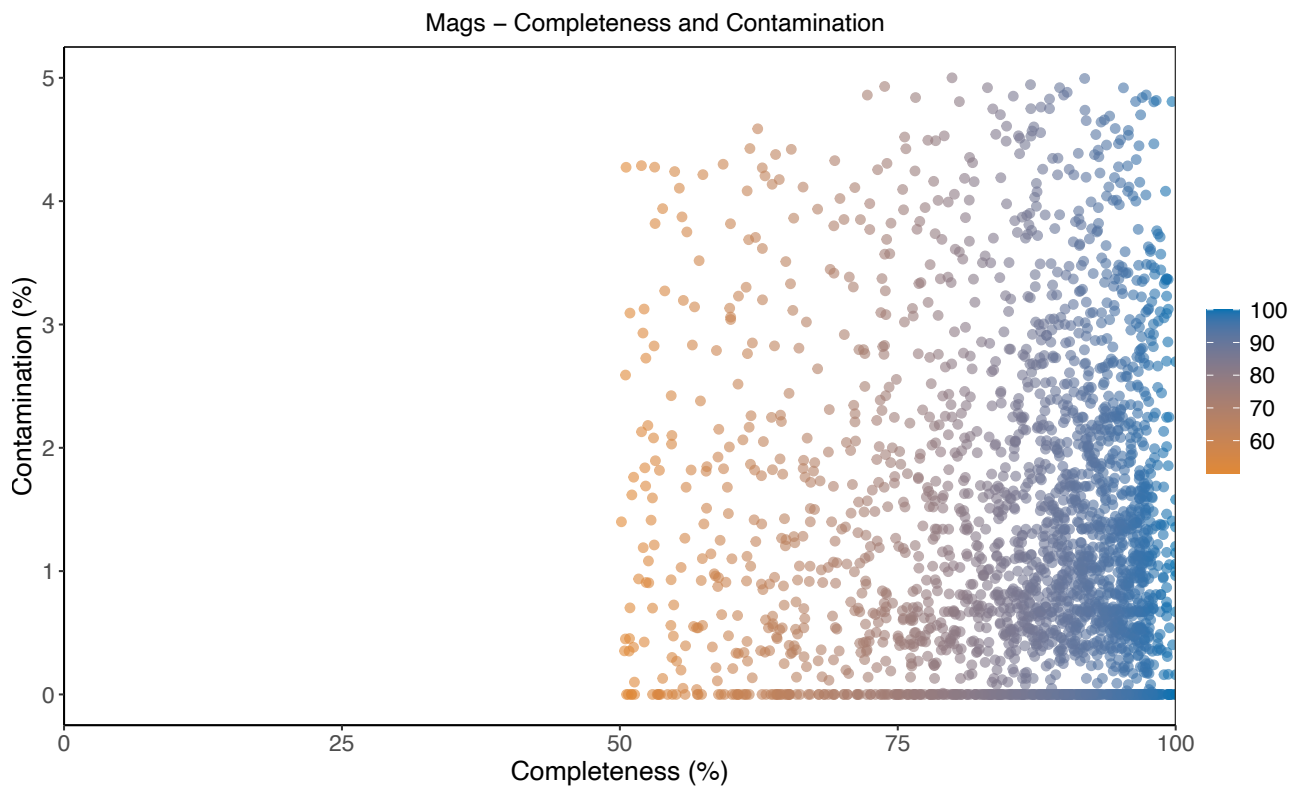


Figure 7.1: This figure illustrates the assessment of completeness and contamination levels in MAGs following quality control procedures. It provides insights into the integrity and reliability of the assembled genomes, with completeness reflecting the extent of the genomic representation and contamination indicating the presence of extraneous or erroneous sequences. The results are critical for evaluating the quality of MAGs used in downstream analyses.

7.1.4.2.3 GTDB-Tk classification (post-quality control)

[illegible]

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bin.340.gh07	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_SUG1186;s
bin.592.gv02	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_SUG1186;s
bin.71.gh	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_SUG1186;s
bin.6.sub.gv30	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UBA9715;s
bin.120.gh08	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1502;s
bin.152.gv06	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1502;s
bin.165.gv03	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1502;s
bin.298.gv09	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1502;s
bin.301_sub.gv07	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1502;s
bin.373.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1502;s
bin.6.gv04	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1502;s
bin.73.gv02	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1502;s
bin.215.gv03	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1519;s
bin.334.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1519;s
bin.3_sub.gv07	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1519;s
bin.586.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_UMGS1519;s
bin.157.sh10	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_W1P20-047;s
bin.253.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_W1P20-047;s
bin.291_sub.gv09	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_W1P20-047;s
111_sub.gv04	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
14.gv08	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
308.gv03	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
80.gv07	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
92.gv10	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.1.gv05	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.116.gv01	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.171.sh10	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.206.gv04	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.208_sub.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.242_sub.gv03	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.292.gv03	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.311.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.368.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.381.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.43_sub.gv02	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.537.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.56.gv02	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.6.gv08	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_.s
bin.133.gv04	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_CASD001;s
bin.44.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_CASD001;s
bin.56.gv07	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_CASD001;s
bin.70.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_QAMH01.g_CASD001;s
bin.110.gv10	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_UMGS124.g_UMGS124;s
bin.173.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_UMGS124.g_UMGS124;s
bin.19.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_UMGS124.g_UMGS124;s
bin.202.gv07	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_UMGS124.g_UMGS124;s
bin.273.gv	d_Bacteria;p_Actinomycetota;_Coriobacteriia;o_Coriobacteriales;f_UMGS124.g_UMGS124;s
15.gv02	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_.g_.s
198.gv06	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_.g_.s
201_sub.gv10	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_.g_.s
65_sub.gv	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_.g_.s
bin.308.gv03	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_.g_.s
maxbin_039_sub.gv	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_.g_.s
maxbin_043.gv07	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_.g_.s
65.gv03	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
73.gv02	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
bin.153.gv01	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
bin.166_sub.gv09	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
bin.185.gv07	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
bin.186_sub.gv08	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
bin.200.gv05	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
bin.41.gv	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
bin.95_sub.gv10	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
bin.98_sub.gv06	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
maxbin_090.gv	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
maxbin_106_sub.gv04	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_.s
bin.46.gv	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_Aristaeella;s
bin.89.gv30	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_Aristaeella;s
bin.127.gv01	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_CAKUFA01;s
bin.136.gv05	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_CAKUFA01;s
bin.264.gv10	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae.g_CAKUFA01;s
bin.97_sub.gv08	d_Bacteria;p_Bacillota_Ac_Clostridia;o_Christensenellales;f_Aristaeellaceae

bin.311.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_Fimadaptatus;s_
 maxbin.177_sub.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_Fimadaptatus;s_
 165.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_Fimadaptatus;s_Fimadaptatus sp900553645
 300_sub.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_Fimadaptatus;s_Fimadaptatus sp900553645
 bin.468.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_Firm-10;s_
 bin.1.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_RUG11247;s_
 bin.218.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_RUG11247;s_
 bin.100_sub.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFHK01;s_
 bin.224_sub.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFHK01;s_
 bin.291_sub.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFHK01;s_
 304_sub.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_
 49_sub.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_
 bin.15.gh09 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_
 bin.221.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_
 bin.156_sub.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_
 bin.264.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_
 bin.265_sub.gh06 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_
 bin.51.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_
 bin.624.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_
 bin.88.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_
 159_sub.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_SFM101 sp004556155
 bin.84.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFM101;s_SFM101 sp004556155
 bin.195_sub.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFH01;s_
 bin.225_sub.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFH01;s_
 bin.38_sub.gh09 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFH01;s_
 maxbin.051_sub.gw08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFH01;s_
 maxbin.075_sub.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_SFH01;s_
 bin.103.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_
 bin.136.gh06 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_
 bin.166.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_
 bin.172.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_
 bin.244.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_
 bin.260_sub.gh09 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_
 bin.332.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_
 bin.35.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_
 bin.54.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_UBA11524 sp000437595
 160.hc19 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_UBA11524 sp000437595
 77.hc18 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_UBA11524 sp000437595
 bin.258.hh15 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_UBA11524 sp000437595
 bin.269.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_UBA11524 sp000437595
 bin.76.hc16 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Aristaeellaceae;g_UBA11524;s_UBA11524 sp000437595
 maxbin.152.g026 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_Scatosoma;s_
 bin.216.hh15 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_UBA10281;s_UBA10281 sp021635425
 93_sub.hh12 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_UBA10281;s_UBA10281 sp900556195
 51.hh14 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_UBA10281;s_UBA10281 sp900556195
 maxbin.152.hc17 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_UBA10281;s_UBA10281 sp900556195
 maxbin.385.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_UBA10281;s_UBA10281 sp900767815
 maxbin.202_sub.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_UBA1259;s_
 293_sub.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_UBA1259;s_
 bin.201_sub.gh06 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_UBA1259;s_
 bin.272_sub.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_UBA1259;s_
 bin.293_sub.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Bordfalkiaceae;g_UBA1259;s_
 137.hh12 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-1252;g_RUG14300;s_
 maxbin.175.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-1252;g_RUG14300;s_
 bin.353.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_CAG-1024;s_CAG-1024 sp000432015
 bin.629.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_CAG-1024;s_CAG-1024 sp000432015
 12.hc17 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_PeH17;s_PeH17 sp000435055
 126.hh12 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_PeH17;s_PeH17 sp000435055
 16.hc19 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_PeH17;s_PeH17 sp000435055
 203.hh15 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_PeH17;s_PeH17 sp000435055
 234.hc20 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_PeH17;s_PeH17 sp000435055
 28.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_PeH17;s_PeH17 sp000435055
 82.hh11 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_PeH17;s_PeH17 sp000435055
 bin.2.hh13 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_PeH17;s_PeH17 sp000435055
 maxbin.248_sub.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_PeH17;s_PeH17 sp000435055
 0_sub.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 183_sub.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 215.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 22.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 298.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 308_sub.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 33.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 50.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 98.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 bin.110.gh09 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 maxbin.011.gh06 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_Phil1;s_
 273.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_RUG472;s_RUG472 sp900545265
 bin.31.hh13 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_SFD801;s_SFD801 sp004558825
 bin.92.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_SFD801;s_SFD801 sp004558825
 112_sub.gw27 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_SFEL01;s_
 218_sub.gw26 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_SFEL01;s_
 210.hc20 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_SFEL01;s_SFEL01 sp004557245
 bin.104.hh13 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_SFEL01;s_SFEL01 sp004557245
 bin.406.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_SFEL01;s_SFEL01 sp004557245
 bin.414.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_SFEL01;s_SFEL01 sp004557245
 bin.72.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_SFEL01;s_SFEL01 sp004557245
 bin.103.gw28 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_UBA3792;s_
 86.gw29 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-138;g_UBA3792;s_UBA3792 sp902792295

78.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-314;g_Fimimonas;s_

79.gh09 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-314;g_Fimimonas;s_

bin.164_sub.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-314;g_Fimimonas;s_

bin.22.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-314;g_Fimimonas;s_

maxbin.079.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-314;g_Fimimonas;s_

maxbin.094.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-314;g_Fimimonas;s_

maxbin.097.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-314;g_Fimimonas;s_

maxbin.113_sub.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-314;g_Fimimonas;s_

maxbin.171_sub.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-314;g_Fimimonas;s_

164.hc20 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-1138;s_CAG-1138 sp000434675

bin.179.hh12 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-1138;s_CAG-1138 sp000434675

bin.383.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-1138;s_CAG-1138 sp000434675

bin.438.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-1138;s_CAG-1138 sp000434675

bin.49.hh13 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-1138;s_CAG-1138 sp000434675

12.hh14 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-349;s_CAG-349 sp003539515

170.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-349;s_CAG-349 sp003539515

254.sub.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-349;s_CAG-349 sp003539515

bin.111.hc17 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-349;s_CAG-349 sp003539515

bin.58.hh12 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-349;s_CAG-349 sp003539515

bin.59.hh15 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-349;s_CAG-349 sp003539515

maxbin.022.hh11 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-349;s_CAG-349 sp003539515

maxbin.086.hh13 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-349;s_CAG-349 sp003539515

172_sub.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_

221.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_

bin.165_sub.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_

bin.176_sub.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_

bin.213.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_

bin.219.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_

bin.87.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_

maxbin.099_sub.gh06 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_

maxbin.135_sub.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_

bin.133.hh11 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_CAG-475 sp002478945

maxbin.281.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_CAG-475 sp002478945

5_sub.hc20 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_CAG-475 sp900550915

bin.54.hc19 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_CAG-475 sp900550915

maxbin.353_sub.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_CAG-475;s_CAG-475 sp900550915

133.gp27 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_RIGI4097;s_RIGI4097 sp017461985

260.gp d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_RIGI4097;s_RIGI4097 sp017461985

42.gp28 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_RIGI4097;s_RIGI4097 sp017461985

bin.62.gp29 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CAG-917;g_RIGI4097;s_RIGI4097 sp017461985

bin.154.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CALWSW01;g_JAEYF001;s_

bin.324.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_CALWSW01;g_JAEYF001;s_

bin.453.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Christensenellaceae;g_s_

147.gh09 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_DTU072;g_s_

147.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_DTU072;g_s_

242.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_DTU072;g_s_

249.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_DTU072;g_s_

250_sub.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_DTU072;g_s_

bin.428.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Maliibacteriaceae;g_RIGI9107;s_

bin.14.hh13 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Pumilbacteriaceae;g_CAG-552;s_CAG-552 sp000435495

bin.57.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Pumilbacteriaceae;g_CAG-552;s_CAG-552 sp000435495

292_sub.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_Pumilbacteriaceae;g_UBA10677;s_

bin.253.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_QALW01;g_UMGS1322;s_

bin.190.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_Caccovivens;s_Caccovivens sp900753315

bin.86.hh12 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_Caccovivens;s_Caccovivens sp900753315

bin.297.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_CAKVLG01;s_CAKVLG01 sp934756675

maxbin.171_sub.hc18 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_CAKVLG01;s_CAKVLG01 sp934756675

114_sub.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_CASFBJ01;s_

268.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_CASFBJ01;s_

bin.196.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_CASFBJ01;s_

bin.283.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_CASFBJ01;s_

11.hc18 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_HGM11372;s_HGM11372 sp900767715

bin.222.hh15 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_Onthoplasma;s_

72.gh06 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_RUG666;s_

bin.122.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_RUG666;s_

bin.95.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_RUG666;s_

167.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_UBA5893;s_

bin.523.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_UBA5893;s_

bin.545.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_UBA5893;s_

200.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_UBA7584;s_UBA7584 sp946635125

84.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_UBA7584;s_UBA7584 sp946635125

maxbin.149.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_UBA7584;s_UBA7584 sp946635125

maxbin.324.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_UBA7584;s_UBA7584 sp946635125

maxbin.354.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_UBA7584;s_UBA7584 sp946635125

104.hc18 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_UMGS2069;s_UMGS2069 sp900554955

36_sub.hh15 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA1242;g_UMGS2069;s_UMGS2069 sp900554955

maxbin.189_sub.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA3700;g_s_

bin.121_sub.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Christensenellales;t_UBA3700;g_UBA3700;s_

bin.195.hh12 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Clostridiales;t_Clostridiaceae;g_Clostridium;s_Clostridium sp900540255

bin.202.hh14 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Clostridiales;t_Clostridiaceae;g_Clostridium;s_Clostridium sp900540255

bin.26.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Clostridiales;t_Clostridiaceae;g_Clostridium;s_Clostridium sp900540255

bin.55.hh15 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Clostridiales;t_Clostridiaceae;g_Clostridium;s_Clostridium sp900540255

291.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Eubacteriales;t_Anaerofustaceae;g_s_

253.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Eubacteriales;t_Anaerofustaceae;g_RUG14186;s_

maxbin.114.gh09 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Eubacteriales;t_Anaerofustaceae;g_RUG14186;s_

maxbin.183.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Eubacteriales;t_Anaerofustaceae;g_RUG14186;s_

maxbin.194_sub.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Eubacteriales;t_Anaerofustaceae;g_RUG14186;s_

203.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Lachnospirales;t_Lachnospiraceae;g_s_

240_sub.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Lachnospirales;t_Lachnospiraceae;g_s_

28.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Lachnospirales;t_Lachnospiraceae;g_s_

3.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Lachnospirales;t_Lachnospiraceae;g_s_

