

**Genomic identification of rare and low-prevalence enteric bacterial pathogens in Canada:
implications for taxonomy and reference laboratories**

by

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*To my husband,
for believing in me every step of the way,
and to my parents,
for always encouraging my love of science.*

Abstract

Accurate identification of enteric bacteria is essential for public health surveillance, outbreak detection, and clinical decision-making. While whole genome sequencing (WGS) has increasingly allowed us to replace traditional diagnostic and characterization methods for common pathogens, its applications for rare and low-prevalence enteric bacteria remains poorly characterized. Traditional approaches such as 16S rRNA gene sequencing and phenotypic profiling, still used by diagnostic and reference laboratories, often lack sufficient resolution for species-level identification of closely related or uncommon taxa. Furthermore, WGS-based workflows introduce challenges related to sequencing platform choice, bioinformatic tool selection, reference database stability, and taxonomy. Evidence guiding the implementation of WGS for the identification of uncommon enteric bacteria in reference laboratory settings is limited.

This study evaluated the performance of multiple WGS-based workflows relative to traditional identification methods using a retrospective collection of 331 rare and low-prevalence bacterial isolates submitted to Canada's National Microbiology Laboratory for identification from 1995 to 2023, together with 34 type strains. Isolates were sequenced using Illumina short-read and Oxford Nanopore long-read platforms and analyzed with bioinformatic workflows incorporating multiple taxonomic classification tools. Results were compared with 16S rRNA gene sequencing and biochemical identification methods. Concordance analyses assessed agreement across methods, characterized discordant classifications, and evaluated taxonomic resolution and accuracy.

Results from WGS-based approaches consistently achieved higher taxonomic resolution than traditional methods, particularly at the species level. However, classification outcomes

varied substantially across sequencing platforms and bioinformatic workflows. Discordance was frequently observed among closely related taxa and organisms with limited or unstable representation in reference databases. Illumina-based taxonomic classifications demonstrated higher concordance and more consistent species-level classifications, whereas Nanopore-based workflows produced a greater proportion of genus-level, ambiguous, or unresolved classifications. Across all methods, unresolved and discordant results were associated with read or assembly quality, taxonomic reclassification, nomenclatural inconsistencies, or incomplete reference database coverage.

Overall, these findings show that while WGS-based methods offer advantages for identifying rare enteric bacteria, diagnostic utility strongly depends on the sequencing platform used, its analytical workflow design, and reference database curation quality. Together, these data identify the technical and taxonomic priorities that must be addressed for reliable implementation of WGS-based identification in public health and reference laboratories.

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List of Abbreviations

ATCC	American Type Culture Collection	MALDI-TOF	matrix-assisted laser desorption/ionization time-of-flight
ANI	average nucleotide identity	MS	mass spectrometry
CDC	United States Centers for Disease Control and Prevention	NESP	National Enteric Surveillance Program
CI	confidence interval	NI	no identity
CNDSS	Canadian Notifiable Disease Surveillance System	NML	National Microbiology Laboratory
DDH	DNA-DNA hybridization	OL3.0	OmniLog Data Collection 3.0 software
DIST	distance	ONT	Oxford Nanopore Technologies
ECA	enterobacterial common antigen	PE	paired end
FIORP	Canada's Foodborne Illness Outbreak Response Protocol	PHAC	Public Health Agency of Canada
GTDB	Genome Taxonomy Database	QC	quality control
GTDB-Tk	Genome Taxonomy Database Toolkit	RDS	Reference and Diagnostic Services
HPB	Health Products and Food Branch	SIM	similarity
ICNP	International Code of Nomenclature of Prokaryotes	STEC	Shiga-toxin producing <i>E. coli</i>
IF	inoculating fluid	TYGS	Type Strain Genome Server
IRIDA	Integrated Rapid Infectious Disease Analysis	WGS	whole genome sequencing
LMIC	low- and middle-income countries	WHO	World Health Organization
LPSN	List of Prokaryotic names with Standing in Nomenclature	16S rRNA	16S ribosomal RNA

Author Contributions

Unless otherwise stated, the study design, wet lab procedures and data generation, bioinformatic analyses, statistical analyses, data interpretation, figure preparation, and thesis writing were completed by the author. The project was conducted under the supervision of Dr. Celine Nadon (Director of the Division of Enteric Diseases (DED), NML). Contributions from collaborators are outlined below.

Project Conception and Study Design: The overall research was developed by Dr. Celine Nadon and Sara Christianson (Manager of Reference and Diagnostic Services, DED, NML) as part of ongoing efforts to modernize identification of enteric bacterial isolates at the NML. The author developed the detailed study design, analytical framework, performance evaluation strategy, and comparative methodology under their supervision. James Robertson (Innovation and Application Development, DED, NML), Matthew Wells (Data Analytics and Algorithm Development, DED, NML), and Matthew Walker (Innovation and Application Development, DED, NML) provided consultation during study planning regarding the selection and implementation of the bioinformatic workflows evaluated in the thesis.

Traditional Identification Methods: Historical 16S rRNA gene sequence data were available for many isolates prior to this study. Additional sequencing for isolates lacking historical data was performed by Cristal Cizik (Reference and Diagnostic Services, DED, NML) and Lindsey Lamboo (Reference and Diagnostic Services, DED, NML).

Whole Genome Sequencing: Genomic DNA extraction for Illumina sequencing was performed by Sierra Ives (Reference and Diagnostic Services, DED, NML). Library preparation and sequencing was completed by the Genomics Core Facility of the NML using validated institutional protocols.

Figures and Visualization: All figures were created by the author using BioRender, Microsoft PowerPoint, R, RStudio, and associated R packages. Figures adapted from published sources have been redrawn and appropriately referenced.

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Chapter 1: Introduction

1.1 Enteric Bacterial Infections: Global Burden, Canadian Context, and Beyond

1.1.1 Health and Economic Impact of Enteric Infections

Enteric diseases remain among the most common and impactful infectious illness worldwide, disproportionately affecting children, the elderly, and immunocompromised individuals (1–5). These infections are caused by a broad group of bacterial, viral, and parasitic pathogens transmitted primarily through the fecal-oral route, often via contaminated food, water, direct person-to-person contact, or through fomites (1, 5–10). Despite advances in sanitation and clinical microbiology, enteric infections continue to contribute significantly to global morbidity and mortality. Low- and middle-income countries (LMICs) experience the highest burden of disease (4, 11–15), while countries with robust healthcare and surveillance systems still report substantial morbidity and economic impact from foodborne pathogens (3, 10, 14, 16–20).

Globally, diarrheal disease accounts for nearly 1.6 million deaths annually, with most death occurring in children under five years of age (19, 21). This number represents only the most severe cases; millions more are estimated to experience prolonged or recurrent enteric infections that lead to malnutrition, growth stunting, and reduced educational and economic outcomes (1, 15, 21–23). The burden is concentrated in regions with poor water and sanitation infrastructure (4, 15, 24–26), but enteric disease also poses a significant challenge in countries with strong public health systems, where foodborne pathogens continue to account for a high incidence of illness (3, 10, 12, 14, 17–20, 27, 28). Foodborne transmission accounts for a major share of this burden: in the United States, it is estimated that one in six individuals experiences a foodborne illness each year, translating to more than 48 million cases (23), although counts vary (17, 29, 30). In Canada, one in eight individuals is affected annually, representing an estimated five million cases of domestically acquired foodborne illness (10). National estimates can be

contextualized against global data by comparing pathogen-specific burden (Fig. 1) and these examples highlight that even in countries with robust public health systems, the risk of enteric disease remains high.

The impact of enteric pathogens can be illustrated through historical large-scale outbreaks that highlight both disease severity and surveillance gaps. In Walkerton, Ontario, in 2000, contamination of the municipal water supply with *Escherichia coli* O157:H7 and *Campylobacter* led to over 2,300 illnesses and seven deaths (31, 32). This outbreak revealed vulnerabilities in water safety oversight and remains a defining example of the public health consequences of enteric pathogens in Canada (32, 33). In Germany, a rare Shiga toxin-producing *E. coli* (STEC) O104:H4 outbreak in 2011 caused over 3,800 cases and 54 deaths, traced to contaminated fenugreek sprouts, highlighting global trade related risks and challenges in detecting rare strains (34, 35). The cholera epidemic in Haiti (2010-2019) resulted in over 820,000 cases and 10,000 deaths (36–38), emphasizing the devastating consequences of enteric pathogens in settings with fragile infrastructure.

Surveillance data consistently underestimate the true incidence of enteric disease. Many infected individuals do not seek healthcare, and even when care is sought, stool and other clinical specimens are often not collected. Diagnostic sensitivity varies widely, and confirmed case counts typically represent only a fraction of total infections (39). Public health agencies therefore apply multipliers to estimate the true burden from confirmed cases. Multipliers vary by pathogen and jurisdiction, reflecting differences in healthcare-seeking behaviour, sample collection, and laboratory detection rates. These multipliers quantify the gap between reported cases and actual incidence, providing a more accurate picture of the burden of disease (10, 27, 30, 40) (Table 1).

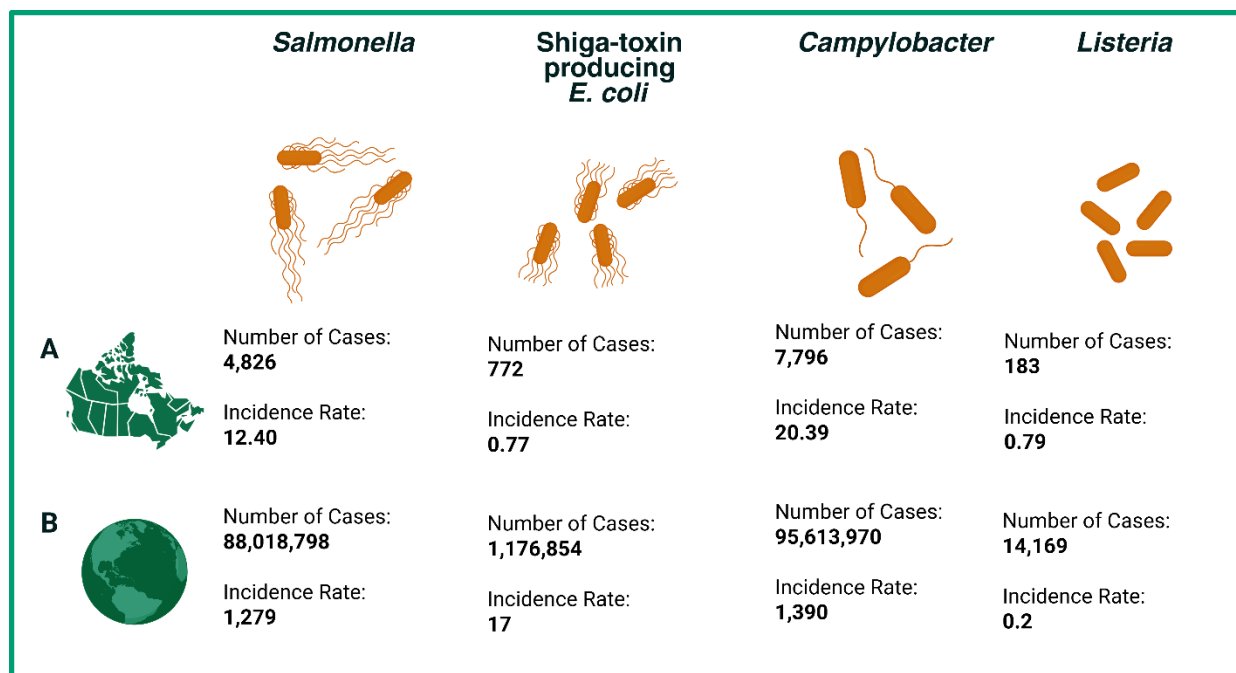


Figure 1. Incidence and global burden of foodborne illness caused by *Salmonella*, STEC, *Campylobacter*, and *Listeria*. *Salmonella*, STEC, *Campylobacter*, and *Listeria* are the leading pathogens associated with foodborne illness in Canada and globally. (A) In 2021, the Canadian Notifiable Disease Surveillance System (CNDSS) reported 4826 cases of salmonellosis, 772 cases of STEC infection, 7,796 cases of campylobacteriosis, and 183 cases of listeriosis, with incidence rates per 100,000 population of 12.40, 0.77, 20.39, and 0.79, respectively. *Campylobacter* isolates are not routinely forwarded to provincial public health or central reference laboratories, resulting in significant underrepresentation in CNDSS data (41). (B) In 2010, the World Health Organization reported global estimates of 88,018,798 cases of salmonellosis, 1,176,854 cases of STEC infection, 95,613,970 cases of campylobacteriosis, and 14,169 cases of *L. monocytogenes* infection. The corresponding global incidence rates per 100,000 population were 1,279, 17, 1,390, and 0.2, respectively (19).

Table 1. Estimated multipliers to adjust confirmed case data for enteric bacterial pathogens in Canada and the United States.

<i>Pathogen</i>	<i>Approximate Case Multiplier (Canada)</i>	<i>Approximate Case Multiplier (United States)</i>	<i>Notes</i>
<i>Salmonella</i> (27, 30, 42)	×26	×29	High underreporting due to mild, self-limiting illness
<i>STEC O157</i> (30)	not available	×~ 40	Higher healthcare-seeking rates in Canada reduce underreporting
<i>Campylobacter</i> (10, 30)	×27	×30	Most common pathogen but rarely confirmed
<i>Listeria</i> (10, 30, 40)	×2	×2	More likely to be reported due to severity

Note. Multipliers are derived from Thomas et al. (2013, 2014) for Canada and Scallan Walter et al. (2025) and Mead et al. (1999) for the United States.

An example of this reduction from community infections to confirmed and reported cases is presented in Figure 2.

In Canada, foodborne illness costs exceed \$3 billion annually, accounting for direct medical care and productivity losses (43). Sequelae such as Guillain-Barre syndrome following *Campylobacter* infection (44) and hemolytic uremic syndrome following STEC infection (9, 45) add to the long-term consequences and burden of enteric illness. Globally, unsafe food costs LMICs more than \$100 billion annually in lost productivity and trade (15, 46), illustrating the broader societal impact of enteric pathogens.

Enteric pathogens therefore represent a paradox for modern public health as they are ancient and persistent, disproportionately affect vulnerable populations, and remain capable of large-scale outbreaks even in settings with strong public health systems. While global estimates highlight substantial morbidity and mortality, these figures obscure the larger hidden burden of disease caused by underreporting and limited surveillance. Recognizing the true scale of disease burden is essential for designing prevention strategies, prioritizing public health interventions, and evaluating surveillance systems.

1.1.2 Global Epidemiology and Burden of Foodborne Enteric Illness

Foodborne illnesses represent a significant and preventable public health burden. The World Health Organization (WHO) estimates that nearly 600 million people, or one in ten globally, fall ill each year from contaminated food, resulting in 420,000 deaths (22). In Canada, the Public Health Agency of Canada (PHAC) estimates that one in eight Canadians will acquire

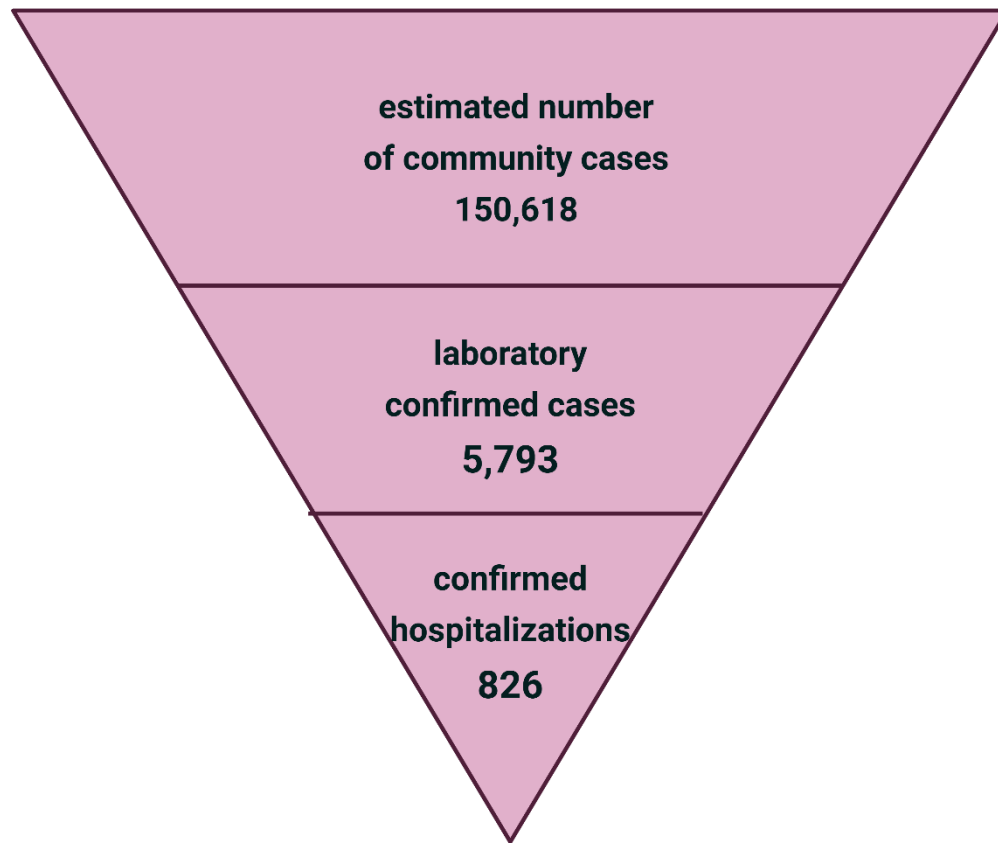


Figure 2. Underreporting pyramid for *Salmonella* in Canada (2006). Each tier represents a stepwise reduction from estimated community incidence to confirmed cases and hospitalizations through public health surveillance. Numbers were inferred using the Canadian *Salmonella* case multiplier (Table 1) and corresponding PHAC reports (10, 42). The pyramid illustrates the substantial underreporting that must be considered when estimating the true burden of *Salmonella* and other underreported enteric infections.

a foodborne illness annually (47). Accurately estimating the burden of foodborne disease is challenging due to underdiagnosis and underreporting. The result is a surveillance picture that underrepresents the true incidence of disease. As shown in Table 1 and Figure 2, surveillance data substantially underrepresents the true incidence of community infections (10, 27, 42), underscoring the limitations of surveillance data.

Even in high-income countries with well-developed surveillance systems, case counts remain only a fraction of the true incidence. Canadian programs such as the National Enteric Surveillance Program (NESP) (41, 48, 49) and PulseNet Canada (50, 51) strengthen detection and outbreak response yet estimates consistently show that the real burden is several times higher than reported. At the global level, different modeling frameworks contribute additional uncertainty. The WHO notes that mortality estimates for enteric diseases differ substantially between groups such as the Institute for Health Metrics and Evaluation and the Maternal Child Epidemiology Estimation group, due to differences in analytic approach and ongoing changes in diagnostic technology (20).

Despite these limitations, enteric bacterial pathogens remain a clear driver of morbidity and mortality worldwide. Building on the pathogens highlighted in Figure 1, Canadian and global data consistently identify *Salmonella*, *Campylobacter*, STEC, *L. monocytogenes*, and *Shigella* as leading causes of foodborne illness. They are responsible for a wide spectrum of disease, from self-limiting gastroenteritis to invasive complications such as hemolytic uremic syndrome or bacteremia, and they can cause large outbreaks (5, 9, 10, 19, 27, 39, 42, 52, 53). These pathogens represent the core targets of current surveillance systems not only because of their clinical and public health significance but also because they are the organisms most amenable to standardized laboratory detection methods.

While advancements in diagnostics and modeling have improved burden estimates, large gaps remain. Bridging these gaps will require enhanced laboratory capacity, improved surveillance methodologies, and broader public engagement with food safety practices. For now, public health systems necessarily concentrate on a limited number of high-priority enteric pathogens. This prioritization, while pragmatic, also means that rare and emerging bacterial causes of enteric illness remain understudied. Recognizing this limitation provides the rationale for expanding future surveillance frameworks, and it sets the stage for the present study, which aims to build toward greater inclusion of rare and low-prevalence enteric bacteria within the broader landscape of foodborne disease.

1.1.3 Reservoirs and Transmission Routes of Enteric Bacteria

Enteric pathogens circulate in diverse reservoirs and reach humans through multiple transmission routes, making prevention complex. Reservoirs include animals, including livestock (54), poultry (54, 55), wildlife (56), and pets (10), as well as environmental sources such as freshwater (57), groundwater (28), and soil. Plants also can serve as important reservoirs when enteric bacteria adhere to or internalize within edible foliage, evading surface-level decontamination (58). Recognizing these reservoirs is central to designing effective prevention strategies.

Transmission routes are equally varied and extend beyond foodborne exposure. A Canadian expert elicitation (2015) highlighted that some enteric bacteria, like *Yersinia enterocolitica* are primarily foodborne, while *Shigella* spreads mainly person-to-person. Others, including *Campylobacter*, *L. monocytogenes*, *Salmonella*, and *E. coli* span multiple routes, notably foodborne and waterborne routes (55). Further resolution from a 2016 Canadian study

highlighted raw produce and seafood as leading foodborne sources, private wells as key waterborne pathways, and farm animals as important contributors to the transmission of enteric bacterial pathogens (54). These findings underscore the need for prevention strategies tailored to specific exposures, such as improving produce safety, protecting private water sources, educating community members regarding food and water safety, and minimizing farm animal exposure risks.

Transmission risks are not uniformly distributed across populations. Indigenous communities in Canada face heightened vulnerability due to a combination of environmental and social factors, including reliance on game meats, traditional fermentation practices, overcrowded housing, food-sharing customs, and ongoing challenges with safe water access (26). Such contexts illustrate the importance of considering both biological and socio-cultural drivers of exposure.

While Canadian studies clarify local pathways, global evidence highlights how transmission dynamics vary by region. WHO analyses show that foodborne routes dominate in developed regions, while waterborne transmission routes remain critical in many developing communities (52). Local factors such as hygiene practices, water storage, and fomites such as exposure to animal feces also play an important role in transmission, as highlighted in recent studies from India (4) and Laos (25). These findings stress the importance of tailoring interventions to regional contexts rather than assuming uniform exposure pathways.

In Canada, source attribution studies and expert elicitations highlight the complexity of transmission dynamics for enteric pathogens, with overlapping roles of foodborne, waterborne, animal contact, and person-to-person routes. The diversity is illustrated in Figure 3 showing reservoirs with major transmission pathways and human infection. Together with Canadian-

specific evidence presented here, this framework underscores the need for interventions that address both common and context-specific exposures, such as raw produce, private wells, or traditional food practices in Indigenous communities.

Understanding reservoirs and transmission routes is essential for preventing infection, guiding public health interventions, and improving surveillance. While common pathogens such as *Salmonella*, *E. coli*, *Shigella*, *Campylobacter*, and *Listeria* are well characterized, there remain substantial knowledge gaps for rare and low-prevalence enteric bacteria. These pathogens may occupy poorly understood reservoirs or follow atypical transmission routes besides well-understood food- and waterborne transmission, making them harder to detect and control. Expanding research to include these organisms will be key for strengthening diagnostics and surveillance systems.

1.1.4 Epidemiology of Major Enteric Pathogens in Canada

In Canada, the bulk of reported enteric bacterial infections involve *Salmonella*, *Campylobacter*, STEC, *L. monocytogenes*, and *Shigella*. *Campylobacter* consistently holds the highest case counts (10, 41, 42, 48, 49), while *Salmonella* and STEC frequently appear in outbreaks, particularly those tied to produce, poultry, and processed foods. Although less frequent, *L. monocytogenes* carries substantial severity, with higher rates of hospitalization and mortality in outbreak settings.

Recent Canadian outbreaks underscore the ongoing public health threat of common pathogens. In 2025, a *Salmonella* outbreak linked to salami and deli-meats caused 90 illnesses

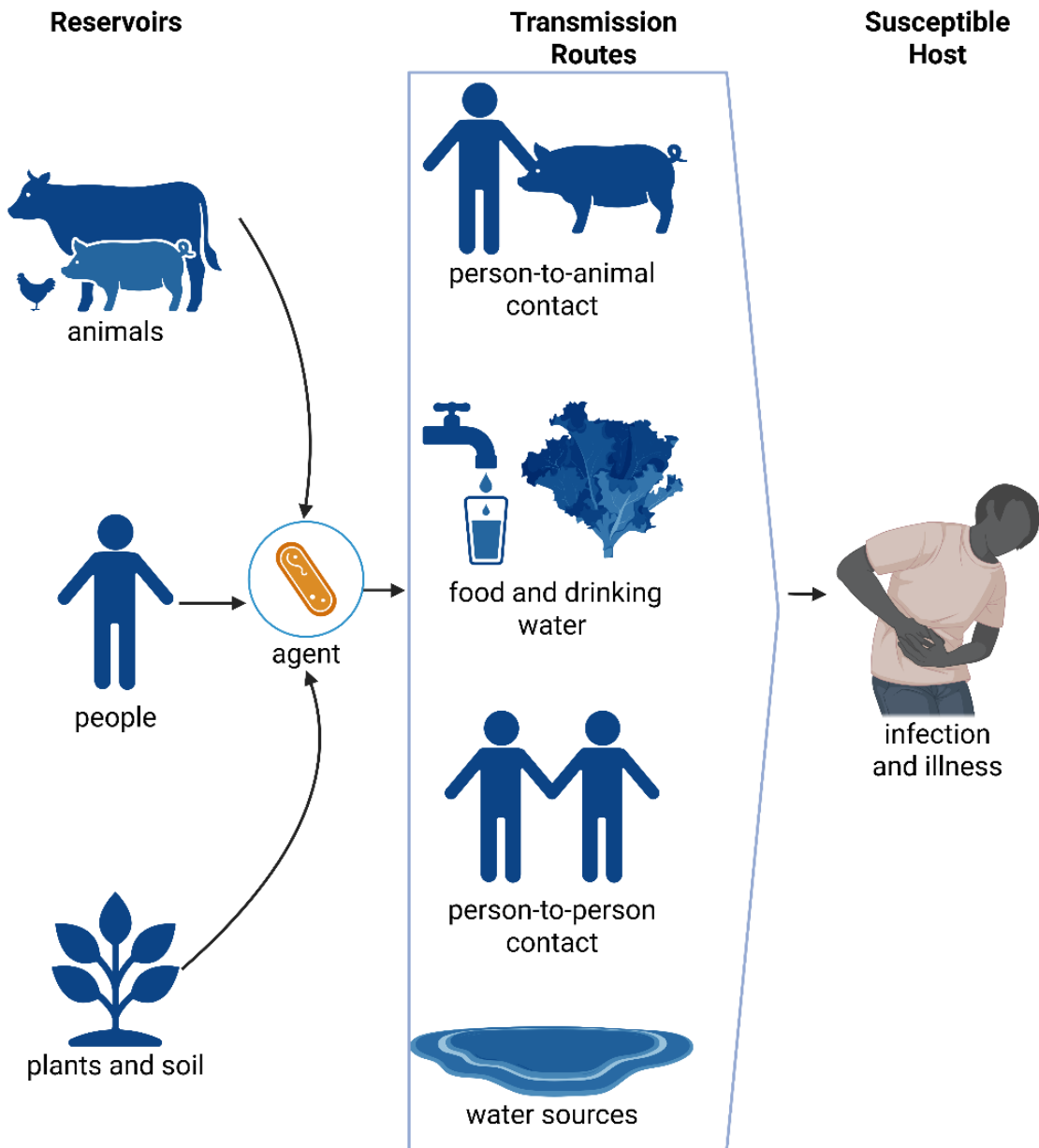


Figure 3. Conceptual framework of reservoirs and transmission routes for enteric pathogens. Reservoirs such as animals, humans, plants, and soil serve as sources of pathogens that spread via multiple transmission routes including food and drinking water, direct or indirect animal contact, person-to-person contact, and contaminated water sources, leading to human infection and illness (28, 55–58). Adapted for Canadian context to highlight the interconnectedness of reservoirs and transmission pathways.

across multiple provinces. Among the 90 laboratory-confirmed cases, several hospitalizations occurred, and no deaths were reported (59). In 2024, a Canadian *L. monocytogenes* outbreak linked to plant-based milks caused 20 cases across provinces resulting in 15 hospitalizations and 3 deaths (60). These events highlight that outbreaks tied to processed foods remain a continuing challenge in Canada.

Canada's surveillance systems provide robust monitoring for major pathogens, but only where diagnostic capacity is sufficient. Rare and low-prevalence enteric bacteria often evade reliable detection because case numbers are typically small, diagnostic assays may not target them, and outbreak recognition is less likely. So, while epidemiological data for common enteric bacteria are well defined, knowledge regarding rarer species remains poorly studied. Expanding genomic surveillance, improving isolate-level testing, and integrating more sensitive diagnostics are essential to capture the full spectrum of enteric bacterial disease in Canada.

1.1.5 Canadian Surveillance and Outbreak Response Systems for Enteric Pathogens

Public health surveillance provides the foundation for detecting and controlling enteric bacterial disease. By systematically tracking infections and analyzing trends, surveillance systems enable early outbreak detection, resource allocation, and timely interventions. In Canada, three complementary programs underpin this framework: NESP, PulseNet Canada, and the Foodborne Illness Outbreak Response Protocol (FIORP). Together, they support both routine monitoring and coordinated responses to emerging public health threats.

NESP, coordinated by PHAC in partnership with provincial laboratories, compiles weekly and annual reports on enteric pathogens. These reports highlight national and regional trends, provide early warnings, and support multi-provincial outbreak detection. Despite its

value, NESP data face well-recognized limitations. Certain pathogens, particularly *Campylobacter*, are underrepresented as not all isolates are forwarded for full characterization (48). The COVID-19 pandemic further disrupted reporting, with Canadian data showing sharp declines in reported cases of *Salmonella*, *Shigella*, and STEC, while *Listeria* incidence remained stable (50, 61). These findings illustrate both the strengths and vulnerabilities of laboratory-based surveillance in Canada.

PulseNet Canada, launched in 2000 as a part of the global PulseNet network, serves as the country's molecular early warning system for enteric outbreaks. Coordinated by the NML, it uses whole genome sequencing (WGS) and other molecular subtyping tools to rapidly detect clusters of *Salmonella*, *E. coli*, *Listeria*, *Shigella*, and other foodborne pathogens. By linking laboratories across provinces in real-time, PulseNet accelerates outbreak investigations and strengthens Canada's capacity to identify sources of contamination (50, 51). WGS has become a backbone of this system, enabling unprecedented taxonomic resolution for outbreak tracking (50).

Outbreaks that cross provincial or national boundaries are managed under FIORP, a formal network that coordinates PHAC, Health Canada, the Canadian Food Inspection Agency, and provincial/territorial health authorities. FIORP standardizes collaboration, communication, and response measures, ensuring that food recalls, public advisories, and risk assessments are issued in a timely and coordinated fashion. The framework has proven critical in managing increasingly complex, multi-jurisdictional outbreaks tied to the global food supply chain (62).

While WGS-based surveillance has transformed outbreak detection for common pathogens, significant gaps remain for rare and low-prevalence enteric bacteria. Current reference databases are heavily biased toward high-prevalence, well-characterized pathogens

(e.g. *Salmonella* and *E. coli*), leaving many uncommon taxa underrepresented or misclassified. Bioinformatics pipelines that have been optimized for high-prevalence organisms often fail to resolve closely related rare species (63–66). As a result, unusual pathogens may be misidentified, incompletely characterized, or overlooked during outbreak investigations.

Traditional diagnostic methods continue to fill these gaps but are limited in resolution. 16S ribosomal RNA (16S rRNA) gene sequencing provides broad taxonomic coverage but cannot reliably differentiate closely related organisms (67–75). Biochemical profiling is inexpensive but often fails to distinguish organisms beyond the genus-level (76, 77) and can vary due to the biologic plasticity of metabolic traits (75). Proteomic approaches, such as matrix-assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry (MS) offer rapid, high-throughput identification of common pathogens, but struggle with rarer organisms that lack robust spectral databases (77–80). These limitations restrict reliable identification of rare and low-prevalence enteric bacteria using traditional diagnostic approaches, particularly for Enterobacterales, where shifting species boundaries and reclassification complicate classification further.

Expanding reference databases, developing rare pathogen-inclusive bioinformatics pipelines, and integrating WGS more fully into clinical diagnostics would represent major advances for Canadian surveillance. Addressing these limitations will broaden outbreak detection beyond common enteric bacteria, strengthen epidemiological tracking, and enhance public health preparedness.

1.1.6 Beyond Acute Infection: Chronic Disease and Cancer Links

Enteric pathogens are most often recognized for their role in acute gastrointestinal illness and foodborne outbreaks. However, accumulating evidence suggests that they may also contribute to chronic inflammatory disease, bacteremia and wound infections, malignancies, and other severe outcomes.

Members of the Enterobacteriaceae family, particularly *E. coli* and *Proteus* have been investigated as contributors to chronic inflammatory disorders. *E. coli* strains have been implicated in Crohn's disease and ulcerative colitis (81), while studies in pediatric Crohn's patients have reported an overabundance of *Proteus* in the intestinal microflora (82). These associations remain under investigation, but they highlight a potential role for enteric bacteria in shaping chronic disease. *Proteus* has also been studied in the context of rheumatoid arthritis, a chronic inflammatory joint disease influenced by both host genetics and microbial exposures (83). Furthermore, acute infections with *E. coli* or *Yersinia* can trigger reactive arthritis (84), reinforcing the possibility that enteric pathogens serve as catalysts for long-term immune-mediated conditions.

The relationship between enteric bacteria and cancer remains an emerging area of research. Dysbiosis of the intestinal microbiome, including overrepresentation of Enterobacteriaceae, has been also associated with increased cancer risk (7). Patients with *Klebsiella pneumoniae*-associated pyogenic liver abscess, for example, have shown an elevated incidence of colorectal cancer (85). Similarly, higher abundances of *Enterobacter*, *Shigella*, and *Escherichia* isolates have been reported in patients with primary liver cancer compared to cirrhosis controls (86). While these organisms are unlikely to be direct causative agents, they may act as important cofactors or biomarkers of underlying malignancies (85, 86).

Beyond inflammatory disease and cancer, certain enteric pathogens are associated with additional systemic complications. *Campylobacter* infections are linked to Guillain-Barre syndrome, myocarditis, pericarditis, and reactive arthritis (44). *Helicobacter pylori* can cause peptic ulcer disease and is a well-established risk factor for gastric carcinoma (87, 88). Furthermore, enteric infections have been associated with a growing range of long-term health consequences, including human metabolic (89, 90), neurological (91–93), and cardiovascular disorders (94, 95), as well as other post-infectious sequelae such as chronic kidney damage (96–98) and ankylosing spondylitis (99, 100). These complications contribute substantially to long-term morbidity and, in some cases, mortality.

These associations highlight that the impact of enteric bacterial pathogens extends well beyond acute gastroenteritis and outbreak settings. Recognizing their potential role in chronic disease and malignancy underscores the importance of continued surveillance and detailed genomic characterization. As Canada moves towards modernizing its public health and reference laboratory systems, expanding the scope of genomic surveillance to include rare and low-prevalence pathogens will not only improve outbreak detection but also elucidate their broader contributions to human health and longevity.

1.2 Overview of Enteric Pathogens and Their Classification

The Enterobacteriaceae family has long stood at the centre of enteric pathogen research due to its role in foodborne illness, zoonoses, diverse clinical conditions, and recurrent outbreaks. Genera such as *Escherichia*, *Salmonella*, *Shigella*, *Klebsiella*, *Enterobacter*, and *Citrobacter* exemplify this diversity, while historically recognized groups such as *Yersinia* and *Serratia* further illustrate the evolving boundaries of the family (7, 101). Beyond their clinical relevance,

these bacteria have shaped molecular biology, serving as model systems for gene function and microbial pathogenicity (102).

Although enteric bacteria were recognized in the 19th century, formal classification of the Enterobacteriaceae only emerged in 1937 when Rahn introduced the family name, initially encompassing a single genus, *Enterobacter* (102, 103). Early typing schemes relied heavily on a narrow set of phenotypic traits (Gram-negative staining, glucose fermentation, and nitrite reduction), but taxonomic consistency was hindered by limited biochemical data, non-standardized testing, and the absence of formal taxonomic guidelines (7, 101, 102). Efforts by the US Centers for Disease Control (CDC) during the 1960-1970s introduced more structured biochemical panels, and, eventually, a polyphasic approach incorporating morphology, culture, and genetics (7, 104). Even with such progress, challenges to the family's validity persisted, and debates over genus- and family-level assignments continue today (6–8, 102). Bergey's Manual, the major bacteriological reference guide, notes differences in the taxonomic frameworks it uses to define taxonomic boundaries (105). The manual notes that it may adhere to the List of Prokaryotes with Standing in Nomenclature (LPSN), which is primarily based on historically published nomenclature and taxonomic rules (101, 106), it may adhere to Genome Taxonomy Database-based (GTDB) taxonomy, which uses whole genome phylogeny to reorganize bacterial relationships based on genomic similarity (63), or may not use either of these. Even amongst major reference guides and formal recommendations, disagreement persists (105). Despite these challenges, this review will adhere to the formal name, Enterobacteriaceae, defined the 2022 revision of the International Code of Nomenclature of Prokaryotes (ICNP) (106) and the 2026 version of the LPSN (101).

1.2.1 Definitions and Scope of Enteric Bacteria

The term *enteric bacteria* is used inconsistently across the literature, sometimes to denote habitat (gut-associated bacteria), sometimes pathogens that cause gastrointestinal illness, and sometimes as shorthand for the taxonomic group such as Enterobacteriaceae (family) or Enterobacterales (order). This variability reflects both the historical prominence of Enterobacteriaceae in enteric disease research and the recognition that other families may contain species with enteric relevance.

To illustrate this heterogeneity, Table 2 summarizes a selected set of published definitions of “enteric bacteria” or “enteric pathogen”. These highlight both overlap and divergence, some emphasize pathogenicity, others ecology, and other taxonomy. In this review, we adopt a functional definition: human enteric bacterial pathogens are bacteria capable of causing acute gastrointestinal disease in humans, whether or not they fall within Enterobacteriaceae.

1.2.2 Taxonomic Refinements and Diagnostic Features of Enteric Bacteria

Key features still define Enterobacteriaceae, most notably the enterobacterial common antigen (ECA), a carbohydrate structure largely unique to this group. While its function remains unclear, ECA has been implicated in membrane permeability, motility, and virulence, reinforcing its diagnostic importance (109). Morphologically, Enterobacteriaceae members appear as Gram-negative bacilli and are often microscopically indistinguishable, making biochemical and molecular assays for differentiation necessary (7, 8).

The advent of genomic testing has revealed further complexities and identified numerous exceptions to long-standing classification criteria and have driven recent taxonomic

Table 2. Definitions of “enteric bacteria” and “enteric pathogen” across the literature.

Definition	Scope	Source
An enteric pathogen may be classified as any microbe that is able to cause enteric disease	Broad, disease-based definition	Kolling et al., 2012 (107)
Enteric Gram-negative bacilli are organisms inhabiting the intestinal tract of humans and animals, including both pathogens and commensals	Clinical microbiology framing, links to disease relevance	Ryan et al., 2021 (108)
Enteric bacteria are pathogenic and can produce disease in normal individuals on a regular basis... most are harmless; others can produce disease	Distinguishes harmless versus pathogenic gut bacteria (Accessed from: https://safetyservices.ucdavis.edu/units/occupational-health/surveillance-system/enteric-bacteria)	UC Davis Occupational Health
Enteric bacteria are bacteria that typically exist in the intestines of animals and humans. They can be either harmless or pathogenic	Habitat-based, acknowledges dual roles (Accessed from: https://www.osmosis.org/answers/enteric-bacteria)	Osmosis.org (educational source)
Enteric bacteria may refer to gut flora, enteric pathogens, or members of Enterobacteriaceae	Explicit taxonomic/ ecological/ functional overlap (Accessed from: https://en.wikipedia.org/wiki/Enterobacteriaceae)	Wikipedia disambiguation

reassignments such as the transfer of *Yersinia* and *Serratia* into the newly defined Yersiniaceae family, alongside other restructured lineages (101, 110). These refinements are shown in Figure 4, which illustrates the placement of *Enterobacteriaceae* within the order Enterobacterales (101, 110). This visualization underscores the breadth of enteric-associated taxa and highlights that clinically relevant human pathogens extend well beyond the classical Enterobacteriaceae.