311.gh09 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 49_sub.gh07 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 51.gw05 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 78.gh06 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 bin.249.gh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 bin.252.gw04 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 bin.260.gh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 bin.266.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 bin.293.gw03 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 bin.542_sub.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 bin.75.gh09 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 bin.95.gw26 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 maxbin.048.gw01 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 maxbin.213.gw02 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 maxbin.225.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 maxbin.281.gh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_s_
 bin.175.gh09 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Agathobacter;s_
 bin.253_sub.gh07 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Agathobacter;s_
 bin.128.gw04 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Alectryococcobium;s_
 bin.149_sub.gw02 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Alectryococcobium;s_
 bin.343.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Alectryococcobium;s_
 bin.40.gw03 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Alectryococcobium;s_
 bin.511_sub.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Alectryococcobium;s_
 bin.570.gh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Alectryococcobium;s_
 bin.110.go d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Allitcatomonas;s_
 bin.164.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerobutyricum;s_
 bin.390.gh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerobutyricum;s_
 196_sub.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerostipes;s_
 222.gh09 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerostipes;s_
 bin.217.gw04 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerostipes;s_
 maxbin.147.gh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerostipes;s_
 254_sub.hh15 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anthropogastromicrobium;s_Anthropogastromicrobium sp934292725
 bin.105.hh12 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anthropogastromicrobium;s_Anthropogastromicrobium sp934292725
 bin.195_sub.hc18 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anthropogastromicrobium;s_Anthropogastromicrobium sp934292725
 bin.132_sub.gw03 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Avilachnospira;s_
 bin.215.gw02 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Avilachnospira;s_
 bin.569.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Avilachnospira;s_
 maxbin.218_sub.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Avilachnospira;s_
 bin.113.gw27 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Bariatricus;s_
 bin.135_sub.gh09 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia;A;s_
 bin.298_sub.gh10 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia;A;s_
 bin.2_sub.gh07 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia;A;s_
 bin.589_sub.gh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia;A;s_
 bin.86_sub.gw05 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia;A;s_
 bin.88_sub.gh08 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia;A;s_
 maxbin.097_sub.gw01 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia;A;s_
 bin.100_sub.gw03 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia;A;s_
 bin.177.hc20 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Bovifimicola;s_Bovifimicola ammoniilytica
 112_sub.hh13 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A crossotus
 184_sub.hh14 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A crossotus
 35.hh15 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A crossotus
 bin.161.hh12 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A crossotus
 bin.344.hh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A crossotus
 bin.42.hc19 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A crossotus
 bin.58_sub.hc18 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A crossotus
 bin.65.hc20 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A crossotus
 maxbin.063.hh11 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A crossotus
 bin.223.hh15 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A sp000431815
 bin.496.hc d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A sp000431815
 bin.5.hc18 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A sp000431815
 maxbin.174_sub.hh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyriyibrio;A;s_Butyriyibrio A sp000431815
 78.gw28 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-303;s_
 bin.48.gw30 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-303;s_
 bin.128_sub.gw29 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-303;s_CAG-303 sp017412055
 bin.254.hh15 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-303;s_CAG-303 sp900539455
 bin.351.hh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-303;s_CAG-303 sp900539455
 bin.33_sub.gw27 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-411;s_
 104.hh14 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-510;s_CAG-510 sp000434615
 249_sub.hc17 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-510;s_CAG-510 sp000434615
 bin.6.hc19 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-510;s_CAG-510 sp000434615
 bin.10_sub.gw02 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_
 bin.125.hh12 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_
 bin.267_sub.gh09 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_
 bin.309_sub.gh07 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_
 bin.75_sub.ca23 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_
 bin.93.gh08 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_
 maxbin.117.gh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_
 maxbin.133.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_
 maxbin.139_sub.gw05 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_
 111.hh13 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_CAG-791 sp000431495
 12.hc19 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_CAG-791 sp000431495
 bin.105.hc20 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_CAG-791 sp000431495
 bin.21.hh11 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_CAG-791 sp000431495
 bin.281_sub.hc17 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_CAG-791 sp000431495
 bin.82.hh14 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-791;s_CAG-791 sp000431495
 bin.179.gw10 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAKRJP01;s_
 bin.385.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAKRJP01;s_
 bin.285_sub.gw d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Choladousia;s_
 bin.627.gh d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Choladousia;s_
 bin.193.hh14 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Choladousia;s_Choladousia sp902363135
 226.gh08 d_Bacteria;p_Bacillota;A_c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Chordicoccus;s_

bin.256.gh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Chordicoccus;s_
 bin.315.gh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Chordicoccus;s_
 bin.318_sub.gh07 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Chordicoccus;s_
 bin.45.gh09 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Chordicoccus;s_
 bin.515.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Chordicoccus;s_
 maxbin.265_sub.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Chordicoccus;s_
 bin.275.hh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Clostridium_A/s_Clostridium_AI sp934438135
 bin.375.gh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_COE1;s_
 bin.458_sub.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_COE1;s_
 218.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coproccoccus_A/s_
 bin.219.gh07 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coproccoccus_A/s_
 bin.290.gh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coproccoccus_A/s_
 129_sub.gh08 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_C/s_
 190_sub.gh06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_C/s_
 bin.112.gh09 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_C/s_
 bin.201_sub.gw02 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_C/s_
 bin.235.gh10 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_C/s_
 bin.281.gv03 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_C/s_
 bin.29.gw04 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_C/s_
 bin.30.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_C/s_
 bin.556.gh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_C/s_
 maxbin.127.gh07 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_C/s_
 93_sub.hc20 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_F sp003491505
 bin.351_sub.hc d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_F/s_Eubacterium_F sp003491505
 bin.205.hh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_F/s_Eubacterium_F sp900539115
 196_sub.gh10 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_FD2005;s_
 bin.107.gh07 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_FD2005;s_
 bin.179.gw02 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_FD2005;s_
 maxbin.072_sub.gh06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_FD2005;s_
 maxbin.078.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_FD2005;s_
 89_sub.hc18 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Fusicatenibacter saccharivorans
 bin.97.hh11 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Fusicatenibacter;s_Fusicatenibacter saccharivorans
 bin.20.gv027 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_JALENY01;s_
 161.gh06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_JAUS01;s_
 bin.276.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnoclostridium_B/s_
 maxbin.267.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnoclostridium_B/s_
 bin.248.hc17 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospira;s_Lachnospira hominis
 maxbin.067.hh13 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospira;s_Lachnospira pectinoschiza_A
 bin.571.hc d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospira;s_Lachnospira sp000437735
 bin.193.gv03 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Oribacterium;s_
 bin.353.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Oribacterium;s_
 bin.44.gh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Oribacterium;s_
 bin.584.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Oribacterium;s_
 bin.3_sub.gv05 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Pararoseburia;s_
 bin.6_sub.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Pararoseburia;s_
 20_sub.gh06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG3528;s_
 bin.12.gv03 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG3528;s_
 bin.174_sub.gw02 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG3528;s_
 bin.45.gv04 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG3528;s_
 bin.83.gh09 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG3528;s_
 bin.106.gv01 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.122.gv05 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.181.gh07 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.22.gw02 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.223.gv03 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.265.gv09 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.285.gv09 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.315.gv07 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.57.gv08 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.71.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.72.gv06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 maxbin.040.gv10 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 maxbin.044_sub.gv08 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 maxbin.048.gv04 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 maxbin.048_sub.gv06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 maxbin.049.gv d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 maxbin.232.gv d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 maxbin.327.gv d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RIG5612;s_
 bin.14.hc18 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Roseburia_C/s_Roseburia_C amytophila
 bin.469.hc d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Roseburia_C/s_Roseburia_C amytophila
 189_sub.gv09 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 209_sub.gv d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 288_sub.gv10 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 bin.114.gv05 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 bin.176_sub.gv02 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 bin.228.gv04 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 bin.240_sub.gv10 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 bin.331_sub.gv d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 bin.42_sub.gv06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 bin.79.gv07 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 bin.86.gv01 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 maxbin.119.gv01 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 maxbin.186_sub.gv03 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 maxbin.208.gv d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 maxbin.265.gv d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG14243;s_
 bin.126.go d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG191;s_
 bin.196.ca d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG191;s_
 bin.205_sub.gv02 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_G/s_
 bin.210_sub.gv04 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_G/s_
 bin.295.gv03 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_G/s_
 bin.372.gv d_Bacteria;p_Bacillota_Acc_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Ruminococcus_G/s_

maxlin.132.gh07	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_Ruminococcus_G.s
maxlin.159.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_Ruminococcus_G.s
bin.131.gw01	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_Scatomonass
bin.211.gw09	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_Scatomonass
bin.232.gh10	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_Scatomonass
bin.269.gw02	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_Scatomonass
bin.548_sub.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_Scatomonass
bin.56.gw26	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_SFDP01.s_SFDP01.sp017520155
bin.560.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_SUG1684.s
maxlin.087.hh11	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_Sulimilivens;s_Sulimilivens.sp000436115
219_sub.gw01	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.116_sub.gw06	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.13.gw01	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.14.gw03	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.17.gw02	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.185_sub.gw04	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.202.gw06	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.212.gw09	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.231.gw05	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.234_sub.gw07	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.274.gw09	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.299.gw03	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.356.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.40.gw04	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.427_sub.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.83.gh10	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
maxlin.038.gh08	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
maxlin.049.gh10	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
maxlin.063.gw07	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
maxlin.125.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
maxlin.129_sub.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA1258;s
bin.60.hc20	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA2821.s_UBA2821.sp002763335
bin.38.hh15	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA2882.s_UBA2882.sp000549665
179.gw03	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA3633;s
bin.489_sub.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_UBA4285;s
73.hc	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_VSOB01.s_VSOB01.sp934432885
bin.102.gw08	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_WOPF3-017;s
bin.115.gw01	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_WOPF3-017;s
bin.179.gw09	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_WOPF3-017;s
bin.192.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_WOPF3-017;s
bin.237.gw03	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_WOPF3-017;s
bin.247.gw07	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_WOPF3-017;s
bin.39.gw02	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_WOPF3-017;s
bin.46.hc20	d_Bacteriap_Bacillota_Ac	Clostridia_o_Lachnospirales_f_Lachnospiraceae_g_Wujia;s_Wujia.chipingensis
102.gw09	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_s
180.gw04	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_s
262.gw01	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_s
302_sub.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_s
bin.360.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_s
bin.655.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_s
bin.87_sub.gw01	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_s
maxlin.194.gw	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_s
138_sub.gw02	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s
155_sub.gw06	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s
161.gw04	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s
173_sub.gw05	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s
183_sub.hh13	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s
275_sub.gw01	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s
bin.24.gh10	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s
maxlin.011.gw30	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s
maxlin.032_sub.gw07	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s
maxlin.037.gw08	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s
102.hh14	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s_CAG-177.sp000431775
235.hh14	d_Bacteriap_Bacillota_Ac	Clostridia_o_Oscillospirales_f_Acutalibacteraceae_g_CAG-177;s_CAG-177.sp000431775

bin.91.hh14 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_CAG-964:s_CAG-964.sp000435335
bin.137.hh d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_CAKSST01.sp934489895
152_sub.g_h09 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_
281_sub.gw03 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_
bin.123_sub.gw02 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_
bin.363.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_
maxbin_286_sub.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_
154.hh15 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp000433975
bin.100.hc19 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp000433975
bin.25.hc16 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp000433975
bin.335.hh d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp000433975
bin.440.hc d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp000433975
223_sub.hh14 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp000434995
200.hh12 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp000436835
218.hc20 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp000436835
214.hh15 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp003526845
335_sub.hc d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp003526845
170_sub.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp00764665
maxbin_342_sub.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp00764665
32_sub.hh11 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp00772705
25_sub.hc19 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Eubacterium_R.s_Eubacterium_R.sp00772705
bin.230_sub.g_h09 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Fimencus_
bin.52.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Fimencus_
53.hc16 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Fimencus_Fimencus.sp000432435
bin.213.hh d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Fimencus_Fimencus.sp000432435
bin.215.hc17 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Fimencus_Fimencus.sp000432435
100.g026 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Fimencus_Fimencus.sp017399405
bin.121.hh11 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Fimencus_Fimencus.sp017399405
bin.564.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_HGM12789:s_HGM12789.sp934667845
bin.145.hc20 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Hominiterrimicrobium_Hominiterrimicrobium mulieris
12.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Limousia_
188.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Limousia_
bin.193.gw02 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Limousia_
bin.29.g_h08 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Limousia_
182_sub.hc16 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Pseudoruminococcus_Pseudoruminococcus massiliensis
249.hc19 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Pseudoruminococcus_Pseudoruminococcus massiliensis
bin.30_sub.hc18 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Pseudoruminococcus_Pseudoruminococcus massiliensis
135.ca23 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
201_sub.g027 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
bin.2.ca21 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
bin.339.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
bin.38.g029 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
bin.47.ca25 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
bin.59.g030 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
bin.62.g026 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
bin.7.ca22 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
maxbin.009.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
maxbin.055.g_h07 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG420:s_
bin.31.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG612:s_
bin.464.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG612:s_
129_sub.g_h09 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG806:s_
129_sub.g_h07 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG806:s_
293_sub.g_h06 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG806:s_
306_sub.g_h10 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG806:s_
bin.147_sub.g_h08 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG806:s_
bin.180_sub.gw01 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG806:s_
bin.492_sub.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG806:s_
maxbin.012_sub.gw03 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG806:s_
bin.176_sub.hh d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_RUG806:s_RUG806.sp16297645
117.g029 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_
bin.9.g029 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_
5_sub.hc16 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.bromii_B
maxbin.013.hc19 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.bromii_B
maxbin.048_sub.hh11 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.bromii_B
bin.35_sub.hh11 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.intestinalis
bin.52.hc16 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp000543095
bin.634.hh d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp000543095
maxbin.035.hh12 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp000543095
maxbin.001.g029 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp002776185
d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp002776185
maxbin.184.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp002776185
197_sub.hh12 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp934476515
85_sub.hh13 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp934476515
bin.140.hc19 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp934476515
bin.153.hh11 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp934476515
bin.67_sub.hc16 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_Ruminococcus_E.s_Ruminococcus_E.sp934476515
79.g029 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_SIG588:s_
205_sub.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_SIG603:s_
264.gw04 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_SIG603:s_
298_sub.gw d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_SIG603:s_
bin.136.gw03 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_SIG603:s_
bin.139.g_h06 d_Bacteriap_Bacillota_Ac_Clostridia_Oscillospirates_f_Acutalibacteraceae_SIG603:s_
bin.148

bin.218_sub.gh10 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1227;s_
 bin.233_sub.gh06 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1227;s_
 bin.262_sub.gw04 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1227;s_
 bin.29.gw02 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1227;s_
 bin.341.gh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1227;s_
 bin.416.gw d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1227;s_
 bin.68.gw03 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1227;s_
 maxbin.142_gh07 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1227;s_
 147.hh14 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA6857;s_UBA6857_sp934511365
 198.hh12 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UMGS1279;s_UMGS1279_sp900550315
 287.hh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UMGS1279;s_UMGS1279_sp900550315
 300_sub.gh06 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Butyricoccus_A;s_
 bin.167_sub.gh09 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Butyricoccus_A;s_
 maxbin.039_gh08 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Butyricoccus_A;s_
 189_sub.hh15 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Butyricoccus_A;s_Butyricoccus_Aintestinisimiae
 bin.278.hc17 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Butyricoccus_A;s_Butyricoccus_Aintestinisimiae
 bin.39.hh12 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Butyricoccus_A;s_Butyricoccus_Aintestinisimiae
 bin.56_sub.hh11 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Butyricoccus_A;s_Butyricoccus_Aintestinisimiae
 199.gw03 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_RGIG1902;s_
 maxbin.285.gw d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_RGIG1902;s_
 maxbin.391.gh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_RGIG1902;s_
 bin.133.hc18 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-390;s_CAG-390_sp000437015
 bin.68.hc d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-390;s_CAG-390_sp000437015
 156.gw04 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_
 21.gh06 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_
 bin.138.gw05 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_
 bin.191.gh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_
 bin.207_sub.gw03 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_
 bin.238_sub.gh07 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_
 bin.254.gw01 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_
 bin.265_sub.gw02 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_
 bin.425.gw d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_
 155.hh15 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_CAG-448_sp003150135
 43_sub.hh13 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_CAG-448_sp003150135
 bin.141.hc d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_CAG-448_sp003150135
 bin.207.hc18 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_CAG-448_sp003150135
 bin.32.hh14 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_CAG-448_sp003150135
 bin.489.hh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-448;s_CAG-448_sp003150135
 51.hh12 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-724;s_CAG-724_sp905202255
 bin.184.hc d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-841;s_CAG-841_sp900544285
 bin.229.hh15 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAG-841;s_CAG-841_sp900544285
 144_sub.gw d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAKSQF01;s_
 269_sub.gh09 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAKSQF01;s_
 81_sub.gw05 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_CAKSQF01;s_
 bin.213.gw d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_DTU064;s_
 150.hh15 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_RGIG3994;s_RGIG3994_sp934378145
 bin.638.hh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_RGIG3994;s_RGIG3994_sp934378145
 bin.105.hh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UBA1740;s_
 bin.127_sub.gw03 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1312;s_
 bin.20.gh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1312;s_
 bin.242.gw02 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1312;s_
 maxbin.261.gw d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1312;s_
 63.gw05 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 bin.121.gh09 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 bin.193.gw05 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 bin.260.gh10 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 bin.294.gh10 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 bin.43.gh08 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 bin.61.gw04 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 bin.77_sub.gh09 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 bin.92.gw03 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 maxbin.047_gh06 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 maxbin.056_sub.gw02 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 maxbin.062_sub.gw04 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 maxbin.064.gw01 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 maxbin.077.gw03 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 maxbin.086.gw02 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 maxbin.109.gh06 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 maxbin.121.gh07 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 maxbin.122.gw01 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 maxbin.142_sub.gh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1696;s_
 178.gw02 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1865;s_
 27.gh10 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1865;s_
 34.gh06 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1865;s_
 39.gw03 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1865;s_
 61_sub.gw01 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1865;s_
 bin.400.gh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1865;s_
 bin.88.gw d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-272.g_UMGS1865;s_
 bin.186_sub.hh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1206;s_UBA1206_sp000433115
 143_sub.gw04 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 194.gw05 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 bin.1.gw02 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 bin.16.gw d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 bin.19.gh06 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 bin.246_sub.gw01 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 bin.257.gh10 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 bin.51.gh08 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 bin.57.gh07 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 bin.65.gh09 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 maxbin.097.gw03 d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_
 maxbin.123.gh d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_CAG-382.g_UBA1752;s_

bin.90.hh11	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_CAG-382.g_UMGS1387.s_UMGS1387 sp34446675
bin.103.gw01	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
bin.105.g_h08	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
bin.124.g_h10	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
bin.131.gw04	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
bin.27.g_h09	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
bin.37.gw03	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
bin.404.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
bin.437.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
maxbin.051_sub.g_h10	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
maxbin.076.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
maxbin.081_sub.g_h07	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
maxbin.081_sub.g_h09	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
maxbin.109_sub.g_h08	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
maxbin.130_sub.g_h04	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.s
bin.449_sub.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_.CAG-170.s_CAG-170 sp002404795
bin.105_sub.g_h10	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAJOG01.s_CAJOG01 sp934597255
bin.122.g_h08	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAJOG01.s_CAJOG01 sp934597255
bin.132.gw05	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAJOG01.s_CAJOG01 sp934597255
bin.136.g_h09	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAJOG01.s_CAJOG01 sp934597255
bin.41.gw01	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAJOG01.s_CAJOG01 sp934597255
bin.44.gw06	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAJOG01.s_CAJOG01 sp934597255
maxbin.093.g_h07	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAJOG01.s_CAJOG01 sp934597255
maxbin.098_sub.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAJOG01.s_CAJOG01 sp934597255
maxbin.148.g_w	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAJOG01.s_CAJOG01 sp934597255
bin.151.gw02	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAKSPX01.s
bin.95.gw05	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAKSPX01.s
bin.147_sub.g_h09	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAKSPX01.s_CAKSPX01 sp934515035
bin.667.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAKSPX01.s_CAKSPX01 sp934515035
bin.190.g_w	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAKTEQ01.s
bin.47.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CAKTEQ01.s
bin.186_sub.g_h09	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CALXCOR01.s
bin.55.g_w	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CALXCOR01.s
maxbin.312_sub.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_CALXCOR01.s
bin.100_gw01	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s
bin.15.g_h08	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s
bin.215.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s
bin.289.g_h09	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s
bin.61.gw03	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s
bin.67.gw02	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s
bin.80.g_h07	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s
bin.455.h_c	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s_Evtepia sp004556345
110_sub.g_h10	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s_Evtepia sp934567745
bin.109.g_h08	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s_Evtepia sp934567745
bin.144.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s_Evtepia sp934567745
bin.596.g_w	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s_Evtepia sp934567745
bin.92_sub.g_h07	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Evtepia.s_Evtepia sp934567745
131_sub.g_h08	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
24_sub.g_w	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
bin.134.g_h06	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
bin.164_sub.g_h07	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
bin.189.gw02	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
bin.201.g_h09	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
bin.227.gw05	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
bin.254.gw03	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
bin.277.gw03	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
bin.332.g_h07	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
bin.593.g_w	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
bin.86.gw04	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
maxbin.010_sub.gw02	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
maxbin.016_sub.g_w	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s
256.hh14	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s_F23-B02 sp003533405
273.h_c	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s_F23-B02 sp003533405
90.hh15	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s_F23-B02 sp003533405
bin.466_sub.hh11	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_F23-B02.s_F23-B02 sp004556755
bin.211.hh14	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Faecousia.s
bin.136.g_h	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Faecousia.s
bin.191.gw02	d_Bacteriap__Bacillota_Ac_Clostridia_Oscillospirales_f_Oscillospiraceae.g_Faecousia.s
bin.213.g_h09	

bin.233.gw02 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UMGS1766;s_
bin.240.g07 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UMGS1766;s_
bin.484.g0 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UMGS1766;s_
bin.4_sub.gw03 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UMGS1766;s_
bin.58_sub.g06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UMGS1766;s_
bin.58_sub.gw01 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UMGS1766;s_
bin.594_sub.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UMGS1766;s_
bin.69.gw05 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UMGS1766;s_
245_sub.g09 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Vescimonas;s_
bin.222.g0 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Vescimonas;s_
bin.5.hh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_QAMX01;g_QAMX01;s_QAMX01 sp004555605
100.go d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_QAMX01;g_RUG11797;s_RUG11797 sp015068345
bin.360.go d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_QAMX01;g_SIG499;s_SIG499 sp015067715
bin.264.g0 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_s_
bin.82.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_s_
60_sub.hh12 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_CAG-115;s_CAG-115 sp002304735
bin.13.hc17 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_CAG-115;s_CAG-115 sp003516865
bin.38.hc d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_CAG-115;s_CAG-115 sp003516865
127.g10 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_
20_sub.g09 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_
44.gw01 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_
bin.104.gw04 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_
bin.261.gw03 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_
bin.97_sub.g06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_
maxbin.074.gw02 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_
maxbin.116_sub.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_
102.g027 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faeciplasma;s_
bin.117_sub.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecivivens;s_
bin.15_sub.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
bin.177.g06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
bin.191.g10 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
bin.224.g09 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
bin.250.gw04 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
bin.320_sub.g0 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
bin.42.g08 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
bin.47_sub.gw01 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
bin.48.gw05 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
bin.81.gw02 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
maxbin.092_sub.g07 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
maxbin.101_sub.g0 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fimivivens;s_
135_sub.hc18 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger quicubialis
137.hc d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger quicubialis
172.hh15 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger quicubialis
201.hc20 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger quicubialis
201_sub.hc19 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger quicubialis
46.hc17 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger quicubialis
5.hh11 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger quicubialis
bin.105.hc16 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger quicubialis
bin.160_sub.hh12 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger quicubialis
bin.23.hh14 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger quicubialis
235_sub.hc17 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Hominimerdicola;s_Hominimerdicola sp934435205
bin.41.hc20 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Hominimerdicola;s_Hominimerdicola sp934435205
111.hc19 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Huintestnicola;s_Huintestnicola butyrica
172.hc18 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Huintestnicola;s_Huintestnicola butyrica
170_sub.hh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Huintestnicola;s_Huintestnicola butyrica
69.hh12 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Huintestnicola;s_Huintestnicola butyrica
bin.199.hh14 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Huintestnicola;s_Huintestnicola butyrica
bin.39.hh15 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Huintestnicola;s_Huintestnicola butyrica
maxbin.222_sub.hc d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Huintestnicola;s_Huintestnicola butyrica
265.g0 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Huintestnicola;s_Huintestnicola sp945867875
47.hc19 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Huintestnicola;s_Huintestnicola sp945867875
109_sub.g06 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
155.gw03 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
290.g08 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
34.gw05 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
90.g09 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
bin.223.gw01 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
maxbin.104_sub.gw02 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
maxbin.117.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
maxbin.120.gw04 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
maxbin.137.g10 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
maxbin.143.g0 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
maxbin.155.g07 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_JAUNBN01;s_
bin.461.hh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Merdivicinus;s_Merdivicinus sp900555435
15.hc19 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Porcipelethomonas;s_Porcipelethomonas sp900554975
190.g028 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_RGIG4131;s_RGIG4131 sp017466865
bin.19_sub.hc18 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminiclostridium_E;s_Ruminiclostridium_E siraeum
bin.260_sub.hc17 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminiclostridium_E;s_Ruminiclostridium_E siraeum
201_sub.gw d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C;s_
130.hc19 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C callidus
166_sub.hh d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C callidus
92.hh11 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C callidus
bin.42_sub.hc20 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C callidus
10.hc16 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C sp000433635
107.hc20 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C sp000433635
109_sub.hh15 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C sp000433635
134.hc19 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C sp000433635
206_sub.hh12 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C sp000433635
208_sub.hc18 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C sp000433635
bin.151.hh13 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C sp000433635
bin.161_sub.hh11 d_Bacteria;p_Bacillota_Acc_Clostridia;o_Oscillospirales;f_Ruminococcus_C;s_Ruminococcus_C sp000433635

maxbin.060_sub.hh14 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C;s_Ruminococcus_C sp000433635
 bin.162.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C;s_Ruminococcus_C sp900770195
 bin.295.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C;s_Ruminococcus_C sp900770195
 bin.33.hh13 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C;s_Ruminococcus_C sp900770195
 bin.318.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_F;s_Ruminococcus_F champanelensis
 bin.607.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_F;s_Ruminococcus_F champanelensis
 bin.10.hc18 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp002438605
 bin.143_sub.hc20 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp002438605
 bin.170.hh13 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp002438605
 bin.179.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp002438605
 bin.192.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp002438605
 bin.374.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp002438605
 bin.606.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp002438605
 bin.625.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp002438605
 bin.85.hh12 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp002438605
 bin.99.hh15 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp002438605
 223_sub.hh13 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp900540005
 360_sub.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp900540005
 bin.164_sub.hc20 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp900540005
 bin.176.hc17 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp900540005
 bin.357_sub.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp900540005
 bin.427_sub.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp900540005
 bin.602.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp900540005
 bin.81_sub.hh15 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp900540005
 bin.463.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp934474025
 bin.192.hh15 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus;s_Ruminococcus sp934481385
 135.gh06 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_SFIE01;s
 211.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_SFIE01;s
 222.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_SFIE01;s
 228.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_SFIE01;s
 66.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_SFIE01;s
 80.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_SFIE01;s
 bin.126.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_SFIE01;s
 maxbin.313.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_SFIE01;s
 bin.408.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_SFIE01;s_SFIE01 sp004555405
 25.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s
 bin.125.gh09 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s
 bin.146.gh06 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s
 bin.165.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s
 bin.245.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s
 bin.273.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s
 bin.63.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s
 bin.94.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s
 maxbin.141.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s
 123_sub.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s_UBA5884 sp018376535
 266_sub.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s_UBA5884 sp018376535
 38.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s_UBA5884 sp018376535
 45_sub.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s_UBA5884 sp018376535
 14.hc17 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s_UBA5884 sp934444765
 bin.403.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s_UBA5884 sp934444765
 maxbin.432.hh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA5884;s_UBA5884 sp934444765
 bin.283.hc17 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UMGS1889;s_UMGS1889 sp900556055
 maxbin.070.hc18 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UMGS363;s_UMGS363 sp900541495
 174_sub.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_YE71;s_YE71 sp000434695
 19.gw28 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_SIG627;g_SIG685;s
 bin.103.ca d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA644;g_HGM12619;s_HGM12619 sp904502105
 222_sub.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA644;g_UBA644;s
 bin.147_sub.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA644;g_UBA644;s
 maxbin.334.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UBA644;g_UBA644;s
 bin.176.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Oscillospirales;f_UMGS1384;g_JAAZKA01;s
 110_sub.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 148_sub.gh06 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 204_sub.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 245.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 248.gh09 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 285.gw01 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 288_sub.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 305.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 33.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 60.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 73.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 bin.12_sub.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 bin.15.gh06 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 bin.173_sub.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 bin.195.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 bin.200.gh08 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 bin.39.gw05 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 bin.77.gw03 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 bin.92.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 maxbin.019.gh10 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 maxbin.032.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 maxbin.100.gh09 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_s
 226_sub.hc d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_CAKQOE01;s_CAKQOE01 sp934255545
 bin.101_sub.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s
 bin.127.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s
 bin.146.gh07 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s
 bin.153.gw02 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s
 bin.153.gw04 d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s
 bin.280.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s
 bin.496.gw d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s
 bin.50_sub.gh d_Bacteria;p_Bacillota;Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s

bin.61.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_

bin.72.gh10 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_

maxbin.159_sub_gh07 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_

maxbin.167_gh07 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_

maxbin.241_sub_gh d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_

110_sub.go29 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_Lentihominibacter sp017416795

18_sub.go27 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_Lentihominibacter sp017416795

220_sub.go28 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_Lentihominibacter sp017416795

bin.187_sub.gw05 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Mogibacterium_Ac_

maxbin.200.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Mogibacterium_Ac_

maxbin.269_sub.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Mogibacterium_Ac_

maxbin.291_sub.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Mogibacterium_Ac_

maxbin.317_gh d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Mogibacterium_Ac_

137_sub.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

158_gw05 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

259_sub.gh10 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

281_sub.gh06 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

37_sub.gw03 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

62_sub.gh07 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

70_sub.gw01 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

75_gh09 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

79_gw02 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

bin.18.g030 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

maxbin.007_gh08 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

maxbin.008_gw04 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

maxbin.011_sub_gh d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_

bin.215.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UBA1739;s_

bin.644_gh d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UBA1739;s_

289_gh06 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

bin.155.gw04 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

bin.18.gh10 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

bin.197_gh08 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

bin.237_gw05 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

bin.46.gh07 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

bin.61.gh09 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

bin.97_gw03 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

maxbin.112_gh d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

maxbin.168.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

maxbin.175_gw02 d_Bacteria;p_Bacillota_Ac_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UMGS973;s_

bin.123.go29 d_Bacteria;p_Bacillota_Ac_Clostridia;o_TANB77f_CAG-465;g_CAG-465;s_

bin.44.hc18 d_Bacteria;p_Bacillota_Ac_Clostridia;o_TANB77f_CAG-465;g_CAG-465;s_CAG-465 sp000433755

bin.11_sub.hh14 d_Bacteria;p_Bacillota_Ac_Clostridia;o_TANB77f_CAG-508;g_CAG-273;s_CAG-273 sp003534295

bin.160.hc19 d_Bacteria;p_Bacillota_Ac_Clostridia;o_TANB77f_CAG-508;g_CAG-492;s_CAG-492 sp900553225

bin.134_sub.hh14 d_Bacteria;p_Bacillota_Ac_Clostridia;o_TANB77f_CAG-508;g_CAG-492;s_CAG-492 sp934180065

bin.104.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_TANB77f_CAG-508;g_HGM13634;s_HGM13634 sp934177485

bin.6.gw01 d_Bacteria;p_Bacillota_Ac_Clostridia;o_TANB77f_CAG-508;g_UMGS1901;s_UMGS1901 sp900556135

bin.530.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_TANB77f_RIGI9151;g_RIGI9151;s_

bin.178_sub.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_TANB77f_UBA1234;g_HGM13618;s_

bin.199.gh d_Bacteria;p_Bacillota_Ac_Clostridia;o_TANB77f_UBA1234;g_HGM13618;s_

260_sub.gw d_Bacteria;p_Bacillota_Ac_Clostridia;o_UMGS1883;f_JAAYJM01;g_s_

bin.601.gw d_Bacteria;p_Bacillota_B;c_Peptococcia;o_Peptococcales;f_Peptococcaceae;g_QAKL01;s_

4.ca24 d_Bacteria;p_Bacillota_B;c_Peptococcia;o_Peptococcales;f_Peptococcaceae;g_UBA7185;s_UBA7185 sp017383785

bin.50_sub.ca25 d_Bacteria;p_Bacillota_B;c_Peptococcia;o_Peptococcales;f_Peptococcaceae;g_UBA7185;s_UBA7185 sp017383785

bin.51.ca23 d_Bacteria;p_Bacillota_B;c_Peptococcia;o_Peptococcales;f_Peptococcaceae;g_UBA7185;s_UBA7185 sp017383785

bin.223_sub.go d_Bacteria;p_Bacillota_B;c_Peptococcia;o_Peptococcales;f_Peptococcaceae;g_UBA7185;s_UBA7185 sp017622155

164.ca25 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_JAHUH01;s_JAHUH01 sp937901335

bin.4_sub.ca24 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_JAHUH01;s_JAHUH01 sp937901335

maxbin.021.ca21 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_JAHUH01;s_JAHUH01 sp937901335

146_sub.gh d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascalarctobacterium_Ac_

92.gw04 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascalarctobacterium_Ac_

bin.172_gh09 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascalarctobacterium_Ac_

bin.418.gh d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascalarctobacterium_Ac_

maxbin.238_sub.gw01 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascalarctobacterium_Ac_

150_sub.hc18 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascalarctobacterium_Ac_Phascalarctobacterium_Ac sp934190775

275_sub.gh d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Anaerovibrio;s_

108.hh14 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Anaerovibrio;s_Anaerovibrio sp900548165

196.hc17 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Anaerovibrio;s_Anaerovibrio sp900548165

13.hh15 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Anaerovibrio;s_Anaerovibrio sp900548165

154.hh13 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Megamonas;s_Megamonas funiformis

27.hh13 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Mitsuokella;s_Mitsuokella multacida

29.hc17 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Mitsuokella;s_Mitsuokella multacida

70.hc19 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Mitsuokella;s_Mitsuokella multacida

82.hh12 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Mitsuokella;s_Mitsuokella multacida

bin.200.hh d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Mitsuokella;s_Mitsuokella multacida

bin.214.hc18 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Mitsuokella;s_Mitsuokella multacida

119.hc19 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Selenomonas_Ac_Selenomonas_Ac sp900769615

72.hh12 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Selenomonas_Ac_Selenomonas_Ac sp900769615

bin.225.hh d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Selenomonas_Ac_Selenomonas_Ac sp900769615