Beyond Enterobacteriaceae, other taxonomic groups contribute significantly to enteric disease. Within the Campylobacteraceae (Campylobacterales order) family, *C. jejuni*, *C. coli*, and *C. lari* represent leading causes of bacterial gastroenteritis worldwide. Infection is typically foodborne, associated with undercooked poultry, raw milk, and contaminated water. Infection presents with fever, diarrhea, abdominal pain, and in rare cases, serious complications and sequelae such as Guillain-Barre syndrome or reactive arthritis. Diagnosis relies on culture or molecular assays, and treatment is usually supportive, with antibiotics reserved for severe cases (9, 44, 111).

The Helicobacteraceae, (Campylobacterales order) while taxonomically distinct, similarly colonize vertebrate gastrointestinal tracts. The most common species, *H. pylori*, produces urease to survive gastric acid and is associated with gastritis, peptic ulcers, and gastric carcinoma. Other species, including *H. pullorum* and *H. fennelliae* are less common but underscore the pathogenic breadth of the genus. Like *Campylobacter*, their ability to evade host immunity complicates both pathogenesis and treatment (87, 88).

Aeromonadaceae provides another example of emerging enteric pathogens. *Aeromonas* are widely distributed in aquatic environments, share a Gram-negative bacillus morphology with other enteric bacteria but belong to a distinct order (Aeromonadales). They are increasingly recognized in human gastroenteritis, especially among children, though they remain

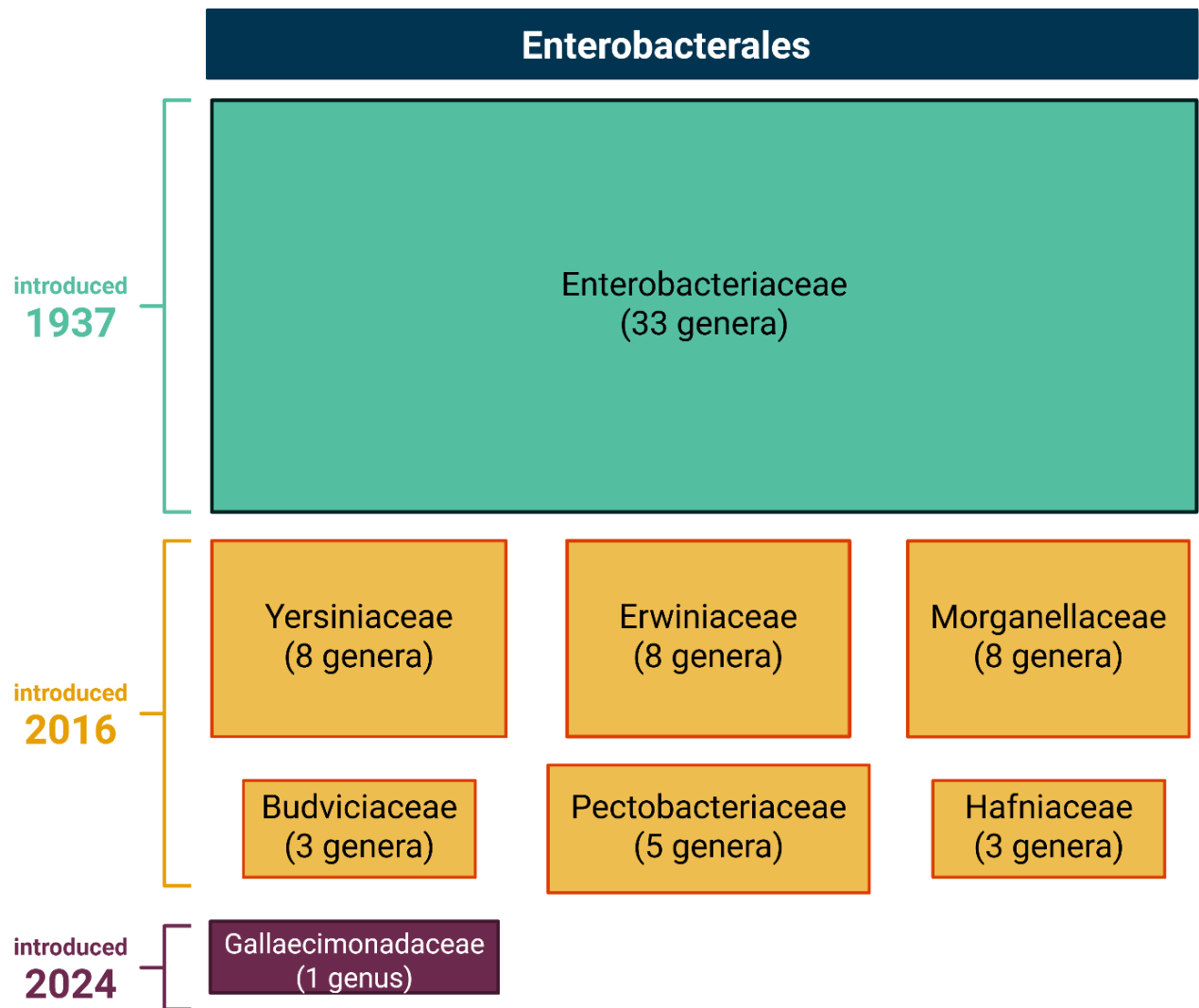


Figure 4. Contemporary classification of order Enterobacterales. Enterobacteriaceae is the oldest and largest family in the order, formally established in 1937 and currently including 33 genera. A major taxonomic restructuring in 2016 led to the creation of six additional families: Yersiniaceae (8 genera), Erwiniaceae (8 genera), Morganellaceae (8 genera), Pectobacteriaceae

underdiagnosed in routine laboratories. Recent large-scale studies have identified *Aeromonas* as a common enteric bacterial pathogen in pediatric patients, highlighting the importance of accurate detection (112, 113). (5 genera), Budviciaceae (3 genera), and Hafniaceae (3 genera). Most recently, in 2024, Gallaecimonadaceae, comprising a single genus, was added to the order. [Adapted from Janda and Abbot, 2024] (7, 101, 110).

Collectively, these examples illustrate the fluid boundaries of what constitutes an enteric pathogen. Defining what constitutes an enteric pathogen remains a complex and evolving challenge, as numerous bacterial genera across diverse taxonomic groups can cause infections of the gastrointestinal tract. The wide range of phenotypic, genetic, and ecological characteristics shared by these organisms, coupled with ongoing advances in molecular and genomic identification methods, have led to multiple, sometimes overlapping, definitions of enteric pathogens in the literature. This variability complicates efforts to establish consistent classification criteria, highlighting the need for continued research and taxonomic consensus-building to better understand and manage these important public health threats.

1.3 Isolation and Identification of Enteric Pathogens

The rapid and accurate identification of pathogenic bacteria is critical for infection control, clinical treatment, and public health surveillance. Historically, classification relied on morphological, physiological, and biochemical traits, which provided essential but often time-consuming and sometimes imprecise results. The advent of molecular biology and genomics introduced alternatives such as 16S rRNA gene sequencing, MALDI-TOF MS, and WGS, each offering greater speed and accuracy. The following sections trace this progression, outlining how each methodological advance reshaped our ability to detect, classify, and track enteric pathogens

and establishes the foundation for evaluating emerging technologies and guiding modernization of enteric pathogen identification.

1.3.1 Culture-based Methods for Enteric Bacteria

Isolation of enteric pathogens has historically depended on culture-based techniques, which remain foundational in both microbiology. Enteric bacteria such as *E. coli*, *Salmonella*, *Shigella*, and *Yersinia* are routinely cultured from stool, food, or water samples on selective and differential media. For example, MacConkey agar distinguishes lactose fermenters like *E. coli* from non-fermenters like *Salmonella* and *Shigella* through colony colouration (114, 115). Likewise, xylose lysine deoxycholate agar facilitates the recognition of *Salmonella* by hydrogen sulfide production, yielding black-centred colonies (116). These approaches exploit physiological traits and metabolic pathways to differentiate among organisms (115, 117).

Although traditional culture provides isolates for downstream testing, it is labour-intensive and often slow. Furthermore, some enteric bacteria, including many *Campylobacter* species, can be fastidious, with relatively poor growth in aerobic and microaerophilic cultures, raising concerns about sensitivity. Despite its utility, culture typically requires 18-72 hours for colony development (44, 118), delaying actionable results and limiting its role in fast-paced decision-making. Nevertheless, culture remains indispensable as it generates viable isolates for confirmatory identification, antimicrobial susceptibility testing, and molecular epidemiology.

1.3.2 Biochemical Identification Systems in Enteric Diagnostics

Once isolates are cultured, biochemical testing provides the next layer of identification. Biochemical assays enable identification by evaluating metabolic traits. Classical tube tests

typically detect colorimetric changes (pH shifts or substrate utilization), or gas production, collectively indicating enzyme activity. These tests are flexible but labour-intensive. However, panel-based systems have largely replaced individual tube tests in modern laboratories (119–121) (Fig. 5).

The API 20E system was one of the earliest commercial platforms offering standardized biochemical panels with colorimetric endpoints. More recently, automated systems such as VITEK 2 (bioMérieux, Marcy-l'Étoile, France) and Biolog MicroPlates (Biolog Inc., Hayward, USA) have gained in popularity. VITEK (bioMérieux, Marcy-l'Étoile, France) identifies bacteria through fluorogenic and colorimetric substrates and links results to an extensive database for species-level assignments (122–125). Biolog instead measures patterns of carbon source utilization and chemical sensitivity, creating “metabolic fingerprints” that can differentiate closely related organisms (126–128).

Biochemical systems are relatively inexpensive, standardized, and compatible with routine workflows. However, their performance can be limited for unusual strains or emerging pathogens poorly represented in reference commercial data sets and cannot be routinely curated or updated by end users. Continued efforts to improve phenotype-based identification are ongoing. For example, BacDoc, introduced in 2026, combines culture characteristics with biochemical interpretation to enhance diagnostic performance, although its current scope remains relatively limited (129). Biochemical testing also requires isolates from pure culture, which can delay identification. These tests often generate ambiguous results, especially for closely related taxa (119, 120). In practice, this can mean misidentification of pathogens during outbreaks, leading to delays in control measures.

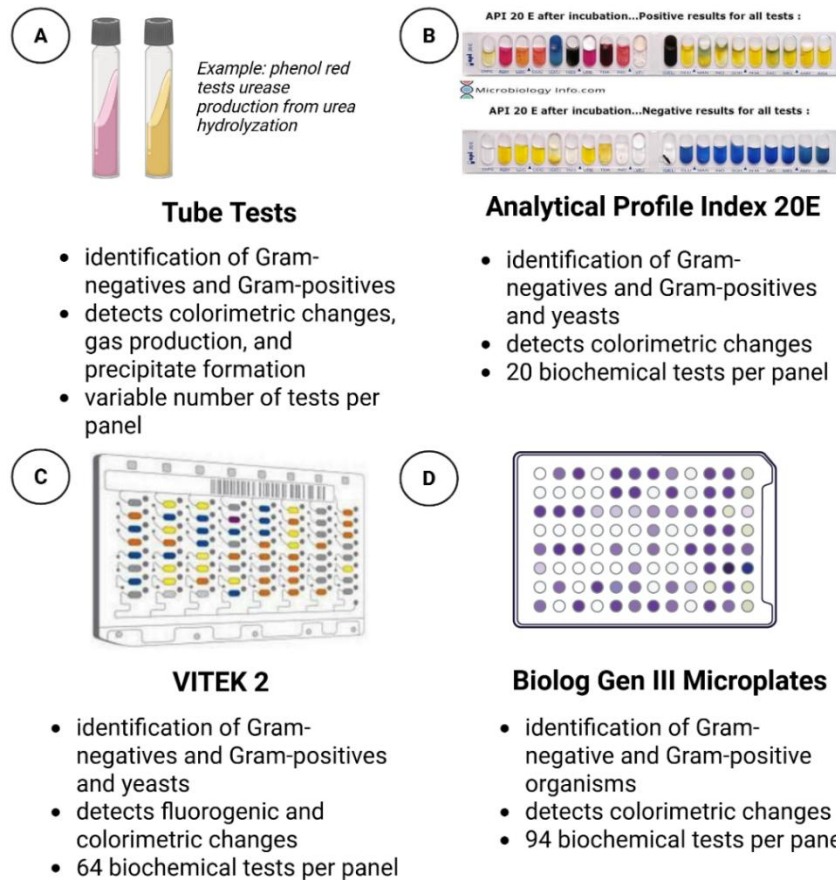


Figure 5. Biochemical test platforms for bacterial identification. A range of platforms are used for bacterial identification based on metabolic and biochemical phenotypes. **[A]** Tube-based biochemical tests are manually selected and interpreted by laboratory technicians, with colorimetric changes, gas production, or precipitate formation used to infer metabolic traits. **[B]** The API 20E (bioMérieux, Marcy-l'Étoile, France) standardizes 20 biochemical reactions into a strip-based format, interpreted by colorimetric changed and compared against reference databases with 20 reactions per strip (122, 123, 125). **[C]** VITEK 2 (bioMérieux, Marcy-l'Étoile, France) automates biochemical testing using fluorogenic and colorimetric assays with 64 reactions per card (122–125). **[D]** Biolog Gen III Microplates (Biolog Inc., Hayward, USA) expand testing capacity to 94 reactions, detecting colorimetric responses to carbon utilization and chemical sensitivity (126–128).

1.3.3 Serological Assays for Enteric Pathogen Detection

Serological methods identify enteric pathogens by detecting surface antigens using specific antisera. Historically, slide agglutination tests for O (somatic) and H (flagellar) antigens have been central to differentiating *Salmonella* serovars, as codified in the Kauffmann-White scheme (130). Similar serological panels are applied for *E. coli* pathotypes and *Shigella* serogroups. In clinical contexts, these tests are rapid and inexpensive, often yielding results within minutes. Despite their utility, serological assays are limited by cross-reactivity, subjectivity in reading results, and the requirement for highly trained personnel (116, 131, 132). They are increasingly used as confirmatory reference tests rather than primary diagnostic tools (116, 131, 132) and have largely been replaced by molecular and genomic approaches, particularly by Canadian public health labs (133–135) and the CDC (136). This has been particularly important for *Salmonella* serovar identification in outbreak settings, where serotyping remains a key surveillance parameter.

1.3.4 DNA-DNA Hybridization and Average Nucleotide Identity

Before the widespread adoption of gene sequencing, bacterial taxonomy relied heavily on DNA-DNA hybridization (DDH). In this method, genomic DNA from two organisms was denatured and allowed to reassociate, and the percentage of hybridization was used to infer genetic relatedness (137–139). A 70% DDH value became the conventional threshold for delineating species (140). While this approach provided a much-needed quantitative framework, it was technically demanding, poorly reproducible across laboratories, and limited in scalability (139, 141, 142).

The introduction of sequencing technologies enabled a more precise analogue of DDH, average nucleotide identity (ANI). ANI calculated the mean nucleotide identity of orthologous genomic regions shared between two isolates, with a threshold of approximately 95-96% ANI corresponding to the traditional 70% DDH cutoff (143). ANI is computationally simple, highly reproducible, and easily scalable to thousands of genomes within a reference database. As a result, it has largely replaced DDH as the genomic gold standard for species delineation. However, ANI is not without its limitations. ANI is dependent on high-quality assemblies and reference databases, debates persist around threshold cutoffs, and incomplete genomes can yield misleading values (144–146).

1.3.5 16S rRNA Gene Sequencing: Utility and Limitations

The sequencing of the 16S rRNA gene revolutionized bacterial taxonomy by providing a universal genetic marker (67). The gene's mosaic of conserved and hypervariable regions (Fig. 6) allows amplification across nearly all bacteria, while also permitting differentiation between taxa (138, 147, 148). Early studies using Sanger sequencing of the 16S rRNA gene provided the first comprehensive phylogenetic frameworks, leading to a major restructuring of bacterial systematics in the late 20th century (6, 68, 138, 148). The widespread adoption of 16S sequencing provided a standardized method for species identification and phylogenetic analysis (67, 68, 148). Its strengths lie in its universality, relatively low cost, and compatibility with historical datasets (67, 68).

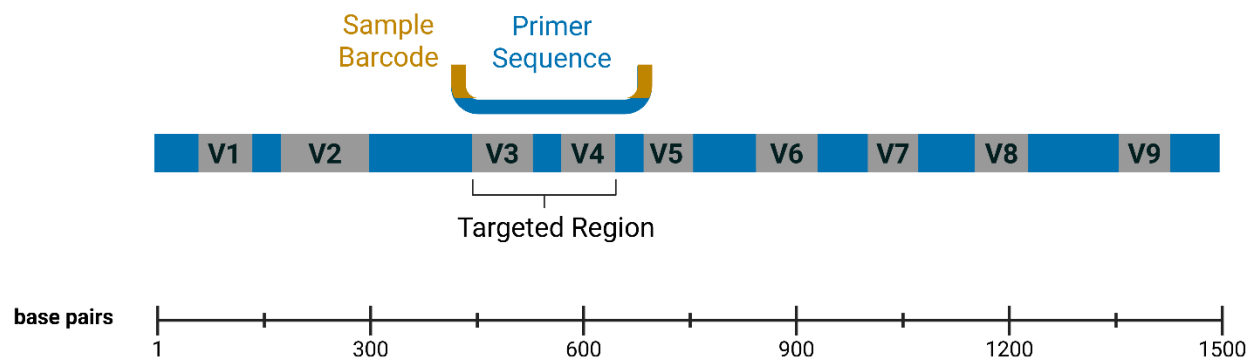
Despite its transformative role, 16S rRNA sequencing has important limitations. First, the gene evolves extraordinarily slowly, leading to insufficient resolution for closely related species, particularly among Enterobacterales (67, 69, 72). Secondly, some species share nearly identical

16S rRNA sequences despite clear differences in whole genome content, ecological niches, or taxonomic borders making species-level discrimination unreliable (68, 74, 147). Finally, horizontal gene transfer, intragenomic heterogeneity, and sequencing artifacts can complicate interpretation (70, 73, 74, 138, 151). Even though 16S has been a gold standard (67, 146), its inability to distinguish pathogenic vs. non-pathogenic strains of the same species undercuts its reliability in guiding clinical management.

Comparative studies have shown that 16S rRNA sequence similarity thresholds of 97-99% often fail to resolve species accurately when benchmarked against ANI and DDH (67, 68, 145–147) (Table 3). To illustrate this, Table 3 compares cutoff values and performance characteristics for DDH, ANI, and 16S rRNA sequence similarity. Collectively, these observations highlight the lasting role of 16S rRNA sequencing as a first-line tool, but also its limitations relative to whole-genome-based approaches. Importantly, these challenges are amplified when attempting to identify highly related rare or low-prevalence bacteria, which may not be included in reference databases or are insufficiently characterized in the literature, resulting in ambiguous or misleading identifications, leaving 16S rRNA sequencing unable to provide reliable species-level resolution.

1.3.6 MALDI-TOF MS

MALDI-TOF MS has become a transformative tool in clinical microbiology laboratories. The technique involves ionizing proteins extracted directly from whole bacterial cells, generating a spectral fingerprint that can be compared against a reference database. The post-culture



CONSERVED REGIONS: non-specific function

VARIABLE REGIONS: taxon-specific function

Figure 6. Conserved and hypervariable regions of the 16S rRNA gene. The 16S rRNA gene (~1500 bps), is a conserved gene found in all bacteria that encodes the 16S subunit of the ribosome and is composed of nine hypervariable regions (V1-V9, shown in grey) interspersed between conserved regions (blue). The conserved regions enable primer binding for PCR amplification (example barcode and primer shown), while the variable regions facilitate phylogenetic or taxonomic classification of microorganisms at the genus or species level (147, 149). [Adapted from Fakuda *et al*, 2016 (150)].

Table 3. Comparison of thresholds used in DDH, ANI, and 16S rRNA sequencing for bacterial taxonomic classification

<i>Method</i>	<i>Threshold</i>	<i>Resolution</i>	<i>Advantages</i>	<i>Limitations</i>
<i>DDH</i> (139–141)	$\geq 70\%$	Moderate	• Historical standard • Species-level cutoff	• Labour intensive • Poor reproducibility
<i>ANI</i> (143–146)	$\geq 95\text{-}96\%$	High	• Reproducible • Scalable • Genome-wide	• Requires whole genome sequences
<i>16S rRNA</i> <i>sequence</i> <i>similarity</i> (67, 68, 145–147)	$\geq 97\text{-}99\%$	Low-moderate	• Universal marker • Cost effective	• Poor resolution among closely related species • Horizontal gene transfer • Intragenomic heterogeneity

process, from sample preparation to result, typically requires only minutes, offering a rapid alternative to both biochemical and molecular assays (79, 152, 153).

The advantages of MALDI-TOF MS include its speed, low per-sample cost, and ability to manage large sample volumes with minimal consumables. It has been particularly impactful for routine diagnostics, enabling same-day identification of pathogens that would otherwise require biochemical or molecular testing (78, 79). Nonetheless, MALDI-TOF MS has limitations. While transformative for routine pathogens, its reliance on existing spectral libraries leaves public health laboratories blind to rare or emerging organisms, precisely those that matter most in outbreak investigations (78–80).

Another important consideration is that MALDI-TOF is a proteomic rather than genomic method. It identifies organisms based on expressed proteins, which reflect the current physiological state of the isolate. As a result, culture conditions, growth phase, and environmental stressors can influence the spectrum obtained. By contrast, WGS provides information about an organism's genetic potential, often independent of environmental conditions (79, 152, 153). This distinction underlines the complementary but non-equivalent nature of proteomic and genomic identification strategies. Despite these constraints, MALDI-TOF MS represents a major advance in diagnostic microbiology bridging the gap between traditional phenotype-based approaches and genomic methods.

1.3.7 Whole Genome Sequencing

WGS has rapidly become the most powerful tool for bacterial identification, classification, and epidemiological tracking. By capturing the complete genetic blueprint of an organism, WGS surpasses earlier methods in taxonomic resolution, providing the ability to

define species boundaries, infer evolutionary relationships, and detect clinically relevant genetic determinants (154). The impact of WGS has been particularly pronounced in infectious disease surveillance. Genomic data can link cases across outbreaks, identify transmission pathways, identify enhanced risk alleles (155, 156), and uncover reservoirs of antimicrobial resistance (157–165). Public health agencies worldwide now integrate WGS into their workflows for pathogen surveillance and outbreak investigation (50, 154, 158, 164, 166–168), marking a fundamental shift from phenotypic to genomic epidemiology.

The evolution of sequencing technologies has aided this transformation. Early Sanger sequencing (Applied Biosystems, Foster City, USA) provided the first bacterial genomes in the 1990s, but its low throughput and high cost limited broader application (169). The advent of next-generation sequencing platforms, particularly Illumina’s sequencing by synthesis chemistry (San Diego, USA), represented a turning point, offering massively parallel sequencing at reduced cost and high accuracy. Illumina has since become the primary global platform for microbial genomics (161, 170–172). Meanwhile, other short-read platforms such as IonTorrent (Thermo Fisher Scientific, Waltham, MA, USA), and SOLiD (Applied Biosystems, Foster City, USA) provided early competition, though both are used less frequently due to limitations in accuracy, throughput, and ongoing manufacturer support (171, 173), as described in Tables 4 and 5.

The introduction of long-read technologies has further expanded the genomic toolkit. Pacific Biosciences (PacBio; Menlo Park, USA) developed the Single Molecule, Real-Time sequencing, producing long, high accuracy “HiFi” reads well suited for *de novo* genome assemblies (174, 175). More recently, Oxford Nanopore (ONT; Oxford, UK) introduced portable, real-time sequencing devices capable of producing ultra-long reads (176–181). ONT’s ability to deliver rapid results directly in the field has made it a unique complement to Illumina,

Table 4. Summary of commonly used platforms for bacterial genomics. [Adapted from Garrido-Cardenas *et al*, 2017] (182).

Sequencing Platform	Read Type	Read Length	Accuracy	Time (h)	Cost per Gigabase	Throughout
Sanger (169)	capillary	500-1000 bp	99.9% (Q30)	72	not applicable	Low
Illumina (161, 170–172)	short-read	50-500 bp	99.9% (Q30)	72	\$10	Very high
IonTorrent (183)	short-read	100-400 bp	99% (Q20)	2	\$100	Moderate
SOLiD (173)	short-read	35-75 bp	99.9% (Q30)	7 days	\$10	High
Element Biosciences AVITI (184–188)	short-read	150-300 bp	99.999% (Q50)	17-60	\$5-7	Moderate
PacBio (HiFi) (174, 175)	long-read	10-25 kb	90% (Q10)	3	\$600	Moderate
Oxford Nanopore (176–181)	long-read	>4 Mb	90% (Q10)	72	\$50-2000	High

Table 5. Description, advantages and limitations of common WGS platforms. [Adapted from Garrido-Cardenas *et al*, 2017] (182).

<i>Platform</i>	<i>Key Features</i>	<i>Advantages</i>	<i>Limitations</i>
<i>Sanger</i> (169)	• Historical standard	• High accuracy • Widely adopted	• Low throughput • Consensus read • Labour, time, and cost intensive
<i>Illumina</i> (161, 170–172)	• Sequencing by synthesis	• Low cost per base • Low raw error rate • Widely adopted	• Short reads limit downstream assembly • Longer run time
<i>IonTorrent</i> (171)	• Sequencing by synthesis and semiconductor detection	• Cost effective • Short run time	• Lower accuracy in homopolymers • Poor coverage in AT- and GC-rich regions
<i>Solid</i> (173)	• Two-base encoding and ligation-based approach	• High accuracy • High throughput • Cost effective	• Largely discontinued
<i>Element Biosciences AVITI</i> (184–188)	• Avidite base chemistry • Flexible, high-accuracy PE sequencing	• Near-perfect accuracy • Cost effective	• Short reads limit downstream assembly • New platform with small user base
<i>PacBio (HiFi)</i> (174, 175)	• First widely used long read sequencing platform	• Long, high accuracy reads • Good for de novo assembly	• High cost
<i>Oxford Nanopore</i> (176–181)	• Portable devices • Leader in benchtop workflows	• Ultra long reads	• Lower raw read accuracy • High cost

particularly in outbreak investigations and resource-limited settings. Together, Illumina and ONT now dominate microbial genomics with their complementary strengths in accuracy and read length, making them central to modern bacterial genomics (183, 189, 190). Tables 4 and 5 summarize the characteristics of these major sequencing platforms relevant to bacterial genomics.

The AVITI platform has emerged as an additional and novel short-read sequencing technology. AVITI employs avidite chemistry, in which multivalent nucleotide ligands improve signal persistence and reduce background noise, enabling high sequencing accuracy while maintaining throughput and cost comparable to existing short-read platforms (Tables 4-5) (184–188). Although adoption within microbial genomics remains relatively limited, AVITI represents a promising addition to the expanding landscape of bacterial whole-genome sequencing technologies.

Beyond the sequencing itself, the analysis of WGS data requires robust computational pipelines. A typical bioinformatic workflow for WGS data includes quality control (QC), optional genome assembly or read mapping, annotation, and downstream analysis such as phylogenetics, resistance gene detection, or taxonomic classification. These workflows are generally carried out stepwise, where the output of one tool serves as the input for the next. Automation reduces the need for manual intervention, but challenges remain regarding computational infrastructure, software compatibility, and user expertise (191, 192). Open-source platforms such as Galaxy have communized access to bioinformatics pipelines (193), while containerization tools (e.g. Singularity (194)) and workflow managers (e.g. Nextflow (195)) are increasingly used to standardize and streamline analyses. Despite these advances, public health

laboratories must carefully evaluate tools and pipelines for accuracy, reproducibility, and scalability.

Altogether, WGS offers unprecedented power for bacterial identification and characterization, but it also introduces new and ongoing challenges related to infrastructure, expertise, and data governance. WGS-based approaches promise to resolve the limitations in sequencing and downstream analysis, but implementation barriers inhibit large-scale deliverability (162–164, 196–201). Nonetheless, the trajectory of the field suggests that WGS will continue to replace earlier methods, ultimately serving as the central framework for microbial taxonomy and clinical microbiology. However, these methods illustrate a persistent gap: our most widely used diagnostic tools are optimized for common pathogens yet fall short in precisely those scenarios where accurate identification is most critical for uncommon and emerging bacteria. This gap highlights the importance of evaluating, validating, and modernizing WGS approaches.

1.4 Applications of WGS In Clinical and Public Health Microbiology for Enteric Pathogens

The use of WGS data has rapidly emerged as a transformative tool in clinical and public health microbiology. Falling sequencing costs and improved throughput suggest it may soon outpace traditional molecular methods, yet routine implementation remains limited (159, 163). At present, WGS approaches are mostly applied in public health and tertiary care laboratories, where it enables high resolution typing, epidemiological surveillance and outbreak investigation.

Despite its promise, WGS adoption faces technical and practical hurdles. Current analyses typically rely on genome content analysis by comparing to a reference genome, but outcomes are highly sensitive to sequencing quality, assembly completeness, and reference

selection (202). Broader analyses of all genomic loci can improve resolution but are computationally demanding. Importantly, WGS captures genetic potential rather than gene expression, limiting direct clinical interpretation. These limitations are compounded by a lack of large-scale validation studies, leaving uncertainty about clinical utility and hindering evidence-based adoption (159, 163).

Current reference databases and bioinformatic tools present additional challenges for accurate bacterial identification. Most databases are heavily weighted toward common enteric pathogens, with high-quality reference genomes available for only a narrow set of organisms. This imbalance reduces the ability to classify rare or low-prevalence pathogens with accuracy, leading to misclassification or incomplete identification. As a result, uncommon pathogens can be difficult to distinguish from closely related species, impeding timely outbreak response and obscuring the true spectrum of enteric disease (196, 198, 203). Moreover, widely used bioinformatics pipelines for genome assembly and taxonomic classification have not been systematically optimized for rare pathogens, further constraining their diagnostic resolution (63–66). PulseNet Canada and NESP have made significant progress in tailoring tools for outbreak investigation (48, 50), but the challenge of resolving rare taxa underscores the need for expanded genomes, reference libraries, and refined analytical workflows.

Standardization remains a critical challenge. Uniform benchmarks for sequencing run quality, genome assembly accuracy, and typing schemes are still under development. Without harmonized criteria, data generated across laboratories is difficult to compare, complicating surveillance and outbreak response. International coordination will be essential to establish shared pipelines, reference databases, and QC frameworks.

Financial and infrastructural barriers also remain significant. Costs extend well beyond sequencing reagents, encompassing sample preparation equipment, bioinformatics infrastructure, data storage, and highly trained personnel. While automation and cloud-based solutions may ease some burdens, they introduce new concerns around data security, confidentiality, and inoperability. These barriers currently confine WGS primarily to specialized centres rather than frontline diagnostic use (154, 157, 159, 163, 191, 192, 198, 199, 201).

Nonetheless, the long-term trajectory is clear. WGS offers unparalleled resolution for pathogen detection and epidemiological investigation. As costs decline, workflows streamline, and quality standards solidify, WGS has the potential to transition from a supplementary tool into a cornerstone of both clinical diagnostics and public health microbiology. Yet, its full potential remains limited, particularly for the identification of rare and low-prevalence pathogens that continue to evade reliable identification. Bridging this gap is essential if WGS is to truly deliver on its potential in frontline diagnostics and public health surveillance.

1.5 Current Study

To date, gold-standard bacterial identification methods have included genomic approaches such as 16S rRNA gene sequencing, phenotypic methods based on biochemical profiling of bacterial metabolism, and proteomic techniques such as MALDI-TOF MS. While these methods typically allow identification at the family or genus level, they struggle to achieve species-level resolution, especially for rare and low-prevalence pathogens, such as *Aeromonas*, *Cronobacter*, and *Proteus*, although these examples are not exhaustive. These approaches remain foundational in clinical and public health microbiology, but their limited discriminatory power restricts reliable differentiation of closely related organisms, particularly uncommon taxa that are

underrepresented in reference databases and infrequently encountered in routine reference laboratory practice. This creates a persistent gap in taxonomic resolution for organisms that are underrepresented in references databases and lack well-curated genomic reference sequences.

WGS has emerged as a powerful alternative by comparing entire bacterial genomes rather than a single gene or phenotypic characteristics, enabling higher-resolution taxonomic classification based on genome-wide similarity. However, its application to rare and low-prevalence pathogens remains limited by incomplete representation of these organisms in reference databases, and differences among bioinformatic workflows in their underlying algorithms, confidence thresholds, and reference database used. As a result, even genome-based diagnostic approaches may yield inconsistent or ambiguous results for uncommonly sequenced or infrequently identified bacteria. These challenges highlight that improved resolution alone does not fully resolve the complexities of bacterial identification, particularly where taxonomy itself is dynamic.

This study explores these limitations by evaluating WGS-based identification methods in the context of rare and low-prevalence enteric bacteria, with a particular emphasis on both classification performance and their impacts on bacterial taxonomy and diagnostic interpretation. This study hypothesized that modernizing WGS-based bacterial identification methods would improve species-level identification of rare and low-prevalence enteric bacterial pathogens and increase diagnostic accuracy relative to the traditional identification methods evaluated in this study. This study recognizes that genome-based classification may challenge or refine existing taxonomic frameworks and introduce new considerations for how diagnostic “truth” is defined and applied. The primary objectives of this thesis are to: [1] evaluate WGS-based techniques and bioinformatic tools for rare pathogen identification, [2] compare WGS-based diagnostics to

traditional methods such as 16S rRNA sequencing and biochemical tests, and [3] provide recommendations for the application of genomics in clinical laboratories, with a focus on improving public health surveillance and patient care.

Improving WGS-based methods for the identification of rare and low-prevalence enteric bacterial pathogens has the potential to strengthen public health surveillance systems, support timely outbreak detection and response, and guide more accurate, evidence-based clinical decision-making. More broadly, this work contributes to the ongoing efforts to integrate genomics into bacterial taxonomic and diagnostic practice, where classification is increasingly shaped by genome-based evidence rather than historical frameworks. The subsequent chapters outline the methods used in this investigation, followed by the presentation and discussion of results.

Chapter 2: Methods

2.1 Sample Selection and Inclusion Criteria

This study analyzed a retrospective convenience sample of 365 bacterial isolates, including 331 clinical isolates submitted to the Reference and Diagnostic Services (RDS) laboratory at Canada's NML. The RDS serves as the national reference laboratory for enteric bacterial pathogens, receiving isolates referred by provincial and territorial public health laboratories when organisms cannot be confidently identified using routine diagnostic methods. Reasons for referral include limited laboratory infrastructure, lack of specialized equipment or expertise, inability to culture fastidious organisms, or the need for advanced characterization such as WGS and bioinformatic analysis (48, 50, 51, 204).

Archived RDS submissions were selected because they represent the diagnostically challenging organisms encountered during routine national reference laboratory practice, directly aligning with the objective of evaluating identification methods for difficult-to-classify enteric bacteria. Clinical isolates submitted between 1995 and 2023 were eligible for inclusion; thus, the isolates spanned 28 years. Isolates that had been definitively identified by the RDS as *Salmonella*, *E. coli*, or *Shigella* were excluded because these common enteric pathogens are routinely identified using well-established laboratory workflows and therefore do not represent the diagnostic challenges addressed in this study.

Throughout this thesis, the terms *rare*, *low-prevalence*, and *uncommon* refer to organisms that were infrequently encountered within routine Canadian reference laboratory submissions rather than organisms classified according to national disease incidence. Because the dataset was assembled retrospectively from archived clinical referrals, no predefined numerical threshold was used to define rarity. Instead, the collection represents the spectrum of diagnostically challenging enteric bacteria referred for specialized identification over nearly three decades of

routine reference laboratory service. Consequently, the findings are intended to inform diagnostic practice within reference laboratory settings rather than estimate the population prevalence of enteric bacterial pathogens in Canada.

The final dataset comprised 331 clinical isolates recovered from stool, blood, urine, cerebrospinal fluid, wound, and other clinical specimens. An additional 34 type strains from the American Type Culture Collection (ATCC) and Health Products and Food Branch (HPB) culture collections were included as reference organisms for accuracy assessment. These type strains represented taxa present within the clinical isolate collection and had previously been evaluated during internal method development to establish the feasibility of the laboratory and bioinformatic workflows applied in this study.

The isolate collection represented substantial taxonomic diversity. Based on the original laboratory identifications assigned at the time of submission, the dataset included five bacterial orders comprising 13 families, 35 genera, and 85 named species (Fig. 7). Original taxonomic assignments were generated using biochemical testing, 16S rRNA gene sequencing, MALDI-TOF MS, WGS, or combinations of these methods based on availability and laboratory procedure at the time of submission. Diagnostic uncertainty was common within the archived collection, with 36 clinical isolates (10.9%) lacking genus-level identification and 113 isolates (34.1%) lacking species-level identification before inclusion in this study. This diversity and baseline diagnostic uncertainty provided an appropriate framework for evaluating the performance of WGS-based identification methods across a broad range of uncommon enteric bacterial pathogens.