102_sub.gw d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

145_sub.gw02 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

182_sub.gw03 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

29_sub.gh06 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

bin.205.gw03 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

bin.57_sub.gw01 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

maxbin.020_gw01 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

maxbin.022_gh07 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

maxbin.024_gw04 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

maxbin.024_sub_gh09 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

maxbin.025_gh08 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

maxbin.026_gw02 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

maxbin.027_sub.gw05 d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_s_

maxbin.033.gv	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Dialisteraceae.g_s_
maxbin.035.gv#6	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Dialisteraceae.g_s_
maxbin.054.gv#4	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Dialisteraceae.g_s_
146.hc17	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Dialisteraceae.Dialisters._
bin.227.gv	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Dialisteraceae.Dialisters._
bin.477.gv	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Dialisteraceae.Dialisters._
bin.62.gv#1	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Dialisteraceae.Dialisters._
214.hc19	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Megasphaeraee.g_Megasphaera:Megasphaera elsdonii
29.hc20	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Megasphaeraee.g_Megasphaera:Megasphaera elsdonii
234_sub.hh13	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Megasphaeraee.g_Megasphaera:Megasphaera sp934193515
247.hh14	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Megasphaeraee.g_Megasphaera:Megasphaera sp934193515
268.hh15	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Megasphaeraee.g_Megasphaera:Megasphaera sp934193515
38.hc17	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Megasphaeraee.g_Megasphaera:Megasphaera sp934193515
98.hc20	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Megasphaeraee.g_Megasphaera:Megasphaera sp934193515
bin.55.hc	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Megasphaeraee.g_Megasphaera:Megasphaera sp934193515
86_sub.hc18	d_Bacteriap.	Bacillota_Cyc_Negativicuteso_Veillonellalesf_Veillonellatae_Veillonella_Veillonella sp900538355
bin.448.hg	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Achloplasmatalesf_Anaroplasmataceae_g_Anaroplasma:_Anaroplasma sp934216145
bin.10.hc16	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Achloplasmatalesf_Anaroplasmataceae_g_CAG-307s_CAG-307 sp901916215
bin.528.hc	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Achloplasmatalesf_Anaroplasmataceae_g_CAG-307s_CAG-307 sp901916215
bin.29.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Achloplasmatalesf_Anaroplasmataceae_g_UBA3206s_
bin.9.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Achloplasmatalesf_Anaroplasmataceae_g_UBA3206s_
172.hh14	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Coproballiaceae_g_Catenibacterium:_Catenibacterium sp900764565
bin.107.hh12	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Coproballiaceae_g_Catenibacterium:_Catenibacterium sp900764565
bin.171.hc20	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Coproballiaceae_g_Catenibacterium:_Catenibacterium sp900764565
103_sub.gv#27	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Coproballiaceae_g_CATOPA01s_
bin.98.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Coproballiaceae_g_Faecalibacillus_
151_sub.hc20	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Coproballiaceae_g_Faecalibacillus:_Faecalibacillus intestinalis
213.hc19	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Coproballiaceae_g_Faecalibacillus:_Faecalibacillus intestinalis
bin.18.gv#27	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Coproballiaceae_g_Kandleria:_Kandleria vitulina
bin.99.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Coproballiaceae_g_Kandleria:_Kandleria vitulina
30_sub.gv#4	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Abscisococcus_
75_sub.gv#3	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Abscisococcus_
214_sub.gv#6	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.11.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.197.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.231.gv#3	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.236.gv#4	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.273.gv#2	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.279.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.305.gv#3	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.338.ca	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.52.gv#4	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.57.gv#5	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.575.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.69.gv#2	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
maxbin.035.gv#7	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
maxbin.047.gv#8	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
maxbin.057.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
maxbin.064.gv#6	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
maxbin.065.gv#9	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
maxbin.069_sub.gv#1	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia_
bin.257.hh15	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia:_Bulleidia sp934725105
bin.50.hc20	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia:_Bulleidia sp934725105
bin.60_sub.hh12	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia:_Bulleidia sp934725105
bin.67.hc	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia:_Bulleidia sp934725105
bin.97_sub.hh14	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia:_Bulleidia sp934725105
bin.591.hg	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Bulleidia:_Bulleidia sp934754415
bin.200_sub.gv#3	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Holdemanelia_
bin.70.gv#4	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Holdemanelia_
bin.78.gv#2	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_Holdemanelia_
221.gv#2	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_UBA1783s_
296_sub.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_UBA1783s_
bin.100.gv	d_Bacteriap.	Bacillota_Cyc_Bacilli_Aoo_Erysipelotrichalesf_Erysipelotrichaceae_g_UBA1783s_
bin.126.gv#4	d_Bacteriap.	

bin.109.gw05	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RF39;f_UBA660;g_CAG-877;s_
bin.156.gh08	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RF39;f_UBA660;g_CAG-877;s_
bin.184.gw03	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RF39;f_UBA660;g_CAG-877;s_
bin.213_sub.gw02	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RF39;f_UBA660;g_CAG-877;s_
bin.22.gh06	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RF39;f_UBA660;g_CAG-877;s_
bin.509.gw	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RF39;f_UBA660;g_CAG-877;s_
bin.510_sub.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RF39;f_UBA660;g_CAG-877;s_CAG-877 sp934162125
bin.637.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RF39;f_UBA660;g_RUG591;s_RUG591 sp934119955
bin.355.gw	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RF39;f_UBA660;g_Scybalousia;s_
bin.21.go29	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RF39;f_UBA660;g_SIG200;s_
215_sub.hc	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_CAG-568;s_CAG-568 sp000434395
232_sub.hh13	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_CAG-568;s_CAG-568 sp000434395
54_sub.hc19	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_CAG-568;s_CAG-568 sp000434395
bin.101.hh14	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_CAG-568;s_CAG-568 sp000434395
bin.187.hc20	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_CAG-568;s_CAG-568 sp000434395
bin.275.hc17	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_CAG-568;s_CAG-568 sp000434395
bin.5.hh15	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_CAG-568;s_CAG-568 sp000434395
maxbin.028_sub.hh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_CAG-568;s_CAG-568 sp000434395
292.gh10	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
323_sub.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.125.gw	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.162.gh08	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.177_sub.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.181.gw05	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.247.gw02	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.267.gw03	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.33.gw01	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.36.gw04	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.506_sub.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.525.gw	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
bin.7.gh09	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
maxbin.151_gh06	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
maxbin.260.gh07	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_
252_sub.hh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_Enterosoma sp021621525
109.hc17	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_Enterosoma sp900549915
191.hc16	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_Enterosoma sp900549915
bin.133.hh12	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_Enterosoma sp900549915
bin.143.hh14	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_Enterosoma sp900549915
bin.600.hh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_Enterosoma sp900549915
100.hc	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_Enterosoma sp900763245
163_sub.hc17	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_Enterosoma sp900763245
47.hh15	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_Enterosoma sp900763245
bin.455.hh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Enterosoma;s_Enterosoma sp900763245
bin.327.gw	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-288;g_Scatoplasma;s_
bin.140.gh07	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-449;g_UBA3210;s_
bin.203.gw03	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-449;g_UBA3210;s_
bin.294.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-449;g_UBA3210;s_
bin.43.gh06	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-449;g_UBA3210;s_
bin.245.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-631;g_CAKPXW01;s_
bin.28.gw	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-631;g_CAKPXW01;s_
bin.308_sub.gh07	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-631;g_CAKPXW01;s_
bin.201.gw01	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_s_
bin.230.gh10	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_s_
bin.296.gh07	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_s_
bin.39.gh06	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_s_
bin.505.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_s_
180_sub.hc	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
197.hh13	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
226_sub.gw	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
37.hc20	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
bin.148.gh10	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
bin.280_sub.gw	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
bin.304.gh07	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
bin.475.hh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
maxbin.100_sub.gh08	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
maxbin.132_sub.gh06	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
maxbin.184.gw02	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Enteromonas;s_
bin.150.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Onthovivens;s_
bin.198.gw	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Onthovivens;s_
bin.75.gw02	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Onthovivens;s_
bin.81.gw	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Onthovivens;s_
bin.93.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_Onthovivens;s_
288_sub.gw03	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_RUG13091;s_
bin.423_sub.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_RUG13091;s_
bin.151_sub.hh11	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_RUG131;s_RUG131 sp900315885
bin.202.hh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_RUG131;s_RUG131 sp900315885
186_sub.gh10	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
190_sub.gh09	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
214.hh11	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
30_sub.gw02	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
75.hh15	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
93_sub.gw03	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
bin.122.gw03	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
bin.13.gh07	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
bin.142.gw01	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
bin.15.gh07	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
bin.152_sub.gw05	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
bin.159.gh06	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
bin.164.gh06	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
bin.170_sub.gh	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_
bin.184.gh08	d_Bacteria;p_Bacillota.l;c_Bacilli.Ao_RFN20;f_CAG-826;g_UBA4951;s_

bin.191.gh08 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.227.gw02 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.229.gw03 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.258.gh d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.263_sub.gw01 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.28.gw04 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.281.gh10 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.3.gh10 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.339.gh07 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.39_sub.gh09 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.421_sub.gw d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.50.gh06 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.53.gw03 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.82.gh07 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.85_sub.gw02 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.93.gh06 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 bin.93_sub.gw02 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 maxbin.083.gw05 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 maxbin.105.gw01 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 maxbin.155_sub.gh d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_
 103.hc18 d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_UBA4951 sp900540385
 bin.194.hc d_Bacteria;p_Bacillota;l;c_Bacilli_Ao_RFN20f_CAG-826;g_UBA4951;s_UBA4951 sp900540385
 bin.60_sub.gw02 d_Bacteria;p_Bacillota;c_Bacilli;o_Bacillales;D;f_Amphibacillaceae;g_Virgibacillus;f_Virgibacillus;f_halotolerans
 49.hh15 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus;B;s_Enterococcus;B_lactis
 bin.116.hh13 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus;B;s_Enterococcus;B_lactis
 bin.118.hc19 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus;B;s_Enterococcus;B_lactis
 bin.136.hh d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus;B;s_Enterococcus;B_lactis
 bin.205_sub.hc18 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus;B;s_Enterococcus;B_lactis
 bin.246.hc17 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus;B;s_Enterococcus;B_lactis
 bin.32.hc20 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus;B;s_Enterococcus;B_lactis
 bin.77.hc16 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus;B;s_Enterococcus;B_lactis
 61.hc d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus;s_Lactobacillus;f_delbrueckii
 67_sub.hc19 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus;s_Lactobacillus;f_delbrueckii
 bin.52.hc17 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus;s_Lactobacillus;f_delbrueckii
 bin.93_sub.hc19 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Leuconostoc;s_Leuconostoc;f_lactis
 204.hh13 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Ligilactobacillus;s_Ligilactobacillus;f_ruminis
 30.hc19 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Ligilactobacillus;s_Ligilactobacillus;f_ruminis
 333_sub.hc d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Ligilactobacillus;s_Ligilactobacillus;f_ruminis
 maxbin.017.hc17 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Ligilactobacillus;s_Ligilactobacillus;f_ruminis
 maxbin.029.hc16 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Ligilactobacillus;s_Ligilactobacillus;f_ruminis
 maxbin.032.hh12 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Ligilactobacillus;s_Ligilactobacillus;f_ruminis
 maxbin.038.hc20 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Ligilactobacillus;s_Ligilactobacillus;f_ruminis
 maxbin.067.hc18 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Ligilactobacillus;s_Ligilactobacillus;f_ruminis
 maxbin.101.hh d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Ligilactobacillus;s_Ligilactobacillus;f_ruminis
 93.hc19 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Umosilactobacillus;s_Umosilactobacillus;f_fermentum
 maxbin.363_sub.hc d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Umosilactobacillus;s_Umosilactobacillus;f_fermentum
 38.gw09 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Umosilactobacillus;s_Umosilactobacillus;f_gorillae
 bin.114.gw d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Umosilactobacillus;s_Umosilactobacillus;f_gorillae
 bin.115.gw04 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Umosilactobacillus;s_Umosilactobacillus;f_gorillae
 bin.336.gh d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Umosilactobacillus;s_Umosilactobacillus;f_gorillae
 bin.54.gh06 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Umosilactobacillus;s_Umosilactobacillus;f_gorillae
 maxbin.026.gh08 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Umosilactobacillus;s_Umosilactobacillus;f_gorillae
 maxbin.086.gh d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Weissella;s_Weissella;f_confusa
 198.hh13 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus;s_Lactococcus;f_lactis
 bin.35.hc19 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus;s_Lactococcus;f_petauri
 bin.179.hc19 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus;s_Lactococcus;f_petauri
 bin.517_sub.hh d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus;s_Lactococcus;f_petauri
 bin.539.hc d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus;s_Lactococcus;f_petauri
 165_sub.gh07 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_
 181.gw03 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_
 253.gh08 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_
 319.gh d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_
 69_sub.gh d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_
 81.gh06 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_
 85.gw02 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_
 bin.17.ca d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_Streptococcus;f_equinus;B
 bin.39.hh11 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_Streptococcus;f_infantarius
 bin.15_sub.hh12 d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_Streptococcus;f_macedonicus
 bin.118.gw04 d_Bacteria;p_Bacillota;c_Bacilli;o_Staphylococcales;f_Staphylococcaceae;g_Staphylococcus;s_Staphylococcus;f_equorum
 bin.221.gw03 d_Bacteria;p_Bacillota;c_Bacilli;o_Staphylococcales;f_Staphylococcaceae;g_Staphylococcus;s_Staphylococcus;f_equorum
 bin.366_sub.gw d_Bacteria;p_Bacillota;c_Bacilli;o_Staphylococcales;f_Staphylococcaceae;g_Staphylococcus;s_Staphylococcus;f_equorum
 bin.2_sub.ca25 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Alloprevotella;s_
 54_sub.hh13 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Alloprevotella;s_Alloprevotella;f_sp900540885
 bin.21_sub.hh14 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Alloprevotella;s_Alloprevotella;f_sp900540885
 bin.64.hc d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Alloprevotella;s_Alloprevotella;f_sp934255485
 140.hh13 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides;s_Bacteroides;f_fragilis
 bin.149.hc17 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides;s_Bacteroides;f_ovatus
 bin.124_sub.hc20 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides;s_Bacteroides;f_uniformis
 bin.6.gw26 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_HGM04593;s_HGM04593;f_sp015060965
 bin.131_sub.gw28 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_HGM04593;s_HGM04593;f_sp017416705
 bin.101_sub.gw28 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Paraprevotella;s_Paraprevotella;f_sp017937925
 bin.532.go d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Paraprevotella;s_Paraprevotella;f_sp017937925
 bin.154_sub.gh d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Phocaeicola;f_A;s_
 bin.253_sub.gw05 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Phocaeicola;f_A;s_
 bin.279_sub.gw d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Phocaeicola;f_A;s_
 bin.195.hc20 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Phocaeicola;s_Phocaeicola;f_dorei
 bin.191.hc17 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Phocaeicola;s_Phocaeicola;f_sp000434735
 bin.50.hc18 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Phocaeicola;s_Phocaeicola;f_vulgatus
 bin.55.hc17 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Phocaeicola;s_Phocaeicola;f_vulgatus
 bin.108.gw03 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Prevotella;s_
 bin.122.gh10 d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Prevotella;s_

bin.141_sub.gv05	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.199_sub.gv04	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.211.gv10	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.224.gv07	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.278_sub.gv10	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.387.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.416_sub.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.54.gv08	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.64_sub.gv02	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.8.gv01	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.8.gv04	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
bin.89.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_s
maxbin.019_sub.hc16	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp000434975
bin.141_sub.hc17	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp002251295
bin.65_sub.hc16	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp002262626
bin.18.hk14	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp002296635
bin.26_sub.hh11	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp002299363
maxbin.025.hc20	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp002299635
148_sub.hc16	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp003447235
52.hh15	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp003447235
75_sub.hh12	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp003447235
bin.176.hh11	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp003447235
bin.147.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp017410365
bin.33.gv29	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp017410365
maxbin.050.gv28	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp017410365
193.hk	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp900771975
bin.138.hh11	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp900771975
bin.196.hh13	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp900771975
bin.1_sub.hh15	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp900771975
bin.41.hh12	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp900771975
bin.62_sub.hc20	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp900771975
maxbin.007_sub.hc17	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp900771975
bin.157.hc18	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp934254985
bin.19.hk14	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp934254985
bin.2.hh12	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_Prevotella_Prevotella sp934254985
22.ca	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA1179_s_UBA1179 sp017556585
bin.144.gv08	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA1786_s_UBA1786
bin.189_sub.gv04	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA1786_s_UBA1786
bin.229.gv10	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA1786_s_UBA1786
bin.289.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA1786_s_UBA1786
bin.62.gv09	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA1786_s_UBA1786
bin.97.gv01	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA1786_s_UBA1786
bin.105.gv02	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA2918_s_UBA2918
bin.152.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA2918_s_UBA2918
bin.217.gv03	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA2918_s_UBA2918
bin.456.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA2918_s_UBA2918
bin.520.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA2918_s_UBA2918
bin.198.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA4334_s_UBA4334 sp017507385
179_sub.gv07	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA4372_s_UBA4372
bin.340.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA4372_s_UBA4372
bin.35_sub.ca21	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA4372_s_UBA4372
bin.73.gv29	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA4372_s_UBA4372 sp017622815
maxbin.034_sub.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA4372_s_UBA4372 sp017622815
110.hc16	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA4372_s_UBA4372 sp900543815
6.hc20	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA4372_s_UBA4372 sp900543815
bin.26.hh13	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA4372_s_UBA4372 sp900543815
bin.49.ca25	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA4372_s_UBA4372 sp900770805
bin.118.gv09	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6382_s_UBA6382
bin.155.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6382_s_UBA6382
bin.323.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6382_s_UBA6382
bin.54.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6382_s_UBA6382
bin.64_sub.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6382_s_UBA6382
bin.261.hk	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6382_s_UBA6382 sp900557555
bin.51.gv07	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6398_s_UBA6398
maxbin.173_sub.gv	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6398_s_UBA6398
193.hc17	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6398_s_UBA6398 sp003150315
58.hk14	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6398_s_UBA6398 sp003150315
193.gv26	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6398_s_UBA6398 sp003150315
57.gv26	d_Bacteriap_Bacteroidotac_Bacteroidia_Bacteroidales_Bacteroidaceae_UBA6398_s_UBA6398 sp003150315

maxbin.059_sub.gh10 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Marinilabiliaceae;g__W3P20-009;s__
maxbin.065_sub.gw02 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Marinilabiliaceae;g__W3P20-009;s__
maxbin.079_gw03 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Marinilabiliaceae;g__W3P20-009;s__
maxbin.314_sub.gw d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Marinilabiliaceae;g__W3P20-009;s__
110.hh14 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873;s__CAG-873 sp900540625
146.hh13 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873;s__CAG-873 sp900540625
171.hh11 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873;s__CAG-873 sp900540625
267_sub.hh d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873;s__CAG-873 sp900540625
2.hc16 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAIUPY01;s__CAIUPY01 sp022768005
253.hc17 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAIUPY01;s__CAIUPY01 sp022768005
bin.39.hc d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAIUPY01;s__CAIUPY01 sp022768005
127.ca22 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Lepagella;s__
153.go27 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Lepagella;s__Lepagella sp015061085
bin.461.go d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Lepagella;s__Lepagella sp015061085
221.hh14 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Limisoma;s__Limisoma sp000437795
59_sub.hc16 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Limisoma;s__Limisoma sp000437795
bin.149.hh15 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Limisoma;s__Limisoma sp000437795
bin.24.hc19 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Limisoma;s__Limisoma sp000437795
bin.70_sub.hh11 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Limisoma;s__Limisoma sp000437795
130.gw04 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__SFTJ01;s__
158_sub.gw02 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__SFTJ01;s__
23.g08 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__SFTJ01;s__
311.g07 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__
312_sub.gw03 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__
79.g03 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__
bin.367.gw d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__
bin.595.gw d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__
maxbin.356_sub.gh d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__
140.hh14 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__Sodaliphilus sp004557565
156.hc16 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__Sodaliphilus sp004557565
156.hc17 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__Sodaliphilus sp004557565
237.hc20 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__Sodaliphilus sp004557565
274.hh15 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__Sodaliphilus sp004557565
335.hh d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__Sodaliphilus sp004557565
35.hh13 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Sodaliphilus;s__Sodaliphilus sp004557565
bin.163.hc19 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__UBA7173;s__UBA7173 sp900546835
bin.199.hc18 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__UBA7173;s__UBA7173 sp900546835
bin.360.hc d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__UBA7173;s__UBA7173 sp900546835
148.ca25 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Onthomorpha;s__Onthomorpha sp002358855
bin.16.ca21 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Onthomorpha;s__Onthomorpha sp002358855
bin.42.ca23 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Onthomorpha;s__Onthomorpha sp002358855
bin.200.ca d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Onthomorpha;s__Onthomorpha sp017559135
126.g03 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
163.g04 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
97_sub.gh d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
bin.119.gh10 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
bin.149.gh09 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
bin.152.gh07 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
bin.214.gh06 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
bin.31.gh08 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
bin.40.gw01 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
bin.82.gw02 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
maxbin.062_sub.gw05 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__Phl12;s__
128.gw d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
166.g07 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
214.gw02 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
95.gw04 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
95.gw05 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
bin.112.g08 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
bin.139.gw01 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
bin.217.g09 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
maxbin.012.gh06 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
maxbin.018.gw03 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
maxbin.023_gh10 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3_g__UBA1711;s__
25.go27 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Aphodosoma;s__
bin.108.go26 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Aphodosoma;s__
222_sub.gw01 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Enterocola;s__
bin.108.gw d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Enterocola;s__
bin.245.gw03 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Enterocola;s__
bin.63.g01 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Enterocola;s__
bin.22.go26 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Enterocola;s__Enterocola sp017508305
bin.236.go d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Enterocola;s__Enterocola sp017508305
105.go27 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Enterocola;s__Enterocola sp017517845
bin.199.go d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Enterocola;s__Enterocola sp017517845
bin.220.gw d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__RF16;s__
bin.28.g08 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__RF16;s__
bin.81.gw01 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__RF16;s__
maxbin.223_sub.gh d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__RF16;s__
169.hc17 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__RF16;s__RF16 sp900556095
201.hh13 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__RF16;s__RF16 sp900556095
233.hh15 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__RF16;s__RF16 sp900556095
86.ca23 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__RGIG9608;s__RGIG9608 sp017652785
bin.185.ca d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__RGIG9608;s__RGIG9608 sp017652785
141_sub.g09 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__UBA1181;s__
284_sub.g010 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__UBA1181;s__
324_sub.g01 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__UBA1181;s__
70.gw05 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__UBA1181;s__
bin.163.gw d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__UBA1181;s__
bin.199.g06 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__UBA1181;s__
bin.241_sub.gw04 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__UBA1181;s__
bin.260_sub.gw02 d_Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__UBA1181;s__

bin.280_sub.gw01	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_UBA1181;s
bin.292.gw07	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_UBA1181;s
bin.8.gw08	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_UBA1181;s
bin.98_sub.gw03	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_UBA1181;s
336_sub.gw07	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_UBA363;s
bin.108.gw07	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
bin.127.gw10	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
bin.129.gw06	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
bin.13.gw04	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
bin.258.gw02	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
bin.573.gw	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
bin.84.gw05	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
maxbin.033.gw03	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
maxbin.039.gw01	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
maxbin.041.gw08	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
maxbin.044.gw	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
maxbin.047.gw09	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Paludibacteraceae;g_W0P28-013;s
35_sub.gw30	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s
maxbin.004.ca21	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s
bin.427_hc	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes putredinis
132.gw30	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp015059805
150.gw02	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp015060115
maxbin.003_sub.gw27	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp015060115
111_sub.gw29	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017410165
124_sub.gw28	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017410165
55_sub.gw30	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017437045
45.gw27	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017442365
bin.142.gw28	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017442365
bin.97.gw30	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017442365
maxbin.027_sub.gw29	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017442365
139.gw29	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017624955
178.gw27	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017624955
191.gw28	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017624955
191.ca23	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp00769045
maxbin.001.gw30	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp017624955
maxbin.004.gw29	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Alistipes;s_Alistipes sp037880705
bin.142.ca	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_CAIGB011;s
120.ca22	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Tidjaniabacter;s
158_sub.gw08	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Tidjaniabacter;s
198.ca23	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Tidjaniabacter;s
bin.145.gw05	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Tidjaniabacter;s
bin.206.gw10	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Tidjaniabacter;s
bin.72.gw	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Tidjaniabacter;s
10.gw	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Tidjaniabacter;s_Tidjaniabacter sp017396085
129.gw27	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Tidjaniabacter;s_Tidjaniabacter sp017396085
bin.70.gw28	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Rikenellaceae;g_Tidjaniabacter;s_Tidjaniabacter sp017396085
bin.149.gw	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Tannerellaceae;g_Parabacteroides;s
bin.161.gw03	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Tannerellaceae;g_Parabacteroides;s
bin.295.gw	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Tannerellaceae;g_Parabacteroides;s
bin.430.gw	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Tannerellaceae;g_Parabacteroides;s
36_sub.hc	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_Tannerellaceae;g_Parabacteroides;s_Parabacteroides distans
bin.104_sub.gw02	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
bin.164.gw10	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
bin.197.gw03	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
bin.203.gw06	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
bin.228.gw09	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
bin.269.gw04	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
bin.478.gw	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
maxbin.005_sub.gw05	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
maxbin.011_sub.gw08	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
maxbin.027_sub.gw07	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
maxbin.042_sub.gw10	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s
66.gw28	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s_UBA1757 sp017468435
bin.495.gw	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA1402;g_UBA1757;s_UBA1757 sp017468435
210_sub.gw10	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA3663;g_UBA3663;s
26_sub.gw08	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA3663;g_UBA3663;s
66_sub.gw04	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA3663;g_UBA3663;s
89.gw05	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UBA3663;g_UBA3663;s
bin.121_sub.gw03	d_Bacteriap_Bacteroidota;c_Bacteridiao_Bacteroidales_f_UB

[illegible]

bin.156.hh15 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_D_s_Campylobacter_D sp900539255
 bin.85_sub_hh14 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_D_s_Campylobacter_D sp900539255
 bin.98.hc17 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_D_s_Campylobacter_D sp900539255
 maxbin.046.hh12 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_D_s_Campylobacter_D sp900539255
 maxbin.142.hh11 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_D_s_Campylobacter_D sp900539255
 bin.144.hc16 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_D_s_Campylobacter_D sp900539255
 11_sub_gh10 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s
 160_sub_gw d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s
 228_sub_gh d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s
 292.gh06 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s
 308_sub_gw04 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s
 38_sub_gh07 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s
 bin.167.gw02 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s
 bin.202.gh09 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s
 bin.276.gw03 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s
 maxbin.190.gh08 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s
 56.hh12 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter infans
 bin.22.hc16 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter infans
 bin.304.hh d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter infans
 bin.512.hc d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter infans
 bin.63.hh11 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter infans
 bin.67.hc17 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter infans
 maxbin.082_sub_hc18 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter infans
 211.gw29 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter ovis
 bin.111.gw26 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter ovis
 bin.101.g02 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter ovis
 maxbin.030.g02 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter ovis
 maxbin.030.g03 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter ovis
 maxbin.035.g0 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter ovis
 198.ca22 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter sp017646085
 maxbin.327.ca d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Campylobacteraceae_g_Campylobacter_s_Campylobacter sp017646085
 32.gw02 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Helicobacteraceae_g_NHYM01_s
 45.gh d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Helicobacteraceae_g_NHYM01_s
 50_sub_gw03 d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Helicobacteraceae_g_NHYM01_s
 7_sub.gw d_Bacteriap_Campylobacterota_c_Campylobacteriay_Campylobacterales_f_Helicobacteraceae_g_NHYM01_s
 bin.128.gw01 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 bin.194.gh08 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 bin.199_sub_gw03 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 bin.217.gw02 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 bin.272_sub_gh06 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 bin.76.gw05 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 bin.93.gh09 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 maxbin.009_sub_gw04 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 maxbin.013_sub_gh0 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 maxbin.013.g02 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 maxbin.014_sub_gh10 d_Bacteriap_Chloroflexota_c_Anaerolineae_o_Anaerolineales_f_Anaerolineaceae_g_Flexilinea_s
 bin.183_sub_hh14 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_QHMH01_s_QHMH01 sp003258795
 bin.368.hh d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_QHMH01_s_QHMH01 sp003258795
 132.hc19 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_RUG841_s_RUG841 sp900772035
 18_sub_hc20 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_RUG841_s_RUG841 sp900772035
 234_sub_hh d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_RUG841_s_RUG841 sp900772035
 bin.73.hh12 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_RUG841_s_RUG841 sp900772035
 maxbin.075.hh11 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_RUG841_s_RUG841 sp900772035
 200_sub_hh11 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_Scotosia_s_Scotosia sp900321895
 85_sub_hh14 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_Scotosia_s_Scotosia sp900321895
 bin.219_sub_hc d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_Scotosia_s_Scotosia sp900321895
 bin.27.hc17 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_Scotosia_s_Scotosia sp900321895
 bin.18.hc18 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_Stercorosia_s
 97.hh13 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_UBA2883_s_UBA2883 sp900768915
 bin.184.hh11 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_UBA2883_s_UBA2883 sp900768915
 bin.446.hc d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_UBA2883_s_UBA2883 sp900768915
 43_sub_hh12 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_UBA6984_s_UBA6984 sp003258725
 bin.136_sub_hc18 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_UBA6984_s_UBA6984 sp900550295
 bin.159_sub_hh d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_UMGS1585_s_UMGS1585 sp005053205
 137_sub_hc16 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_Zag111_s_Zag111 sp002103105
 147_sub_hc18 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_Zag111_s_Zag111 sp002103105
 43.hh15 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_Zag111_s_Zag111 sp002103105
 bin.135.hc16 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_Zag111_s_Zag111 sp002587535
 195_sub_hc17 d_Bacteriap_Cyanobacteriota_c_Vampirovibrionia_o_Gastranaerophilales_f_Gastranaerophilaceae_g_Zag111_s_Zag111 sp00458955
 bin.128.gw d_Bacteriap_Desulfobacter

bin.106.hc19 d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900540405
 bin.106.hh11 d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900540405
 bin.21.hh13 d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900540405
 maxbin.068.hh15 d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900540405
 maxbin.118.hh d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900540405
 maxbin.182.hc d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900541355
 14_sub.hh13 d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900541355
 bin.284.hc17 d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900541355
 maxbin.197.hh15 d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900541355
 maxbin.198_sub.hc20 d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900541355
 maxbin.206.hh d_Bacteria;p_Elusimicrobiota;c_Elusimicrobia;o_Elusimicrobiales;f_Elusimicrobiales;g_Avelusimicrobium;s_Avelusimicrobium;sp900541355
 310_sub.hh d_Bacteria;p_Eremiobacterota;c_Xenobia;o_Xenobiales;f_Xenobiaceae;g_Bruticola;s_Bruticola;sp004554425
 7.hc17 d_Bacteria;p_Eremiobacterota;c_Xenobia;o_Xenobiales;f_Xenobiaceae;g_Bruticola;s_Bruticola;sp004554425
 62.hc20 d_Bacteria;p_Eremiobacterota;c_Xenobia;o_Xenobiales;f_Xenobiaceae;g_Bruticola;s_Bruticola;sp934644775
 176.gw01 d_Bacteria;p_Fibrobacterota;c_Fibrobacteria;o_Fibrobacteriales;f_Fibrobacteraceae;g_Hallerella;s_Hallerella;s
 220.hh13 d_Bacteria;p_Fibrobacterota;c_Fibrobacteria;o_Fibrobacteriales;f_Fibrobacteraceae;g_Hallerella;s_Hallerella;s
 63.gw04 d_Bacteria;p_Fibrobacterota;c_Fibrobacteria;o_Fibrobacteriales;f_Fibrobacteraceae;g_Hallerella;s_Hallerella;s
 95_sub.gw02 d_Bacteria;p_Fibrobacterota;c_Fibrobacteria;o_Fibrobacteriales;f_Fibrobacteraceae;g_Hallerella;s_Hallerella;s
 bin.71.gw03 d_Bacteria;p_Fibrobacterota;c_Fibrobacteria;o_Fibrobacteriales;f_Fibrobacteraceae;g_Hallerella;s_Hallerella;s
 maxbin.223.gw d_Bacteria;p_Fibrobacterota;c_Fibrobacteria;o_Fibrobacteriales;f_Fibrobacteraceae;g_Hallerella;s_Hallerella;s
 22.hc20 d_Bacteria;p_Fibrobacterota;c_Fibrobacteria;o_Fibrobacteriales;f_Fibrobacteraceae;g_Hallerella;s_Hallerella;s
 29_sub.gw d_Bacteria;p_Fusobacteriota;c_Fusobacteriota;o_Fusobacteriales;f_Fusobacteriaceae;g_s_s
 276.g10 d_Bacteria;p_Myxococcota;c_Bradymonadia;o_UBA4248;f_UBA4248;g_UBA4248;s_UBA4248;s
 97.gw02 d_Bacteria;p_Myxococcota;c_Bradymonadia;o_UBA4248;f_UBA4248;g_UBA4248;s_UBA4248;s
 bin.239.gw d_Bacteria;p_Myxococcota;c_Bradymonadia;o_UBA4248;f_UBA4248;g_UBA4248;s_UBA4248;s
 15.hc20 d_Bacteria;p_Myxococcota;c_Bradymonadia;o_UBA4248;f_UBA4248;g_UBA4248;s_UBA4248;sp004554395
 maxbin.504.hc d_Bacteria;p_Myxococcota;c_Bradymonadia;o_UBA4248;f_UBA4248;g_UBA4248;s_UBA4248;sp004554395
 234.gw d_Bacteria;p_Myxococcota;c_Myxococcia;o_Myxococcales;f_UBA5297;g_UBA1203;s_UBA1203;s
 bin.219_sub.gw d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_Nanosyncoccus;s_Nanosyncoccus;s
 bin.51.gw03 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_Nanosyncoccus;s_Nanosyncoccus;s
 bin.55.g10 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_Nanosyncoccus;s_Nanosyncoccus;s
 bin.64.gw d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_Nanosyncoccus;s_Nanosyncoccus;s
 bin.86.gw d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_Nanosyncoccus;s_Nanosyncoccus;s
 maxbin.033_sub.g10 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_Nanosyncoccus;s_Nanosyncoccus;s
 maxbin.048_sub.gw d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_Nanosyncoccus;s_Nanosyncoccus;s
 maxbin.051_sub.gw02 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_Nanosyncoccus;s_Nanosyncoccus;s
 maxbin.094_sub.gw05 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_Nanosyncoccus;s_Nanosyncoccus;s
 bin.117.gw05 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 bin.197.g10 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 bin.270.gw02 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 bin.363.gw d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 bin.522.gw d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 maxbin.015_sub.g10 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 maxbin.030.gw01 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 maxbin.033.g10 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 maxbin.039_sub.g10 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 maxbin.085_sub.gw08 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 maxbin.089_sub.gw03 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 maxbin.240_sub.gw d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;s
 bin.204.hc18 d_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Nanosyncoccaceae;g_UBA2834;s_UBA2834;sp004561445
 bin.369.gw d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG3701;s_RUG3701;sp01793795
 109.g10 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 155.g10 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 191.g10 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 225.g10 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 239.gw01 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 255.gw05 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 267.g10 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 273.g10 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 298.gw02 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 36.gw03 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 63.gw d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 91.gw04 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;s
 58.g029 d_Bacteria;p_Plantomycetota;c_Plantomycetia;o_Pirellulales;f_Thermoguttaceae;g_RUG369;s_RUG369;sp017937485
 bin.13.hh14 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_CAAFY01;s_CAAFY01;sp937920765
 bin.156.hc18 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_CAAFY01;s_CAAFY01;sp937920765
 bin.267.hc d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_CAAFY01;s_CAAFY01;sp937920765
 bin.429.hh d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_CAAFY01;s_CAAFY01;sp937920765
 maxbin.082.hh13 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_CAAFY01;s_CAAFY01;sp937920765
 77_sub.hh13 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_RUG410;s_RUG410;sp900769705
 bin.163.hc20 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_RUG410;s_RUG410;sp900769705
 148.hc19 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_RUG410;s_RUG410;sp934271715
 249.hh12 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_RUG410;s_RUG410;sp934271715
 bin.101.hc d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_CAKQWA01;s_CAKQWA01;sp934277945
 bin.57.hc17 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_CAKQWA01;s_CAKQWA01;sp934277945
 bin.36.hh13 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA11549;s_UBA11549;sp002440235
 58.g10 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA11549;s_UBA11549;sp900550445
 134_sub.hh14 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA11549;s_UBA11549;sp900768185
 226_sub.hh13 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900768465
 86_sub.hh12 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900768465
 132_sub.hc20 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900768875
 bin.100.hc16 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900768875
 bin.130.hh14 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900768875
 bin.79.hc18 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900768875
 bin.89_sub.hh15 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900768875
 maxbin.181_sub.hh maxbin.188.hc d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900768875
 21.hc18 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900772625
 234_sub.hh14 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900772625
 maxbin.637_sub.hc d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp900772625
 90.hh13 d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_RF32;f_CAG-977;g_UBA2903;s_UBA2903;sp934202735