Taxonomic Diversity of Study Isolates Original taxonomic assignments ; area proportional to isolate count

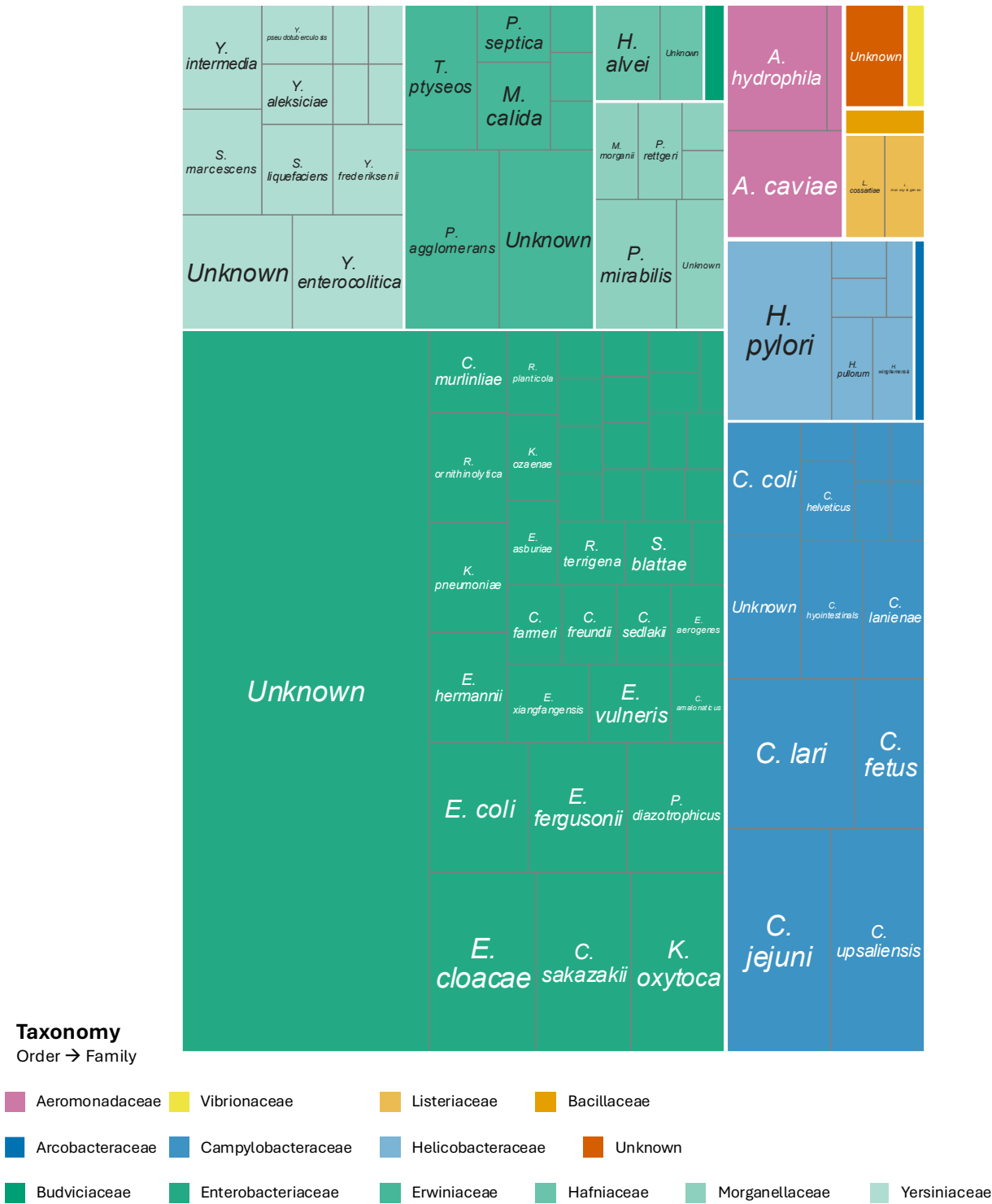


Fig. 7, part 1 of 2

Figure 7. Taxonomic diversity of the bacterial isolate collection based on original laboratory identification (1995-2023). Hierarchical treemap shows the taxonomic composition of the 365 isolates included in this study at the order, family, and species levels. Tile area is proportional to the number of isolates represented. Orders are distinguished by colour, with families shown as related shades within each order. Species labels are displayed only for taxa represented by more than one isolate to improve readability, and isolates lacking species- or genus-level identification at the time of submission were grouped as "unknown" within their respective family. The collection comprised five bacterial orders: Enterobacterales (n=267), Campylobacterales (n=76), Caryophanales (n=5), Aeromonadales (n=13), and Vibrionales (n=1). Enterobacterales included Enterobacteriaceae (n=184), Yersiniaceae (n=34), Erwiniaceae (n=29), Morganellaceae (n=14), Hafniaceae (n=5), and Budviciaceae (n=1). Campylobacterales comprised Campylobacteraceae (n=59), Helicobacteraceae (n=16), and Arcobacteraceae (n=1). Caryophanales included Listeriaceae (n=4) and Bacillaceae (n=1), Aeromonadales included Aeromonadaceae (n=13), and Vibrionales included Vibrionaceae (n=1). Three isolates had not been taxonomically classified and only a Gram status was available. Taxonomic classifications reflect the original laboratory identifications assigned at the time of sample submission (1995-2023).

2.2 Recovery and Cultivation of Bacterial Isolates from Frozen Stocks

Isolates were cryopreserved at -80°C in 50% v/v glycerol peptone or 19% w/v skim milk broth following initial submission (1995-2023) (6). Submissions arrived as clinical specimens (e.g. stool), from which the organism of interest was first isolated via agar plating prior to storage. For recovery, isolates were revived using culture conditions tailored to their preliminary identification or suspected identity at the time of submission. Media, incubation conditions, and atmospheric requirements for organism groups are summarized in Table 6.

Isolates of microaerophilic organisms were incubated in anaerobic jars supplemented with custom gas mixtures labeled MO₂ (composition: 5% O₂, 10% CO₂, and the balance N₂) and ↑H₂ (composition: 3% O₂, 7% CO₂, 7% H₂, and the balance N₂). Consistent with internal protocols and quality assessments, *Campylobacter* isolates were recovered with MO₂ and *Helicobacter* with MO₂ and ↑H₂ to account for their fastidious growth. Aerobic and facultative anaerobic organisms were incubated under standard atmospheric conditions.

Following incubation, cultures were inspected for colony morphology and purity. Isolates displaying mixed morphologies or signs of contamination were streaked for isolation and re-incubated until a pure culture aligning with expected phenotypic characteristics was obtained. Subculturing was performed as necessary to generate sufficient biomass for downstream analysis. If recovery was unsuccessful, cultivation strategies were adapted according to the suspected organism, including changes to media, incubation time, temperature, or atmospheric composition. Once viability and purity were confirmed, isolates were subcultured into fresh 19% w/v skim milk broth and preserved at -80°C until DNA extraction and subsequent testing was performed.

Table 6. Culture conditions used in this study to cultivate bacterial isolates from frozen stocks.

Organism Type	Media	Temperature (°C)	Time	Oxygen Requirements
<i>Listeria</i>	Brain Heart infusion agar	34-36	24-48 h	Facultative anaerobe
<i>Salmonella</i>	MacConkey agar	34-36	24-48 h	Facultative anaerobe
<i>Campylobacter</i>	Meuller-Hinton agar with 10% sheep's blood	34-36 or 44-46	3-5 d	Microaerophilic
<i>Helicobacter</i>	Meuller-Hinton agar with 10% sheep's blood	34-36 or 44-46	3-5 d	Microaerophilic
Others	1.5% nutrient agar	34-36	24-48 h	Aerobic or Facultative anaerobe

2.3 Whole Genome Sequencing

Two complementary WGS platforms were employed in this study. Illumina short-read sequencing (San Diego, USA) provides high per-base accuracy but lower real-time throughput, whereas Oxford Nanopore Technologies long-read sequencing (Oxford, UK) offers rapid turnaround and greater read length at the expense of a higher raw error rate (172, 183, 190, 197, 205). By combining these technologies, we leveraged the accuracy of Illumina reads with the long-range information of ONT reads to generate platform specific assemblies (183, 190). The subsequent bioinformatic analyses described in Section 2.4, therefore, includes workflows tailored to Illumina data and ONT data.

2.3.1 DNA Preparation: Extraction and Evaluation of Genomic DNA

Bacterial isolates were cultured as described in Section 2.2, and approximately one inoculating loopful of fresh biomass was used per extraction. DNA extraction protocols were selected based on the predicted Gram status of each isolate, inferred from preliminary identification records rather than direct Gram staining, to guide the use of Gram-positive or Gram-negative specific DNA extraction kits, as outlined in Table 7. Extraction blanks (reagent-only) were included periodically as contamination controls but were not sequenced.

To ensure sufficient yield for downstream sequencing, gDNA was quantified using fluorescence-based assays, PicoGreen (Thermo Fisher Scientific, Waltham, MA, USA) or Qubit (Thermo Fisher Scientific, Waltham, MA, USA), with the choice dependant on throughput requirements. Samples not meeting a platform's specific thresholds (≥ 0.2 ng/uL for Illumina (San Diego, USA) and ≥ 20 ng/uL for ONT (Oxford, UK)), were concentrated using centrifugal filters

Table 7. DNA extraction and quantification workflows for bacterial isolates used in this study.

<i>Workflow</i>	<i>Kit / Assay</i>	<i>Sample Type / Throughput</i>	<i>Key Steps</i>	<i>Notes</i>
Gram-negative DNA extraction	Qiagen DNeasy Blood & Tissue (spin column or 96-well format) (Valencia, USA)	Gram-negative isolates (n=360)	proteinase K lysis (55°C, 1-2h), RNase A treatment, silica binding, wash, elution in Buffer EB	spin-column for ≤36 samples; 96-well plate for high throughput
Gram-positive DNA extraction	Lucigen MasterPure Complete DNA & RNA Purification Kit (Middleton, USA)	Gram-positive isolates (n=5)	lysozyme + RNase A lysis, Proteinase K digestion, protein precipitation, ethanol wash, resuspension (37°C, 3.5h),	single tube format due to low sample number
Quantification (high throughput)	Quant-iT™ PicoGreen dsDNA Assay (Thermo Fisher Scientific, Waltham, MA, USA)	≥36 samples	fluorescence-based quantification on FilterMax F5 plate reader (Molecular Devices, San Jose, CA, USA)	background corrected to reagent-only blanks
Quantification (low throughput / confirmatory)	Qubit™ dsDNA Broad Range Assay (Thermo Fisher Scientific, Waltham, MA, USA)	≤36 samples or critical samples	fluorescence detection on Qubit 4 fluorometer (Thermo Fisher Scientific, Waltham, MA, USA) with calibration standards	higher accuracy, lower throughput
DNA concentration (as needed)	Amicon Ultra-0.5 50kDA centrifugal filters (Sigma-Aldrich, Burlington, MA, USA)	as required for low concentration samples	centrifugation to reduce volume, re-measured on the Qubit 4 fluorometer (Thermo Fisher Scientific, Waltham, MA, USA)	used if DNA concentration fell below platform thresholds

and gDNA was collected from the filters centrifugally. Extracted gDNA was aliquoted and stored at 5°C±2°C until library preparation. The extraction and quantification workflows are summarized in Table 7.

2.3.2 Short-read Sequencing: Illumina MiSeq and NextSeq Platforms

Short-read sequencing was performed by the NML's Genomics Core Facility using Illumina MiSeq and NextSeq platforms (San Diego, USA). To ensure adequate coverage, approximate genome sizes were assumed for different groups: *Campylobacter* (~1.5Mb), *Listeria* (~3Mb), and other bacteria (~5Mb), with all sequencing runs targeting 50X coverage.

Genomic DNA was normalized by the Genomics Core Facility (NML, Winnipeg) prior to library preparation according to their validated sequencing workflow. Shotgun libraries were prepared using an internally validated reduced-volume implementation of the Nextera XT DNA Library Preparation kit (Illumina, San Diego, USA). Use of the MiSeq or NextSeq was based on instrument availability at the time of sequencing. MiSeq runs generated 301bp paired-end (PE) reads, whereas NextSeq runs generated 151bp PE reads. Approximately 30 libraries were pooled per sequencing run according to project requirements and sequencing platform requirements. Pooled libraries underwent selection using a BluePippin (Sage Science, Beverly, USA) to remove adapter dimers and small fragments prior to sequencing. Library fragment size distributions were evaluated using an Agilent 4200 TapeStation with Genomic DNA ScreenTape (Agilent Technologies, Santa Clara, CA, USA), and pooled library concentrations were confirmed using the Qubit High Sensitivity dsDNA Assay (Thermo Fisher Scientific, Waltham, MA, USA).

Average library fragment sizes and cluster loading concentrations were adjusted according to organism group, with smaller average fragment-sized libraries and lower instrument loading concentrations used for *Campylobacter* and *Listeria* than for other organisms to accommodate their smaller genome sizes and optimize cluster generation based on library validation. On average, each sample yielded 1.2-1.6 million PE reads, sufficient for downstream assembly and analysis.

The resulting short-read data were uploaded to the Integrated Rapid Infectious Disease Analysis (IRIDA) platform (version 21.9) (206). These Illumina-derived paired-end sequencing reads were used for standalone short-read genome assembly and taxonomic classification (Section 2.4.1). The overall Illumina sequencing workflow is illustrated in Figure 8 and key run parameters are summarized in Table 8.

2.3.3 Long-read Sequencing: ONT MinION and GridION

ONT (Oxford, UK) long-read sequencing was performed using MinION (n=149 samples) and GridION (n=307 samples) platforms, though >365 samples were sequenced in total due to repeat sequencing required for low quality whole genome sequences. DNA libraries were prepared using ONT's Rapid Barcoding Kit 24 according to the manufacturer's protocol. R10.4.1 flow cells (ONT, Oxford, UK) were used for all runs, meeting ONT's minimum pore threshold of ≥ 800 active pores prior to library loading. Sequencing was conducted for the full 72-hour runtime with live basecalling disabled as real-time basecalling introduced computational instability during initial trials. Instead, raw signal files in ONT POD5 file format were collected and subsequently basecalled using Dorado v0.9.0 (207). Run control and pore monitoring were performed using MinKNOW v24.06.16 and v24.11.8 (ONT, Oxford, UK), depending on

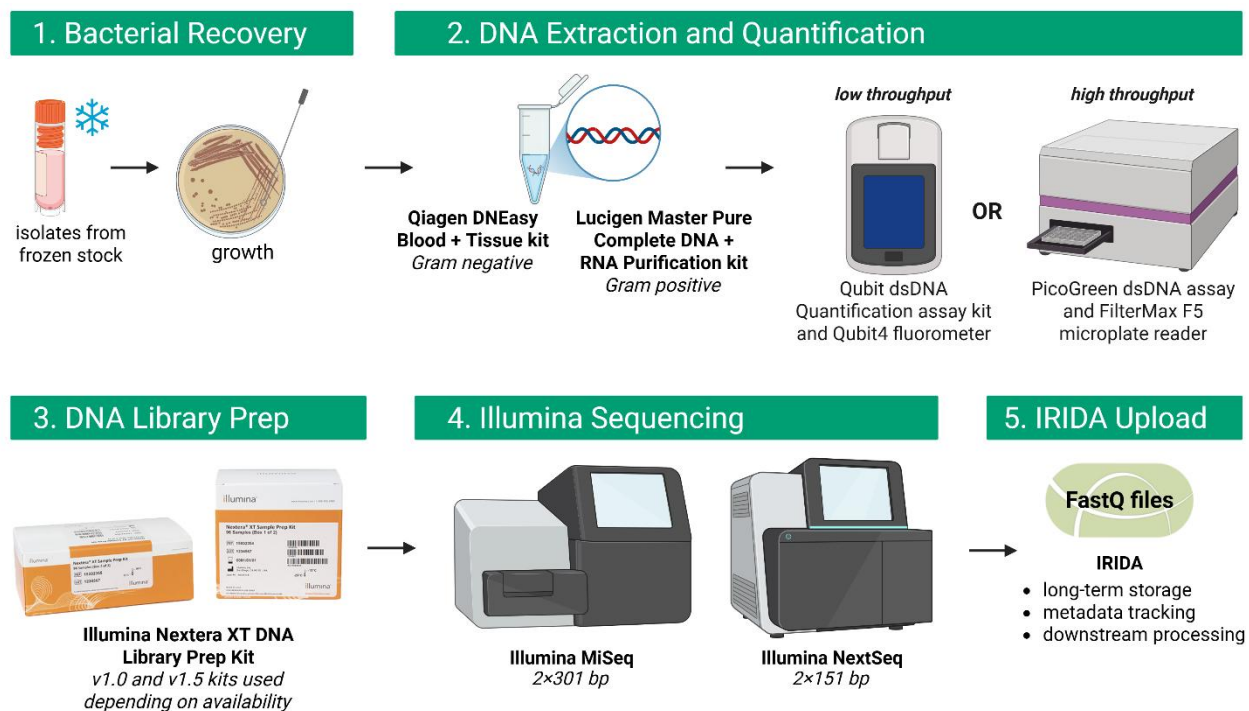


Figure 8. The Illumina sequencing workflow used in this study. Isolates were recovered from frozen stock (Section 2.2), genomic DNA was extracted using Gram-specific kits and quantified using Qubit and PicoGreen assays (Section 2.3.1), normalized, and libraries prepared using an internally validated reduced-volume Nextera XT DNA library preparation workflow. Sequencing was performed on Illumina MiSeq (301 bp PE reads) or NextSeq (151 bp PE reads) instruments, with resulting FASTQ files uploaded to IRIDA for storage and downstream analysis (206).

Table 8. The Illumina sequencing parameters used in this study.

Parameter	<i>Campylobacter</i> Isolates	<i>Listeria</i> Isolates	<i>Other</i> <i>Isolates</i>	<i>Notes</i>
Estimated genome size	~1.5 Mb	~3 Mb	~ 5 Mb	incorporated during sequencer run configuration
Target coverage	50X			across all runs
Library kit	Nextera XT			NML Genomics Core Facility library procedure deviates from manufacturer protocol
<i>Sequencing kit</i>	(v1.0 300-cycle, v1.0 500-cycle, v1.5 300-cycle)			Sequencing kit selected by the NML Genomics Core Facility
Read length	301 bp PE (MiSeq)		301 bp PE (MiSeq) or 151 bp PE (NextSeq)	platform dependent
Average library size	~250 bp		700-900 bp	N/A
Cluster loading concentration	6-12 pM		12-20 pM	N/A
Yield per sample	~1.2-1.6 million PE reads			

software version availability at the time of sequencing. The resulting FastQ files were then integrated into downstream bioinformatic analyses (Section 2.4.2). The overall workflow for ONT sequencing is summarized in Figure 9, with platform-specific run parameters outlined in Table 9.

2.4 Bioinformatic Analyses of WGS-derived Data: Quality Control, Assembly, and Taxonomic Classification

2.4.1 Illumina (San Diego, USA) WGS-derived Data Processing: Workflow Management, Quality Control, Assembly, Quality Assessment, and Taxonomic Classification

Illumina sequencing produced paired-end FastQ files for 362 bacterial isolates (Section 2.3.2). To ensure consistent taxonomic classification, raw sequencing reads for 362 isolates underwent *de novo* genome assembly and the genome assembly was analyzed with six taxonomic classifiers that produced 2,190 taxonomic assignments (Fig. 10, Table 10). Raw reads were first uploaded to IRIDA (206) for centralized data management, then processed in Mikrokondo v0.5.0 (Nextflow v24.10.4) (194, 195, 208, 209). The workflow incorporated standard QC (211–219), *de novo* assembly (220), and polishing steps, after which Kraken 2 v2.1.2 (kraken2 Standard Database, release 2024-12-28) (210) provided initial taxonomic classifications.

To verify taxonomic classifications, the resulting assemblies were analyzed with complementary tools: Mash (221) (Mikrokondo module (194, 195, 208, 209), GTDB Mash Sketch 2023-10-03/r214); GTDB Toolkit (GTDB-Tk) using both FastANI v 2.3.2 (144) (GTDB R214) and skANI v 2.4.1 (222) (GTDB R226), Type Strain Genome Server (TYGS) v401

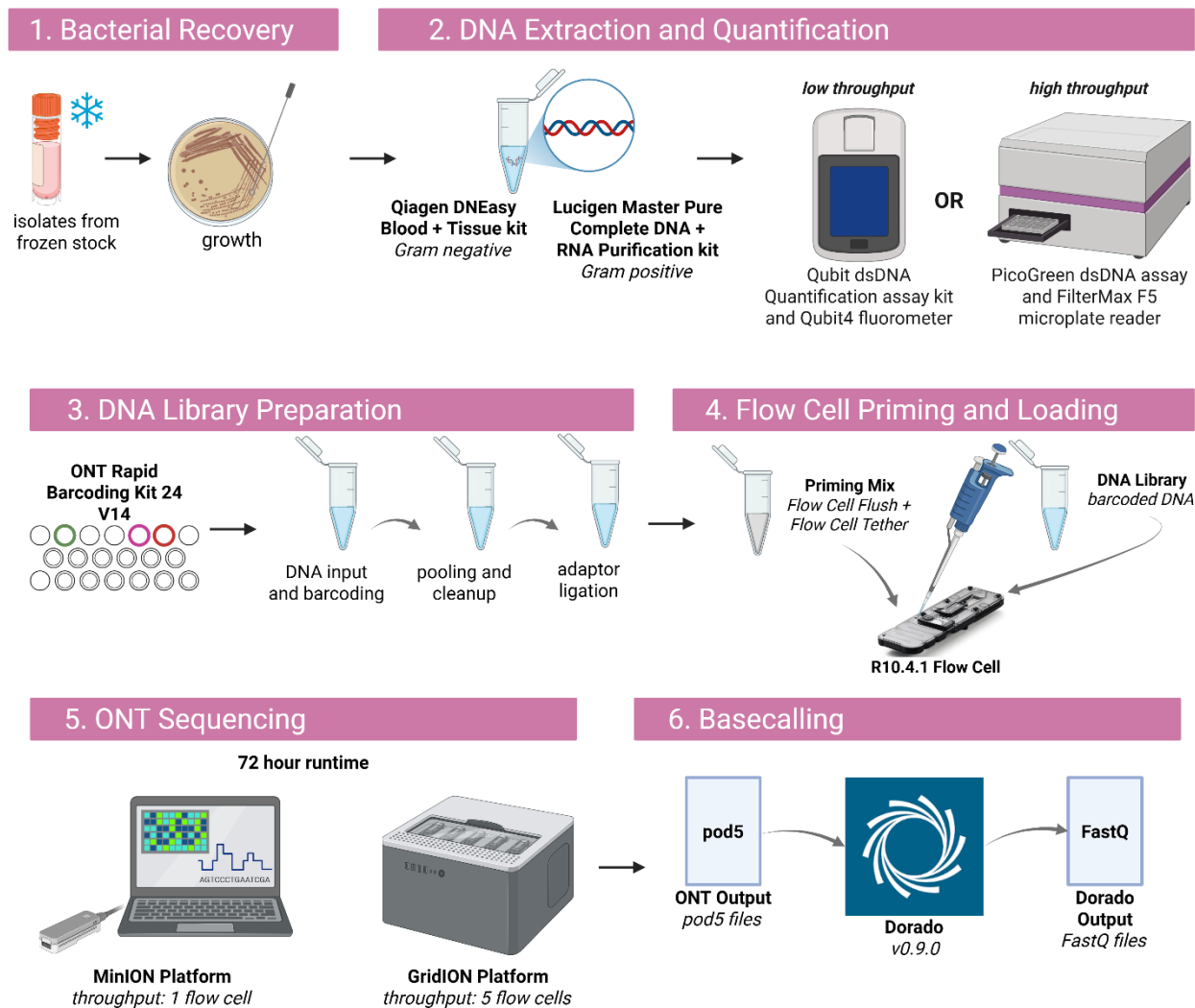


Figure 9. The ONT sequencing workflow used in this study. Isolates were revived from frozen stocks and genomic DNA was extracted using Gram-specific kits and quantified using Qubit and PicoGreen assays (Section 2.3.1). DNA was barcoded with the ONT Rapid Barcoding Kit 24 V14 (Oxford, UK). Libraries were pooled, cleaned, ligated to adapters, and loaded onto R10.4.1 flow cells (≤ 24 samples/flow cell). Sequencing was performed on MinION (single flow cell) or GridION (up to 5 flow cells) ONT platforms (Oxford, UK) for 72 hours. Raw signal data (POD5 format) were basecalled using Dorado v0.9.0 to generate FastQ files for downstream analysis.

Table 9. The ONT sequencing run parameters used in this study.

Parameter	MinION	GridION	Notes
Number of samples processed	149	307	>365 total attempted (repeats included)
Library preparation	ONT Rapid Barcoding Kit 24 V14 (ONT, Oxford, USA)		barcoding capacity: 24 samples/flow cell
Flow cell chemistry	R10.4.1 (FLO-MIN114) (ONT, Oxford, USA)		dual reader head, updated motor protein
Flow cell capacity	1 per device	5 per device	use depended on batch size
Runtime	72 h		live basecalling disabled
Sequencing software	MinKNOW v24.06.16, v24.11.8 (ONT, Oxford, USA)		version varied by run due to software updates during the study period
Basecalling software	Dorado v0.9.0	Dorado v0.9.0	offline basecalling post-run

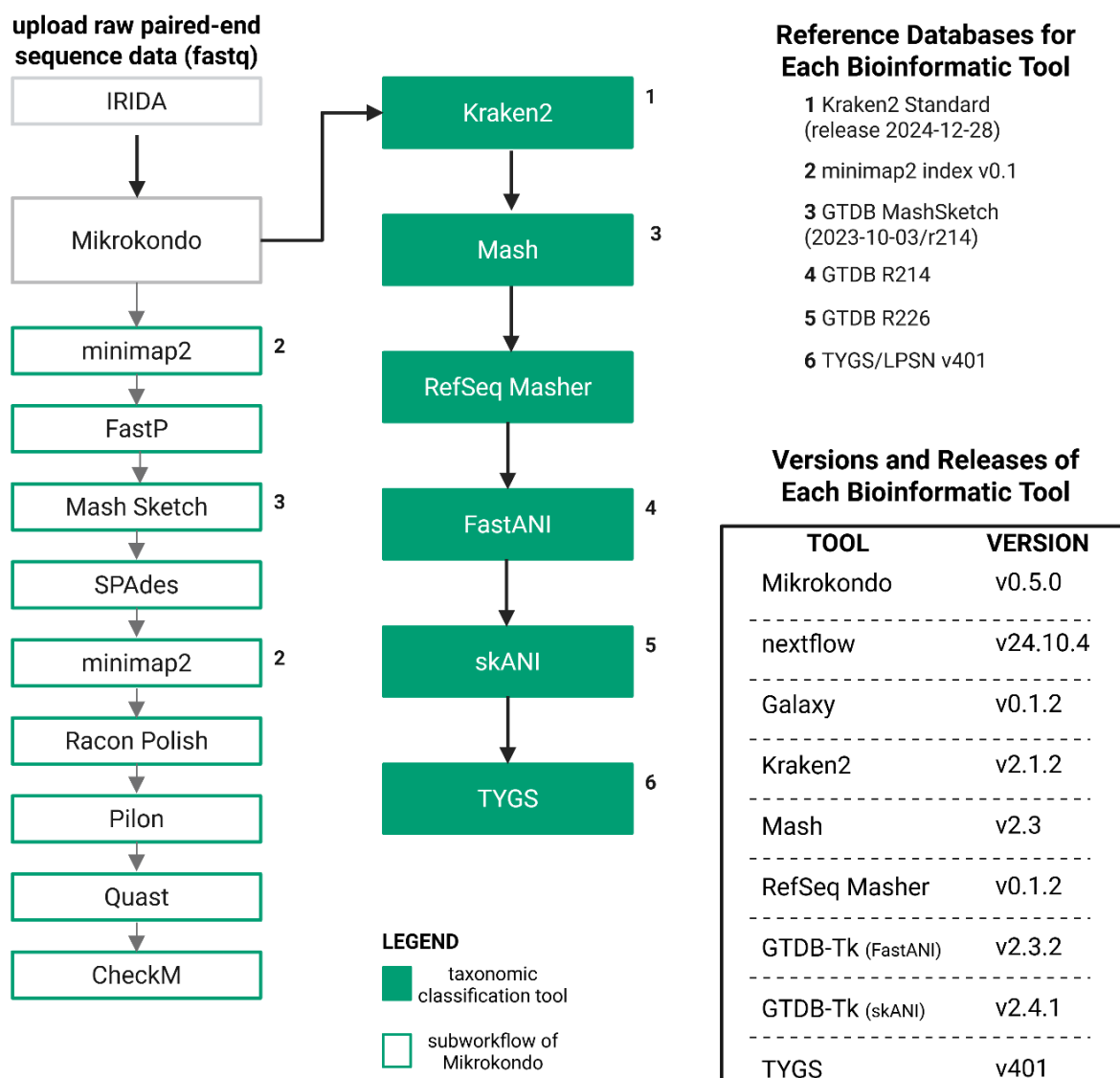


Figure 10. Bioinformatic workflow for Illumina WGS-derived sequence data. [A] Flowchart of the Illumina WGS bioinformatic analysis pipeline. Raw PE reads were uploaded to IRIDA (206), processed in Mikrokondo (194, 195, 208, 209) with Kraken2 (210) for initial classification, and passed through sub-workflows for QC (211–219), genome assembly (220), and quality assessment (212, 218, 219). Complementary classification tools included Mash (Mikrokondo module) (194, 195, 208, 209, 221), RefSeq Masher, GTDB-Tk (FastANI (144) and skANI (222)) (223–226), and TYGS (101, 227). **[B]** Reference databases corresponding to each bioinformatic tool. **[C]** Versions/releases of taxonomic classification tools used in the workflow.

Table 10. Reference databases used for taxonomic classification in Illumina and Nanopore workflows used in this study.

Tool / Workflow Step	Illumina WGS-derived Data	ONT WGS-derived Data	Reference Database
Basecalling	N/A	Dorado v0.9.0 (207)	N/A
Read Filtering	FastP v0.23.4 (213) *	Filtlong v0.3.0 (228) FastP v0.23.4 (213) *	N/A
Primary Workflow Manager	Mikrokondo v0.5.0 (208) (Nextflow v24.10.4) (194, 195, 209) (208) (194, 195, 209)		N/A
Initial Taxonomic Classification	Kraken 2 v2.1.2 (210) (210)		Kraken2 Standard DB (release 2024-12-28)
Genome Assembly	Spades v3.15.5 * (220) Pilon (no version statement listed) (229)*	Flye (230) * Pilon (no version statement listed) (229) *	N/A
Quality Assessment	QUAST v5.2.0 (218) * + CheckM1 v1.2.2 (212) * (218) (212)		N/A
Genome Similarity (fast k-mer)	Mash v2.3 (221) * (221)		Mash Sketch DB (2023-10-03/r214)
Genome Similarity (ANI)	GTDB -Tk v2.3.2 GTDB-Tk v2.4.1 (144, 222–224)	Excluded v2.3.2 GTDB-Tk v2.4.1 (222–224)	GTDB R214 GTDB R226
Phylogenomic Placement	TYGS V401 (101, 227)	Excluded	proprietary reference database
RefSeq-based Comparison	RefSeq Masher v0.1.2 (231) (Galaxy) (193)	Excluded	RefSeq Complete Genomes (232)

* run as a workflow or sub-workflow of Mikrokondo

provided phylogenomic placement and taxonomic assignments (223–226) using LPSN references (101, 227), and RefSeq Masher (Galaxy v0.1.2, RefSeq complete genomes) (193, 231, 232) (Fig. 9). This multi-tool approach increased confidence in species assignments and enabled cross-validation across classification workflows (detailed in Section 2.6). Taxonomic assignments generated by each method were standardized against the LPSN (26 January 2026) to ensure consistency in valid taxonomic nomenclature and to minimize the impact of synonymy and legacy taxon names.

2.4.2 ONT (Oxford, UK) WGS-derived Data Processing: Workflow Management, Quality Control, Assembly, Quality Assessment, and Taxonomic Classification

ONT sequencing generated POD5 signal files for 310 isolates, sequenced on MinION and GridION platforms (Section 2.3.3). Like the bioinformatic workflow applied to Illumina data, Nanopore reads for 310 retained isolates were assembled *de novo* and resulting genome assemblies were analyzed with three taxonomic classifiers, producing 1,460 taxonomic assignments (Fig. 11, Table 10), providing a complementary dataset for cross-platform comparison and method concordance analyses (Section 2.6). Raw signals were basecalled with Dorado v0.9.0 (207) producing FastQ files, which were then filtered with Filtlong v0.3.0 (228) to remove the shortest 10% of reads. Because Nanopore sequencing generates reads of variable length and quality, Filtlong v0.3.0 (228) was used to remove the shortest 10% of reads before assembly. Equivalent read-length filtering was unnecessary for Illumina data because paired-end reads are generated at fixed lengths and undergo quality filtering within the Mikrokondo workflow. Processed reads from each isolate were concatenated into a single FastQ file before further analysis.

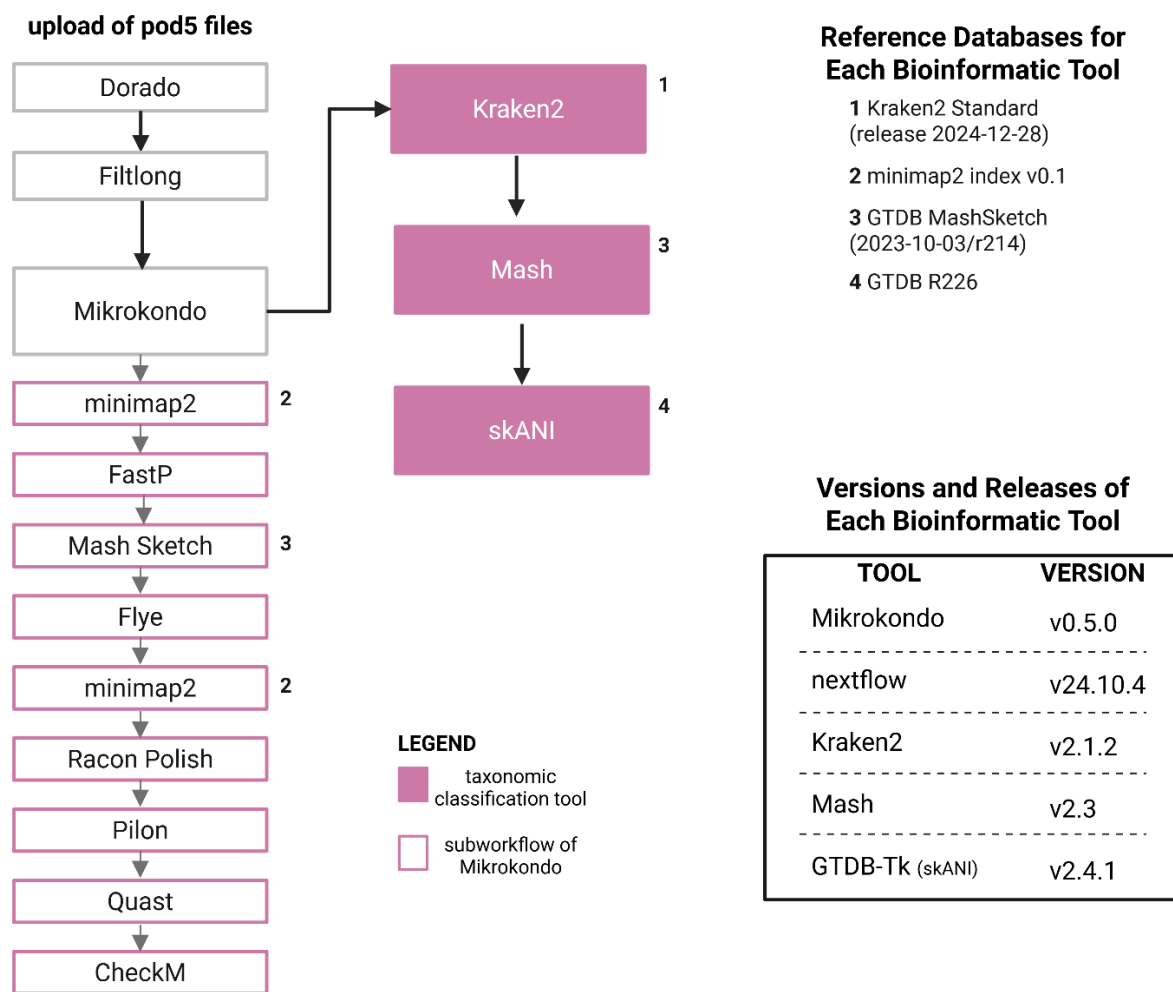


Figure 11. Bioinformatic workflow for Nanopore WGS derived sequence data. [A]

Flowchart of the Nanopore taxonomic classification workflow. Raw POD5 files were basecalled with Dorado (207) and filtered with Filtlong (228) before concatenation and downstream processing in Mikrokondo (194, 195, 208, 209, 211–219, 230). Kraken2 (210) was used for initial classification and passed through sub-workflows for QC, genome assembly, and quality assessment. This was followed by complementary analysis with Mash (221) and GTDB-Tk (skANI) (222–226). **[B]** Reference databases corresponding to each bioinformatic tool. **[C]** Versions/releases of taxonomic classification tools used in the workflow.

Bioinformatic analysis followed the same overall framework as the Illumina data, with adjustments specific to Nanopore reads. Reads were analyzed in Mikrokondo v0.5.0 (Nextflow v24.10.4) (194, 195, 208, 209, 211–219, 230) with Kraken2 v2.1.2 enabled (Kraken2 Standard database, release 2024-12-28) (210) providing initial classifications and genome assemblies. Complementary analyses of assemblies used Mash (Mikrokondo module, database 2023-10-03/r214) (194, 195, 208, 209, 211–219, 221) and GTDB-Tk using skANI v2.4.1 (222) (GTDB R226) (223–226) (Fig. 11). Taxonomic assignments generated by each method were standardized against the LPSN (26 January 2026) to ensure consistency in valid taxonomic nomenclature and to minimize the impact of synonymy and legacy taxon names.

In contrast to the Illumina workflow, FastANI was excluded from Nanopore analysis because GTDB-Tk transitioned to skANI for genome similarity estimation in later software releases, reflecting updates in the GTDB-Tk framework and associated reference database. (GTDBTk Changelog, www.ecogenomics.github.io/GTDBTk/changelog.html, accessed January 2026). RefSeq Masher and TYGS also were excluded based on performance observations in the Illumina dataset, where it provided limited taxonomic resolution and a high number of no identity classifications for the study organisms. Restricting Nanopore workflow to tools aligned with current GTDB-Tk implementation and those demonstrating sufficient discriminatory power in preliminary analyses allowed the workflow to remain consistent while avoiding propagation of unreliable or low-resolution results.

2.5 Traditional Identification Methods

In addition to WGS, traditional identification methods were used to characterize bacterial

isolates. Two complementary approaches were used; (1) 16S rRNA gene sequencing, widely regarded as the molecular “gold standard”(71, 233–235), and (2), phenotypic profiling with the Biolog OmniLog Gen III system, which provides biochemical fingerprints for species-level classification.

2.5.1 16s rRNA Gene Sequencing and Taxonomic Classification

Of the 365 isolates included in this study, 65 required new 16S rRNA sequencing, while the remaining 300 had existing 16S rRNA gene sequences generated by the NML from 1995 and 2023. New sequencing was required for isolates submitted prior to routine implementation of 16S rRNA sequencing at the NML, when this method was not yet part of standard identification workflows. Since reference databases and bacterial taxonomy have been extensively revised during this period, all isolates were subjected to a unified (re)analysis using NCBI’s BLASTn v 2.14.1 (National Institutes of Health, USA, <https://blast.ncbi.nlm.nih.gov/Blast.cgi>, (236)) to ensure consistency in taxonomic classification.

For isolates whose 16S rRNA gene was sequenced in this study, genomic DNA was extracted as described in Section 2.3.1 and used for PCR amplification of the near full-length 16S rRNA gene with universal primers containing Nextera XT adapter overhang sequences to produce sequencing-ready amplicons (Table 11). For newly generated sequences, universal pA and pH primers (237) were synthesized with 5’ Nextera XT adapter overhangs to produce sequencing-ready amplicons while preserving the full 16S rRNA gene target sequence. Each 100 µL PCR reaction contained 10 µL of 10X PCR buffer with MgCl₂, 2 µL of 10 mM dNTPs, 10 µL of forward primer (Nextera adapted pA, 10 µM) (237), 10 µL of reverse primer

Table 11. Universal primers used for 16S rRNA gene amplification (237).

Primer	Sequence
<i>Forward Primer (pA)</i>	AGA GTT TGA TCC TGG CTC AG
<i>Reverse Primer (pH)</i>	AAG GAG GTG ATC CAG CCG CA

Note. For newly generated sequences, Illumina Nextera XT adapter sequences were appended to the 5' ends of the universal pA and pH primers during oligonucleotide synthesis to produce sequencing-ready amplicons. The 16S rRNA gene target remained unchanged; only the sequencing workflow differed from historical Sanger-generated amplicons.

(Nextera adapted pH, 10 μ M) (237), 0.4 μ L of Taq polymerase (5 U/ μ L), and 64.6 μ L of nuclease-free water, with 3 μ L of template DNA. *C. jejuni* ssp. *jejuni* T6 CCUG 12066 (Culture Collection University of Gothenburg, Gothenburg, Sweden) was used as a positive control, and a no-template negative control were included in each run to verify reaction integrity and monitor for contamination. Thermocycling conditions were optimized to balance yield and specificity and are presented in Table 12.

Following amplification, amplicons were quantified using the Qubit High Sensitivity dsDNA assay (Thermo Fisher Scientific, Waltham, MA, USA), as described in Section 2.3.1, and standardized to 50 ng/ μ L. Gel electrophoresis (1.5% agarose in 0.5X TBE, stained with GelRed nucleic acid stain (Sigma-Aldrich, Burlington, MA, USA)) was used to verify amplicon size and assess specificity, with the 100 bp Invitrogen TrackIt ladder (Thermo Fisher Scientific, Waltham, MA, USA) serving as a molecular marker. These QC steps ensure amplicon quality prior to sequencing, minimizing downstream errors in assembly and taxonomic assignment.

Amplicons containing the Illumina XT adapter overhangs (San Diego, USA) were submitted to the NML's Genomics Core Facility for sequencing. Because sequencing adapters had already been incorporated during PCR primer synthesis, library preparation consisted of indexing PCR using KAPA HiFi HotStart ReadyMix, (Roche Diagnostics, Laval, Quebec, Canada). Amplicon libraries were quantified with PicoGreen (Thermo Fisher Scientific, Waltham, MA, USA), as described in Section 2.3.1, to allow equimolar pooling. Fragment size verification was conducted on an Agilent TapeStation (Agilent Technologies, Santa Clara, CA, USA) using the Genomic DNA ScreenTape (Agilent Technologies, Santa Clara, CA, USA), and library concentrations were confirmed via Qubit High Sensitivity assays (Thermo Fisher Scientific, Waltham, MA, USA). Amplicon sequencing was carried out on an Illumina NextSeq

Table 12. PCR thermocycling conditions used for 16S rRNA gene amplification.

Initial Denature	No. of Cycles	Cycle			Final Extension	Vol (uL)
		Denature	Anneal	Extend		
95°C for 5 min	32	94°C for 30 sec	50°C for 20 sec	72°C for 2 min	72°C for 5 min	50

1000/2000 platform using the NextSeq P1 600 XLEAP SBS kit, generating 2×300 bp PE reads (cycle parameters 301-10-10-301) (San Diego, USA). These parameters were chosen by the Genomics Core Facility.

Consensus sequences were assembled in SeqMan Pro (DNASTAR Lasergene v7.0.1) (DNASTAR, Inc., Madison, WI, USA) and aligned against the NCBI RefSeq rRNA database (National Institutes of Health, USA) (232) using BLASTn v2.14.1 (National Institutes of Health, USA, <https://blast.ncbi.nlm.nih.gov/Blast.cgi> (236)). BLASTn, a nucleotide alignment tool optimized for detecting genomic regions of high local similarity, was selected for its reliability in distinguishing bacterial isolates based on sequence similarity in regions of the 16S rRNA gene and of reference strains. The approach accommodated both historical full-length 16S rRNA gene sequences, predominantly generated by Sanger sequencing, and newly generated near-full-length Illumina amplicon sequences following quality trimming, enabling standardized taxonomic analysis across the complete dataset. Alignments were filtered using stringent parameters, including an e-value of 0 and sorting by maximum score to prioritize the most significant matches.

Taxonomic assignments were determined using identity thresholds of $\geq 98\%$ for species, 95-98% for genus, and 90-95% for family (138, 145–147). These thresholds reflect commonly used but not universally accepted cutoffs in 16S rRNA gene-based taxonomy. In cases where multiple top hits exceeded these thresholds but corresponded to different taxa, isolates were assigned to the highest shared taxonomic level. This was done unless the top hit, sorted by max score, had a query coverage of 100%, a percent identity of 100%, and e-value reported as 0.0 by BLASTn (i.e., below computational threshold); this was considered a perfect match. Species-, genus-, and family-level assignments were made using predefined identity thresholds. Sequences

that produced no significant BLASTn alignments (“no significant similarity found”) were reported as “*no identity*”. When multiple significant alignments exceeded the relevant threshold but corresponded to different taxa, the isolate was assigned to the lowest common ancestor supported by the predefined thresholds.

Taxonomic assignments generated by each method were standardized against the LPSN (accessed on 26 January 2026) to ensure consistency in valid taxonomic nomenclature and to minimize the impact of synonymy and legacy taxon names. Although 16S rRNA gene sequencing alone offers limited resolution for closely related taxa, the application of standardized thresholds with conservative filtering provided a framework for taxonomic classification of the study isolates, enabling direct comparison between traditional 16S-based approaches and phenotypic and WGS-based methods.

This 16S rRNA sequencing workflow therefore integrated both newly generated and historical datasets, with all isolates analyzed under a consistent and up-to-date taxonomic framework using NCBI’s nucleotide BLAST (National Institutes of Health, USA). Of the 365 total isolates included, only the 65 isolates without prior sequence data underwent the full wet-lab workflow, including DNA extraction, PCR amplification of the 16S rRNA gene, amplicon purification, gel electrophoresis, Illumina amplicon sequencing. In contrast, the remaining 300 isolates, which already had historical sequences that were generated by the NML between 1995 and 2023, predominantly using Sanger sequencing of full-length 16S rRNA gene amplicons generated according to the protocols in use at the time. These existing sequences were not regenerated but were reanalyzed using a standardized BLASTn (National Institutes of Health, USA) workflow to ensure consistency in taxonomic assignment using modern and up-to-date taxonomy and nomenclature. While 16S rRNA gene-based sequencing alone is inherently

limited in its resolution of closely related or rare bacterial strains, its inclusion in this study provides an essential benchmark against which WGS-based approaches can be evaluated. By re-analyzing both historical and newly generated sequences within a standardized taxonomic framework and generating species-level assignments where possible, this method enables direct comparison with WGS-based pipelines and highlights both the strengths and limitations of 16S rRNA sequencing in the identification of rare and low-prevalence enteric bacteria.

2.5.2 Biochemical Identification using the Biolog OmniLog Gen III System

Biochemical identification of bacterial isolates was carried out using the Biolog OmniLog system (Biolog Inc., Hayward, USA) (238). This system uses a panel of 94 biochemical tests to generate phenotypic fingerprints that can be matched to an internal reference database for species-level identification. We used the OmniLog incubator (Biolog Inc., Hayward, USA) and OmniLog Data Collection 3.0 software (OL3.0; Biolog Inc., Hayward, USA), Gen III MicroPlates (Biolog Inc., Hayward, USA), and inoculating fluids (IF; Biolog Inc., Hayward, USA) according to the manufacturer's protocol to generate biochemical and metabolic profiles for each isolate. Profiles were compared against the GenIII reference database v2.8 (Part No. 00P188 Rev G, 2016) by MicroLog Secure software version 6.2 (Biolog Inc., Hayward, USA) which was used for data interpretation. Type strains were used as described in Section 2.1 to validate system performance.

All isolates were cultured according to the procedures outlined in Section 2.2. After revival from -80 °C storage in 19% skim milk broth, they were plated on appropriate agar and incubated under the conditions described in Table 4 to generate fresh, healthy growth for downstream biochemical analyses. Growth was assessed for colony morphology, isolation of

single colonies, and absence of mixed colony types before downstream testing. If mixed growth or insufficient biomass was observed, isolates were streaked for isolation or subcultured under varied conditions until single colonies with expected morphology and adequate biomass were obtained.

For Biolog testing, isolates were suspended in IF to the cell density required by one of four manufacturer-recommended protocols: A, B, C1, or C2. Protocol A was used for the majority of isolates. Protocol B was used for isolates that produced a false positive result in the negative control well (A1) under Protocol A, which is often observed in strongly reducing or capsulated strains. Protocol B was also used for isolates preliminarily identified as *Aeromonas*. Protocol C2 was used for fastidious, capnophilic, or oxygen-sensitive species that showed insufficient growth or yielded poor reactions under Protocols A and B. This included isolates preliminarily identified as *Campylobacter* or *Helicobacter*. Protocol C1 was not used, unless specified by the OL3.0 software (Biolog Inc., Hayward, USA), typically when Protocol C2 failed due to rapid growth. A summary of the inoculation protocols used is provided in Table 13. Organism names reflect the preliminary identifications recorded at the time of original submission and testing from 1997 to 2023.

Inocula were prepared using freshly grown colonies. A sterile cotton-tipped swab was used to collect approximately 3 mm of single colony growth, which was suspended in the designated IF and adjusted to the target turbidity using a calibrated turbidimeter. The suspension was mixed thoroughly to remove clumps and achieve a homogeneous solution. Cell density was rechecked and adjusted as needed by adding more cells or IF. Each isolate was tested once under each applicable protocol; replicate testing was performed only when initial testing failed, as indicated by OL3.0 (Biolog Inc., Hayward, USA). Uninoculated IF controls were included

Table 13. Summary of Biolog Gen III Microplate inoculation protocols and number of isolates processed by protocol.

Protocol	Inoculating Fluid	Target Cell Density (% transmittance)	Criteria for Use	Number of Isolates Tested (including repeats)
A	IF-A	90-98% T	Default protocol for most isolates	267
B	IF-B	90-98% T	For <i>Aeromonas</i> isolates and for other isolates when Protocol A failed	50
C2	IF-C	40% T and 62-68% T	For fastidious and oxygen-sensitive isolates including <i>Campylobacter</i> and <i>Helicobacter</i>	68
C1	IF-C	92-95% T	For isolates when Protocol C2 failed	2

Note. Organism names and classifications (e.g., Aeromonas, Campylobacter, Helicobacter) reflect the preliminary identification assigned at the time of original submission (1995–2023). Counts include both initial testing and retesting following protocol failures.

periodically to monitor for contamination. These were not included with every batch due to the cost of reagents, but no unexpected background activity was observed.

A total of 100 μ L of cell suspension was dispensed into each of the 96 wells of the Gen III MicroPlate (Biolog Inc., Hayward, USA). The inoculated plate was covered and loaded into the OmniLog incubator (Biolog Inc., Hayward, USA) for automated incubation and plate reading. Incubation was carried out at 33 °C for 22 hours in the incubator, as recommended by the Gen III protocol (Biolog Inc., Hayward, USA). For isolates preliminarily identified as *Campylobacter* or *Helicobacter*, incubation was extended up to 48 hours to ensure a visible reaction pattern could develop, due to their slow growth and fastidious nature.

Following incubation, data were processed and analyzed with OL3.0 (Biolog Inc., Hayward, USA) and MicroLog Secure software v6.2 (Biolog Inc., Hayward, USA). The system compared the phenotypic/metabolic profile of each isolate to Biolog's internal species library and generated a similarity index (SIM) and distance estimation (DIST) for each identification result. Thresholds for species-level identification were defined according to the manufacturer's criteria: $SIM \geq 0.5$ and $DIST \geq 5.0$. Each well was scored as positive, negative, or borderline depending on its color intensity, in accordance with the manufacturer's guidelines. The layout of the Gen III MicroPlate, including carbon source utilization and chemical sensitivity wells, is shown in Figure 12.

All isolates were tested using the Biolog system regardless of whether their preliminary identification was included in the Gen III reference database (Biolog Inc., Hayward, USA). These historical identifications, recorded at the time of submission (1995-2023), were not used to interpret Biolog results due to potential changes in identification methods and bacterial taxonomy over time. If an isolate failed to yield an identification using Protocol A, it was

A1 Negative Control	A2 Dextrin	A3 D-Maltose	A4 D-Trehalose	A5 D-Cellobiose	A6 Gentiobiose	A7 Sucrose	A8 D-Turanose	A9 Stachyose	A10 Positive Control	A11 pH 6	A12 pH 5
B1 D-Rifanose	B2 α -D-Lactose	B3 D-Melibiose	B4 β -Methyl-D-Glucoside	B5 D-Salicin	B6 N-Acetyl-D-Glucosamine	B7 N-Acetyl- β -D-Mannosamine	B8 N-Acetyl-D-Galactosamine	B9 N-Acetyl Neuraminic Acid	B10 1% NaCl	B11 4% NaCl	B12 8% NaCl
C1 α -D-Glucose	C2 D-Mannose	C3 D-Fructose	C4 D-Galactose	C5 3-Methyl Glucose	C6 D-Fucose	C7 L-Fucose	C8 L-Rhamnose	C9 Inosine	C10 1% Sodium Lactate	C11 Fusidic Acid	C12 D-Serine
D1 D-Sorbitol	D2 D-Mannitol	D3 D-Arabitol	D4 myo-Inositol	D5 Glycerol	D6 D-Glucose -6-PO ₄	D7 D-Fructose -6-PO ₄	D8 D-Aspartic Acid	D9 D-Serine	D10 Troleando-mycin	D11 Rifamycin SV	D12 Minocycline
E1 Gelatin	E2 Glycyl-L-Proline	E3 L-Alanine	E4 L-Arginine	E5 L-Aspartic Acid	E6 L-Glutamic Acid	E7 L-Histidine	E8 L-Pyroglutamic Acid	E9 L-Serine	E10 Lincomycin	E11 Guanidine HCl	E12 Niaproof 4
F1 Pectin	F2 D-Galacturonic Acid	F3 L-Galactonic Acid Lactone	F4 D-Gluconic Acid	F5 D-Glucuronic Acid	F6 Glucuronamide	F7 Mucic Acid	F8 Quinic Acid	F9 D-Saccharic Acid	F10 Vancomycin	F11 Tetrazolium Violet	F12 Tetrazolium Blue
G1 p-Hydroxy-Phenylacetic Acid	G2 Methyl Pyruvate	G3 D-Lactic Acid Methyl Ester	G4 L-Lactic Acid	G5 Citric Acid	G6 α -Keto-Glutaric Acid	G7 D-Malic Acid	G8 L-Malic Acid	G9 Bromo-Succinic Acid	G10 Nalidixic Acid	G11 Lithium Chloride	G12 Potassium Telluride
H1 Tween 40	H2 γ -Amino-Butyric Acid	H3 α -Hydroxy-Butyric Acid	H4 β -Hydroxy-D,L-Butyric Acid	H5 α -Keto-Butyric Acid	H6 Acetoacetic Acid	H7 Propionic Acid	H8 Acetic Acid	H9 Formic Acid	H10 Azetreonam	H11 Sodium Butyrate	H12 Sodium Bromate

Fig. 12, part 1 of 2

Figure 12. Gen III MicroPlate layout for biochemical identification of bacterial isolates. The 96-well plate contains a diverse panel of substrates and chemical sensitivity assays organized by functional groups. Wells across the plate assess utilization of carbohydrates (C1-C4, C6-C8), oligosaccharides and disaccharides (A2-A9, B2-B5), sugars and phosphorylated sugars (F1-F5, D6-D7, C5), amino acids and peptides (D8-D9, E1-E9, G2, H2-H5, H10) carboxylic and organic acids (F2-F9, G1, G3-G8, H6-H9), and other metabolic compounds (D4-D5, H1). Additional wells evaluate tolerance to osmotic stress (NaCl series; B10-B12), pH tolerance (A11-A12), and inhibitory or selective compounds including antibiotics, dyes, and salts (C11-12, D10-12, E10-12, F10-12, G9-G12M H10-12). Well A1 serves as a negative control and A10 as a positive control. Colourimetric changes driven by cellular respiration reduce tetrazolium dyes and well reactions were interpreted according to manufacturer guidelines to generate metabolic fingerprints for taxonomic classification. [Adapted from Biolog Inc.]

retested using Protocol B and then Protocol C2, but only if its preliminary identification suggested it was represented in the Gen III database. If no identification was obtained and the original identification was not listed in the database, the isolate was not retested under alternative protocols and was recorded as “*no identity*”. This avoided unnecessary retesting of organisms outside the scope of the Biolog OmniLog system (Biolog Inc., Hayward, USA) and helped conserve reagents and technician time. Identification results from Biolog were compared to 16S rRNA gene sequencing data (Section 2.5.3) to evaluate concordance between traditional identification methods and were later evaluated against WGS-based results (Section 2.6). Taxonomic assignments generated by each method were standardized against the LPSN (accessed on 26 January 2026) to ensure consistency in valid taxonomic nomenclature and to minimize the impact of synonymy and legacy taxon names.

2.5.3 Resolution of Conflicting Traditional Identifications

This section describes the approach used to resolve cases where biochemical identifications from the Biolog protocol and 16S rRNA-based taxonomic classifications were discordant at the species level (Fig. 13). Only isolates with discordant species-level assignments are considered here, isolates with concordant assignments are excluded. The goal of this workflow was to assign a single, reconciled traditional identification to each isolate, combining information from both biochemical profiles and 16S rRNA gene sequencing-based analysis results according to the defined confidence thresholds. Since downstream analyses included a single taxonomic label per isolate, discordant traditional identifications were reconciled into a

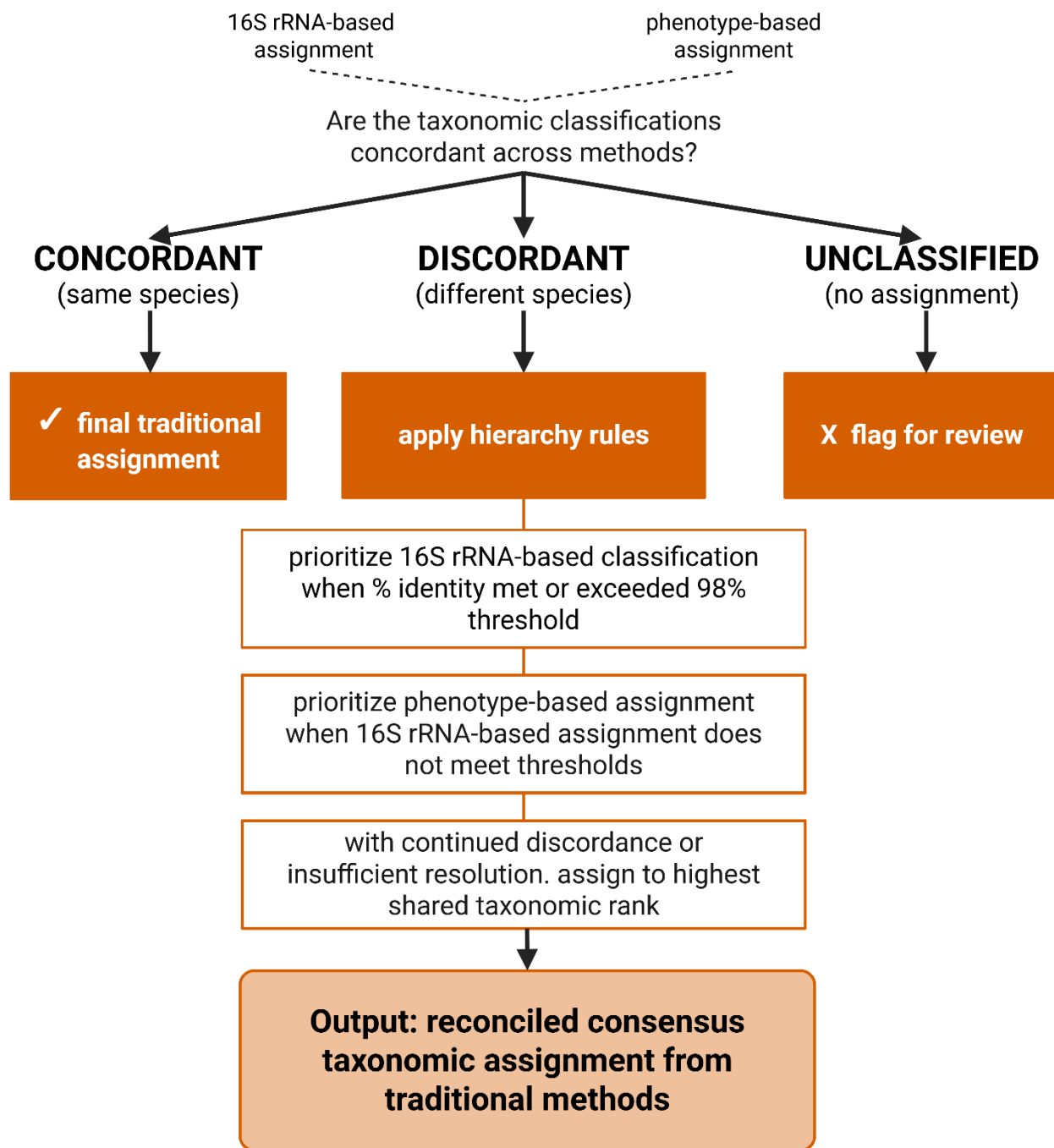


Figure 13. The decision workflow used to resolve discordant taxonomic classifications between 16S rRNA gene-based classification and biochemical profiling.

unified consensus assignment. This approach ensured analytical consistency by enabling one-to-one comparisons of traditional method-based assignments with WGS-based outputs and reflects real-world diagnostic practice in which a single final identification must be reported. By applying a transparent and reproducible decision framework, the consensus classification further provided a stable reference point for benchmarking WGS performance, allowing concordance, discordance, and improvements in taxonomic resolution and accuracy to be evaluated quantitatively.

For isolates with conflicting classifications, priority was given to the highest-confidence taxonomic assignment within our defined thresholds via 16S rRNA-based taxonomic classification using BLASTn ($\geq 98\%$ identity for species-level, 95-98% for genus-level, and $\geq 90\%$ for family-level). When multiple top hits exceeded the threshold but corresponded to different taxa, the isolate was assigned to the highest shared taxonomic level (e.g., genus rather than species) to ensure a conservative and reproducible classification. In cases where the 16S rRNA gene-based assignment fell below the confidence thresholds or remained ambiguous, the biochemical profile-based identification was used if it met the thresholds; otherwise, the isolate was labeled “no identity” and flagged for further review.

This workflow allowed for systematic resolution of discordant identifications while maintaining consistency with the criteria applied to the broader 16S rRNA dataset (NCBI BLASTn, National Institutes of Health, USA) and the Gen III reference database (Biolog Inc., Hayward, USA). The resulting reconciled identifications provided a robust framework for comparing traditional biochemical methods with genotypic approaches, highlighting both agreement and limitations at the species level.

2.6 Comparative Analysis of Traditional and WGS-based Identification Methods

To evaluate the performance of identification approaches, results generated by traditional laboratory identification methods and WGS-based classification workflows were compared across taxonomic resolution, concordance among identification methods, classification failures, and identification accuracy. Traditional methods included 16S rRNA gene sequencing and phenotypic profiling using the Biolog OmniLog system. WGS-based identification was performed using multiple bioinformatic workflows applied to whole genome assemblies generated from both Illumina and ONT sequencing platforms.

To assess the comparability of taxonomic classification approaches, results from WGS were evaluated alongside traditional identification methods including 16S rRNA gene sequencing, Biolog phenotypic profiling, and the consensus approach, which were treated as an additional tool rather than a gold standard. Comparative analyses therefore focused on quantifying agreement between methods, identifying patterns of discordance and evaluating differences in classification performance across analytical workflows and taxonomic groups. Statistical analyses were performed in R using RStudio (239). Statistical significance was defined as $p > 0.05$.

2.6.1 Analysis of Traditional Identification Methods

Taxonomic resolution was defined as the lowest taxonomic rank assigned to an isolate by a given identification method. For traditional identification approaches, taxonomic assignments generated 16S rRNA sequencing, Biolog phenotypic profiling, and a consensus classification derived from agreement between the two methods were evaluated. All classifications were categorized to the lowest reported taxonomic rank (species, genus, family, order, or phylum).

Instances in which a method failed to produce a valid classification were categorized as no identity. Differences in taxonomic resolution among the three traditional classification outcomes were evaluated using Pearson's chi-square tests (χ^2) of independence. Where significant associations were identified, standardized residuals were examined to determine which method-rank combinations contributed most strongly to deviations from expected frequencies.

Agreement between 16S rRNA sequencing and Biolog phenotypic profiling was evaluated using isolate-level pairwise comparisons. Comparisons were restricted to isolates for which both methods produced classifications at the same taxonomic rank. Assignments were categorized into the following outcomes: concordant (when both methods produced the same taxonomic assignment at the shared rank), discordant (when both methods produced different taxonomic assignments), 16S only (when only 16S rRNA sequencing produced a classification), Biolog only (when only Biolog phenotypic profiling produced a classification), and both fail (when neither method produced a valid classification).

Changes in discordance across taxonomic ranks were evaluated using a chi-square test for linear trend. Associations between taxonomic rank and classification outcome were assessed using Pearson's chi-square tests and Cramer's V was calculated to estimate the strength of association. To evaluate whether discordance occurred disproportionately within particular taxonomic groups, chi-square tests of independence were used to assess associations between genus-level taxonomic identity and classification outcome. Where significant associations were detected, standardized residuals were examined to identify taxa contributing disproportionately to concordant or discordant classifications.

Accuracy of traditional identification methods was evaluated using type strains with established species identities. For each isolate, the reported taxonomic classification generated

by each method was compared with the known reference designation. Accuracy was calculated as the proportion of isolates correctly identified at the species level and 95% confidence intervals (CI) were estimated using the Wilson method for binomial proportions. Differences in accuracy between identification methods were evaluated using pairwise McNemar's tests for paired categorical outcomes.

2.6.2 Analysis of WGS-based Identification Methods

Taxonomic resolution achieved by WGS-based identification workflows was evaluated by classifying outputs according to the lowest reported taxonomic rank (species or genus). Outputs that did not produce a valid classification were categorized as "no identity". Differences in taxonomic resolution across bioinformatic workflows and sequencing platforms were evaluated using Pearson's chi-square tests of independence. Where significant associations were observed, standardized residuals were examined to identify specific workflow-rank combinations contributing disproportionately to the observed distribution of taxonomic assignments.

Agreement among WGS-based classification workflows was evaluated through pairwise comparisons of taxonomic assignments generated by each workflow applied to the same isolate. Agreement between workflows was quantified using Cohen's kappa coefficient (κ), which measures agreement beyond that expected by chance. Discordant classifications among WGS-based workflows were further examined to determine whether disagreement occurred more frequently for particular taxa. Associations between genus identity and discordance outcomes were evaluated using chi-square contingency analyses, and standardized residuals were examined to identify taxa contributing significantly to discordant classifications.

Instances in which WGS-based classification workflows failed to produce valid taxonomic assignments were categorized as unclassified outcomes. These classification failures were further grouped into categories reflecting potential sources of failure, including reference database limitations, assembly-related limitations, algorithmic or confidence-threshold filtering, or invalid taxonomy outputs. Definitions for these failure categories are provided in Appendix F. Associations between classification status and bioinformatic workflow or sequencing platform were evaluated using Pearson's chi-square tests of independence and standardized residuals were examined to identify specific workflow- or platform-specific effects. Where contingency table cell counts were small, Fisher's exact tests were used, and odds ratios were calculated to estimate the magnitude of associations between workflow characteristics and classification success. To evaluate whether assembly or QC metrics influenced classification success, genome assembly metrics including genome size, sequencing coverage, assembly completeness, and N50 were compared between classified and unclassified isolates using Wilcoxon rank-sum tests.

Accuracy of WGS-based classification workflows was evaluated using isolates corresponding to recognized type strains with established species identities. Species-level assignments generated by each workflow were compared with the known reference designation. Accuracy was calculated as the proportion of isolates correctly classified at the species level with 95% CI estimated using the Wilson method. Differences in classification accuracy between workflows were evaluated using pairwise McNemar's tests.

2.6.3 Evaluation of Notable Taxonomic Patterns

To further investigate organism-specific classification performance, taxonomic assignment outcomes were examined for patterns associated with particular genera or taxonomic

groups. This analysis included evaluation of classifications potentially affected by historical synonymy, differences in nomenclature used in reference databases, and repeated discrepancies in identification among methods. The frequency and distribution of classification outcomes for selected taxa were descriptively summarized. Where differences in classification outcomes between methods were statistically assessed, Fisher's exact tests were used to compare proportions among relevant groups.

Chapter 3: Results

3.1 Traditional Identification Methods: 16S rRNA Sequencing and Phenotypic Profiling

3.1.1 Taxonomic Assignments of Traditional Identification Workflows

Of the 365 isolates included in the study, targeted 16S rRNA gene sequencing (via Sanger or Illumina) was successfully performed for 362 isolates, while Biolog phenotypic profiling was successfully completed for 350 isolates. Three isolates could not be processed by 16S rRNA gene sequencing and 15 could not be evaluated by Biolog because of workflow-related constraints, including contamination, insufficient growth in culture, or failure of fastidious organisms to meet testing requirements. Subsequent analyses for each method therefore used only the isolates for which that method was successfully completed. In total, 364 of 365 isolates in the sample set received at least one taxonomic assignment from 16S rRNA gene sequencing, biochemical profiling, or the consensus approach while the remaining one isolate could not be identified by either method.

For each isolate, taxonomic outputs from both traditional approaches were reviewed and used to generate a consensus assignment when possible. A summary of method-specific outputs (after standardization to valid taxa and synonym correction (Table A13)) and resulting consensus classifications is provided in Table 14. Complete BLASTn alignment reports and detailed Biolog probability outputs are archived and available upon request. Only the final interpreted taxonomic assignments are reported here.

Table 14. Traditional method-based taxonomic assignments and resulting consensus classifications for study isolates. A presentation of the final taxonomic assignment as determined by 16S rRNA gene sequencing (BLASTn-based), Biolog biochemical profiling, and the derived consensus classification after standardization to valid taxa and correction of homotypic synonymy. “Consensus Assignment Method” indicates whether the consensus assignment was supported by both methods or determined primarily by a single method when results differed or when only one method produced an identification.

Isolate	16S rRNA Sequencing Assignment	Phenotypic Profiling Assignment	Consensus Assignment	Consensus Method
JDID-01	<i>Yersinia sp</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia sp</i>	16S
JDID-02	<i>Yersinia sp</i>	no identity	<i>Yersinia sp</i>	16S
JDID-03	Enterobacterales	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	Biolog
JDID-04	<i>Campylobacter sp</i>	<i>Hafnia alvei</i>	<i>Campylobacter sp</i>	16S
JDID-05	<i>Serratia sp</i>	no identity	<i>Serratia sp</i>	16S
JDID-06	<i>Klebsiella sp</i>	<i>Raoultella terrigena</i>	<i>Klebsiella sp</i>	16S
JDID-07	Enterobacteriaceae	<i>Citrobacter gillenii</i>	Enterobacteriaceae	16S
JDID-08	<i>Citrobacter sp</i>	<i>Citrobacter freundii</i>	<i>Citrobacter sp</i>	16S
JDID-09	Enterobacterales	<i>Morganella morganii</i>	<i>Morganella morganii</i>	Biolog
JDID-10	<i>Providencia sp</i>	<i>Providencia rettgeri</i>	<i>Providencia rettgeri</i>	Biolog
JDID-11	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	both
JDID-12	<i>Campylobacter sputorum</i>	no identity	<i>Campylobacter sputorum</i>	16S
JDID-13	<i>Morganella morganii</i>	<i>Tatumella punctata</i>	<i>Morganella morganii</i>	16S
JDID-14	analysis not performed	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	Biolog
JDID-15	no identity	<i>Yersinia mollaretii</i>	<i>Yersinia mollaretii</i>	Biolog
JDID-16	<i>Micrococcus sp</i>	no identity	<i>Micrococcus sp</i>	16S
JDID-17	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-18	<i>Campylobacter sp</i>	<i>Salmonella enterica</i>	<i>Campylobacter sp</i>	16S
JDID-19	<i>Campylobacter sputorum</i>	<i>Citrobacter freundii</i>	<i>Campylobacter sputorum</i>	16S
JDID-20	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-21	<i>Campylobacter sp</i>	<i>Methylobacterium extorquens</i>	<i>Campylobacter sp</i>	16S
JDID-22	<i>Yersinia sp</i>	<i>Yersinia intermedia</i>	<i>Yersinia sp</i>	16S
JDID-23	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-24	<i>Yersinia sp</i>	<i>Yersinia massiliensis</i>	<i>Yersinia sp</i>	16S
JDID-25	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-26	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-27	<i>Campylobacter sp</i>	analysis not performed	<i>Campylobacter sp</i>	16S
JDID-28	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S

JDID-29	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-30	<i>Campylobacter helveticus</i>	no identity	<i>Campylobacter helveticus</i>	16S
JDID-31	<i>Campylobacter concisus</i>	no identity	<i>Campylobacter concisus</i>	16S
JDID-32	<i>Yersinia sp</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia sp</i>	16S
JDID-33	<i>Yersinia sp</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia sp</i>	16S
JDID-34	<i>Campylobacter lanienae</i>	<i>Yersinia massiliensis</i>	<i>Campylobacter lanienae</i>	16S
JDID-35	<i>Campylobacter sp</i>	<i>Yersinia mollaretti</i>	<i>Campylobacter sp</i>	16S
JDID-36	<i>Campylobacter lanienae</i>	<i>Staphylococcus piscifermentans</i>	<i>Campylobacter lanienae</i>	16S
JDID-37	<i>Yersinia sp</i>	<i>Yersinia frederiksenii</i>	<i>Yersinia sp</i>	16S
JDID-38	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-39	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-40	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-41	<i>Yersinia pestis</i>	no identity	<i>Yersinia pestis</i>	16S
JDID-42	<i>Campylobacter sp</i>	analysis not performed	<i>Campylobacter sp</i>	16S
JDID-43	analysis not performed	<i>Morganella morganii</i>	<i>Morganella morganii</i>	Biolog
JDID-44	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-45	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-46	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-47	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-48	<i>Campylobacter sp</i>	<i>Kingella oralis</i>	<i>Campylobacter sp</i>	16S
JDID-49	<i>Campylobacter sp</i>	analysis not performed	<i>Campylobacter sp</i>	16S
JDID-50	<i>Campylobacter sp</i>	<i>Neisseria elongata</i>	<i>Campylobacter sp</i>	16S
JDID-51	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-52	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-53	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-54	<i>Campylobacter sp</i>	<i>Methylobacterium extorquens</i>	<i>Campylobacter sp</i>	16S
JDID-55	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-56	<i>Campylobacter lanienae</i>	no identity	<i>Campylobacter lanienae</i>	16S
JDID-57	Enterobacterales	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	Biolog
JDID-58	Enterobacterales	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	Biolog
JDID-59	<i>Buttiauxella gaviniae</i>	<i>Lelliottia nimipressuralis</i>	<i>Buttiauxella gaviniae</i>	16S
JDID-60	Enterobacteriaceae	<i>Buttiauxella brennerae</i>	<i>Buttiauxella brennerae</i>	Biolog
JDID-61	Enterobacterales	no identity	Enterobacterales	16S
JDID-62	Enterobacterales	no identity	Enterobacterales	16S
JDID-63	Enterobacteriaceae	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	Biolog
JDID-64	<i>Aeromonas sp</i>	<i>Aeromonas veronii</i>	<i>Aeromonas sp</i>	16S
JDID-65	<i>Aeromonas sp</i>	<i>Aeromonas caviae</i>	<i>Aeromonas sp</i>	16S
JDID-66	<i>Aeromonas sp</i>	<i>Aeromonas jandei</i>	<i>Aeromonas sp</i>	16S
JDID-67	<i>Aeromonas sp</i>	<i>Aeromonas caviae</i>	<i>Aeromonas sp</i>	16S
JDID-68	<i>Aeromonas sp</i>	<i>Aeromonas eucrenophila</i>	<i>Aeromonas sp</i>	16S
JDID-69	<i>Aeromonas sp</i>	<i>Aeromonas caviae</i>	<i>Aeromonas sp</i>	16S
JDID-70	<i>Aeromonas sp</i>	<i>Aeromonas caviae</i>	<i>Aeromonas sp</i>	16S
JDID-71	<i>Aeromonas sp</i>	<i>Aeromonas caviae</i>	<i>Aeromonas sp</i>	16S

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JDID-72	<i>Aeromonas sp</i>	<i>Aeromonas jandei</i>	<i>Aeromonas sp</i>	16S
JDID-73	<i>Aeromonas sp</i>	no identity	<i>Aeromonas sp</i>	16S
JDID-74	<i>Aeromonas sp</i>	<i>Aeromonas caviae</i>	<i>Aeromonas sp</i>	16S
JDID-75	<i>Aeromonas sp</i>	<i>Aeromonas caviae</i>	<i>Aeromonas sp</i>	16S
JDID-76	<i>Aeromonas sp</i>	<i>Aeromonas jandei</i>	<i>Aeromonas sp</i>	16S
JDID-77	<i>Listeria sp</i>	<i>Listeria monocytogenes</i>	<i>Listeria sp</i>	16S
JDID-78	<i>Listeria sp</i>	<i>Listeria monocytogenes</i>	<i>Listeria sp</i>	16S
JDID-79	Vibrionaceae	<i>Escherichia coli</i>	<i>Escherichia coli</i>	Biolog
JDID-80	Erwiniaceae	<i>Pantoea dispersa</i>	<i>Pantoea dispersa</i>	Biolog
JDID-81	Enterobacteriaceae	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	Biolog
JDID-82	Enterobacterales	<i>Kosakonia cowanii</i>	<i>Kosakonia cowanii</i>	Biolog
JDID-83	Enterobacterales	<i>Kluyvera intermedia</i>	<i>Kluyvera intermedia</i>	Biolog
JDID-84	Enterobacteriaceae	<i>Kluyvera intermedia</i>	<i>Kluyvera intermedia</i>	Biolog
JDID-85	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-86	Enterobacterales	<i>Enterobacter hormacheii</i>	<i>Enterobacter hormacheii</i>	Biolog
JDID-87	Enterobacteriaceae	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	Biolog
JDID-88	Enterobacterales	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	Biolog
JDID-89	Enterobacteriaceae	<i>Escherichia coli</i>	<i>Escherichia coli</i>	Biolog
JDID-90	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-91	Enterobacterales	no identity	Enterobacterales	16S
JDID-92	Enterobacterales	<i>Citrobacter youngae</i>	<i>Citrobacter youngae</i>	Biolog
JDID-93	Enterobacteriaceae	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	Biolog
JDID-94	Enterobacterales	no identity	Enterobacterales	16S
JDID-95	Enterobacteriaceae	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	Biolog
JDID-96	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-97	Enterobacteriaceae	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	Biolog
JDID-98	<i>Klebsiella sp</i>	no identity	<i>Klebsiella sp</i>	16S
JDID-99	<i>Klebsiella sp</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella sp</i>	16S
JDID-100	<i>Klebsiella sp</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella sp</i>	16S
JDID-101	Enterobacteriaceae	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	Biolog
JDID-102	Enterobacteriaceae	<i>Raoultella sp</i>	<i>Raoultella sp</i>	Biolog
JDID-103	<i>Klebsiella sp</i>	no identity	<i>Klebsiella sp</i>	16S
JDID-104	<i>Klebsiella sp</i>	no identity	<i>Klebsiella sp</i>	16S
JDID-105	Enterobacteriaceae	<i>Raoultella sp</i>	<i>Raoultella sp</i>	Biolog
JDID-106	<i>Citrobacter sp</i>	<i>Citrobacter freundii</i>	<i>Citrobacter sp</i>	16S
JDID-107	<i>Enterobacter ludwigii</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter ludwigii</i>	16S
JDID-108	Enterobacteriaceae	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	Biolog
JDID-109	Enterobacteriaceae	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	Biolog
JDID-110	<i>Scandinavium goetborgense</i>	<i>Buttiauxella noackiae</i>	<i>Scandinavium goetborgense</i>	16S
JDID-111	Enterobacterales	<i>Enterobacter hormacheii</i>	<i>Enterobacter hormacheii</i>	Biolog
JDID-112	<i>Enterobacter sp</i>	<i>Enterobacter hormacheii</i>	<i>Enterobacter sp</i>	16S
JDID-113	Enterobacteriaceae	<i>Enterobacter hormacheii</i>	<i>Enterobacter hormacheii</i>	Biolog
JDID-114	<i>Kluyvera georgiana</i>	<i>Kluyvera cryocrescens</i>	<i>Kluyvera georgiana</i>	16S