bin.180.hhn	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RF32_f_UBA3637g_RIGIG7089_s_RIGIG7089.sp934202735
131.hh	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_CACZYB01g_CACZYB01.sp016297965
237_sub.hc	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_CACZYB01g_CACZYB01.s_CACZYB01.sp016297965
254.hc17	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_CACZYB01g_CACZYB01.sp016297965
bin.111.hh15	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_CACZYB01g_CACZYB01.s_CACZYB01.sp934246625
bin.61.hh	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_CACZYB01g_CACZYB01.s_CACZYB01.sp934246625
6.gn10	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_
maxbin.018.go28	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_
maxbin.060.go30	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_
maxbin.089.go	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_
maxbin.457.gn	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_
maxbin.053.ca24	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_Enterousia.sp01562525
bin.94.gn26	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_Enterousia.sp017436325
bin.7_sub.go	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_Enterousia.sp017472025
187.hc17	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_Enterousia.sp00546225
221.hc16	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_Enterousia.sp00546225
bin.155.hh12	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_Enterousia.sp00546225
maxbin.170.hh11	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_Enterousia.sp00546225
maxbin.015.hh15	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_Enterousia.sp00549365
bin.149.hh14	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RS-D84_f_RS-D84g_Enterousia;s_Enterousia.sp00550495
bin.124.gw02	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RUG11792_f_RUG11792g_MGBC162888;s_
bin.244_sub.gw03	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RUG11792_f_RUG11792g_MGBC162888;s_
bin.349_sub.gn	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RUG11792_f_RUG11792g_MGBC162888;s_
bin.377_sub.gn	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RUG11792_f_RUG11792g_MGBC162888;s_
bin.65.gn08	d_Bacteriap_Pseudomonadota;c_Alphaproteobacteria;o_RUG11792_f_RUG11792g_MGBC162888;s_
110.ca23	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Aphodousia;s_
158.ca25	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Aphodousia;s_
160.ca21	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Aphodousia;s_
maxbin.132.ca24	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Aphodousia;s_
maxbin.393.go	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Aphodousia;s_
169.hh13	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Comonanotus_Comonanotus.kerstarii
142.gw05	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
159.gn08	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
16.gw02	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
303.gw	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
35.gn09	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
bin.140.gn06	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
bin.208.gw03	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
bin.121.gw04	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
bin.73.gw01	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
bin.8_sub.gw07	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
maxbin.169_sub.gn	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_
bin.160.hh15	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_Duodenibacillus.massiliensis
maxbin.114.hh	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_Duodenibacillus.massiliensis
228_sub.hh12	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_Duodenibacillus.sp00544255
bin.94.hh14	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_Duodenibacillus.sp00544255
maxbin.178_sub.hh15	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_Duodenibacillus.sp00544255
maxbin.185_sub.hh	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_Duodenibacillus.sp00544255
bin.580.hh	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Duodenibacillus;s_Duodenibacillus.sp00544335
128.gn03	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
251.gn10	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
42.gw05	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
54.gn06	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
bin.238.gn08	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
bin.240.gn	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
bin.28.gw01	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
bin.93.gw04	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
maxbin.193.gw	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
maxbin.219.gn07	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
maxbin.236.gn	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Burkholderiaceae;g_Oxalobacter;s_
bin.122_sub.hc	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Parauterellalesf_Parauterellaceae;g_Parauterella_Parauterella.excrementihominis
132_sub.gn08	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Rhodocyclaceae;g_SFHR01;s_
206.gn06	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Rhodocyclaceae;g_SFHR01;s_
286.gw04	d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderialesf_Rhodocyclaceae;g_SFHR01;s_
31.gw02	d_Bacteriap_Pseudomonadota;c_Gammaprote

44.hc17 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Pasteurellaceae;g_Haemophilus_D;s_Haemophilus_D sp959600045
 bin.104_sub.g30 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio
 bin.175.ca d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio
 bin.126.g06 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinimonass_s
 bin.350.g07 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinimonass_s
 bin.541.gw d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinimonass_s
 maxbin.176_sub.gw03 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinimonass_s
 157.gh d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s
 maxbin.391.gw d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s
 o_sub.hc18 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 129_sub.hh12 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 160.hc16 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 189_sub.hh13 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 26.h14 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 bin.184.hc20 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 bin.307.hh d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 bin.568.hc d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 bin.64.hh11 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 maxbin.005_sub.hh15 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 maxbin.006_sub.hc17 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 maxbin.007.hc19 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_Succinivibrio_s_Succinivibrio sp000431835
 109_sub.hh13 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 139_sub.hc18 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 141.hc17 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 3.hc20 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 52.hc d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 bin.1.hc19 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 bin.42.hh d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 bin.47.hc16 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 maxbin.009.hh12 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 maxbin.020_sub.hh14 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 maxbin.021.hh15 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 maxbin.056.hh12 d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacteriales_f_Succinivibrionaceae;g_WG-1s_WG-1 sp900539665
 maxbin.151_sub.hh d_Bacteriap_Pseudomonadota;c_Gammaproteobacteria;o_Pseudomonadales_f_Moraxellaceae;g_Acinetobacter_s_Acinetobacter sp003711395
 324_sub.gw d_Bacteriap_Spirochaetota;c_Brachyspirae;o_Brachyspirales_f_Brachyspiraceae;g_Brachyspira;s
 49.gh d_Bacteriap_Spirochaetota;c_Brachyspirae;o_Brachyspirales_f_Brachyspiraceae;g_Brachyspira;s
 237.hh13 d_Bacteriap_Spirochaetota;c_Brachyspirae;o_Brachyspirales_f_Brachyspiraceae;g_Brachyspira;s_Brachyspira aalborgi
 25.hc16 d_Bacteriap_Spirochaetota;c_Brachyspirae;o_Brachyspirales_f_Brachyspiraceae;g_Brachyspira;s_Brachyspira aalborgi
 255.hh d_Bacteriap_Spirochaetota;c_Brachyspirae;o_Brachyspirales_f_Brachyspiraceae;g_Brachyspira;s_Brachyspira aalborgi
 277.hc d_Bacteriap_Spirochaetota;c_Brachyspirae;o_Brachyspirales_f_Brachyspiraceae;g_Brachyspira;s_Brachyspira aalborgi
 59.hh15 d_Bacteriap_Spirochaetota;c_Brachyspirae;o_Brachyspirales_f_Brachyspiraceae;g_Brachyspira;s_Brachyspira aalborgi
 7_sub.hh14 d_Bacteriap_Spirochaetota;c_Brachyspirae;o_Brachyspirales_f_Brachyspiraceae;g_Brachyspira;s_Brachyspira aalborgi
 85.hc17 d_Bacteriap_Spirochaetota;c_Brachyspirae;o_Brachyspirales_f_Brachyspiraceae;g_Brachyspira;s_Brachyspira aalborgi
 14.g028 d_Bacteriap_Spirochaetota;c_GWE2-31-10;g_GWE2-31-10;g_RIG8597_s_RIG8597 sp017624275
 bin.385.g0 d_Bacteriap_Spirochaetota;c_GWE2-31-10;g_GWE2-31-10;g_RIG8597_s_RIG8597 sp017624275
 85_sub.g06 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Sphaerochaetales_f_Sphaerochaetaceae;g_Omithosporichaeta;s
 bin.255.gw02 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Sphaerochaetales_f_Sphaerochaetaceae;g_UBA9732;s
 bin.392.gw d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Sphaerochaetales_f_Sphaerochaetaceae;g_UBA9732;s
 bin.5.gw03 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Sphaerochaetales_f_Sphaerochaetaceae;g_UBA9732;s
 maxbin.044_sub.gw d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Sphaerochaetales_f_Sphaerochaetaceae;g_UBA9732;s
 maxbin.051_sub.gw07 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Sphaerochaetales_f_Sphaerochaetaceae;g_UBA9732;s
 maxbin.052.gw01 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Sphaerochaetales_f_Sphaerochaetaceae;g_UBA9732;s
 maxbin.087.g07 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Sphaerochaetales_f_Sphaerochaetaceae;g_UBA9732;s
 63.hc20 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Sphaerochaetales_f_Sphaerochaetaceae;g_UBA9732_s_UBA9732 sp001940825
 bin.188.hc d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Sphaerochaetales_f_Sphaerochaetaceae;g_UBA9732_s_UBA9732 sp001940825
 303.gh d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_RIG9060;s
 maxbin.299.gw d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_RIG9060;s
 100.gw02 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 160_sub.hh13 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 195.gh10 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 205_sub.g06 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 241_sub.gw01 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 274.gw03 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 28.g08 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 40.g09 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 44.gw04 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 44_sub.g07 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 55.gh10 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 76_sub.g07 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 97_sub.gw05 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D;s
 98.g08 d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Trepon

bin.43.gw05	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
bin.433.g_h	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
bin.452.gw	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
bin.61.gw01	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
bin.664.g_h	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
bin.669.g_h	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
bin.96.gw05	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
maxbin_029_sub.hc20	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
maxbin_036.gw	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
maxbin_095.gw05	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
maxbin_146.gw03	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
maxbin_159.g_h	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
maxbin_200_sub.g_h	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
maxbin_252_sub.gw02	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_
bin.118.hc20	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_berlinense
bin.179.hh15	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_berlinense
bin.209.hc18	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_berlinense
bin.85.hh	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_berlinense
181.hh13	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
269.hc	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
bin.105.hh15	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
bin.123.hc20	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
bin.136.hh12	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
bin.143.hh11	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
bin.168.hh17	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
bin.174.hh14	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
bin.3.hc16	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
bin.576.hh	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
bin.63.hc18	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_peruense
118_sub.hh11	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_sp900541945
153_sub.hc20	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_sp900541945
bin.40.ca21	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_sp900767955
bin.41_sub.gw28	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_sp900767955
bin.98.gw26	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_sp900767955
87_sub.hh14	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_succinifaciens
bin.200.hc20	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_succinifaciens
bin.236_sub.hc	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_succinifaciens
bin.43.hh11	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_succinifaciens
bin.67_sub.hh13	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_succinifaciens
maxbin_016.hc18	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_D.s_Treponema_D_succinifaciens
bin.85.gw27	d_Bacteriap_Spirochaetota;c_Spirochaetia;o_Treponematales_f_Treponemataceae;g_Treponema_F.s_Treponema_F_sp017622135
174_sub.gw08	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_
bin.13.gw05	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_
bin.250.gw07	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_
bin.284.gw10	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_
bin.56.gw06	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_
bin.96.gw09	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_
maxbin_130.gw04	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_
99.hc16	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_RUG572_sp900547945
bin.106.hc20	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_RUG572_sp900547945
bin.108.hc18	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_RUG572_sp900547945
bin.145.hh14	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_RUG572_sp900547945
bin.183.hh11	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_RUG572_sp900547945
bin.185.hh12	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_RUG572_sp900547945
bin.294.hc	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_RUG572_sp900547945
bin.69.hh15	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_RUG572_s_RUG572_sp900547945
bin.11.ca21	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_Spyradenecuss_
bin.179.ca	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_Spyradenecuss_
bin.74.ca24	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_UBA1067_g_Spyradenecuss_
bin.46.gw26	d_Bacteriap_Verrucomicrobiota;c_Kiritimatiellia;o_RFP12_f_

bin.173.gw02	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Oligosphaerales;f_Oligosphaeraaceae;g_UBA1724;s_
bin.216.gw08	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Oligosphaerales;f_Oligosphaeraaceae;g_UBA1724;s_
bin.218.gw09	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Oligosphaerales;f_Oligosphaeraaceae;g_UBA1724;s_
bin.229.gw05	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Oligosphaerales;f_Oligosphaeraaceae;g_UBA1724;s_
bin.247.gw01	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Oligosphaerales;f_Oligosphaeraaceae;g_UBA1724;s_
bin.33.gw03	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Oligosphaerales;f_Oligosphaeraaceae;g_UBA1724;s_
bin.480.gw	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Oligosphaerales;f_Oligosphaeraaceae;g_UBA1724;s_
bin.145.g	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Victivallales;f_UBA1829;s_SIG77;s_SIG77;sp17623265
61.hc17	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Victivallales;f_UBA1829;s_UBA1829;s_UBA1829;sp00549045
105.hc18	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Victivallales;f_UBA1829;s_UBA1829;s_UBA1829;sp00549415
130_sub.hc	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Victivallales;f_UBA1829;s_UBA1829;s_UBA1829;sp00549415
bin.187.hh14	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Victivallales;f_UBA1829;s_UBA1829;s_UBA1829;sp00549415
bin.47.hh13	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Victivallales;f_UBA1829;s_UBA1829;s_UBA1829;sp00549415
bin.90.hh12	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Victivallales;f_UBA1829;s_UBA1829;s_UBA1829;sp00549415
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maxbin.082.hh	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Victivallales;f_UBA1829;s_UBA1829;s_UBA1829;sp00549415
bin.609.hh	d_Bacteriap_Verrucomicrobiota;c_Lentisphaeria;o_Victivallales;f_Victivallaceae;g_Victivallis;s_Victivallis vadensis
119.hh13	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitatales;f_CAG-312g_CAKUIA01;s_CAKUIA01;sp394613415
316.hc	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitatales;f_CAG-312g_CAKUIA01;s_CAKUIA01;sp394613415
bin.211.hh	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitatales;f_CAG-312g_CAKUIA01;s_CAKUIA01;sp394613415
maxbin.064.hc18	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitatales;f_CAG-312g_CAKUIA01;s_CAKUIA01;sp394613415
maxbin.133.hh15	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitatales;f_CAG-312g_CAKUIA01;s_CAKUIA01;sp394613415
bin.126.hh15	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitatales;f_CAG-312g_Merdousia;s_Merdousia;sp900548275
bin.632.hh	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitatales;f_CAG-312g_Merdousia;s_Merdousia;sp900548275
94.gd20	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitatales;f_UBA953g_Spyradosoma;s_Spyradosoma;sp15061905
bin.88.g	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Opitatales;f_UBA953g_Spyradosoma;s_Spyradosoma;sp15061905
164.ca24	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_
bin.38.ca21	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_
104.hh13	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia muciniphila
5.hc19	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia muciniphila
51.hc18	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia muciniphila
60.hc20	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia muciniphila
bin.158.hc17	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia muciniphila
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maxbin.120.hc	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia muciniphila
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bin.104.gw28	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia sp17398355
bin.326.g	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia sp17398355
bin.13.g030	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia sp17399165
bin.14.g029	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia sp17399165
bin.89.g28	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia sp17399165
bin.153.g	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia sp17415995
bin.125.g029	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia sp17435365
bin.70.g027	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia sp17435365
bin.80.g030	d_Bacteriap_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaaceae;g_Akkermansia;s_Akkermansia sp17517805