Continuation of Table 14, part 3 of 9

JDID-115	Enterobacteriaceae	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	Biolog
JDID-116	<i>Klebsiella sp</i>	no identity	<i>Klebsiella sp</i>	16S
JDID-117	<i>Serratia sp</i>	<i>Serratia sp</i>	<i>Serratia sp</i>	both
JDID-118	<i>Serratia sp</i>	<i>Serratia marcescens</i>	<i>Serratia sp</i>	16S
JDID-119	Enterobacteriaceae	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	Biolog
JDID-120	Enterobacterales	<i>Pantoea dispersa</i>	<i>Pantoea dispersa</i>	Biolog
JDID-121	Enterobacterales	no identity	Enterobacterales	16S
JDID-122	Enterobacterales	<i>Raoultella terrigena</i>	<i>Klebsiella terrigena</i>	Biolog
JDID-123	<i>Serratia sp</i>	<i>Serratia marcescens</i>	<i>Serratia sp</i>	16S
JDID-124	<i>Serratia sp</i>	<i>Serratia marcescens</i>	<i>Serratia sp</i>	16S
JDID-125	<i>Serratia sp</i>	<i>Serratia sp</i>	<i>Serratia sp</i>	both
JDID-126	Erwinaceae	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>	Biolog
JDID-127	<i>Mixta sp</i>	<i>Klebsiella sp</i>	<i>Mixta sp</i>	16S
JDID-128	<i>Kluyvera georgiana</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera georgiana</i>	16S
JDID-129	Enterobacteriaceae	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	Biolog
JDID-130	no identity	no identity	no identity	neither
JDID-131	<i>Serratia sp</i>	<i>Serratia sp</i>	<i>Serratia sp</i>	both
JDID-132	Enterobacterales	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	Biolog
JDID-133	<i>Proteus myxofaciens</i>	<i>Proteus myxofaciens</i>	<i>Proteus myxofaciens</i>	both
JDID-134	Enterobacteriaceae	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	Biolog
JDID-135	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	both
JDID-136	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	both
JDID-137	Enterobacterales	<i>Raoultella terrigena</i>	<i>Klebsiella terrigena</i>	Biolog
JDID-138	<i>Klebsiella sp</i>	<i>Tatumella ptyseos</i>	<i>Klebsiella sp</i>	16S
JDID-139	<i>Proteus sp</i>	<i>Proteus penneri</i>	<i>Proteus sp</i>	16S
JDID-140	<i>Proteus myxofaciens</i>	<i>Proteus myxofaciens</i>	<i>Proteus myxofaciens</i>	both
JDID-141	Enterobacteriaceae	<i>Raoultella terrigena</i>	<i>Klebsiella terrigena</i>	Biolog
JDID-142	Enterobacteriaceae	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	Biolog
JDID-143	<i>Enterobacter sp</i>	<i>Kluyvera cryocrescens</i>	<i>Enterobacter sp</i>	16S
JDID-144	<i>Serratia sp</i>	no identity	<i>Serratia sp</i>	16S
JDID-145	Enterobacteriaceae	<i>Escherichia coli</i>	<i>Escherichia coli</i>	Biolog
JDID-146	<i>Buttiauxella sp</i>	<i>Salmonella subterranea</i>	<i>Buttiauxella sp</i>	16S
JDID-147	<i>Enterobacter sp</i>	<i>Kluyvera ascorbata</i>	<i>Enterobacter sp</i>	16S
JDID-148	<i>Enterobacter sp</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter sp</i>	16S
JDID-149	<i>Enterobacter sp</i>	no identity	<i>Enterobacter sp</i>	16S
JDID-150	<i>Citrobacter sp</i>	<i>Citrobacter freundii</i>	<i>Citrobacter sp</i>	16S
JDID-151	<i>Citrobacter talavivensis</i>	<i>Citrobacter gillenii</i>	<i>Citrobacter talavivensis</i>	16S
JDID-152	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-153	<i>Citrobacter sp</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter sp</i>	16S
JDID-154	<i>Enterobacter sp</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter sp</i>	16S
JDID-155	<i>Klebsiella sp</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella sp</i>	16S
JDID-156	Enterobacteriaceae	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	Biolog
JDID-157	Enterobacteriaceae	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	Biolog

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JDID-158	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-159	Enterobacteriaceae	<i>Enterobacter hormacheii</i>	<i>Enterobacter hormacheii</i>	Biolog
JDID-160	<i>Pantoea agglomerans</i>	no identity	<i>Pantoea agglomerans</i>	16S
JDID-161	Erwiniaceae	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	Biolog
JDID-162	Enterobacteriaceae	<i>Leclercia adecarboxylata</i>	<i>Leclercia adecarboxylata</i>	Biolog
JDID-163	<i>Providencia sp</i>	<i>Klebsiella oxytoca</i>	<i>Providencia sp</i>	16S
JDID-164	<i>Yersinia sp</i>	<i>Yersinia massiliensis</i>	<i>Yersinia sp</i>	16S
JDID-165	Enterobacteriaceae	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	Biolog
JDID-166	Enterobacteriaceae	<i>Enterobacter hormacheii</i>	<i>Enterobacter hormacheii</i>	Biolog
JDID-167	<i>Citrobacter sp</i>	<i>Citrobacter freundii</i>	<i>Citrobacter sp</i>	16S
JDID-168	Enterobacteriaceae	<i>Citrobacter youngae</i>	<i>Citrobacter youngae</i>	Biolog
JDID-169	Enterobacteriaceae	<i>Leclercia adecarboxylata</i>	<i>Leclercia adecarboxylata</i>	Biolog
JDID-170	Enterobacteriaceae	<i>Siccibacter turicensis</i>	<i>Siccibacter turicensis</i>	Biolog
JDID-171	Enterobacteriaceae	<i>Raoultella sp</i>	<i>Raoultella sp</i>	Biolog
JDID-172	<i>Pantoea sp</i>	<i>Pantoea agglomerans</i>	<i>Pantoea sp</i>	16S
JDID-173	Enterobacteriaceae	<i>Leclercia adecarboxylata</i>	<i>Leclercia adecarboxylata</i>	Biolog
JDID-174	no identity	analysis not performed	no identity	neither
JDID-175	Enterobacteriaceae	<i>Raoultella sp</i>	<i>Raoultella sp</i>	Biolog
JDID-176	Enterobacteriaceae	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	Biolog
JDID-177	<i>Citrobacter sp</i>	<i>Citrobacter youngae</i>	<i>Citrobacter sp</i>	16S
JDID-178	<i>Citrobacter sp</i>	<i>Citrobacter freundii</i>	<i>Citrobacter sp</i>	16S
JDID-179	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-180	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-181	Enterobacteriaceae	<i>Leclercia adecarboxylata</i>	<i>Leclercia adecarboxylata</i>	Biolog
JDID-182	Enterobacteriaceae	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	Biolog
JDID-183	Enterobacteriaceae	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	Biolog
JDID-184	no identity	no identity	no identity	16S
JDID-185	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	both
JDID-186	Enterobacterales	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>	Biolog
JDID-187	<i>Yersinia sp</i>	<i>Yersinia frederiksenii</i>	<i>Yersinia sp</i>	16S
JDID-188	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-189	Enterobacterales	<i>Leminorella richardii</i>	<i>Leminorella richardii</i>	Biolog
JDID-190	Enterobacteriaceae	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	Biolog
JDID-191	<i>Helicobacter sp</i>	analysis not performed	<i>Helicobacter sp</i>	16S
JDID-192	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-193	<i>Helicobacter sp</i>	no identity	<i>Helicobacter sp</i>	16S
JDID-194	Enterobacteriaceae	<i>Escherichia coli</i>	<i>Escherichia coli</i>	Biolog
JDID-195	<i>Campylobacter sp</i>	analysis not performed	<i>Campylobacter sp</i>	16S
JDID-196	Enterobacteriaceae	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	Biolog
JDID-197	Enterobacteriaceae	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	Biolog
JDID-198	Enterobacteriaceae	<i>Escherichia coli</i>	<i>Escherichia coli</i>	Biolog
JDID-199	<i>Enterobacter quasihormaechei</i>	<i>Kluyvera intermedia</i>	<i>Enterobacter quasihormaechei</i>	16S
JDID-200	Enterobacteriaceae	<i>Kluyvera intermedia</i>	<i>Kluyvera intermedia</i>	Biolog

JDID-201	Enterobacteriaceae	<i>Kluyvera intermedia</i>	<i>Kluyvera intermedia</i>	Biolog
JDID-202	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-203	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-204	Enterobacteriaceae	<i>Leclercia adecarboxylata</i>	<i>Leclercia adecarboxylata</i>	Biolog
JDID-205	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-206	Enterobacteriaceae	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	Biolog
JDID-207	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-208	Enterobacteriaceae	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	Biolog
JDID-209	Enterobacterales	<i>Serratia plymuthica</i>	<i>Serratia plymuthica</i>	Biolog
JDID-210	Enterobacteriaceae	<i>Kluyvera intermedia</i>	<i>Kluyvera intermedia</i>	Biolog
JDID-211	Enterobacteriaceae	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	Biolog
JDID-212	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-213	<i>Campylobacter sp</i>	<i>Klebsiella oxytoca</i>	<i>Campylobacter sp</i>	16S
JDID-214	Enterobacteriaceae	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	Biolog
JDID-215	<i>Helicobacter sp</i>	<i>Klebsiella pneumoniae</i>	<i>Helicobacter sp</i>	16S
JDID-216	Enterobacteriaceae	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	Biolog
JDID-217	Enterobacteriaceae	<i>Raoultella sp</i>	<i>Raoultella sp</i>	Biolog
JDID-218	Enterobacteriaceae	<i>Trabulsiella guamensis</i>	<i>Trabulsiella guamensis</i>	Biolog
JDID-219	Enterobacteriaceae	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>	Biolog
JDID-220	Enterobacteriaceae	<i>Kosakonia cowanii</i>	<i>Kosakonia cowanii</i>	Biolog
JDID-221	Pectobacteriaceae	<i>Lactobacillus paracasei</i>	<i>Lactocaseibacillus paracasei</i>	Biolog
JDID-222	Enterobacteriaceae	<i>Escherichia coli</i>	<i>Escherichia coli</i>	Biolog
JDID-223	<i>Helicobacter sp</i>	analysis not performed	<i>Helicobacter sp</i>	16S
JDID-224	<i>Helicobacter sp</i>	analysis not performed	<i>Helicobacter sp</i>	16S
JDID-225	Enterobacteriaceae	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	Biolog
JDID-226	Enterobacteriaceae	<i>Leclercia adecarboxylata</i>	<i>Leclercia adecarboxylata</i>	Biolog
JDID-227	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-228	<i>Cronobacter sp</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sp</i>	16S
JDID-229	<i>Helicobacter pylori</i>	no identity	<i>Helicobacter pylori</i>	16S
JDID-230	<i>Helicobacter pylori</i>	no identity	<i>Helicobacter pylori</i>	16S
JDID-231	<i>Providencia sp</i>	<i>Providencia rettgeri</i>	<i>Providencia sp</i>	16S
JDID-232	Enterobacteriaceae	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	Biolog
JDID-233	<i>Yokenella regensburgei</i>	<i>Leclercia adecarboxylata</i>	<i>Yokenella regensburgei</i>	16S
JDID-234	<i>Yokenella regensburgei</i>	<i>Leclercia adecarboxylata</i>	<i>Yokenella regensburgei</i>	16S
JDID-235	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-236	<i>Cronobacter sp</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sp</i>	16S
JDID-237	<i>Phytobacter sp</i>	no identity	<i>Phytobacter sp</i>	16S
JDID-238	<i>Pantoea eucrina</i>	no identity	<i>Pantoea eucrina</i>	16S
JDID-239	<i>Enterobacter sp</i>	no identity	<i>Enterobacter sp</i>	16S
JDID-240	Enterobacteriaceae	<i>Cedecea davisae</i>	<i>Cedecea davisae</i>	Biolog
JDID-241	Enterobacteriaceae	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>	Biolog
JDID-242	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-243	<i>Citrobacter sp</i>	<i>Citrobacter freundii</i>	<i>Citrobacter sp</i>	16S

JDID-244	<i>Klebsiella sp</i>	no identity	<i>Klebsiella sp</i>	16S
JDID-245	Enterobacteriaceae	<i>Lelliottia amnigena</i>	<i>Lelliottia amnigena</i>	Biolog
JDID-246	Enterobacteriaceae	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	Biolog
JDID-247	<i>Providencia sp</i>	<i>Providencia rettgeri</i>	<i>Providencia sp</i>	16S
JDID-248	Enterobacteriaceae	<i>Trabulsiella guamensis</i>	<i>Trabulsiella guamensis</i>	Biolog
JDID-249	Enterobacteriaceae	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	Biolog
JDID-250	<i>Enterobacter sp</i>	no identity	<i>Enterobacter sp</i>	16S
JDID-251	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-252	Enterobacteriaceae	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	Biolog
JDID-253	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-254	<i>Mixta sp</i>	<i>Salmonella enterica</i>	<i>Mixta sp</i>	16S
JDID-255	<i>Yersinia sp</i>	no identity	<i>Yersinia sp</i>	16S
JDID-256	<i>Yersinia sp</i>	<i>Yersinia frederiksenii</i>	<i>Yersinia sp</i>	16S
JDID-257	<i>Yersinia sp</i>	<i>Yersinia intermedia</i>	<i>Yersinia sp</i>	16S
JDID-258	<i>Yersinia sp</i>	<i>Yersinia intermedia</i>	<i>Yersinia sp</i>	16S
JDID-259	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-260	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-261	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-262	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-263	Enterobacteriales	<i>Serratia sp</i>	<i>Serratia sp</i>	Biolog
JDID-264	<i>Mixta sp</i>	no identity	<i>Mixta sp</i>	16S
JDID-265	Enterobacteriaceae	<i>Kosakonia cowanii</i>	<i>Kosakonia cowanii</i>	Biolog
JDID-266	<i>Providencia sp</i>	<i>Salmonella enterica</i>	<i>Providencia sp</i>	16S
JDID-267	Enterobacteriales	<i>Yokenella regensburgei</i>	<i>Yokenella regensburgei</i>	Biolog
JDID-268	<i>Helicobacter valdiviensis</i>	<i>Providencia stuartii</i>	<i>Helicobacter valdiviensis</i>	16S
JDID-269	<i>Helicobacter pylori</i>	analysis not performed	<i>Helicobacter pylori</i>	16S
JDID-270	<i>Helicobacter pylori</i>	analysis not performed	<i>Helicobacter pylori</i>	16S
JDID-271	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-272	<i>Campylobacter fetus</i>	<i>Kingella denitrificans</i>	<i>Campylobacter fetus</i>	16S
JDID-273	<i>Campylobacter fetus</i>	no identity	<i>Campylobacter fetus</i>	16S
JDID-274	<i>Campylobacter upsaliensis</i>	no identity	<i>Campylobacter upsaliensis</i>	16S
JDID-275	<i>Campylobacter sp</i>	<i>Campylobacter sp</i>	<i>Campylobacter sp</i>	both
JDID-276	no identity	<i>Providencia stuartii</i>	<i>Providencia stuartii</i>	Biolog
JDID-277	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-278	Enterobacteriaceae	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	Biolog
JDID-279	<i>Pantoea sp</i>	<i>Pantoea agglomerans</i>	<i>Pantoea sp</i>	16S
JDID-280	<i>Pantoea stewartii</i>	no identity	<i>Pantoea stewartii</i>	16S
JDID-281	<i>Bacillus sp</i>	<i>Pantoea ananatis</i>	<i>Bacillus sp</i>	16S
JDID-282	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-283	<i>Mixta sp</i>	<i>Pantoea ananatis</i>	<i>Mixta sp</i>	16S
JDID-284	<i>Serratia sp</i>	<i>Serratia entomophila</i>	<i>Serratia sp</i>	16S
JDID-285	<i>Erwinia sp</i>	<i>Pseudomonas syringae</i>	<i>Erwinia sp</i>	16S
JDID-286	Erwiniaceae	<i>Pantoea dispersa</i>	<i>Pantoea dispersa</i>	Biolog

JDID-287	<i>Campylobacter sp</i>	<i>Escherichia coli</i>	<i>Campylobacter sp</i>	16S
JDID-288	<i>Yersinia sp</i>	<i>Salmonella enterica</i>	<i>Yersinia sp</i>	16S
JDID-289	Enterobacteriaceae	<i>Enterobacter hormacheii</i>	<i>Enterobacter hormacheii</i>	Biolog
JDID-290	<i>Pantoea sp</i>	<i>Pantoea agglomerans</i>	<i>Pantoea sp</i>	16S
JDID-291	<i>Pantoea sp</i>	<i>Pantoea agglomerans</i>	<i>Pantoea sp</i>	16S
JDID-292	<i>Campylobacter lari</i>	no identity	<i>Campylobacter lari</i>	16S
JDID-293	<i>Listeria sp</i>	no identity	<i>Listeria sp</i>	16S
JDID-294	<i>Listeria sp</i>	no identity	<i>Listeria sp</i>	16S
JDID-295	Enterobacteriaceae	<i>Leclercia adecarboxylata</i>	<i>Leclercia adecarboxylata</i>	Biolog
JDID-296	phylum	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>	Biolog
JDID-297	<i>Campylobacter sp</i>	<i>Kytococcus sedentarius</i>	<i>Campylobacter sp</i>	16S
JDID-298	<i>Yersinia sp</i>	<i>Salmonella enterica</i>	<i>Yersinia sp</i>	16S
JDID-299	<i>Yersinia aleksiciae</i>	<i>Salmonella enterica</i>	<i>Yersinia aleksiciae</i>	16S
JDID-300	<i>Pantoea phytostimulans</i>	<i>Salmonella enterica</i>	<i>Pantoea phytostimulans</i>	16S
JDID-301	Enterobacteriaceae	<i>Escherichia coli</i>	<i>Escherichia coli</i>	Biolog
JDID-302	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-303	<i>Arcobacter sp</i>	no identity	<i>Arcobacter sp</i>	16S
JDID-304	<i>Campylobacter sp</i>	no identity	<i>Campylobacter sp</i>	16S
JDID-305	<i>Helicobacter sp</i>	analysis not performed	<i>Helicobacter sp</i>	16S
JDID-306	<i>Helicobacter pylori</i>	no identity	<i>Helicobacter pylori</i>	16S
JDID-307	<i>Campylobacter sp</i>	<i>Citrobacter koseri</i>	<i>Campylobacter sp</i>	16S
JDID-308	<i>Yersinia sp</i>	<i>Yersinia intermedia</i>	<i>Yersinia sp</i>	16S
JDID-309	Enterobacterales	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	Biolog
JDID-310	<i>Helicobacter sp</i>	<i>Yokenella regensburgei</i>	<i>Helicobacter sp</i>	16S
JDID-311	<i>Klebsiella sp</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella sp</i>	16S
JDID-312	Enterobacteriaceae	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	Biolog
JDID-313	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-314	<i>Citrobacter murlinae</i>	<i>Citrobacter murlinae</i>	<i>Citrobacter murlinae</i>	both
JDID-315	<i>Listeria sp</i>	<i>Listeria sp</i>	<i>Listeria sp</i>	both
JDID-316	<i>Listeria sp</i>	<i>Listeria sp</i>	<i>Listeria sp</i>	both
JDID-317	Enterobacteriaceae	<i>Kosakonia cowanii</i>	<i>Kosakonia cowanii</i>	Biolog
JDID-318	<i>Yersinia sp</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia sp</i>	16S
JDID-319	<i>Helicobacter pylori</i>	no identity	<i>Helicobacter pylori</i>	16S
JDID-320	<i>Cronobacter sakazakii</i>	no identity	<i>Cronobacter sakazakii</i>	16S
JDID-321	no identity	analysis not performed	no identity	16S
JDID-322	Enterobacteriaceae	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	Biolog
JDID-323	<i>Klebsiella aerogenes</i>	<i>Raoultella sp</i>	<i>Klebsiella aerogenes</i>	16S
JDID-324	Enterobacteriaceae	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	Biolog
JDID-325	Hafniaceae	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	Biolog
JDID-326	Enterobacterales	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	Biolog
JDID-327	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>	both
JDID-328	<i>Proteus sp</i>	<i>Proteus mirabilis</i>	<i>Proteus sp</i>	16S
JDID-329	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	both

JDID-330	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	both
JDID-331	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	both
JDID-332	Enterobacteriaceae	<i>Escherichia vulneris</i>	<i>Pseudoescherichia vulneris</i>	Biolog
JDID-333	Enterobacteriaceae	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	Biolog
JDID-334	<i>Tatumella sp</i>	<i>Tatumella ptyseos</i>	<i>Tatumella sp</i>	16S
JDID-335	<i>Tatumella sp</i>	<i>Tatumella ptyseos</i>	<i>Tatumella sp</i>	16S
JDID-336	<i>Shimwellia blattae</i>	<i>Klebsiella oxytoca</i>	<i>Shimwellia blattae</i>	16S
JDID-337	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	both
JDID-338	<i>Proteus sp</i>	<i>Proteus penneri</i>	<i>Proteus sp</i>	16S
JDID-339	Enterobacteriaceae	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	Biolog
JDID-340	Enterobacteriaceae	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	Biolog
JDID-341	Enterobacteriaceae	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	Biolog
JDID-342	Enterobacteriaceae	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	Biolog
JDID-343	Enterobacteriaceae	<i>Escherichia vulneris</i>	<i>Pseudoescherichia vulneris</i>	Biolog
JDID-344	Enterobacteriaceae	no identity	Enterobacteriaceae	16S
JDID-345	Enterobacteriaceae	<i>Escherichia vulneris</i>	<i>Pseudoescherichia vulneris</i>	Biolog
JDID-346	Yersiniaceae	<i>Ewingella americana</i>	<i>Ewingella americana</i>	Biolog
JDID-347	Enterobacteriaceae	<i>Escherichia coli</i>	<i>Escherichia coli</i>	Biolog
JDID-348	Enterobacteriaceae	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	Biolog
JDID-349	Enterobacteriaceae	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	Biolog
JDID-350	Enterobacteriaceae	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	Biolog
JDID-351	Enterobacteriaceae	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	Biolog
JDID-352	Enterobacteriaceae	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	Biolog
JDID-353	Enterobacteriaceae	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	Biolog
JDID-354	<i>Yersinia sp</i>	<i>Citrobacter farmeri</i>	<i>Yersinia sp</i>	16S
JDID-355	<i>Citrobacter sp</i>	<i>Escherichia coli</i>	<i>Citrobacter sp</i>	16S
JDID-356	Enterobacteriaceae	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	Biolog
JDID-357	<i>Tatumella sp</i>	<i>Tatumella ptyseos</i>	<i>Tatumella sp</i>	16S
JDID-358	<i>Cronobacter turicensis</i>	<i>Staphylococcus epidermis</i>	<i>Cronobacter turicensis</i>	16S
JDID-359	<i>Cronobacter sp</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sp</i>	16S
JDID-360	<i>Cronobacter sp</i>	no identity	<i>Cronobacter sp</i>	16S
JDID-361	<i>Cronobacter turicensis</i>	analysis not performed	<i>Cronobacter turicensis</i>	16S
JDID-362	<i>Cronobacter sp</i>	analysis not performed	<i>Cronobacter sp</i>	16S
JDID-363	analysis not performed	analysis not performed	analysis not performed	
JDID-364	<i>Proteus sp</i>	<i>Proteus mirabilis</i>	<i>Proteus sp</i>	16S
JDID-365	<i>Proteus sp</i>	<i>Proteus mirabilis</i>	<i>Proteus sp</i>	16S

Note. “analysis not performed” indicates the method or workflow was not applied to that isolate due to culture contamination (16S rRNA gene sequencing, n=3; biochemical profiling, n=15); this is distinct from “no identity”, which indicates that the method was applied but did not produce a valid taxonomic assignment.

3.1.2 Taxonomic Resolution of Traditional Identification Methods

Taxonomic assignments generated by traditional identification methods were categorized according to the highest taxonomic rank at which classification criteria were met: *species*, *genus*, *family*, *order*, *phylum*, or *no identity* when the method failed to provide a taxonomic assignment. Among the 362 isolates successfully processed by 16S rRNA sequencing, 358 (98.9%) produced a reportable taxonomic assignment following BLASTn analysis, while four (1.1%) did not meet reporting criteria and were designated as *no identity*. Species-level assignments were obtained for 53 isolates (14.6%), while the majority were resolved to the genus (156; 43.1%) or family level (122; 33.7%). Lower resolution assignments included 26 (7.2%) isolates resolved to order and one isolate (0.3%) resolved to phylum. Among the 350 isolates successfully evaluated by Biolog phenotypic profiling, 258 (73.7%) produced a reportable taxonomic assignment, while 92 (26.3%) were designated as *no identity*. Most reportable assignments were resolved to the species level (244, 94.6%), with the remaining 14 (5.4%) isolates identified only to the genus level. These findings indicate that when Biolog produced an identification, it generally achieved species-level resolution; however, nearly one-quarter of isolates could not be confidently classified. Consensus assignments were generated using the reconciliation framework described in Section 2.6. Of 364 isolates evaluated, 174 (48.8%) were assigned to the species level, 161 (44.2%) to the genus level, 22 (6.0%) to the family level, and 5 (1.4%) to the order level. Two isolates (0.6%) remained *no identity* (Fig. 14).

Differences in taxonomic resolution across traditional methods were statistically significant (Pearson's $\chi^2 = 625.65$, $df = 10$, $p < 2.2e-16$). Examination of standardized residuals (Table A4) indicates that Biolog assignments were strongly enriched for species-level classifications and *no identity* outcomes, whereas 16S rRNA gene sequencing overrepresents

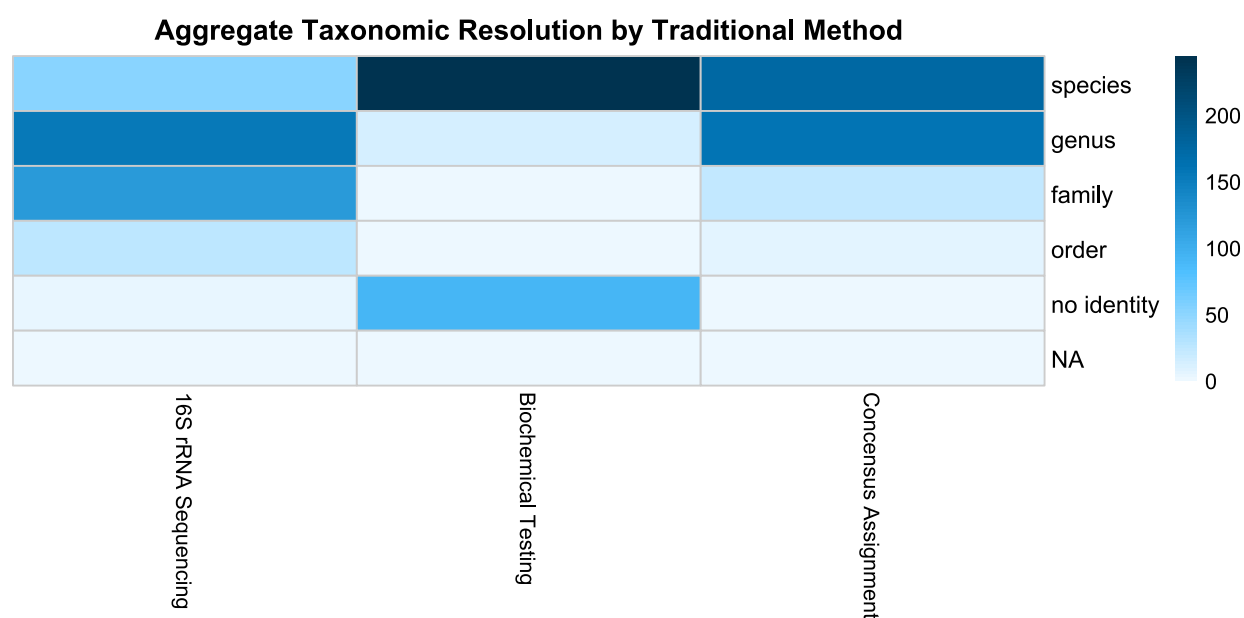


Figure 14. Aggregate taxonomic resolution outcomes across traditional methods. Aggregate heatmap summarizing raw counts of taxonomic resolution outcomes for each methodology across all isolates (n=364) after standardization to valid taxa and correction for taxonomic synonymy. Rows represent taxonomic resolution categories ordered from highest to lowest resolution (species, genus, family, order, or no identity), and columns represent methodology. Colour intensity reflects the number of assignments.

genus and family level assignments. Consensus assignments showed a relative enrichment for genus-level resolution and a reduction in *no identity* classifications (Table A4; Fig. 14). A per-isolate heatmap of taxonomic resolution is shown in Appendix F (Fig. A1).

3.1.3 Concordance Between 16S rRNA-based and Phenotypic Classifications

Agreement between 16S rRNA sequencing and Biolog phenotypic profiling was evaluated using isolates for which both methods produced an assignment at the same taxonomic rank. Analyses were restricted to shared-rank comparisons to avoid inflating concordance through method-specific assignments. Concordance outcomes were categorized as concordant, discordant, or produced by only one method.

Across all evaluated taxonomic ranks (family, *genus*, *species*), both concordant and discordant classifications were observed when 16S rRNA sequencing and phenotypic profiling produced assignments at the same taxonomic level. 197 of 233 shared-rank comparisons (84.5%) at the family level were concordant and concordance declined with increasing taxonomic resolution. At the genus level, 65.6% assignments were concordant while the species level demonstrated 38.7% concordance (n=131) (Table 15). Conversely, discordance proportions increased from 15.5% at the family level to 34.4% at the genus level and 61.3% at the species level (n=31) (Table 15). A formal test for linear trend in discordance across family, genus, and species levels did not detect a statistically significant linear increase in discordance with increasing resolution ($\chi^2 = 2.38$, $df = 1$, $p = 0.123$), indicating that while discordance proportions differed numerically among ranks (Table 13), this pattern did not follow a consistent trend. Accordingly, discordance was interpreted descriptively rather than as a monotonic function of taxonomic resolution.

Table 15. Concordance between 16S rRNA-based and phenotype-based classifications by shared taxonomic rank. Counts of concordant and discordant classifications for isolates where both 16S rRNA sequencing and Biolog phenotypic profiling produced an assignment at the same taxonomic rank*.

Highest Shared Level	Concordant (%)	Discordant (%)	Isolates Compared
Species	12 (38.7)	19 (61.3)	31
Genus	86 (65.6)	45 (34.4)	131
Family	197 (84.5)	36 (15.5)	233

** Taxonomic ranks above family are excluded due to insufficient shared-rank comparisons; only shared-rank comparisons are included.*

Subsequent discordance-focused analyses and visualizations only consider isolates exhibiting discordant classifications and therefore exclude concordant shared-rank comparisons summarized in Table 15. Taxon-specific patterns of discordance were visualized using alluvial plots, which display the flow of discordant assignments (alluvia) between 16S rRNA sequencing and biochemical testing (stratum) (Fig. 15-17).

Across all taxonomic levels, classification outcomes differed significantly in assignments by taxonomic rank (Pearson's $\chi^2 = 89.34$, $df = 8$, $p < 6.3e-16$), indicating a strong association between taxonomic resolution and concordance outcome. Effect size estimation supported this association (Cramer's $V = 0.354$), consistent with a moderate-to-strong relationship between taxonomic level and classification outcome. Standardized residuals (Table A5) revealed resolution-dependent biases in classification behaviour. Species-level comparisons were significantly enriched for discordant outcomes and for Biolog-only assignments or complete failure outcomes but depleted for 16S-only assignments. In contrast, family-level comparisons were strongly enriched for 16S-only assignments and significantly depleted for discordance, indicating greater agreement at broader taxonomic ranks.

Species-, genus-, and family-level discordant classifications were visualized using alluvial plots (Figs. 15-17), which illustrate the magnitude of mismatched assignments between methods. At the species-level, interpretation was limited by the smaller number of shared-rank comparisons ($n=19$; Table 15), and no consistent taxon-specific patterns were evident (Fig. 15).

Genus-level discordance was more broadly distributed across taxa, with distinct asymmetric flows between methods (Fig. 16). A chi-square test assessing the association between genus and outcome category was statistically significant (Pearson's $\chi^2 = 95.73$, $df = 44$, $p < 1.06e-5$), indicating that discordance was not evenly distributed across genera. Standardized

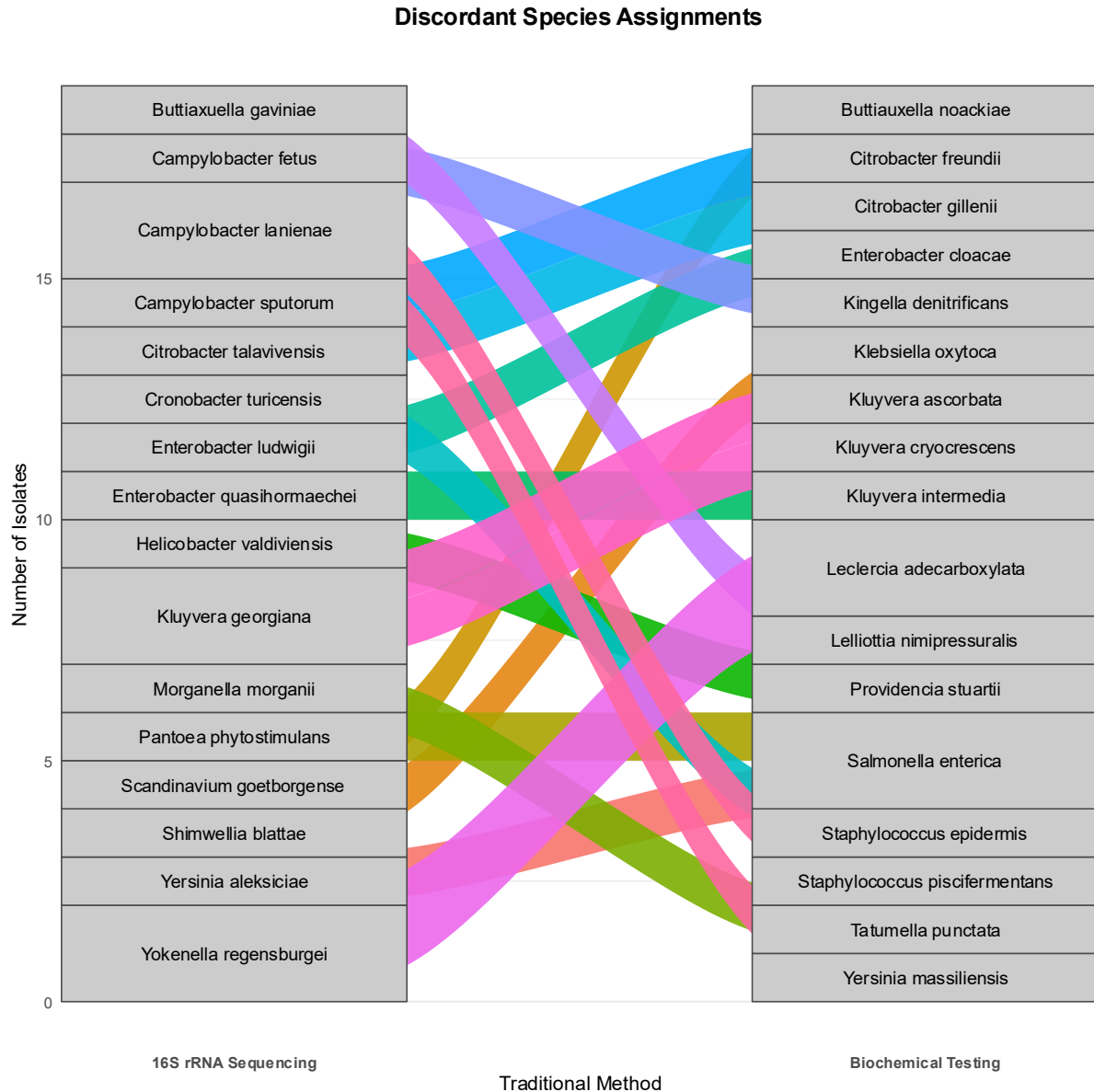


Figure 15. Species-level discordance between 16S rRNA sequencing and phenotypic profiling. Alluvial plot showing discordant species assignments for isolates where both methods returned a species-level identification. Each flow represents the number of isolates assigned to different species by the two methods. Only discordant classifications are shown; 19 (61.3%) isolates species-assigned. Concordant cases and instances where either method failed to produce a species-level identification are excluded. The width of each alluvium is proportional to the number of isolates represented.



Figure 16. Genus-level discordance between 16S rRNA sequencing and phenotypic profiling. Alluvial plot illustrates discordant genus-level assignments between methods. Each flow represents the number of isolates assigned to different genera by the two methods. Only discordant classifications are shown (45 (34.4%) isolates genus-assigned). Concordant cases and instances where either method failed to produce a genus-level identification are excluded. The width of each alluvium is proportional to the number of isolates represented.

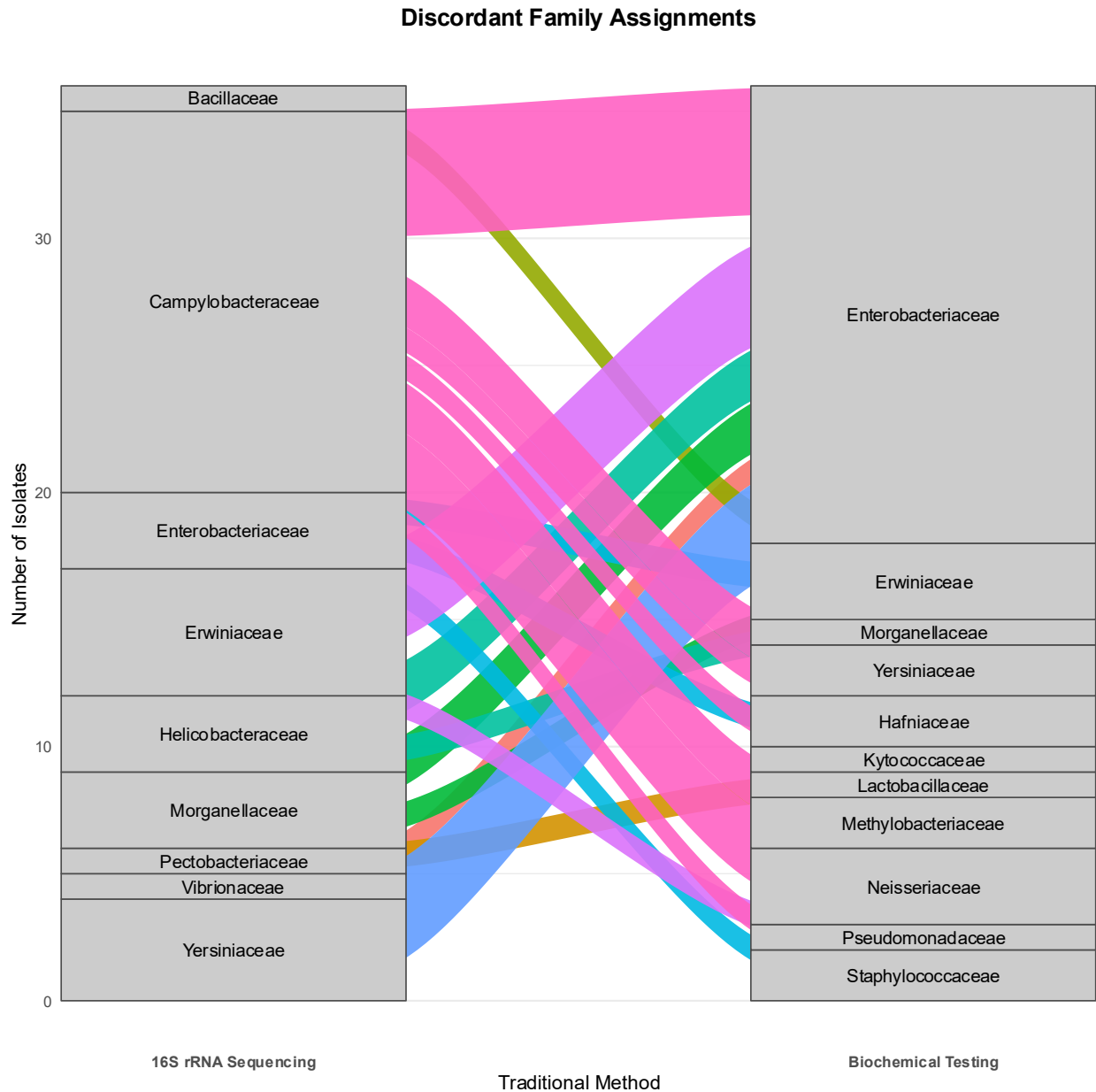


Figure 17. Family-level discordance between 16S rRNA sequencing and phenotypic profiling. Alluvial plot illustrates discordant family-level assignments between methods. Each flow represents the number of isolates assigned to different families by the two methods. Only discordant classifications are shown (36 (15.5%) isolates genus assigned). Concordant cases and instances where either method failed to produce a family-level identification are excluded. The width of each alluvium is proportional to the number of isolates represented.

residuals (Table A6) identified *Aeromonas*, *Citrobacter*, and *Yersinia* as overrepresented in concordant classifications, indicating disproportionate agreement between genotypic and phenotypic assignments. Conversely, *Campylobacter* was underrepresented, indicating disproportionate disagreement in assignments.

The number of taxa in family-level discordance was less frequent than at the genus and species levels (Table 15) and the alluvial plot showed fewer, more concentrated alluvia (Fig. 17), both of which were influenced by the number of isolates compared. These disagreements were concentrated among a small subset of families rather than broadly distributed. A bidirectional pattern was evident between Campylobacteraceae and other families, with 16S rRNA sequencing assigning isolates to Campylobacteraceae that received an alternate classification by phenotypic profiling. Conversely, Enterobacteriaceae assignments were often produced by Biolog phenotypic profiling in cases where 16S rRNA sequencing assigned a different family.

3.1.4 Accuracy of Traditional Methods

Accuracy 16S rRNA sequencing, Biolog phenotypic profiling, and the consensus approach was evaluated using 34 type strains. Accuracy was defined as agreement with the deposited species designation. Phenotypic and the consensus approach each correctly identified 27 of 34 isolates (79.4%; 95% CI: 63.2-89.7%), whereas the 16S-based identification correctly identified 7 of 34 isolates (20.6%; 95% CI: 10.3-36.8%) (Fig. 18). Species-level concordance was limited due to the conservative BLASTn identity and coverage thresholds applied, which frequently resulted in genus-level but not species-level matches. Pairwise McNemar tests showed that 16S-based assignments differed significantly in accuracy from both phenotypic

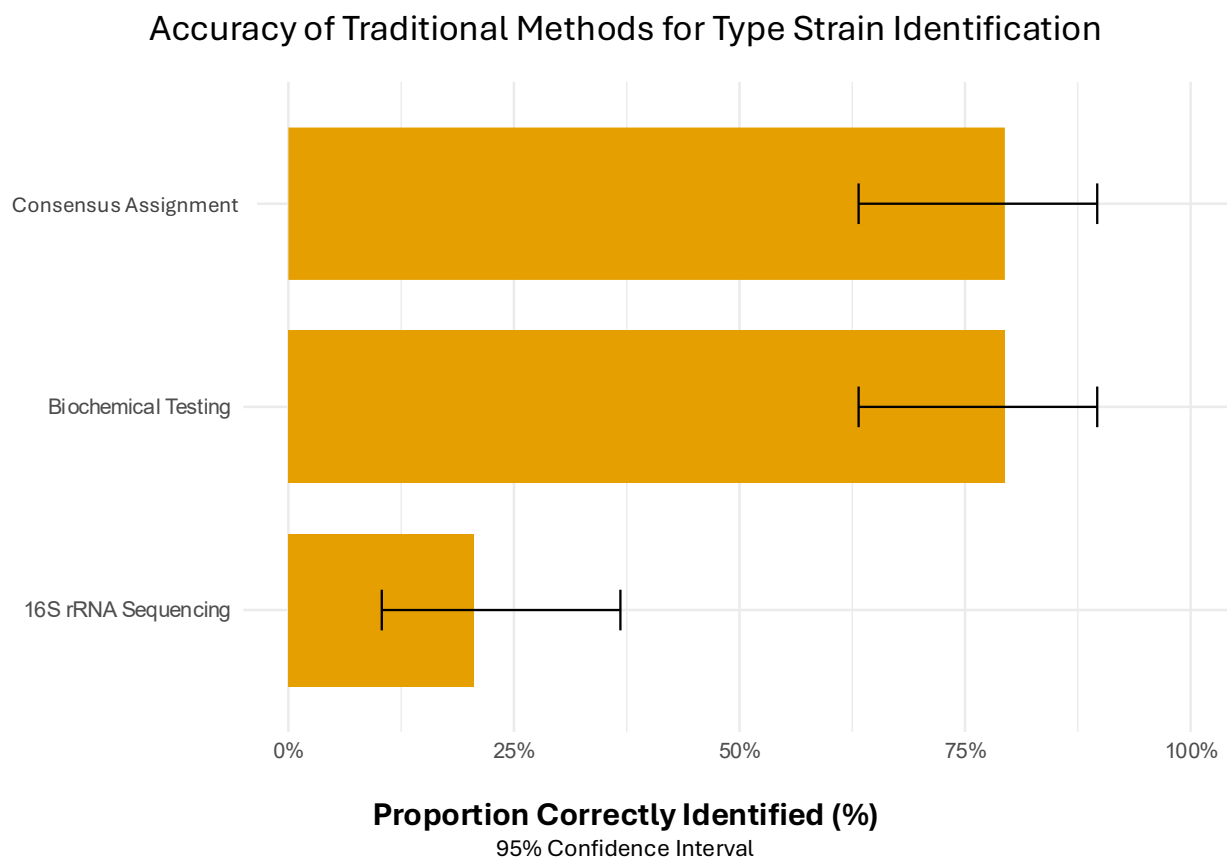


Figure 18. Accuracy of traditional identification methods using type strains. Bar plot showing the proportion of correctly identified type strains (n=34) for each traditional identification methods. Error bars represent 95% Wilson confidence intervals. Accuracy was defined as agreement with the deposited type strain species definition.

($\chi^2 = 15.04$, $p = 1.05\text{e-}4$) and consensus assignments ($\chi^2 = 18.05$, $p = 2.15\text{e-}5$). No significant difference was observed between phenotypic and consensus assignments ($\chi^2 = 0$, $p = 1$).

3.2 WGS-based Classification Methods

3.2.1 Taxonomic Assignments from WGS-based Classification Workflows

WGS data were analyzed using multiple classification workflows applied to Illumina short-read and ONT long-read assemblies. Each workflow generated an independent taxonomic assignment per isolate. Across all isolates, Illumina-based workflows produced 2,172 valid and *no identity* assignments while Nanopore-based workflows produced 930 valid and *no identity* assignments (3,102 total assignments). These total assignments reflect the number of workflows applied per platform (six Illumina-based and three ONT-based taxonomic classifiers) multiplied across the successfully analyzed datasets and include instances where workflows returned “*no identity*”. Of the 365 isolates included in the study, Illumina analyses were completed for 362 isolates following three genome assembly failures. Nanopore analyses were completed for 310 isolates after excluding 16 culture contaminated isolates, 38 failed genome assemblies, and one dataset with insufficient raw read quality for assembly.

Final taxonomic assignments from each workflow are summarized in Table 16 after standardization to valid taxa and synonym correction (Table A13), with complete workflow-specific outputs provided in Appendix Tables A1-A2. To facilitate direct comparison across workflows, subspecies-level classifications were truncated to the species level prior to downstream analyses. This standardized dataset provided the foundation for subsequent comparisons of taxonomic resolution, concordance, classification accuracy, and workflow performance across sequencing platforms and bioinformatic approaches.

Table 16. WGS method-based taxonomic assignments for each isolate by workflow. A presentation of the final taxonomic assignment as determined by individual WGS-based classification workflows applied to Illumina and ONT sequencing data. Each column represents the assignment from a single workflow after standardization to valid taxa and correction of homotypic synonymy. Subspecies classifications were truncated to species level for consistency across tools and taxa.

Isolates	Illumina-based Workflows						ONT-based Workflows		
	Mikrokonodo Kraken2	Mikrokonodo Mash	RefSeq Masher	GTDB-Tk FastANI	GTDB-Tk skANI	TYGS	Mikrokonodo Kraken2	Mikrokonodo Mash	GTDB-Tk skANI
JDID-01	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-02	<i>Yersinia pseudotuberculosis</i>	<i>Yersinia pestis</i>	<i>Yersinia pseudotuberculosis</i>	<i>Yersinia pestis</i>	<i>Yersinia pestis</i>	<i>Yersinia pseudotuberculosis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-03	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>
JDID-04	<i>Campylobacter curvus</i>	<i>Campylobacter curvus</i>	<i>Campylobacter curvus</i>	<i>Campylobacter curvus</i>	<i>Campylobacter curvus</i>	no identity	analysis not performed		
JDID-05	<i>Serratia entomophila</i>	<i>Serratia entomophila</i>	<i>Serratia entomophila</i>	<i>Serratia sp</i>	<i>Serratia sp</i>	no identity	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>
JDID-06	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Providencia rettgeri</i>	<i>Providencia rettgeri</i>	<i>Providencia xianensis</i>
JDID-07	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	no identity	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>
JDID-08	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>
JDID-09	<i>Tatumella ptyseos</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>	<i>Tatumella ptyseos</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>
JDID-10	<i>Providencia rettgeri</i>	<i>Providencia rettgeri</i>	<i>Providencia rettgeri</i>	<i>Providencia rettgeri</i>	<i>Providencia xianensis</i>	<i>Providencia huashanensis</i>	<i>Pantoea piersonii</i>	no identity	no identity
JDID-11	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Serratia entomophila</i>	<i>Serratia entomophila</i>	<i>Serratia sp</i>
JDID-12	<i>Campylobacter sputorum</i>	<i>Campylobacter sputorum</i>	<i>Campylobacter sputorum</i>	<i>Campylobacter sputorum</i>	<i>Campylobacter sputorum</i>	<i>Campylobacter sputorum</i>	<i>Campylobacter sputorum</i>	<i>Campylobacter sputorum</i>	<i>Campylobacter sputorum</i>

JDID-13	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	no identity	no identity	no identity	<i>Proteus mirabilis</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>
JDID-14	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>
JDID-15	<i>Yersinia intermedia</i>	<i>Yersinia rochesterensis</i>	<i>Yersinia rochesterensis</i>	<i>Yersinia rochesterensis</i>	<i>Yersinia rochesterensis</i>	<i>Yersinia rochesterensis</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>
JDID-16	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	analysis not performed		
JDID-17	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	analysis not performed		
JDID-18	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-19	<i>Salmonella enterica</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	no identity	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-20	no identity	no identity	no identity	no identity	<i>Campylobacter vicugnae</i>	<i>Campylobacter vicugnae</i>	<i>Klebsiella pneumoniae</i>	<i>Citrobacter werkmanii</i>	no identity
JDID-21	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	no identity	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>
JDID-22	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Serratia marcescens</i>	<i>Serratia nematodiphila</i>	<i>Serratia nematodiphila</i>
JDID-23	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter peloridis</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>
JDID-24	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	no identity	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-25	<i>Cutibacterium acnes</i>	<i>Campylobacter helveticus</i>	<i>Cutibacterium acnes</i>	<i>Campylobacter helveticus</i>	<i>Campylobacter helveticus</i>	<i>Cutibacterium acnes</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-26	<i>Campylobacter peloridis</i>	<i>Campylobacter peloridis</i>	<i>Campylobacter peloridis</i>	<i>Campylobacter peloridis</i>	<i>Campylobacter peloridis</i>	<i>Campylobacter peloridis</i>	<i>Enterobacter hormaechei</i>	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>
JDID-27	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	no identity	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>
JDID-28	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	no identity	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-29	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	no identity	analysis not performed		
JDID-30	<i>Campylobacter helveticus</i>	<i>Campylobacter helveticus</i>	<i>Campylobacter helveticus</i>	<i>Campylobacter helveticus</i>	<i>Campylobacter helveticus</i>	<i>Campylobacter helveticus</i>	analysis not performed		
JDID-31	<i>Campylobacter concisus</i>	<i>Campylobacter concisus</i>	<i>Campylobacter concisus</i>	<i>Campylobacter concisus</i>	<i>Campylobacter concisus</i>	no identity	analysis not performed		
JDID-32	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>	<i>Hafnia paralvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>
JDID-33	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>	<i>Serratia entomophila</i>	<i>Serratia entomophila</i>	<i>Serratia sp</i>

Continuation of Table 16, part 2 of 19

JDID-34	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>
JDID-35	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	no identity	analysis not performed		
JDID-36	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>
JDID-37	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter intestinihominis</i>
JDID-38	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	no identity	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>
JDID-39	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>
JDID-40	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	analysis not performed		
JDID-41	<i>Yersinia pseudotuberculosis</i>	<i>Yersinia pestis</i>	<i>Yersinia pestis</i>	<i>Yersinia pestis</i>	<i>Yersinia pestis</i>	<i>Yersinia pseudotuberculosis</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>
JDID-42	<i>Campylobacter insulaenigrae</i>	<i>Campylobacter insulaenigrae</i>	<i>Campylobacter insulaenigrae</i>	<i>Campylobacter insulaenigrae</i>	<i>Campylobacter insulaenigrae</i>	no identity	analysis not performed		
JDID-43	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Klebsiella pneumoniae</i>	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>
JDID-44	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	analysis not performed		
JDID-45	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	analysis not performed		
JDID-46	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Providencia rettgeri</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>
JDID-47	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Citrobacter koseri</i>	no identity
JDID-48	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	no identity
JDID-49	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	analysis not performed		
JDID-50	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	analysis not performed		
JDID-51	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	analysis not performed		
JDID-52	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	analysis not performed		
JDID-53	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	no identity	analysis not performed		

Continuation of Table 16, part 3 of 19

JDID-54	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	analysis not performed		
JDID-55	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	analysis not performed		
JDID-56	no identity	no identity	no identity	no identity	<i>Campylobacter vicugnae</i>	<i>Campylobacter vicugnae</i>	<i>Klebsiella pneumoniae</i>	<i>Enterobacter roggenkampii</i>	no identity
JDID-57	<i>Pantoea rwandensis</i>	no identity	no identity	no identity	no identity	no identity	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>
JDID-58	<i>Pantoea rwandensis</i>	no identity	no identity	no identity	no identity	no identity	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-59	<i>Buttiauxella agrestis</i>	no identity	no identity	<i>Buttiauxella sp</i>	<i>Dryocola sp</i>	no identity	<i>Enterobacter hormaechei</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-60	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-61	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Yersinia pseudotuberculosis</i>	<i>Yersinia pestis</i>	<i>Yersinia pestis</i>
JDID-62	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter intestinihominis</i>	<i>Enterobacter hormaechei</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>
JDID-63	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>
JDID-64	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	no identity	analysis not performed		
JDID-65	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>
JDID-66	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>
JDID-67	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>
JDID-68	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-69	<i>Aeromonas media</i>	<i>Aeromonas rivipollensis</i>	<i>Aeromonas rivipollensis</i>	<i>Aeromonas rivipollensis</i>	no identity	no identity	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-70	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	no identity
JDID-71	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Klebsiella pneumoniae</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>
JDID-72	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	no identity	<i>Escherichia coli</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-73	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>

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JDID-74	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-75	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-76	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Tatumella ptyseos</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>
JDID-77	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-78	analysis not performed						<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-79	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Salmonella typhi</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-80	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Klebsiella variicola</i>	<i>Klebsiella variicola</i>	no identity	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>
JDID-81	<i>Klebsiella variicola</i>	<i>Klebsiella variicola</i>	<i>Klebsiella variicola</i>	<i>Phytobacter sp</i>	<i>Phytobacter sp</i>	<i>Klebsiella variicola</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-82	<i>Salmonella enterica</i>	no identity	no identity	<i>Phytobacter sp</i>	<i>Phytobacter sp</i>	no identity	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-83	no identity	no identity	no identity	<i>Phytobacter sp</i>	<i>Phytobacter sp</i>	no identity	<i>Citrobacter freundii</i>	no identity	no identity
JDID-84	no identity	no identity	no identity	<i>Pseudocitrobacter corydidari</i>	<i>Pseudocitrobacter corydidari</i>	no identity	<i>Klebsiella pneumoniae</i>	no identity	no identity
JDID-85	<i>Pseudocitrobacter corydidari</i>	<i>Pseudocitrobacter corydidari</i>	<i>Pseudocitrobacter corydidari</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	no identity	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	no identity
JDID-86	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Klebsiella pneumoniae</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>
JDID-87	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter sp</i>	<i>Enterobacter sp</i>	<i>Enterobacter oligotrophicus</i>	analysis not performed		
JDID-88	<i>Enterobacter cloacae</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	no identity	no identity	no identity	no identity
JDID-89	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Escherichia coli</i>	<i>Kosakonia radicincitans</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-90	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Enterobacter asburiae</i>	<i>Escherichia coli</i>	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>
JDID-91	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter freundii</i>	analysis not performed		
JDID-92	<i>Citrobacter cronae</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	<i>Citrobacter werkmanii</i>	analysis not performed		
JDID-93	no identity	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	no identity	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>

Continuation of Table 16, part 5 of 19

JDID-94	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Citrobacter werkmanii</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-95	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	no identity	no identity	<i>Salmonella typhi</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-96	no identity	no identity	no identity	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	no identity	<i>Klebsiella pneumoniae</i>	<i>Serratia liquefaciens</i>	analysis not performed
JDID-97	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella aerogenes</i>	no identity	no identity	<i>Phytobacter sp</i>
JDID-98	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Sodalis ligni</i>	no identity	<i>Acerihabitans sp</i>
JDID-99	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	no identity	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Hafnia alvei</i>	no identity	no identity
JDID-100	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>
JDID-101	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella quasipneumoniae</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>
JDID-102	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Escherichia coli</i>	<i>Klebsiella ornithinolytica</i>	<i>ornithinolytica</i>
JDID-103	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Serratia liquefaciens</i>	analysis not performed
JDID-104	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella terrigena</i>	<i>Klebsiella terrigena</i>
JDID-105	<i>Klebsiella pneumoniae</i>	<i>Klebsiella terrigena</i>	<i>Klebsiella terrigena</i>	<i>Klebsiella terrigena</i>	<i>Klebsiella terrigena</i>	<i>Klebsiella terrigena</i>	no identity	<i>Khuyvera georgiana</i>	<i>Khuyvera georgiana</i>
JDID-106	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-107	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>
JDID-108	no identity	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>
JDID-109	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Klebsiella quasipneumoniae</i>	<i>Khuyvera ascorbata</i>	<i>Khuyvera ascorbata</i>
JDID-110	<i>Scandinavium goeteborgense</i>	<i>Scandinavium goeteborgense</i>	<i>Scandinavium goeteborgense</i>	<i>Scandinavium goeteborgense</i>	<i>Scandinavium goeteborgense</i>	no identity	<i>Enterobacter kobei</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-111	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Aeromonas media</i>	<i>Aeromonas rivipollensis</i>	no identity
JDID-112	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>

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JDID-113	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-114	no identity	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	no identity	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>
JDID-115	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	no identity	no identity	<i>Leclercia tamurae</i>
JDID-116	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-117	<i>Serratia quinivorans</i>	<i>Serratia quinivorans</i>	<i>Serratia quinivorans</i>	<i>Serratia quinivorans</i>	<i>Serratia quinivorans</i>	<i>Serratia quinivorans</i>	<i>Proteus mirabilis</i>	<i>Proteus myxofaciens</i>	<i>Proteus sp</i>
JDID-118	<i>Serratia marcescens</i>	<i>Serratia ureilytica</i>	<i>Serratia ureilytica</i>	<i>Serratia ureilytica</i>	<i>Serratia ureilytica</i>	<i>Serratia ureilytica</i>	analysis not performed		
JDID-119	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-120	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	no identity	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-121	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	no identity	<i>Kluyvera ascorbata</i>	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>
JDID-122	<i>Leclercia pneumoniae</i>	no identity	no identity	no identity	<i>Leclercia pneumoniae</i>	<i>Leclercia pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-123	<i>Serratia marcescens</i>	<i>Serratia marcescens</i>	<i>Serratia marcescens</i>	<i>Serratia marcescens</i>	<i>Serratia sarumanii</i>	<i>Serratia sarumanii</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-124	<i>Serratia marcescens</i>	<i>Serratia marcescens</i>	<i>Serratia marcescens</i>	<i>Serratia marcescens</i>	<i>Serratia sarumanii</i>	<i>Serratia sarumanii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-125	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>
JDID-126	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	no identity	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-127	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Serratia marcescens</i>	<i>Serratia marcescens</i>	<i>Serratia sarumanii</i>
JDID-128	no identity	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	no identity	no identity	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>
JDID-129	<i>Mixta calida</i>	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	<i>Kluyvera georgiana</i>	no identity	<i>Serratia marcescens</i>	<i>Serratia quinivorans</i>	<i>Serratia quinivorans</i>
JDID-130	<i>Serratia liquefaciens</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Serratia marcescens</i>	no identity	<i>Serratia ureilytica</i>
JDID-131	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-132	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Klebsiella pneumoniae</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbate</i>

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JDID-133	<i>Enterobacter roggkampii</i>	<i>Enterobacter roggkampii</i>	<i>Enterobacter asburiae</i>	<i>Proteus sp</i>	<i>Proteus sp</i>	<i>Enterobacter roggkampii</i>	<i>Klebsiella quasipneumoniae</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>
JDID-134	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter sp</i>
JDID-135	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	no identity	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>
JDID-136	no identity	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-137	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Proteus mirabilis</i>	<i>Proteus myxofaciens</i>	<i>Proteus sp</i>
JDID-138	<i>Proteus columbae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	analysis not performed		
JDID-139	<i>Proteus columbae</i>	no identity	no identity	no identity	no identity	no identity	<i>Proteus columbae</i>	no identity	no identity
JDID-140	<i>Proteus columbae</i>	<i>Proteus myxofaciens</i>	<i>Proteus myxofaciens</i>	<i>Proteus sp</i>	<i>Proteus sp</i>	no identity	<i>Proteus mirabilis</i>	<i>Proteus myxofaciens</i>	<i>Proteus sp</i>
JDID-141	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	analysis not performed		
JDID-142	<i>Raoultella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	no identity	<i>Citrobacter sedlakii</i>	<i>Citrobacter sedlakii</i>
JDID-143	<i>Enterobacter hormaechei</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>
JDID-144	<i>Serratia marcescens</i>	<i>Serratia nevei</i>	<i>Serratia nevei</i>	<i>Serratia nevei</i>	<i>Serratia nevei</i>	no identity	<i>Proteus mirabilis</i>	<i>Proteus myxofaciens</i>	<i>Proteus sp</i>
JDID-145	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter portucalensis</i>
JDID-146	<i>Buttiauxella agrestis</i>	no identity	<i>Buttiauxella agrestis</i>	<i>Buttiauxella gaviniae</i>	<i>Buttiauxella gaviniae</i>	no identity	<i>Klebsiella pneumoniae</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>
JDID-147	<i>Enterobacter asburiae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter roggkampii</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>
JDID-148	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	no identity	<i>Pantoea rwandensis</i>	no identity	no identity
JDID-149	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Leclercia pneumoniae</i>	no identity	<i>Leclercia pneumoniae</i>
JDID-150	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-151	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	no identity	<i>Klebsiella pneumoniae</i>	<i>Pseudocitrobacter corydidiari</i>	<i>Pseudocitrobacter corydidiari</i>
JDID-152	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Salmonella enterica</i>	<i>Escherichia coli</i>

Continuation of Table 16, part 8 of 19

JDID-153	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter sp</i>
JDID-154	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Escherichia coli</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>
JDID-155	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Buttiauxella agrestis</i>	<i>Buttiauxella massiliensis</i>	<i>Buttiauxella gaviniae</i>
JDID-156	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Serratia marcescens</i>	<i>Serratia marcescens</i>	<i>Serratia sarumanii</i>
JDID-157	<i>Citrobacter cronae</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter cronae</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-158	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>
JDID-159	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter intestinihominis</i>
JDID-160	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>
JDID-161	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Erwinia gerundensis</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-162	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	analysis not performed		
JDID-163	<i>Providencia heimbachae</i>	no identity	<i>Providencia alcalifaciens</i>	no identity	no identity	no identity	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-164	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-165	<i>Klebsiella huaxiensis</i>	<i>Klebsiella spallanzanii</i>	no identity	<i>Klebsiella spallanzanii</i>	<i>Klebsiella spallanzanii</i>	<i>Klebsiella spallanzanii</i>	<i>Klebsiella pneumoniae</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-166	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-167	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-168	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-169	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-170	no identity	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	no identity	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>
JDID-171	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-172	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>

Continuation of Table 16, part 9 of 19

JDID-173	no identity	no identity	no identity	no identity	<i>Leclercia tamurae</i>	<i>Leclercia tamurae</i>	no identity	no identity	<i>Leclercia tamurae</i>
JDID-174	no identity	no identity	no identity	no identity	no identity	no identity	analysis not performed		
JDID-175	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-176	<i>Raoultella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-177	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	analysis not performed		
JDID-178	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Escherichia coli</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-179	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>
JDID-180	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	analysis not performed		
JDID-181	<i>Leclercia adecarboxylata</i>	no identity	no identity	no identity	no identity	no identity	<i>Leclercia adecarboxylata</i>	no identity	no identity
JDID-182	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	no identity	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>
JDID-183	<i>Leclercia adecarboxylata</i>	<i>Leclercia adecarboxylata</i>	<i>Leclercia adecarboxylata</i>	<i>Leclercia sp</i>	<i>Leclercia sp</i>	no identity	no identity	<i>Leclercia adecarboxylata</i>	<i>Leclercia sp</i>
JDID-184	no identity	no identity	no identity	no identity	no identity	no identity	<i>Klebsiella pneumoniae</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-185	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Klebsiella ornithinolytica</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-186	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>
JDID-187	<i>Citrobacter portucalensis</i>	<i>Yersinia alsatica</i>	no identity	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Citrobacter portucalensis</i>	<i>Klebsiella planticola</i>	<i>Yersinia alsatica</i>	no identity
JDID-188	<i>Raoultella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-189	<i>Leminorella richardii</i>	<i>Leminorella richardii</i>	<i>Leminorella richardii</i>	<i>Leminorella richardii</i>	<i>Leminorella richardii</i>	<i>Leminorella richardii</i>	analysis not performed		
JDID-190	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>
JDID-191	<i>Helicobacter cinaedi</i>	<i>Helicobacter cinaedi</i>	<i>Helicobacter cinaedi</i>	<i>Helicobacter cinaedi</i>	<i>Helicobacter cinaedi</i>	<i>Helicobacter cinaedi</i>	analysis not performed		
JDID-192	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	no identity	<i>Salmonella enterica</i>	no identity
JDID-193	<i>Helicobacter cinaedi</i>	no identity	no identity	no identity	no identity	no identity	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>

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JDID-194	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Chimaeribacter arupi</i>	<i>Leminorella richardii</i>	no identity
JDID-195	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>
JDID-196	<i>Pseudocitrobacter corydarii</i>	<i>Pseudocitrobacter faecalis</i>	<i>Pseudocitrobacter faecalis</i>	<i>Pseudocitrobacter faecalis</i>	<i>Pseudocitrobacter faecalis</i>	<i>Pseudocitrobacter faecalis</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-197	no identity	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-198	no identity	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	analysis not performed		
JDID-199	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	analysis not performed		
JDID-200	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Campylobacter sputorum</i>	<i>Campylobacter sputorum</i>	<i>Campylobacter sputorum</i>
JDID-201	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-202	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter sp</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	no identity	no identity	<i>Leclercia tamurae</i>
JDID-203	no identity	no identity	no identity	no identity	<i>Leclercia tamurae</i>	<i>Leclercia tamurae</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-204	no identity	no identity	no identity	no identity	<i>Leclercia tamurae</i>	<i>Leclercia tamurae</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-205	<i>Helicobacter pullorum</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	no identity	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-206	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-207	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter rongchengensis</i>	<i>Enterobacter kobei</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>
JDID-208	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter rongchengensis</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>
JDID-209	<i>Serratia plymuthica</i>	<i>Serratia plymuthica</i>	no identity	<i>Serratia plymuthica</i>	<i>Serratia plymuthica</i>	<i>Serratia plymuthica</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-210	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Serratia plymuthica</i>	<i>Serratia plymuthica</i>	<i>Serratia plymuthica</i>
JDID-211	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>
JDID-212	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>
JDID-213	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	analysis not performed		

Continuation of Table 16, part 11 of 19

JDID-214	<i>Enterobacter roggenskampii</i>	<i>Enterobacter roggenskampii</i>	<i>Enterobacter roggenskampii</i>	<i>Enterobacter roggenskampii</i>	<i>Enterobacter roggenskampii</i>	<i>Enterobacter roggenskampii</i>	<i>Salmonella enterica</i>	<i>Enterobacter roggenskampii</i>	<i>Enterobacter roggenskampii</i>
JDID-215	<i>Helicobacter pullorum</i>	<i>Helicobacter pullorum</i>	<i>Helicobacter pullorum</i>	<i>Helicobacter pullorum</i>	<i>Helicobacter pullorum</i>	<i>Helicobacter pullorum</i>	<i>Escherichia coli</i>	no identity	no identity
JDID-216	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-217	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-218	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>
JDID-219	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>
JDID-220	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter intestinihominis</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter intestinihominis</i>
JDID-221	<i>Sodalis ligni</i>	no identity	<i>Pluralibacter gergoviae</i>	<i>Acerihabitans sp</i>	<i>Acerihabitans sp</i>	no identity	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-222	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-223	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	no identity	<i>Campylobacter jejuni</i>	<i>Phytobacter diazotrophicus</i>	no identity
JDID-224	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	no identity	no identity	<i>Phytobacter diazotrophicus</i>	no identity
JDID-225	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-226	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-227	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Aeromonas media</i>	<i>Aeromonas rivipollensis</i>	no identity
JDID-228	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Salmonella enterica</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>
JDID-229	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	no identity	analysis not performed		
JDID-230	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	no identity	analysis not performed		
JDID-231	no identity	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>	<i>Providencia xihuensis</i>	<i>Campylobacter peloridis</i>	<i>Campylobacter peloridis</i>	<i>Campylobacter peloridis</i>
JDID-232	no identity	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	no identity	<i>Hafnia alvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>
JDID-233	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i> ²⁵
JDID-234	<i>Salmonella enterica</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	no identity	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>

Continuation of Table 16, part 12 of 19

JDID-235	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Klebsiella oxytoca</i>	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>
JDID-236	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	analysis not performed		
JDID-237	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-238	<i>Salmonella enterica</i>	<i>Pantoea eucrina</i>	<i>Pantoea eucrina</i>	<i>Pantoea eucrina</i>	<i>Pantoea eucrina</i>	<i>Pantoea eucrina</i>	<i>Pantoea eucrina</i>	<i>Pantoea eucrina</i>	no identity
JDID-239	no identity	no identity	no identity	no identity	no identity	no identity	<i>Enterobacter hormaechei</i>	no identity	no identity
JDID-240	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	no identity	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>	<i>Cedecea neteri</i>
JDID-241	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Hafnia alvei</i>	<i>Kluyvera ascorbata</i>	no identity
JDID-242	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	analysis not performed		
JDID-243	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-244	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter intestinhominis</i>
JDID-245	<i>Pseudesccherichia vulneris</i>	no identity	no identity	no identity	no identity	no identity	<i>Pseudesccherichia vulneris</i>	no identity	no identity
JDID-246	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	no identity	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-247	no identity	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>	<i>Providencia xihuenensis</i>	<i>Providencia alcalifaciens</i>	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>
JDID-248	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-249	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella typhi</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-250	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>
JDID-251	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-252	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Salmonella enterica</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-253	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	no identity	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>
JDID-254	<i>Salmonella enterica</i>	<i>Mixta calida</i>	no identity	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>

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JDID-255	<i>Staphylococcus pseudintermedius</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-256	<i>Yersinia intermedia</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>
JDID-257	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-258	<i>Yersinia intermedia</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	no identity	<i>Yersinia intermedia</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>
JDID-259	<i>Scandinavium goeteborgense</i>	no identity	no identity	<i>Scandinavium sp</i>	<i>Scandinavium sp</i>	no identity	<i>Scandinavium goeteborgense</i>	no identity	no identity
JDID-260	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-261	<i>Escherichia coli</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Escherichia coli</i>	<i>Phytobacter diazotrophicus</i>	no identity
JDID-262	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Escherichia coli</i>	<i>Phytobacter diazotrophicus</i>	no identity
JDID-263	<i>Serratia grimesii</i>	no identity	no identity	no identity	no identity	no identity	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-264	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Pantoea eucrina</i>	<i>Mixta calida</i>	<i>Mixta calida</i>
JDID-265	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter intestinihominis</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	no identity	no identity
JDID-266	<i>Providencia rettgeri</i>	<i>Providencia manganoxydans</i>	<i>Providencia manganoxydans</i>	<i>Providencia manganoxydans</i>	<i>Providencia manganoxydans</i>	<i>Providencia manganoxydans</i>	<i>Salmonella enterica</i>	<i>Providencia manganoxydans</i>	<i>Providencia manganoxydans</i>
JDID-267	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>
JDID-268	<i>Helicobacter canadensis</i>	<i>Helicobacter valdiviensis</i>	<i>Helicobacter valdiviensis</i>	<i>Helicobacter valdiviensis</i>	<i>Helicobacter valdiviensis</i>	<i>Helicobacter valdiviensis</i>	<i>Scandinavium goeteborgense</i>	<i>Hafnia paralvei</i>	no identity
JDID-269	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	no identity	analysis not performed		
JDID-270	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	no identity	analysis not performed		
JDID-271	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter coli</i>	no identity	no identity	no identity	no identity
JDID-272	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-273	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	analysis not performed		
JDID-274	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>
JDID-275	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>

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JDID-276	<i>Cutibacterium acnes</i>	no identity	no identity	<i>Campylobacter</i> sp	<i>Campylobacter</i> sp	no identity	<i>Providencia stuartii</i>	<i>Providencia manganoxydans</i>	<i>Providencia manganoxydans</i>
JDID-277	<i>Campylobacter showae</i>	<i>Campylobacter showae</i>	<i>Campylobacter showae</i>	<i>Campylobacter</i> sp	no identity	no identity	analysis not performed		
JDID-278	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>
JDID-279	<i>Pantoea anthophila</i>	<i>Pantoea anthophila</i>	<i>Pantoea anthophila</i>	<i>Pantoea anthophila</i>	<i>Pantoea anthophila</i>	<i>Pantoea anthophila</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>
JDID-280	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	no identity	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-281	<i>Bacillus velezensis</i>	<i>Bacillus velezensis</i>	<i>Bacillus velezensis</i>	<i>Bacillus velezensis</i>	<i>Bacillus velezensis</i>	<i>Bacillus velezensis</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>
JDID-282	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>
JDID-283	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>
JDID-284	<i>Serratia marcescens</i>	<i>Serratia nematodiphila</i>	<i>Serratia nematodiphila</i>	<i>Serratia nematodiphila</i>	<i>Serratia nematodiphila</i>	<i>Serratia marcescens</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>
JDID-285	no identity	no identity	no identity	no identity	no identity	<i>Erwinia aeris</i>	<i>Providencia rettgeri</i>	<i>Providencia rettgeri</i>	<i>Providencia xianensis</i>
JDID-286	<i>Pantoea piersonii</i>	<i>Pantoea piersonii</i>	<i>Pantoea piersonii</i>	<i>Pantoea piersonii</i>	<i>Pantoea piersonii</i>	<i>Pantoea piersonii</i>	<i>Pantoea agglomerans</i>	<i>Pantoea piersonii</i>	<i>Pantoea piersonii</i>
JDID-287	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	no identity	<i>Serratia proteamaculans</i>	no identity	no identity
JDID-288	<i>Salmonella enterica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Salmonella enterica</i>	no identity
JDID-289	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter intestinihominis</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter intestinihominis</i>
JDID-290	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>
JDID-291	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>
JDID-292	<i>Campylobacter lari</i>	no identity	no identity	no identity	no identity	<i>Campylobacter lari</i>	<i>Pantoea agglomerans</i>	no identity	no identity
JDID-293	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Phytobacter diazotrophicus</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>
JDID-294	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>
JDID-295	no identity	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	no identity	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-296	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>	analysis not performed		

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JDID-297	<i>Kytococcus sedentarius</i>	<i>Kytococcus sedentarius</i>	no identity	<i>Campylobacter</i> sp	no identity	<i>Kytococcus sedentarius</i>	analysis not performed		
JDID-298	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>
JDID-299	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>
JDID-300	<i>Salmonella enterica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>	no identity	<i>Pantoea agglomerans</i>	<i>Salmonella enterica</i>	no identity
JDID-301	<i>Escherichia coli</i>	no identity	no identity	no identity	no identity	no identity	<i>Escherichia coli</i>	no identity	no identity
JDID-302	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Enterobacter cloacae</i>	no identity	no identity
JDID-303	<i>Aliarcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>	<i>Arcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>
JDID-304	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>	no identity	analysis not performed		
JDID-305	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	no identity	<i>Citrobacter koseri</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>
JDID-306	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	no identity	analysis not performed		
JDID-307	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Escherichia coli</i>	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>
JDID-308	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	analysis not performed		
JDID-309	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	analysis not performed		
JDID-310	<i>Helicobacter pullorum</i>	<i>Helicobacter pullorum</i>	<i>Helicobacter pullorum</i>	<i>Helicobacter pullorum</i>	<i>Helicobacter pullorum</i>	<i>Helicobacter pullorum</i>	analysis not performed		
JDID-311	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	analysis not performed		
JDID-312	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>
JDID-313	no identity	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	analysis not performed		
JDID-314	<i>Citrobacter freundii</i>	<i>Citrobacter murlinae</i>	<i>Citrobacter murlinae</i>	<i>Citrobacter murlinae</i>	<i>Citrobacter murlinae</i>	no identity	analysis not performed		
JDID-315	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	no identity	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>
JDID-316	<i>Listeria monocytogenes</i>	no identity	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Pseudocitrobacter corydidari</i>	<i>Pseudocitrobacter faecalis</i>	<i>Pseudocitrobacter faecalis</i>
JDID-317	analysis not performed						analysis not performed		

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JDID-318	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	no identity	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>
JDID-319	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	no identity	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	no identity	analysis not performed		
JDID-320	no identity	no identity	no identity	no identity	no identity	no identity	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-321	analysis not performed						no identity	no identity	no identity
JDID-322	<i>Proteus mirabilis</i>	<i>Enterobacter cloacae</i>	no identity	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>
JDID-323	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>
JDID-324	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>
JDID-325	<i>Proteus mirabilis</i>	<i>Hafnia alvei</i>	no identity	no identity	no identity	<i>Proteus mirabilis</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-326	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Pseudomonas aeruginosa</i>	<i>Pseudomonas aeruginosa</i>	<i>Pseudomonas aeruginosa</i>
JDID-327	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>	<i>Citrobacter koseri</i>
JDID-328	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-329	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-330	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-331	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>
JDID-332	no identity	no identity	no identity	no identity	no identity	no identity	no identity	no identity	no identity
JDID-333	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>
JDID-334	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>
JDID-335	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>
JDID-336	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>	<i>Campylobacter jejuni</i>
JDID-337	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Campylobacter armoricus</i>	<i>Campylobacter lari</i>	<i>Campylobacter lari</i>
JDID-338	<i>Proteus penneri</i>	<i>Proteus penneri</i>	<i>Proteus penneri</i>	<i>Proteus penneri</i>	<i>Proteus penneri</i>	<i>Proteus penneri</i>	analysis not performed		
JDID-339	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>

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JDID-340	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>
JDID-341	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>
JDID-342	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>
JDID-343	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Klebsiella pneumoniae</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>
JDID-344	no identity	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Cronobacter sakazakii</i>	<i>Klebsiella oxytoca</i>	no identity
JDID-345	no identity	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>
JDID-346	<i>Ewingella americana</i>	<i>Ewingella americana</i>	<i>Ewingella americana</i>	<i>Ewingella americana</i>	<i>Ewingella americana</i>	<i>Ewingella americana</i>	<i>Ewingella americana</i>	<i>Ewingella americana</i>	<i>Ewingella americana</i>
JDID-347	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-348	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-349	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>
JDID-350	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Campylobacter fetus</i>	<i>Hafnia alvei</i>	no identity
JDID-351	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-352	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-353	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>
JDID-354	<i>Yersinia mollaretii</i>	<i>Yersinia mollaretii</i>	<i>Yersinia mollaretii</i>	<i>Yersinia mollaretii</i>	<i>Yersinia mollaretii</i>	<i>Yersinia mollaretii</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>
JDID-355	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>
JDID-356	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>	<i>Citrobacter farmeri</i>
JDID-357	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Citrobacter koseri</i>	<i>Campylobacter upsaliensis</i>	<i>Campylobacter upsaliensis</i>
JDID-358	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>
JDID-359	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-360	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>

Continuation of Table 16, part 18 of 19

JDID-361	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>	<i>Citrobacter malonaticus</i>	no identity	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i>
JDID-362	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i>	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>
JDID-363	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-364	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-365	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>

Note. “analysis not performed” indicates the method or workflow was not applied to that isolate due to culture contamination (Nanopore data, n=16), failed assembly (Illumina data, n=3; Nanopore data, n=39), or poor assembly quality (Nanopore data, n=2); this is distinct from “no identity”, which indicates that the method was applied but did not produce a valid taxonomic assignment.