7.1.4.2.4 Shannon's diversity index for pooled samples

Figure 7.2: Shannon diversity index – pooled files

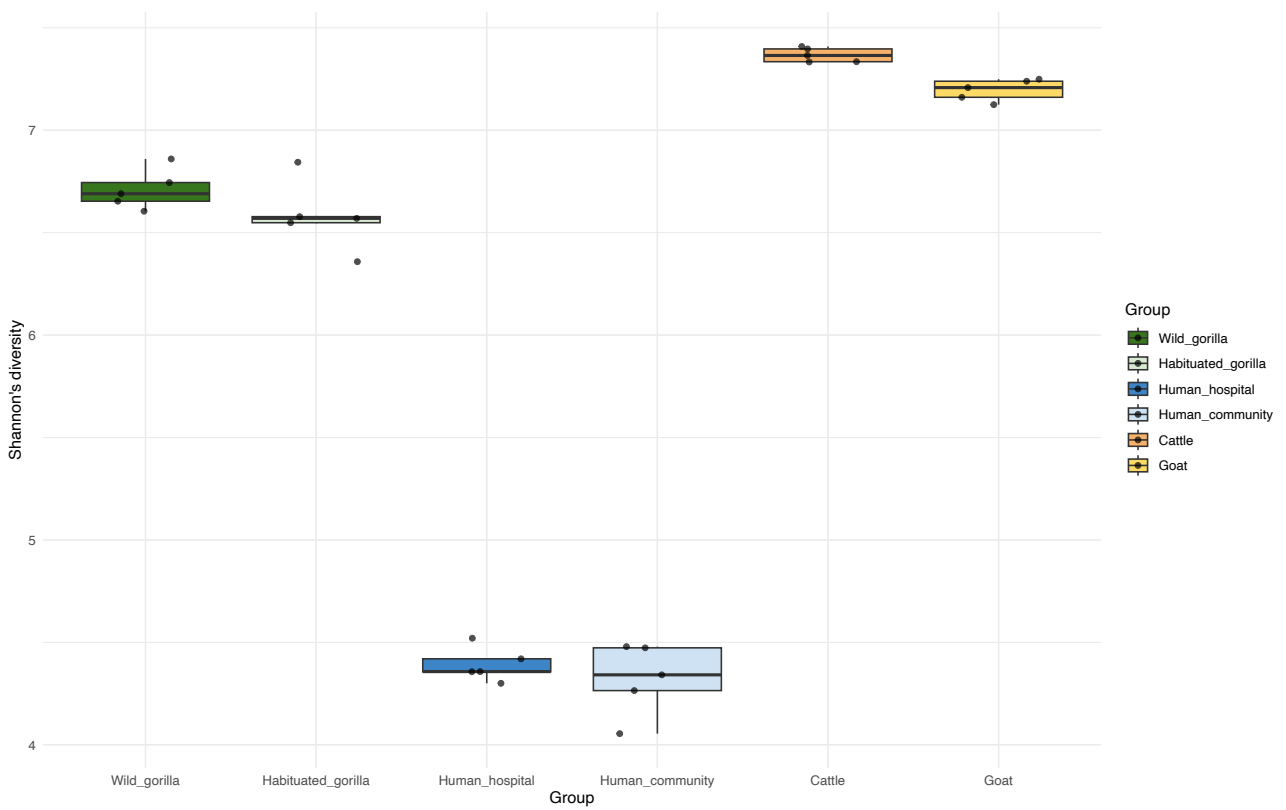


Figure 7.1 - This figure illustrates the Shannon diversity index calculated for pooled gut microbiome samples, providing a measure of species diversity within the dataset.

7.1.4.3 Appendices – Chapter 5

7.1.4.3.1 *Treponema* and *Prevotella* MAGs quality assessment results

Figure 7.3: Completeness and contamination of *Treponema* MAGs

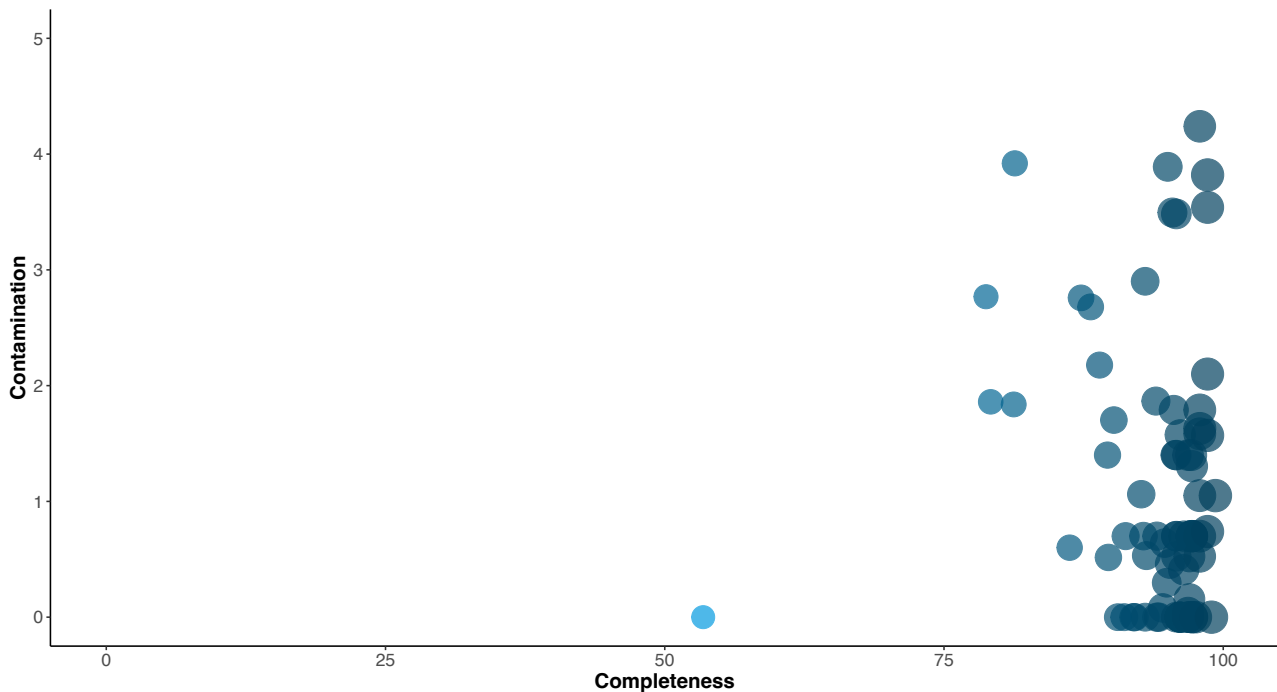


Figure 7.3 - Completeness and contamination of *Treponema* MAGs (%): This figure illustrates the completeness and contamination levels of *Treponema* MAGs, expressed as percentages. It provides insights into the quality of the assembled genomes, with completeness indicating the extent of genomic representation and contamination reflecting the presence of non-target or erroneous sequences.

Figure 7.4: Completeness and contamination levels of *Prevotella* MAGs

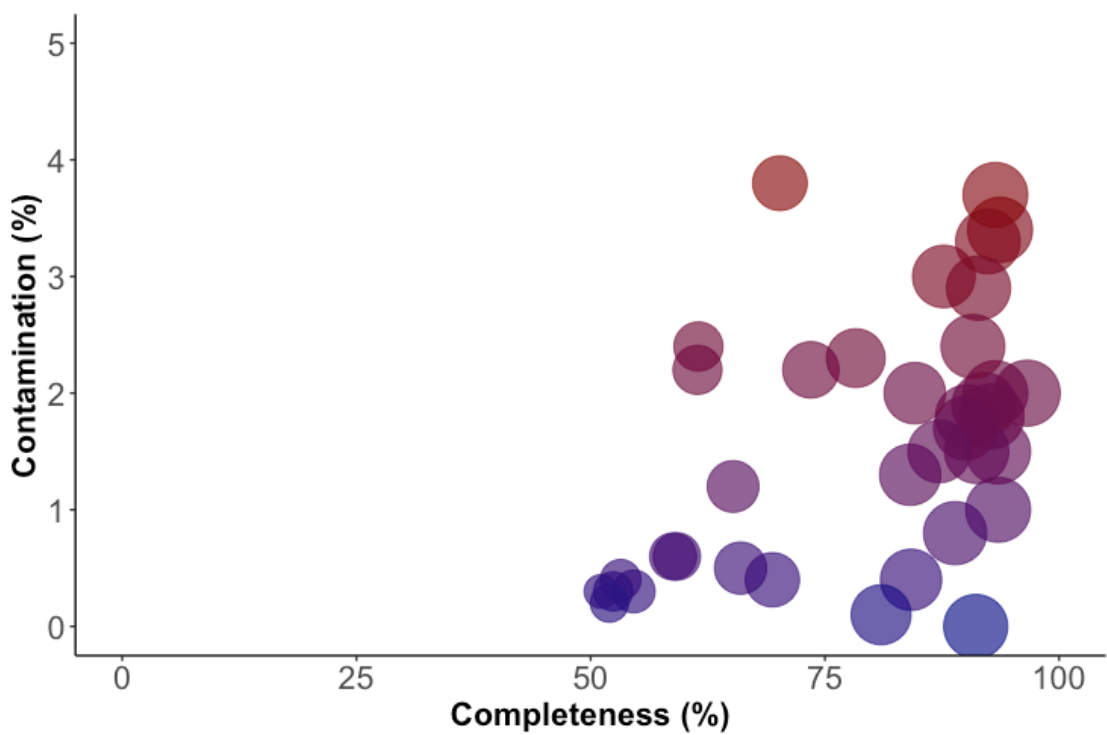


Figure 7.4 - This figure illustrates the completeness and contamination levels of *Prevotella* MAGs, expressed as percentages.

7.1.4.3.2 *Treponema* and *Prevotella* phylogenetic trees

Figure 7.5: Unrooted phylogenetic tree of study MAGs and publicly available *Treponema* genomes

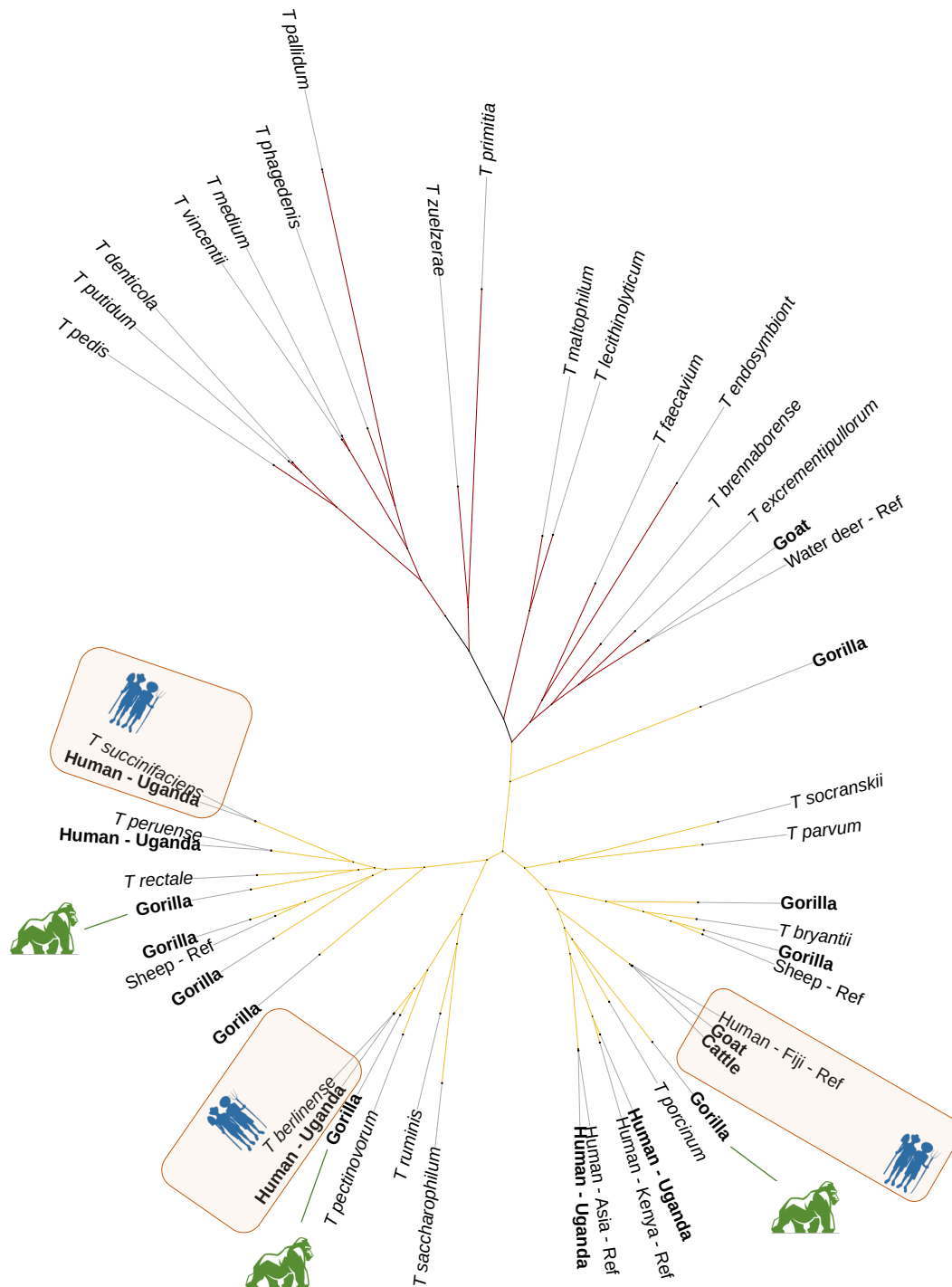


Figure 7.5 - Unrooted phylogenetic tree containing MAGs from this study and publicly available *Treponema* genomes: This figure displays an unrooted phylogenetic tree comparing the MAGs identified in this study with publicly available genomes from known *Treponema* species.

Figure 7.6: Unrooted phylogeny of study MAGs and publicly available *Treponema* genomes

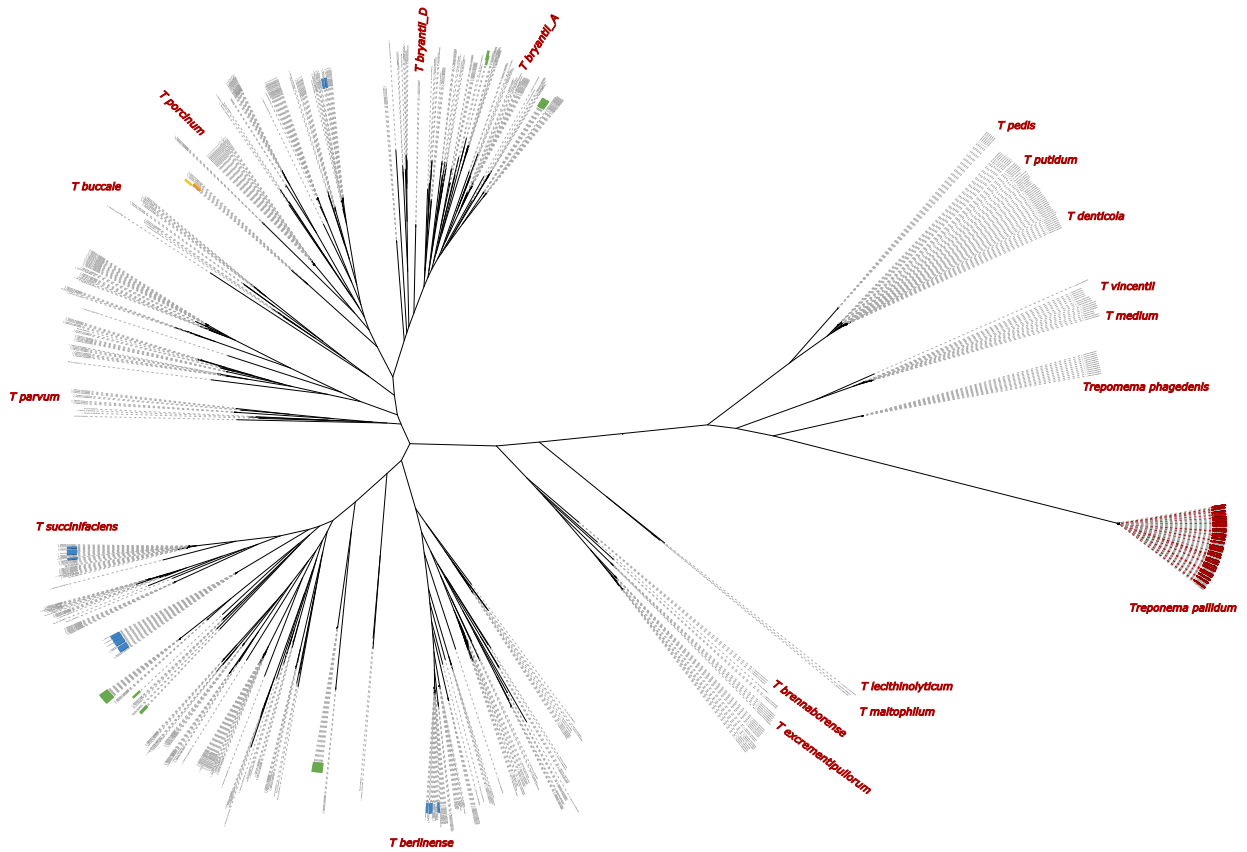


Figure 7.6 - Unrooted phylogenetic tree containing MAGs from this study and reference *Treponema* genomes: This figure displays an unrooted phylogenetic tree comparing the MAGs identified in this study with publicly available from known *Treponema* species.