3.2.2 Quality Assessment and Dataset Retention

QC metrics were assessed separately for Illumina and Nanopore sequencing data that progressed to quality assessment, assembly, and initial screening, including genome completeness, contamination, sequencing coverage, and assembly contiguity (N50). QC metric distributions are shown in Figures 19 and 20. Raw QC metrics are shown in Table A4.

Genome completeness exceeded the 90% threshold for most assemblies, with median completeness values of 99.86% for Illumina assemblies and 99.88% for Nanopore assemblies. Contamination remained below the 3% threshold for most assemblies. The modest increase in contamination among Nanopore assemblies likely reflects the greater sensitivity of long-read assemblies to barcode crosstalk and assembly artifacts in multiplexed sequence runs for lower-quality genome datasets. Coverage depth demonstrated minimal variability for both platforms, with nearly all assemblies achieving $\geq 99\%$ coverage. All retained Illumina and Nanopore assemblies exceeded the predefined thresholds. Median N50 values differed between platforms, with Illumina assemblies showing a median N50 of 186,777 bp and Nanopore assemblies a median N50 of 4,679,609 bp (Fig. 19-20; Table 17), consistent with longer contiguous assemblies expected from long-read sequencing and indicating that most retained Nanopore datasets assembled into highly contiguous genomes. N50 was evaluated descriptively without a predefined threshold, and genome size distributions were similarly summarized descriptively.

Three Illumina datasets, (3 of 365 sequenced; (0.82%)) failed genome assembly and were excluded from downstream analyses. For Nanopore sequencing, 55 isolates (15.1%) were excluded from downstream analyses. 16 isolates (29.1% of excluded isolates) were not sequenced because culture contamination prevented library preparation, one isolate (1.8% of excluded isolates) generated insufficient sequencing output for assembly to be attempted,

Distribution of Quality Control Metrics for Successful Genome Assemblies from Illumina Short-read Data

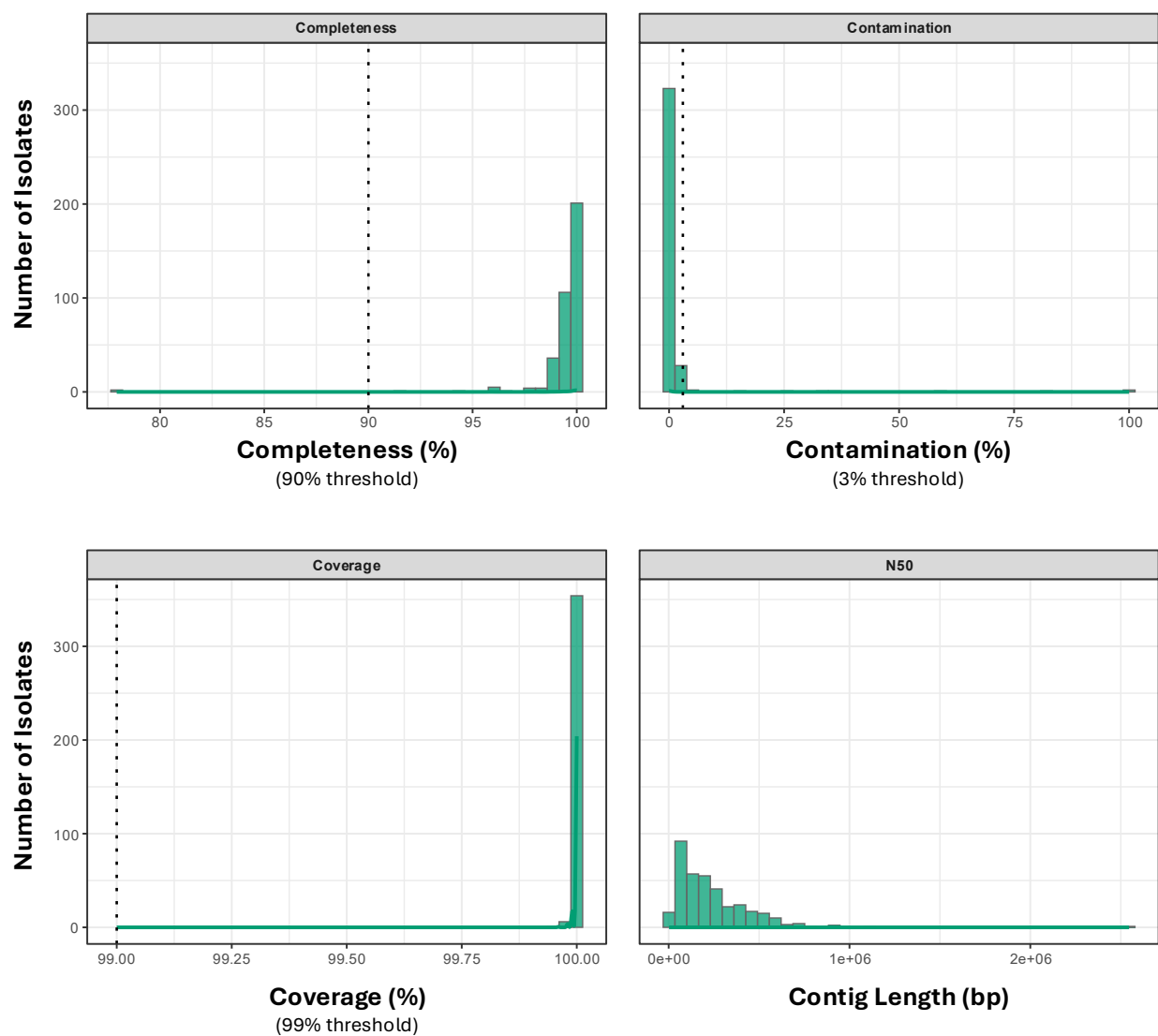


Figure 19. QC metrics for Illumina-based genome assemblies. Distribution of genome assembly completeness (%), contamination (%), genome coverage (%), and N50 (bp). Dotted vertical lines indicate QC thresholds for completeness (90%), contamination (3%), and coverage (99%), shown as percent. N50 values are shown descriptively, as no predefined threshold was applied.

Distribution of Quality Control Metrics for Successful Genome Assemblies from Nanopore Long-read Data

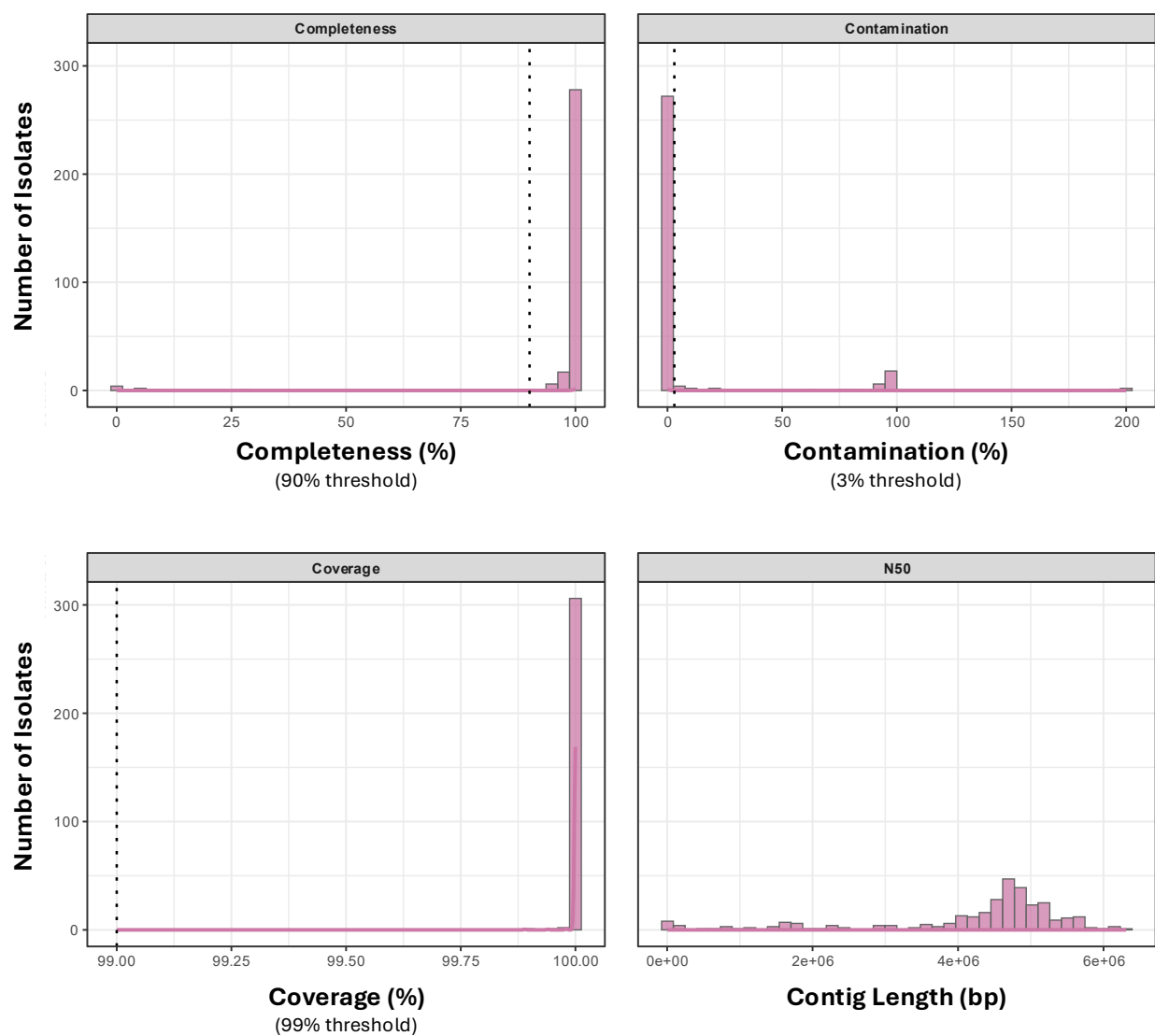


Figure 20. QC metrics for Nanopore-based genome assemblies. Distribution of genome assembly completeness (%), contamination (%), genome coverage (%), and N50 (bp). Dotted vertical lines indicate QC thresholds for completeness (90%), contamination (3%), and coverage (99%), shown as percent. N50 values are shown descriptively, as no predefined threshold was applied.

Table 17. Summary of QC metrics for retained Illumina and Nanopore genome assemblies.

Platform	Metric	Median	IQR	Min	Max	% Meeting Threshold
Illumina (n=362)	Completeness	99.86	0.55	77.92	100	99.4
	Contamination	0.35	0.67	0	100	96.7
	Coverage	100	0	99.96	100	100
	N50	186,775	241,342	2,292	2,546,199	N/A
Nanopore (n=310)	Completeness	99.88	0.61	0	100	97.1
	Contamination	0.41	0.78	0	200	88.1
	Coverage	100	0	99.89	100	100
	N50	4,679,609	894,495.8	5,072	6,312,469	N/A

Note. One Nanopore assembly exhibited exceptionally high contamination (JDID-350; contamination = 200%) and this assembly was reported as “no identity”

and 38 datasets (69.1% of excluded isolates) failed during the assembly step of the Mikrokondo pipeline. Most failed Nanopore assemblies contained substantially fewer sequencing reads than the successful datasets, preventing Flye from generating complete genome assemblies.

Mikrokondo performs genome assembly prior to assembly quality assessment, therefore, these isolate datasets did not proceed to downstream QC analyses and therefore lacked assembly-based QC metrics. Consequently, QC summaries include only retained assemblies which genome reconstruction was successfully completed (Illumina, n=362 (99.2%); ONT, n=310 (84.9%)).

Overall, retained Illumina and Nanopore assemblies consistently met the predefined QC criteria and were considered suitable for downstream taxonomic analysis. Although a subset of Nanopore datasets failed prior to assembly quality assessment, assembly quality among retained genomes was uniformly high, indicating that subsequent differences in taxonomic classification reflected factors beyond assembly quality alone.

3.2.3 Taxonomic Diversity of WGS-based Classifications

Following QC filtering, taxonomic classifications generated across all Illumina- and Nanopore-based workflows for retained isolates (Illumina n=362; Nanopore n=310) were evaluated collectively to characterize the diversity of organisms identified using the WGS-based workflows. Because each retained isolate was classified independently by multiple bioinformatic workflows, this analysis summarizes all valid taxonomic assignments rather than unique isolates.

Across the 362 retained Illumina-based assemblies and 310 retained Nanopore-based assemblies, 3,102 taxonomic classification opportunities were available following dataset retention. Of these, 2,783 (91.3%) resulted in a valid genus- (n=38) or species-level (n=2,745) assignment, whereas 319 (13.5%) were reported as *no identity*, comprising 226 Illumina-derived

and 93 Nanopore-derived *no identity* assignments. Despite these individual workflow failures, every retained isolate received a valid assignment from at least one WGS-based workflow.

The valid assignments represented 164 species across 45 genera. The WGS-based workflows evaluated in this study substantially expanded the taxonomic diversity achieved compared to the original laboratory identifications which identified 85 species across 35 genera and included 36 clinical isolates lacking a genus-level identification (10.9%) and 113 clinical isolates lacking a species-level identification (34.1%) (Fig. 7).

3.2.4 Taxonomic Resolution of WGS-based Classification Workflows

Taxonomic resolution for each workflow-isolate assignment was categorized as species-level, genus-level, or *no identity*. Taxonomic resolution outcomes across workflows are shown in Figure 21. Differences in taxonomic resolution across workflows were significant ($\chi^2 = 172.57$, $df = 16$, $p < 2.2e-16$). Standardized residuals showed positive deviations for species-level outcomes in Illumina ANI-based workflows as well as positive deviations for *no identity* outcomes in Illumina-based TYGS analysis and several ONT-based workflows (Table A7).

When workflows were grouped by sequencing platform, taxonomic resolution outcomes also differed ($\chi^2 = 40.585$, $df = 2$, $p = 1.538e-9$). Illumina-based workflows were associated with higher-than-expected frequencies of species-level resolution, while Nanopore-based workflows contributed more genus-level and *no identity* classifications than expected under independence. However, the magnitude of association was substantially stronger when workflows were considered individually

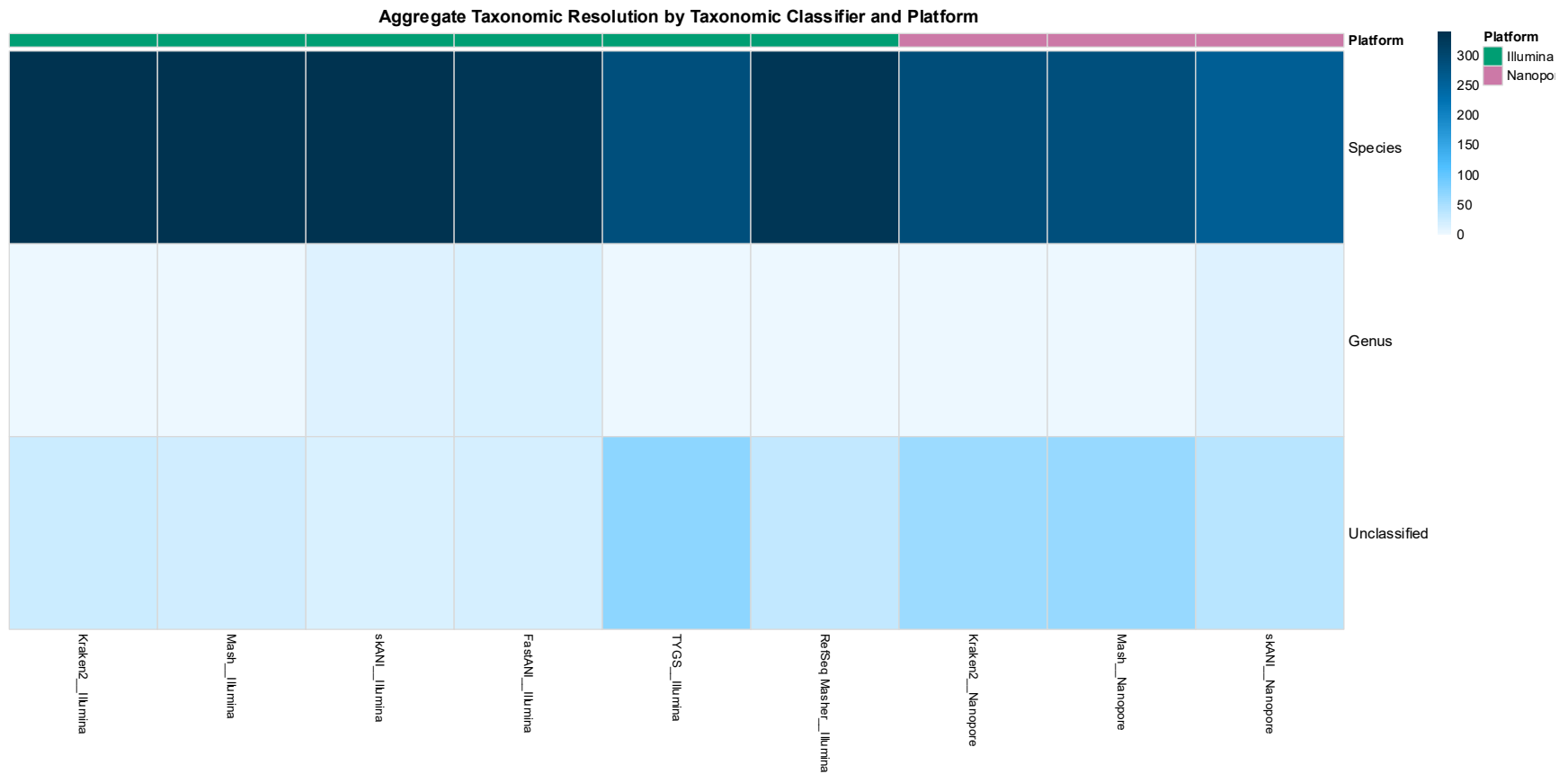


Figure 21. Aggregate taxonomic resolution outcomes across WGS-based classification workflows. Aggregate heatmap summarizing raw counts of taxonomic resolution outcomes for each Illumina- and Nanopore-based workflow across all isolates (n=364). Rows represent taxonomic resolution categories ordered from highest to lowest resolution (species, genus, or *no identity*), and columns represent workflows. Colour intensity reflects the number of assignments.

3.2.5 Concordance Among WGS-based Classifications

Concordance among WGS-based taxonomic classification workflows was evaluated using isolates that received assignments from the workflows under comparison, with isolate-level concordance of assignments visualized in Figure 22. Pairwise Cohen's κ values among Illumina-based workflows ranged from 0.77-0.98. Agreement among ONT-based workflows ranged from 0.64-0.92. Cross-platform comparisons yielded κ values from 0.27-0.40 (Table A8).

Concordance also differed significantly among bioinformatic workflows. The four workflows using GTDB-derived reference databases (Mash, RefSeq Masher, FastANI, and skANI) demonstrated greater agreement with one another than with workflows based on alternative taxonomic frameworks (Kraken2 and TYGS), with standardized residuals exceeding 0.90 for these comparisons (Table A8). This pattern suggests that shared reference database composition and taxonomic framework contributed substantially to classification concordance across otherwise distinct analytical approaches.

To further evaluate the influence of sequencing platform on classification outcomes, pairwise comparisons were performed using Kraken2-, Mash-, and skANI-derived classifications generated from both Illumina and Nanopore assemblies (Fig 23). Concordance between Illumina- and Nanopore-derived classifications was highest for Mash ($\kappa = 0.40$; $n = 261$) and skANI ($\kappa = 0.40$; $n = 253$), whereas Kraken2 showed lower agreement between platforms ($\kappa = 0.31$; $n = 267$), indicating that taxonomic assignments varied according to both sequencing platform and bioinformatic approach.

Within-genus discordance among classified isolates was evaluated for genera represented by ≥ 10 isolates and is visualized with the genus-faceted alluvial plot (Fig. 24). A chi-square test of independence showed significant association between genus and concordance status.

Concordance of Standardized WGS-based Taxonomic Assignments Across Identification Workflows

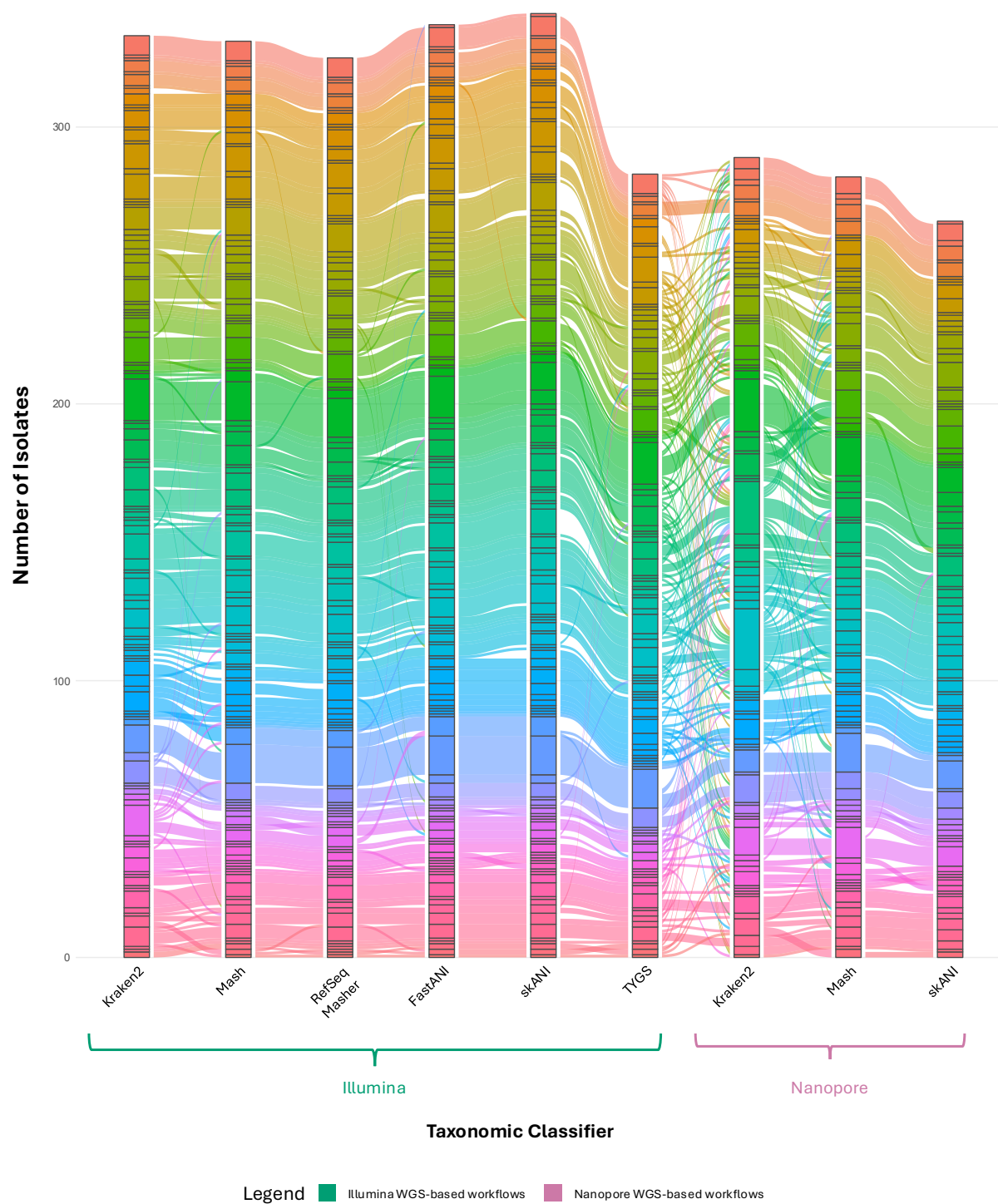


Fig. 22, part 1 of 3

Taxa (Genus or Species)

Acerihabitus sp	Campylobacter jejuni	Cronobacter dublinensis	Erwinia aeris
Aeromonas caviae	Campylobacter lanienae	Cronobacter malonaticus	Erwinia gerundensis
Aeromonas hydrophila	Campylobacter lari	Cronobacter muytjensii	Escherichia coli
Aeromonas media	Campylobacter peloridis	Cronobacter sakazakii	Escherichia fergusonii
Aeromonas rivipollensis	Campylobacter showae	Cutibacterium acnes	Ewingella americana
Aeromonas veronii	Campylobacter sp	Dryocola sp	Hafnia alvei
Aliarcobacter butzleri	Campylobacter sputorum	Enterobacter asburiae	Hafnia paralvei
Atlantibacter hermannii	Campylobacter upsaliensis	Enterobacter cancerogenus	Helicobacter canadensis
Bacillus velezensis	Campylobacter vicugnae	Enterobacter chengduensis	Helicobacter cinaedi
Buttiauxella agrestis	Cedecea neteri	Enterobacter chuandaensis	Helicobacter pullorum
Buttiauxella gaviniae	Chimaeribacter arupi	Enterobacter cloacae	Helicobacter pylori
Buttiauxella sp	Citrobacter amalonaticus	Enterobacter hormaechei	Helicobacter valdiviensis
Campylobacter armoricus	Citrobacter cronae	Enterobacter intestinihominis	Klebsiella aerogenes
Campylobacter coli	Citrobacter farmeri	Enterobacter kobei	Klebsiella huaxiensis
Campylobacter concisus	Citrobacter freundii	Enterobacter ludwigii	Klebsiella michiganensis
Campylobacter curvus	Citrobacter koseri	Enterobacter oligotrophicus	Klebsiella ornithinolytica
Campylobacter fetus	Citrobacter murlinae	Enterobacter roggenkampii	Klebsiella oxytoca
Campylobacter helveticus	Citrobacter portucalensis	Enterobacter rongchengensis	klebsiella planticola
Campylobacter hyointestinalis	Citrobacter sedlakii	Enterobacter soli	Klebsiella planticola
Campylobacter insulaenigrae	Citrobacter werkmanii	Enterobacter sp	Klebsiella pneumoniae
Klebsiella quasipneumoniae	Pantoea anthophila	Providencia xianensis	Serratia sp
Klebsiella spallanzanii	Pantoea eucrina	Providencia xihuensis	Serratia ureilytica
Klebsiella terrigena	Pantoea piersonii	Pseudescherichia vulneris	Shimwellia blattae
Klebsiella variicola	Pantoea rwandensis	Pseudocitrobacter corydarii	Sodalis ligni
Kluyvera ascorbata	Pantoea septica	Pseudocitrobacter faecalis	Staphylococcus pseudintermedius
Kluyvera cryocrescens	Phytobacter diazotrophicus	Pseudoescherichia vulneris	Tatumella ptyseos
Kluyvera georgiana	Phytobacter sp	Salmonella enterica	Tatumella saanichensis
Kosakonia radicincitans	Pluralibacter gergoviae	Salmonella typhi	Yersinia aleksiciae
Kytococcus sedentarius	Proteus columbae	Scandinaviu goeteborgense	Yersinia alsatica
Ledercia adecarboxylata	Proteus mirabilis	Scandinaviu sp	Yersinia enterocolitica
Ledercia pneumoniae	Proteus myxofaciens	Serratia entomophila	Yersinia intermedia
Ledercia sp	Proteus penneri	Serratia grimesii	Yersinia massiliensis
Ledercia tamurae	Proteus sp	Serratia liquefaciens	Yersinia mollaretii
Lelliottia nimipressuralis	Providencia alcalifaciens	Serratia marcescens	Yersinia pestis
Leminorella richardii	Providencia heimbachae	Serratia nematodiphila	Yersinia proxima
Listeria monocytogenes	Providencia huashanensis	Serratia nevei	Yersinia pseudotuberculosis
Mixta calida	Providencia manganoxydans	Serratia plymuthica	Yersinia rochesterensis
Morganella morganii	Providencia rettgeri	Serratia proteamaculans	
Pantoea agglomerans	Providencia stuartii	Serratia quinivorans	
Pantoea ananatis	Providencia vermicola	Serratia sarumanii	

Figure 22. Concordance of standardized taxonomic assignments across WGS-based classification workflows. Alluvial plot illustrating isolate-level concordance of taxonomic assignments across Illumina and ONT WGS-based classification workflows. Each stratum represents a workflow, and each alluvium represents a single isolate tracked across workflows using its standardized taxonomic assignment after normalization of homotypic synonyms and invalid taxon names. Continuous flows indicate concordant classifications whereas branching patterns indicate discordant classifications. White space between strata represents a combination of branching taxonomic assignments across workflows and the omission of invalid or unsuccessful (“*no identity*”) assignments, which were not plotted. Only isolates receiving at least one successful taxonomic assignment were included. A maximum total of 362 of 365 isolates were represented, corresponding to 2,783 successful taxonomic assignments.

Pairwise Comparison of Standardized Taxonomic Assignments for Kraken2, Mash, and skANI for Illumina & Nanopore Assemblies

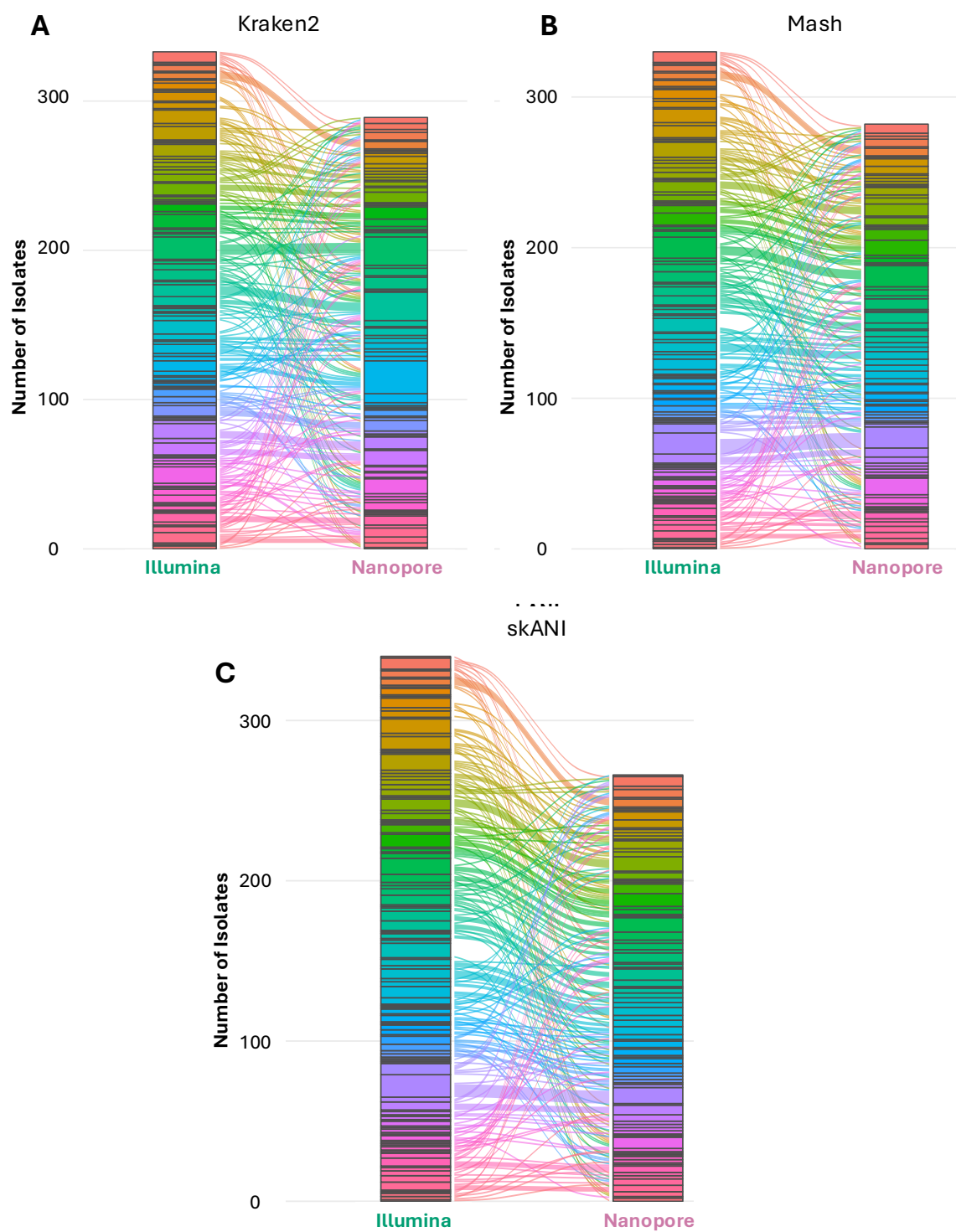


Fig. 23, part 1 of 2

Figure 23. Pairwise comparison of standardized Illumina- and Nanopore-derived taxonomic assignments across selected classification workflows. Three-panel alluvial plots showing isolate-level concordance of the taxonomic assignments generated from Illumina- and Nanopore-derived assemblies using [A] Kraken2, [B] Mash, and [C] skANI. Each alluvium represents a single isolate linking the standardized taxonomic assignment generated from an Illumina-derived assembly to the corresponding taxonomic assignment generated from the Nanopore-derived assembly. Continuous flows indicate concordant classifications whereas branching flows indicate discordant classifications. Assignments recorded as *no identity* were excluded.