Figure 7.7: Rectangular phylogenetic tree of described and putative novel *Treponema* species and their relationship to pig-derived *Treponema*

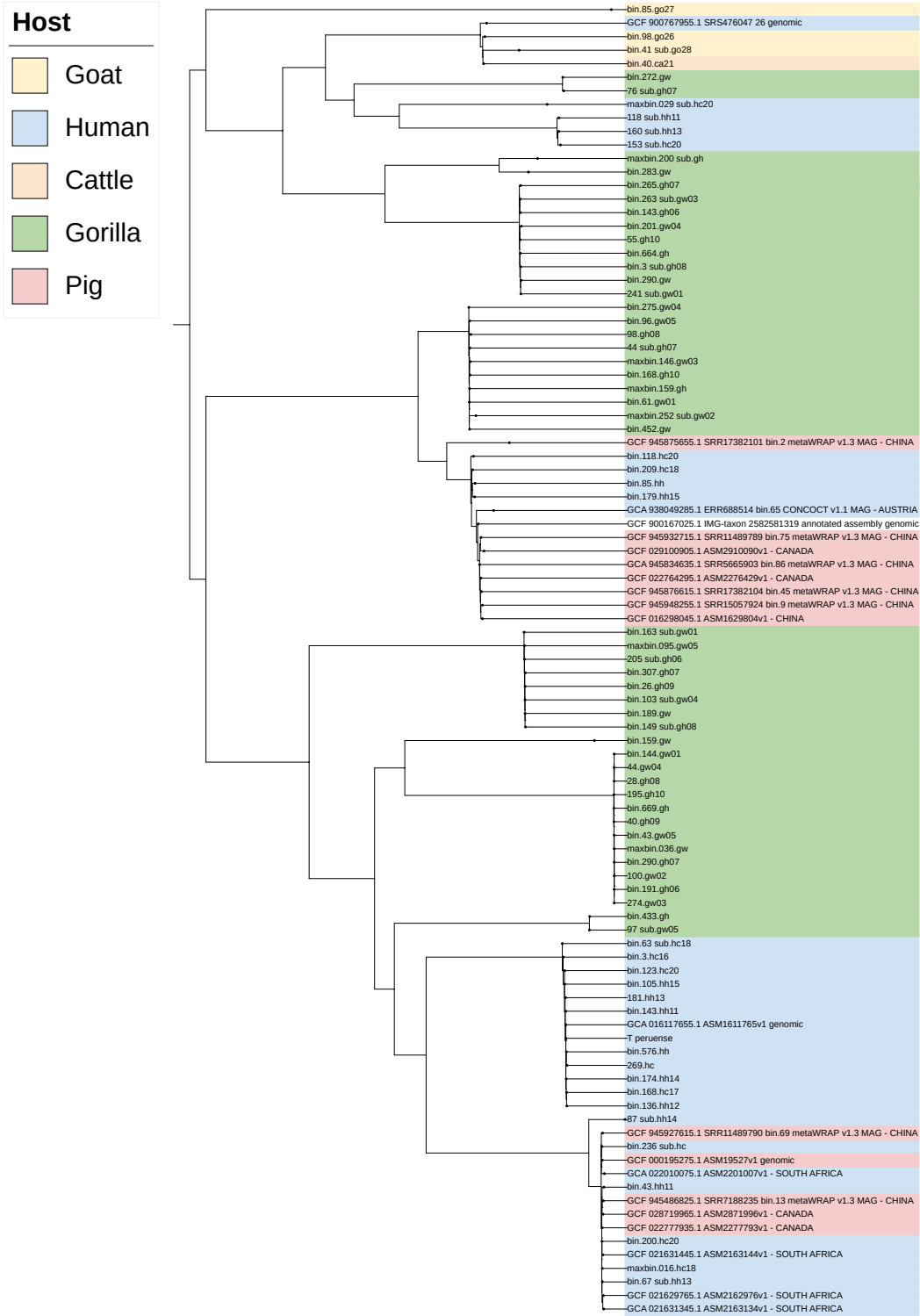


Figure 7.7 - A rectangular phylogenetic tree depicting the described and potential new species of *Treponema* and their relationship with the *Treponema* species recovered from pig samples.

Figure 7.8: Unrooted phylogeny of study MAGs and publicly available *Treponema* genomes

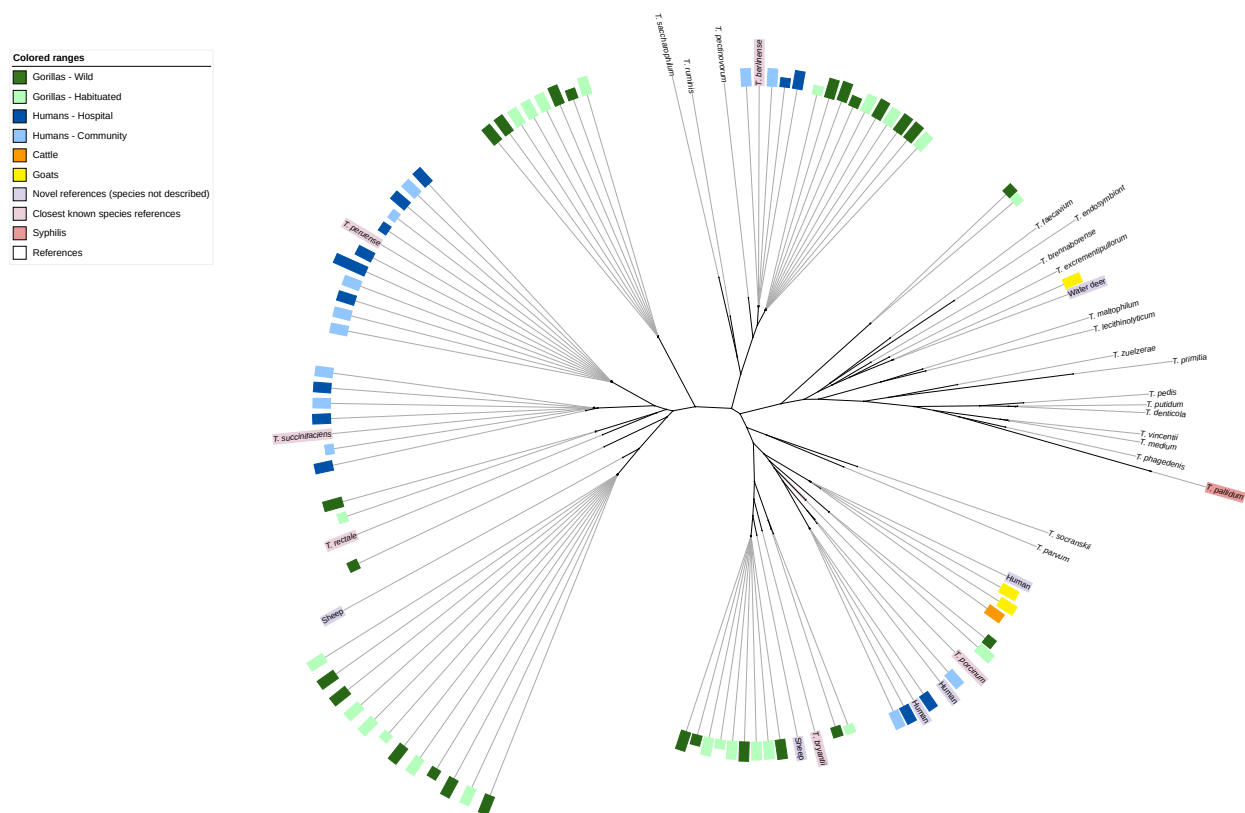


Figure 7.8 - Unrooted phylogenetic tree containing MAGs from this study and publicly available *Treponema* genomes: This figure displays an unrooted phylogenetic tree comparing the MAGs identified in this study with publicly available genomes from known *Treponema* species.

Figure 7.9 - Phylogenetic tree, unrooted, displaying the publicly available and putative novel species of *Prevotella*.



Figure 7.10: Unrooted phylogeny of novel *Prevotella* species

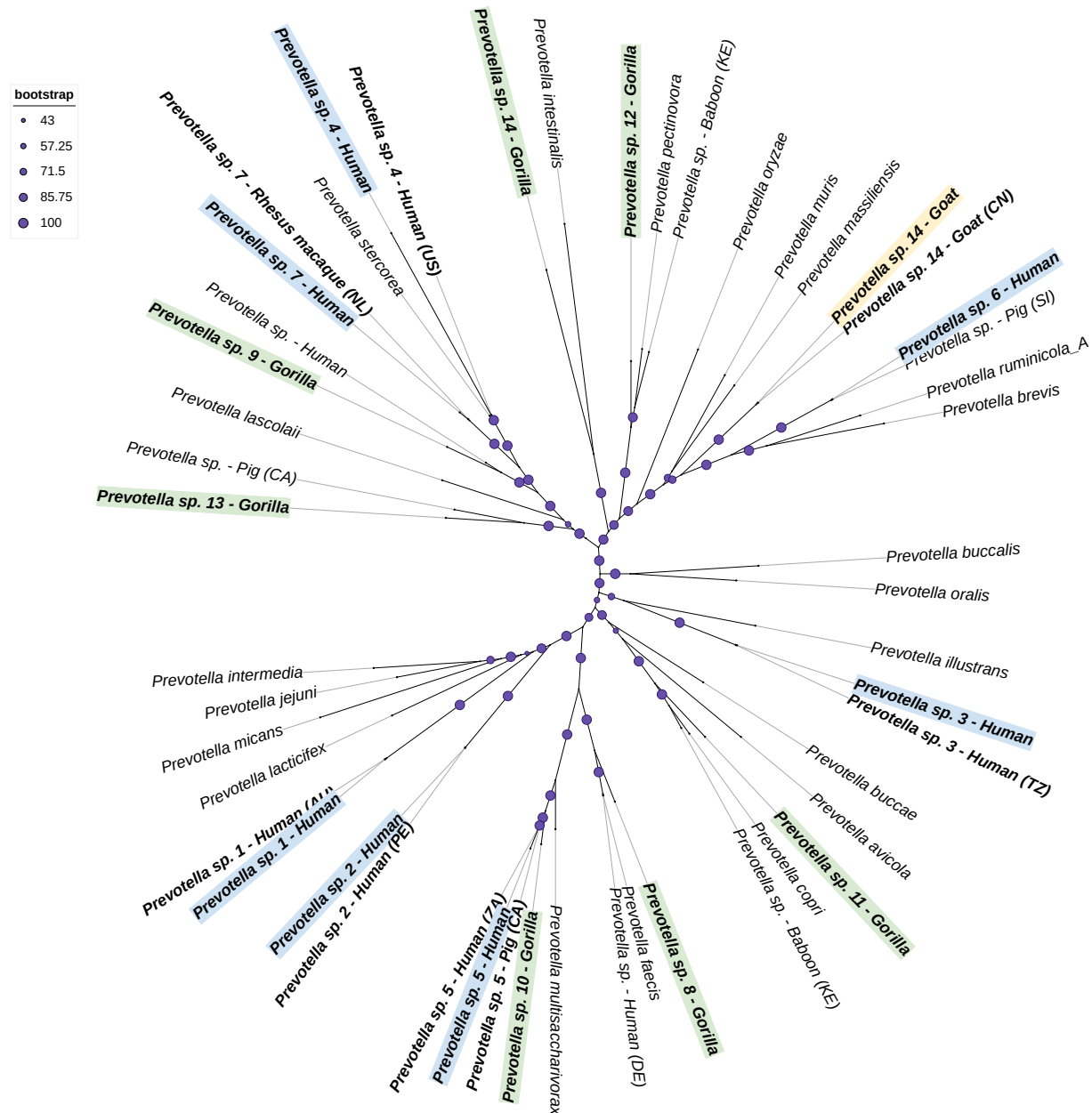


Figure 7.10 - Unrooted phylogenetic tree showing the putative novel *Prevotella* species and publicly available genomes. Bootstrap (1000x).

7.1.4.4 Appendices – Statement of Contribution

7.1.4.4.1 Chapter 4 – Statement of Contribution

 MASSEY UNIVERSITY TE KUNenga o PŪREHUOA UNIVERSITY OF NEW ZEALAND		GRADUATE RESEARCH SCHOOL	
STATEMENT OF CONTRIBUTION DOCTORATE WITH PUBLICATIONS/MANUSCRIPTS			
We, the student and the student's main supervisor, certify that all co-authors have consented to their work being included in the thesis and they have accepted the student's contribution as indicated below in the Statement of Originality.			
Student name:	Valter Almeida		
Name and title of main supervisor:	Professor David Hayman		
In which chapter is the manuscript/published work?	Chapter 4		
Describe the contribution that the student and members of the supervisory team have made to the manuscript/published work: ¹ Valter Almeida – Bioinformatics workflow, metagenomics/genomics analysis, ideas, writing, statistical analysis, data visualisations, and data management. Supervisors: David Hayman – Project creation and management, supervision, ideas, and analysis direction; Matthew Knox – Laboratory work, DNA extraction; All supervisors: Discussions, ideas, writing, reviewing.			
Please select one of the following three options:			
☐	The manuscript/published work is published or in press Please provide the full reference of the research output:		
☐	The manuscript is currently under review for publication Please provide the name of the journal:		
☒	It is intended that the manuscript will be published, but it has not yet been submitted to a journal		
Student's signature:	Valter Almeida Digitally signed by Valter Almeida Date: 2024.10.31 15:20:39 +13'00'	Main supervisor's signature:	David Hayman Digitally signed by David Hayman DN: cn=David Hayman, o=Māsesey University, email=D.L.Hayman@massey.ac.nz, Date: 2024.10.31 16:08:55 +13'00'
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7.1.4.4.2 Chapter 5 – Statement of Contribution

STATEMENT OF CONTRIBUTION DOCTORATE WITH PUBLICATIONS/MANUSCRIPTS

We, the student and the student's main supervisor, certify that all co-authors have consented to their work being included in the thesis and they have accepted the student's contribution as indicated below in the Statement of Originality.			
Student name:	Valter Almeida		
Name and title of main supervisor:	Professor David Hayman		
In which chapter is the manuscript/published work?	Chapter 5		
Describe the contribution that the student and members of the supervisory team have made to the manuscript/published work: ¹ Valter Almeida – Bioinformatics workflow, metagenomics/genomics analysis, ideas, writing, statistical analysis, data visualisations, and data management. Supervisors: David Hayman – Project creation and management, supervision, ideas, and analysis direction; Matthew Knox – Laboratory work, DNA extraction; All supervisors: Discussions, ideas, writing, reviewing.			
Please select one of the following three options:			
☐	The manuscript/published work is published or in press Please provide the full reference of the research output:		
☐	The manuscript is currently under review for publication Please provide the name of the journal:		
☒	It is intended that the manuscript will be published, but it has not yet been submitted to a journal		
Student's signature:	Valter Almeida Digitally signed by Valter Almeida Date: 2024.10.31 15:24:09 +13'00'	Main supervisor's signature:	David Hayman Digitally signed by David Hayman DN: cn=David Hayman, o=Massey University, email=D.L.Hayman@massey.ac.nz Date: 2024.10.31 16:09:24 +13'00'
This form should be placed at the beginning of each relevant thesis chapter.			

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7.1.4.4.3 Chapter 6 – Statement of Contribution



GRADUATE
RESEARCH
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STATEMENT OF CONTRIBUTION DOCTORATE WITH PUBLICATIONS/MANUSCRIPTS

We, the student and the student's main supervisor, certify that all co-authors have consented to their work being included in the thesis and they have accepted the student's contribution as indicated below in the Statement of Originality.			
Student name:	Valter Almeida		
Name and title of main supervisor:	Professor David Hayman		
In which chapter is the manuscript/published work?	Chapter 6		
Describe the contribution that the student and members of the supervisory team have made to the manuscript/published work: ¹ Valter Almeida – Bioinformatics workflow, metagenomics/genomics analysis, ideas, writing, statistical analysis, data visualisations, and data management. Supervisors: David Hayman – Project creation and management, supervision, ideas, and analysis direction; Matthew Knox – Laboratory work, DNA extraction; All supervisors: Discussions, ideas, writing, reviewing.			
Please select one of the following three options:			
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