Within-genus Concordance of Standardized Taxonomic Assignments Across WGS-based Classification Workflows

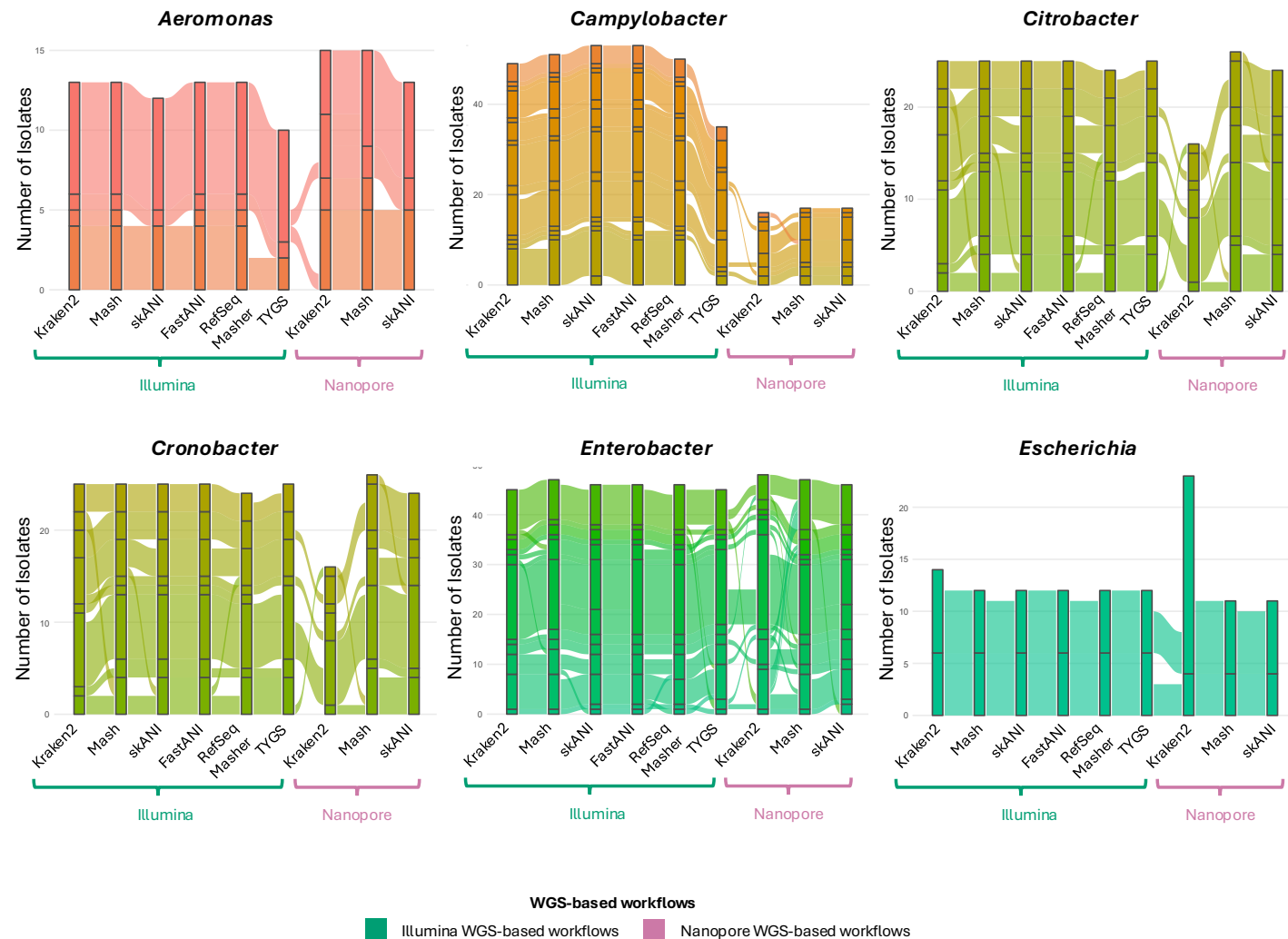
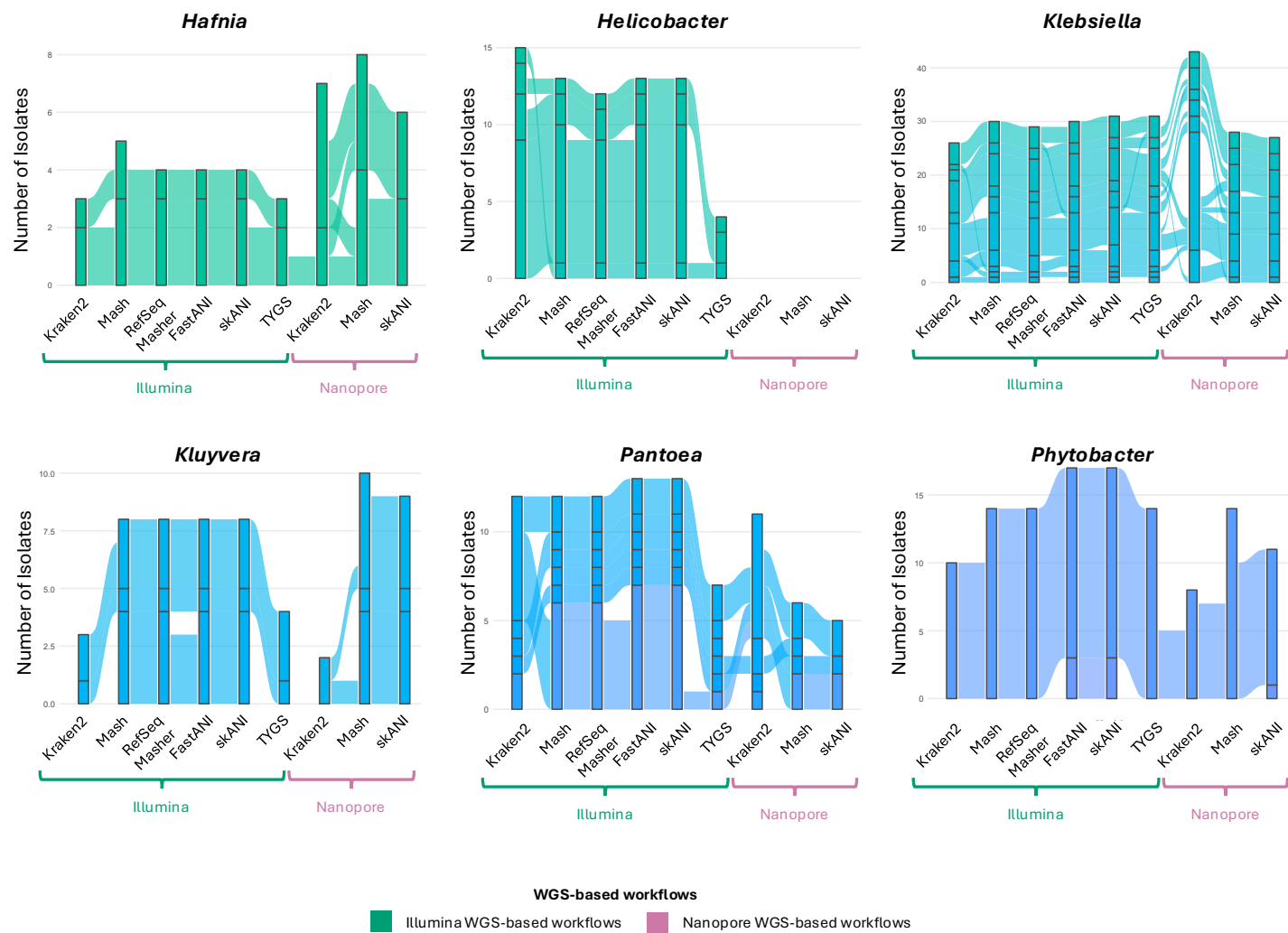


Fig. 24, part 1 of 4



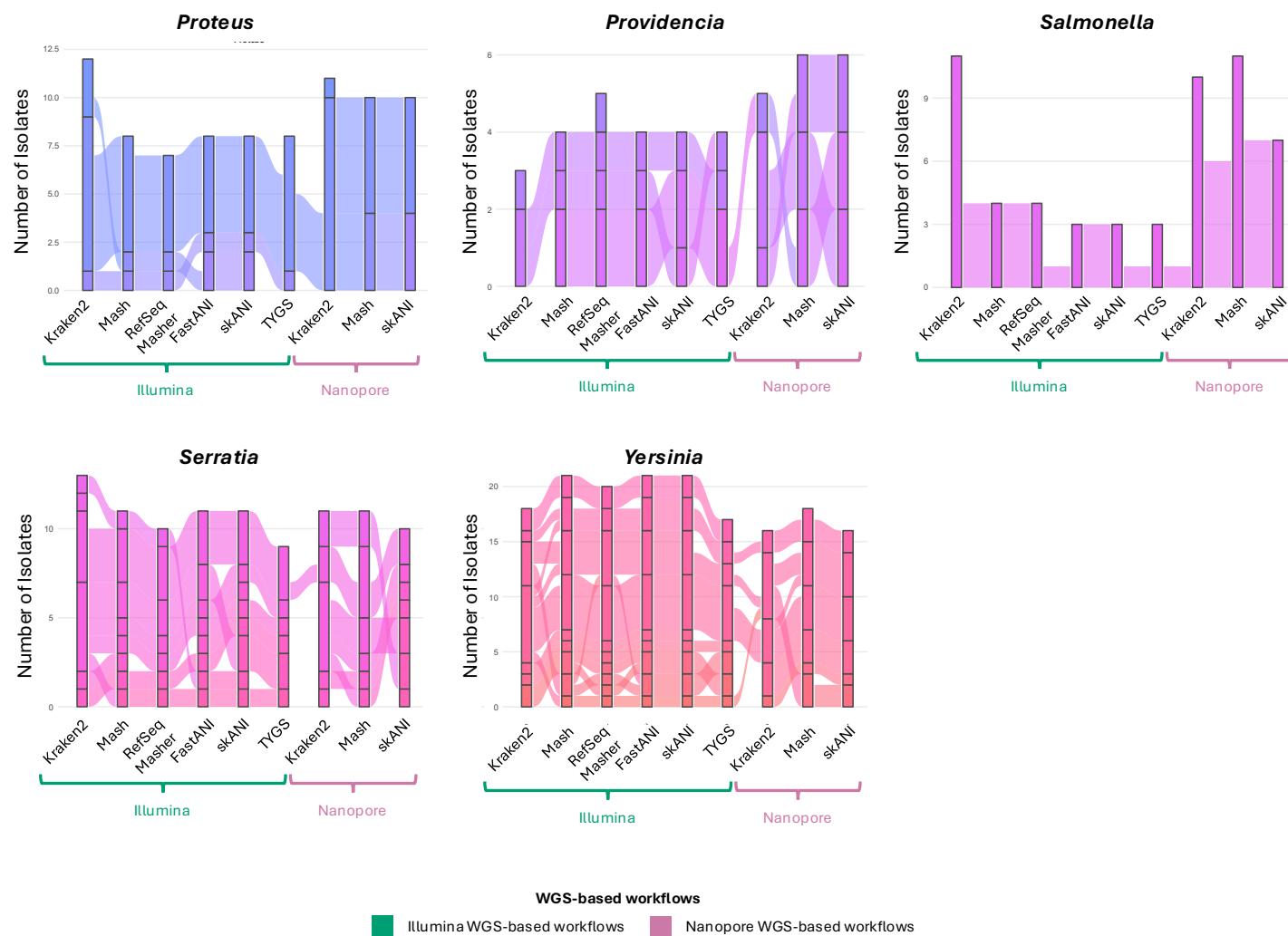


Figure 24. Within-genus concordance of standardized taxonomic assignments across WGS-based classification workflows.

Genus-specific alluvial plots showing standardized isolate-level concordance of taxonomic assignments across Illumina and Nanopore WGS-based classification workflows. Each stratum represents a workflow, and each alluvium represents a single isolate tracked across workflows using its standardized taxonomic assignment after normalization of homotypic synonyms and invalid taxon names. Continuous flows indicate concordant classifications whereas branching patterns indicate discordant classifications. White space between strata represents a combination of branching taxonomic assignments across workflows and the omission of invalid or unsuccessful (“*no identity*”) assignments, which were not plotted. Panels are shown for genera represented by ≥ 10 isolates. Assignments recorded as *no identity* were excluded. Seventeen genera were included (10-79 isolates per genus), representing successful assignments for a maximum total of 362 isolates.

($\chi^2 = 112.75$, $df = 43$, $p = 3.63\text{e-}8$). Examination of standardized residuals revealed that several genera contributed disproportionately to this association. Genera such as *Enterobacter* (standardized residual = -2.84), *Providencia* (-5.00), *Serratia* (-4.54), *Pantoea* (-1.89), *Buttiauxella* (-3.61), and *Yersinia* (-2.33) were overrepresented among discordant classifications, whereas genera including *Escherichia* (+2.65), *Campylobacter* (+2.60), and *Phytobacter* (+2.35) were more frequently classified concordantly across workflows (Table A9). *Providencia* and *Serratia* were among the strongest contributors to discordance, with standardized residuals of +4.94 and +4.46, respectively. Many of the discordant genera comprise closely related species with complex or recently revised taxonomy. In contrast, concordant genera, especially *Escherichia* and *Campylobacter*, are well represented in reference databases compared with many other taxa in the study collection.

Genus-specific pairwise comparisons of Kraken2-, Mash-, and skANI-derived classifications generated from Illumina and Nanopore assemblies were statistically significant and are shown in Figure 25. By comparing classifications generated from different sequencing platforms within the same workflow, these visualizations isolate platform-associated variation while controlling for differences in classification algorithm and reference database composition. The resulting patterns demonstrate that discordance between Illumina- and Nanopore-derived classifications persisted even when the underlying classification workflow remained constant ($\chi^2 = 98.64$, $df = 42$, $p = 1.87\text{e-}6$). As observed in the broader concordance analysis, disagreement was concentrated within a subset of genera rather than being distributed uniformly across taxa.

Within-genus Pairwise Comparison of Standardized Taxonomic Assignments for Kraken2, Mash, and skANI for Illumina & Nanopore Assemblies

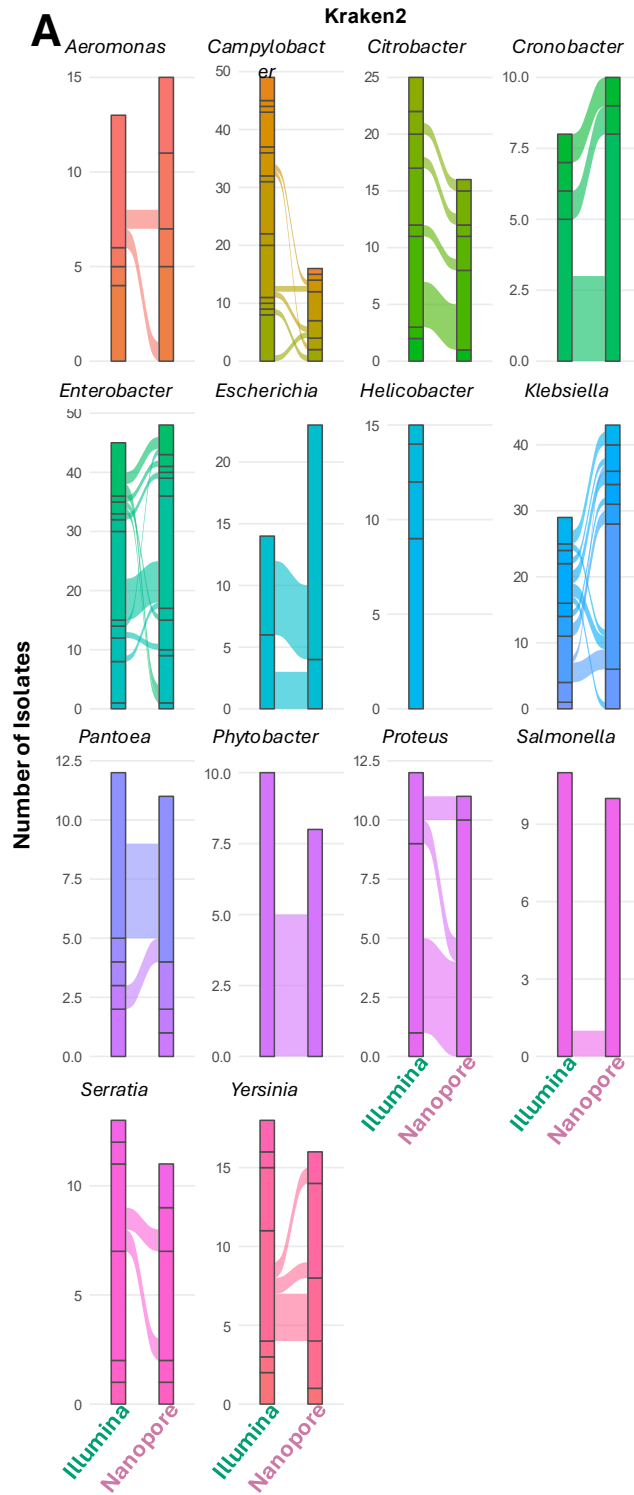
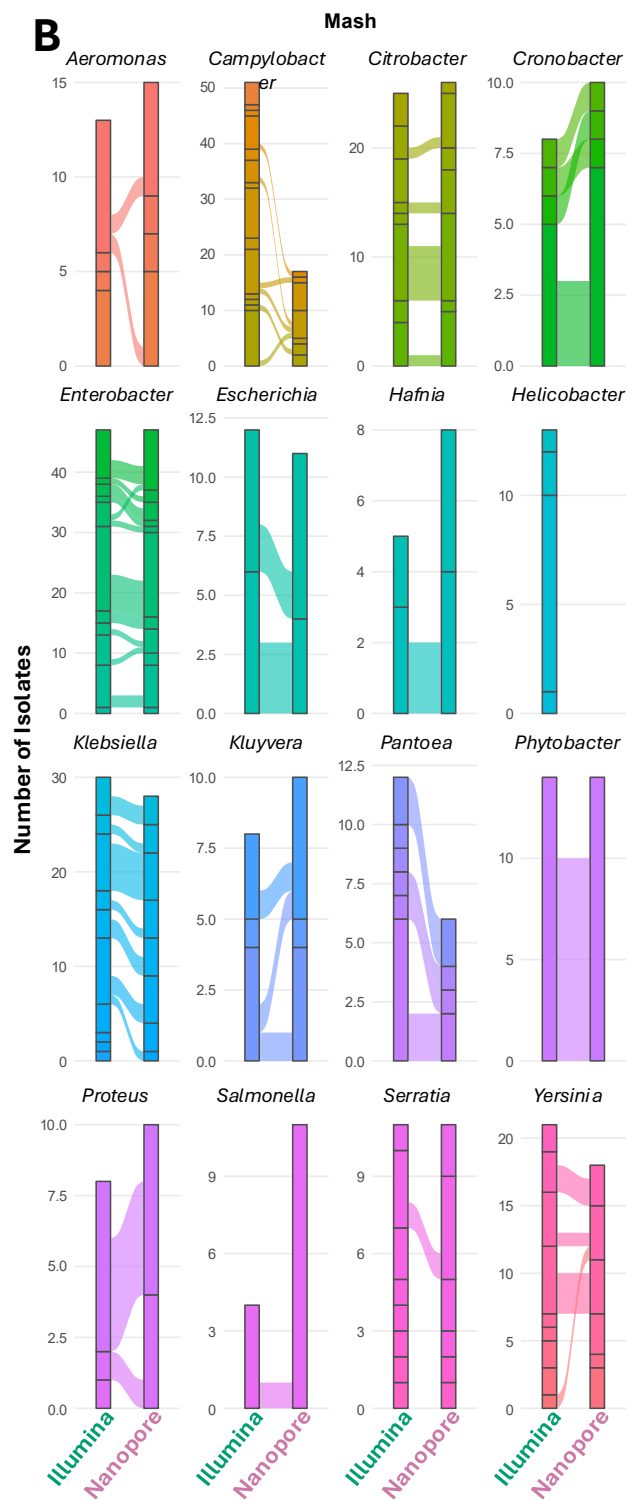


Fig. 25, part 1 of 4



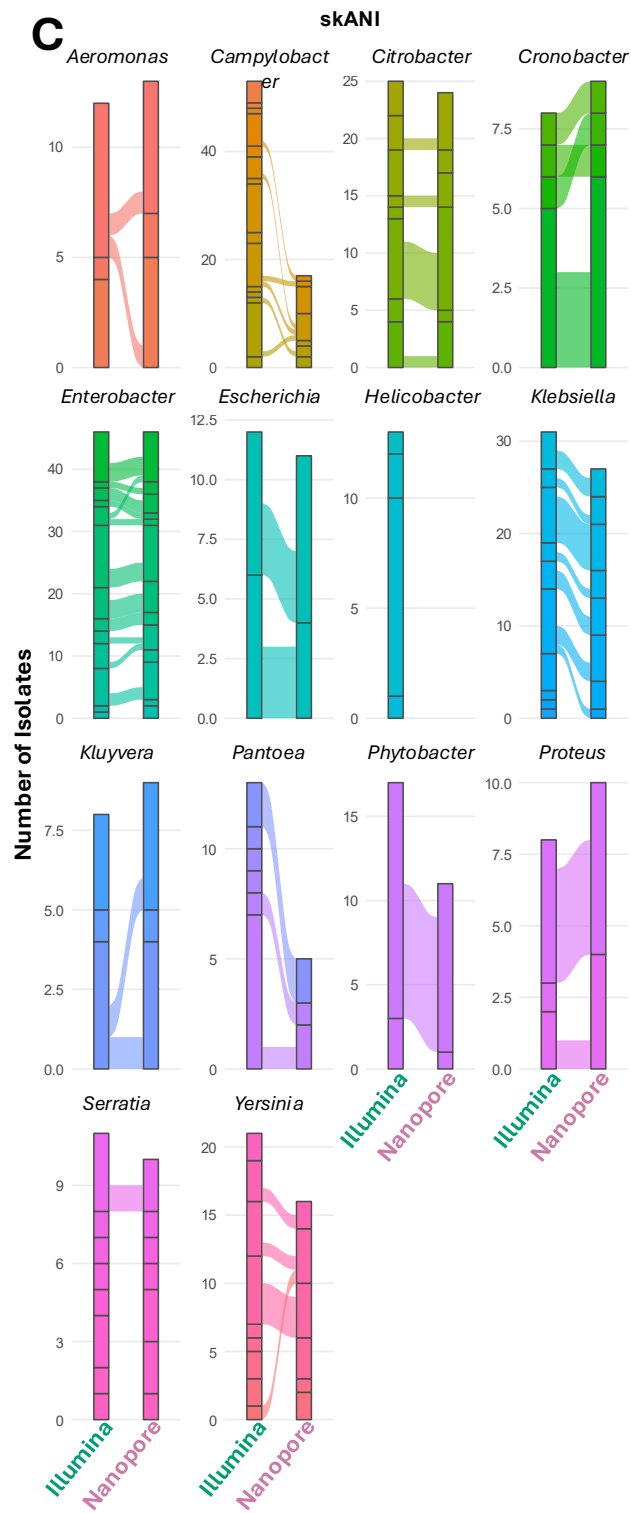


Figure 25. Within-genus pairwise comparison of standardized Illumina- and Nanopore-derived taxonomic assignments across selected classification workflows. Genus-faceted three-panel alluvial plot showing isolate-level concordance of taxonomic assignments using [A] Kraken2, [B] Mash, and [C] skANI. Each alluvium represents a single isolate linking the standardized taxonomic assignment generated from an Illumina-derived assembly to the corresponding taxonomic assignment generated from the Nanopore-derived assembly. Continuous flows indicate the concordant classifications whereas branching flows indicate discordant classifications. Panels are shown for genera represented by ≥ 10 isolates. Assignments recorded as *no identity* were excluded.

3.2.6 Unclassified WGS-based Assignments and Failure Profiles

Of the 2,172 attempted Illumina-based taxonomic classifications, 239 (11.0%) returned no valid assignment and were designated “*no identity*”. Of the 930 attempted Nanopore-based classifications, 179 (19.2%) returned no valid assignment and were designated “*no identity*”. *No identity* classifications were categorized as resulting from reference database limitations, assembly-related limitations, algorithmic or confidence-threshold filtering, and invalid taxonomy (definitions outlined in Appendix F). Distributions of classification failures by platform and workflow are summarized in Tables 18-19 and visually represented in Fig. 26. Failure categories differed significantly across workflows ($\chi^2 = 538.32$, $df = 24$, $p < 2.2e-16$). Examination of standardized residuals revealed distinct workflow-specific failure profiles. Reference database limitations were strongly overrepresented in the RefSeq Masher classifications (Illumina assemblies) whereas algorithmic or confidence-threshold filtering predominated in TYGS-based classifications (Illumina assemblies). Assembly-related limitations were disproportionately associated with Nanopore-based workflows, reflecting the greater frequency of incomplete or unsuccessful genome assemblies among retained ONT datasets (Table 18-19, A10).

When aggregated by sequencing platform, failure categories also differed significantly ($\chi^2 = 111.71$, $df = 3$, $p < 2.2e-16$). Nanopore-based workflows showed an overrepresentation of assembly-related limitations and algorithmic filtering (errors inherent to the sequence reads and assembly), whereas Illumina-based workflows failed more frequently due to reference database limitations and invalid taxonomy (errors beyond assembly quality) (Table 19, A11). Among successful assemblies (Illumina, $n=362$, Nanopore, $n=310$), the overall proportion of classified versus unclassified isolates did not differ significantly between platforms (Fisher’s exact test, odds ratio = 1.62, $p = 7.082e-6$, 95% CI = 1.31-2.00).

Table 18. Platform-specific distribution of classification failure categories among unclassified isolates.

Platform	Reference Database Limitations (n)	Assembly-related Limitations (n)	Algorithmic or Confidence-threshold Filtering (n)	Invalid Taxonomy (n)
Illumina (n=239)	71 (29.7%)	19 (7.9%)	26 (10.9%)	123 (51.4%)
Nanopore (n=179)	8 (4.5%)	83 (46.4%)	37 (20.7%)	51 (28.4%)

Note. Counts (n) represent the number of “no identity” classifications attributed to each failure category. Percentages are calculated within each sequencing platform using the total number of unclassified workflow assignments.

Table 19. Failure category distribution among unclassified isolates by platform and workflow.

<i>Platform</i>	<i>Workflow</i>	<i>Failure Category</i>	<i>n</i>	<i>Proportion</i>
<i>Illumina</i> (<i>n</i> =239)	Mikrokondo – Kraken2	invalid taxonomy	29	1
		assembly-related limitations		
	Mikrokondo - Mash	reference database limitations	2	0.06
		invalid taxonomy	24	0.77
		assembly-related limitations	5	0.16
	RefSeq	invalid taxonomy	15	0.39
	Masher	algorithmic or confidence-threshold filtering	23	0.61
	TYGS	reference database limitations	68	0.77
		invalid taxonomy	6	0.07
		assembly-related limitations	14	0.16
<i>Nanopore</i> (<i>n</i> =179)	Mikrokondo – Kraken2	reference database limitations	1	0.04
		invalid taxonomy	23	0.92
	GTDB-Tk - FastANI	algorithmic or confidence-threshold filtering	1	0.04
		invalid taxonomy	26	0.93
		algorithmic or confidence-threshold filtering	2	0.07
	Mikrokondo – Kraken2	invalid taxonomy	21	0.36
		assembly-related limitations	38	0.64
	Mikrokondo - Mash	invalid taxonomy	14	0.23
		assembly-related limitations	45	0.73
		algorithmic or confidence-threshold filtering	3	0.05
<i>Nanopore</i> (<i>n</i> =179)	GTDB-Tk - skANI	reference database limitations	8	0.14
		invalid taxonomy	16	0.28
		algorithmic or confidence-threshold filtering	34	0.59

Counts (n) and within-workflow proportions are shown for each failure category.

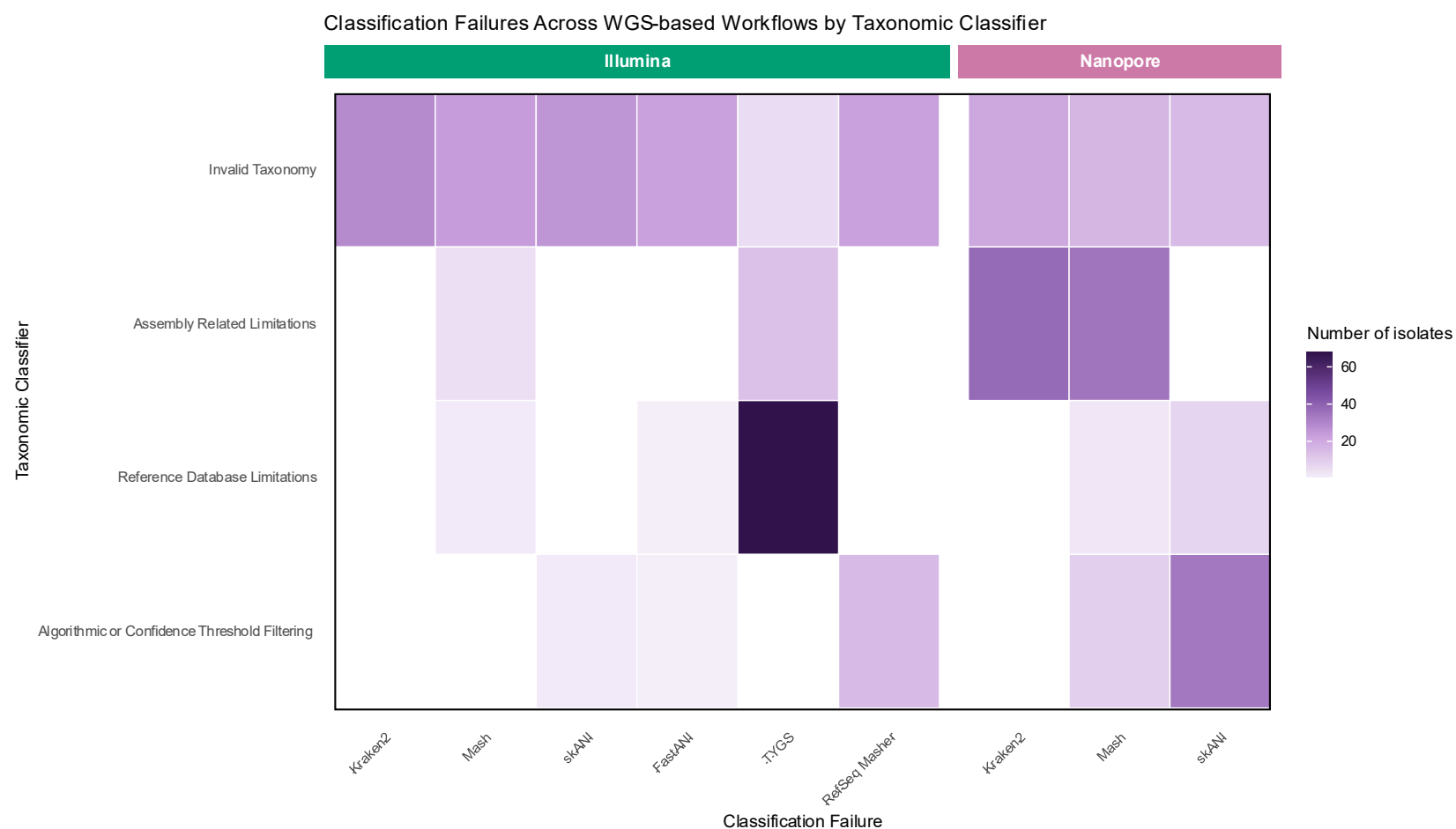


Figure 26. Classification outcomes and failure modes across WGS-based workflows. Stacked tile plot summarizing classification limitations across Illumina- (I:) and Nanopore-based (N:)workflows. Isolates are categorized as unclassified (n=319) due to reference database limitations, assembly-related limitations, algorithmic or confidence-threshold filtering, and invalid taxonomy. Colour intensity reflects the number of isolates per category.

Assembly and QC metrics were compared between classified and unclassified isolates with retained assemblies (Illumina, n=362; Nanopore, n=310) (Table A12). Among the evaluated metrics, including genome size, completeness, contamination, sequencing coverage, and N50, no statistically significant differences were observed between groups (all Wilcoxon rank-sum tests, $p > 0.3$). These findings indicate that once assemblies met predefined quality thresholds, differences in assembly quality alone did not explain classification success or failure. Instead, classification outcomes were more strongly influenced by reference database (coverage) limitations, invalid taxonomy and taxonomic instability, assembly-related limitations (poor assembly), and workflow-specific algorithmic or confidence-threshold filtering.

3.2.7 Accuracy of WGS-based Taxonomic Classifications

The accuracy of WGS-based classification workflows was assessed using 34 type strains with known species identities. Illumina-based approaches showed classification accuracy ranging from 85.3-97.1%. Nanopore-based workflows showed classification accuracy of 67.6% (Table 20; Fig. 27A). The highest-performing workflow, Illumina-based Mash, correctly identified 33 of 34 isolates (accuracy = 97.1%, 95% CI: 85.1-99.5%). Other Illumina-based workflows, including FastANI and skANI, TYGS, and RefSeq Masher, showed similarly strong performance, with classification accuracies ranging from 91.2%-94.1% (Table 20). In contrast, Nanopore-based workflows exhibited lower and more variable classification accuracy. All Nanopore-based workflows correctly identified approximately two thirds of type strains (accuracy = 67.6%; 95% CI:50.8-80.9%) (Table 20; Fig. 27A). Nanopore-based workflows also demonstrated wider confidence intervals than Illumina workflows, reflecting both lower observed accuracy and greater uncertainty in the smaller number of correct classifications.

Table 20. Species-level accuracy and 95% confidence intervals for WGS-based workflows using deposited type strain identities as the reference standard.

Sequencing Platform	Workflow	Number Correctly Identified (n_t = 34)	Accuracy (%)	95% CI (%)
Illumina	MikroKondo – Kraken2	29	85.3	69.9-93.6
	MikroKondo – Mash	33	97.1	85.1-99.5
	TYGS	32	94.1	80.9-98.4
	GTDB-Tk (FastANI)	32	94.1	80.9-98.4
	GTDB-Tk (skANI)	32	94.1	80.9-98.4
	RefSeq Masher	31	91.2	77.0-97.0
Nanopore	MikroKondo – Kraken2	23	67.6	50.8-80.9
	MikroKondo – Mash	23	67.6	50.8-80.9
	GTDB-Tk (skANI)	23	67.6	50.8-80.9

Note. All Nanopore-based workflows correctly identified the same 23 type strains.

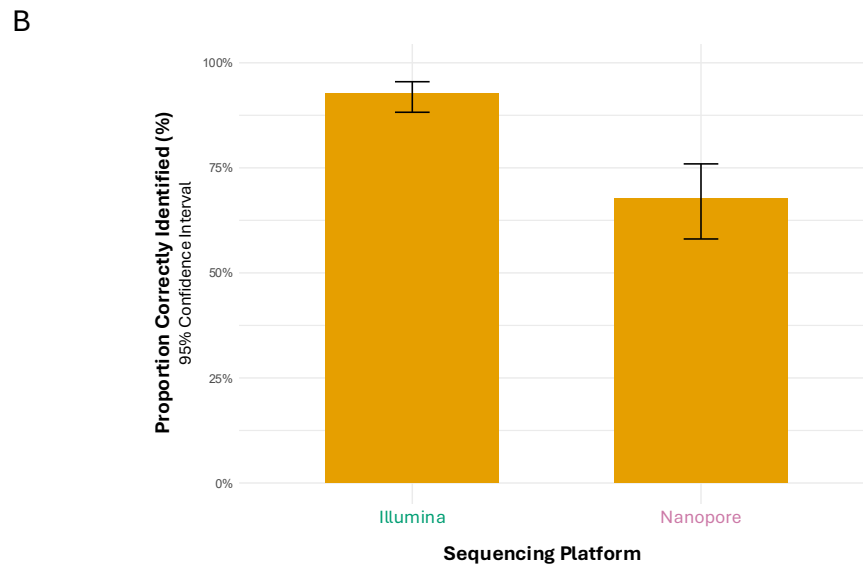
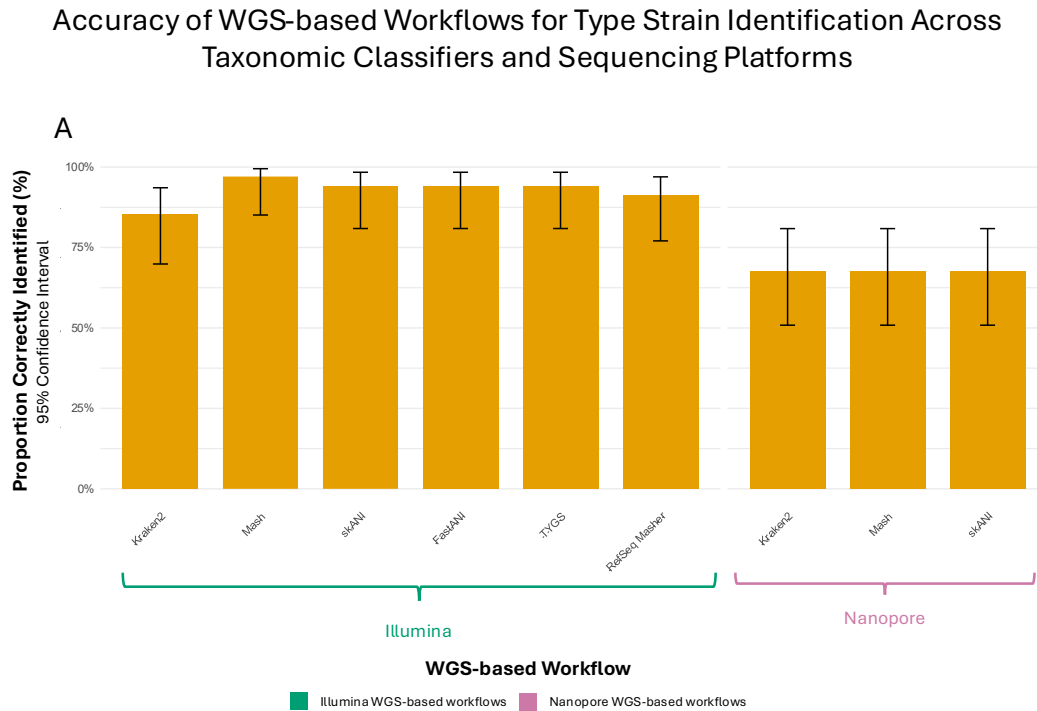


Figure 27. Accuracy of WGS-based workflows using type strains. [A] Accuracy of individual WGS-based classification workflows assessed using 34 type strains. Bars represent the proportion of correct species assignments, with error bars indicating 95% Wilson confidence intervals. **[B]** Pooled accuracy of WGS-based workflows grouped by sequencing platform (Illumina vs. Nanopore).

Pairwise McNemar tests comparing individual WGS-based workflows did not yield statistically significant results, largely due to the limited number of discordant classifications among high-performing Illumina-based workflows and the small sample size of type strains. When pooled by sequencing platform, Illumina-based workflows collectively identified 189 of 204 workflow-isolate combinations (accuracy = 92.6%; 95% CI: 88.2-95.5%), whereas Nanopore-based workflows correctly identified 69 of 102 combinations (accuracy = 67.6%; 95% CI: 58.1-75.9%) (Table 20; Fig. 27B). Pooled taxonomic classification accuracy reflects workflow-isolate combinations rather than unique isolates.

3.3 Notable Classification Patterns

Beyond overall concordance trends, specific classification outcomes with operational or taxonomic implications were identified.

3.3.1 Discordant Species-level Assignments Involving *Yersinia*

Three clinical isolates, originally processed as *Y. pseudotuberculosis* were assigned *Y. pestis* by one or more WGS-based workflows (Table 21). These assignments occurred inconsistently across bioinformatic tools and platforms. For two isolates (JDID-02 and JDID-41), several species assignments to *Y. pestis* were produced by Mash, FastANI, and skANI which share GTDB-derived reference databases, although they differ in database implementation and classification algorithms. Nanopore-based workflows for these isolates produced assignments outside of the *Yersinia* genus, including *Proteus mirabilis* and *Serratia liquefaciens*. For the third isolate (JDID-61), the pattern was reversed: Illumina-based workflows consistently identified *S. liquefaciens*, whereas Nanopore-based workflows included both *Y. pestis* and *Y.*

Table 21. Discordant WGS-based species assignments involving *Y. pestis* and *Y. pseudotuberculosis*.

Isolate	Platform	Workflow	Taxonomic Assignment
JDID-02	Illumina	Mikrokondu Kraken2	<i>Y. pseudotuberculosis</i>
		Mikrokondu Mash	<i>Y. pestis</i>
		gtdb-tk (FastANI)	<i>Y. pestis</i>
		gtdb-tk (skANI)	<i>Y. pestis</i>
		refseq__masher	<i>Y. pseudotuberculosis</i>
		TYGS	<i>Y. pseudotuberculosis</i>
JDID-41	Illumina	Mikrokondu Mash	<i>Y. pestis</i>
		gtdb-tk (FastANI)	<i>Y. pestis</i>
		gtdb-tk (skANI)	<i>Y. pestis</i>
		TYGS	<i>Y. pseudotuberculosis</i>
JDID-61	Nanopore	Mikrokondu Kraken2	<i>Y. pseudotuberculosis</i>
		Mikrokondu Mash	<i>Y. pestis</i>
		gtdb-tk (skANI)	<i>Y. pestis</i>

pseudotuberculosis assignments. Assembly quality metrics for these isolates showed no evidence of poor sequencing quality or elevated contamination that would account for the discordant species assignments. Independent laboratory safety testing performed outside the scope of this study confirmed that these isolates were not *Y. pestis*.

3.3.2 Naming Discordance Associated with Homotypic Synonyms

Species names from all workflows were compared against curated homotypic synonym sets (Appendix E, Table A13) and validated by LPSN (accessed 25 January 2026). Overall, 21.9% of isolates in the dataset were associated with at least one homotypic synonym set. This proportion reflects ongoing taxonomic revision rather than biological disagreement between methods. Prior to downstream taxonomic classification, all assignments were standardized to a single accepted name using the curated synonym set (Table A13). Therefore, nomenclature alone did not contribute to the concordance analyses or alluvial visualizations presented in this thesis.

The most frequently represented synonym-associated taxa were Enterobacterales, particularly genera that have undergone recent restructuring. Examples include *Raoultella* and *Klebsiella* species, *Leclercia adecarboxylata*, and *Lelliottia nimipressuralis*. Reassignments at the genus level were also evident outside Enterobacterales, such as *Cutibacterium acnes* (formerly *Propionibacterium acnes*) and *Alioarcobacter butzleri* (formerly *Arcobacter butzleri*), among others.

3.3.3 Family-level Assignments Reflecting Legacy Enterobacterales Taxonomy

Assignments from Mash workflows (Illumina- and Nanopore-based) included family-level outputs corresponding to pre-2016 Enterobacterales taxonomy. A substantial total of 81

Illumina- and 75 Nanopore-based assignments belonged to genera that are currently classified outside Enterobacteriaceae under revised taxonomy (Table 22). Assignments affected family-level classification only; genus and species names were not affected. These data illustrate the realistic effects of ongoing taxonomic instability withing Enterobacterales when workflows rely on differing reference database versions and taxonomic frameworks.

3.3.4 Discordance of 16S and Phenotypic Assignments for *Campylobacter*

Among 54 isolates assigned to *Campylobacter* by 16S rRNA sequencing, Biolog Gen III did not return a *Campylobacter* assignment in 49 cases (90.7%). The distribution of *Campylobacter* versus non-*Campylobacter* outcomes differed significantly between 16S rRNA sequencing and Biolog phenotypic profiling (Fisher's exact test, $p < 0.001$). Standardized residuals demonstrated that *Campylobacter* contributed disproportionately to the discordance observed between the two methods (standardized residual = -5.12; Table A6). Therefore, under the conditions evaluated, these data highlight a substantial limitation of the Biolog Gen III system for the identification of *Campylobacter*.

Table 22. Legacy Enterobacterales family-level taxonomy in Mikrokondo Mash workflows.

Platform	Mash Output (Family Name)	Updated Family Name (post-2016)	Number of Isolates
Illumina (n=362)	Enterobacteriaceae	Budviciaceae	1
		Hafniaceae	5
		Erwiniaceae	26
		Morganellaceae	14
		Yersiniaceae	35
Nanopore (n=310)	Enterobacteriaceae	Budviciaceae	1
		Hafniaceae	8
		Erwiniaceae	17
		Morganellaceae	18
		Yersiniaceae	31

Chapter 4: Discussion

4.1 WGS Improves Taxonomic Resolution for Rare Enteric Pathogens

This study demonstrates that WGS-based approaches provide substantially improved taxonomic resolution and species-level accuracy for rare and low-prevalence enteric bacteria, compared to the two traditional identification methods evaluated in this study: 16S rRNA gene sequencing and Biolog Gen III phenotypic profiling. Across a large dataset of 331 enteric bacterial isolates collected from cases of illness across Canada between 1995 and 2023 and 34 type strains (Fig. 7), genome-based workflows consistently achieved higher rates of species-level classification, higher concordance, and higher classification accuracy with reference strain identities than either 16S rRNA gene sequencing, phenotypic profiling, or traditional consensus assignments. Species-level resolution exceeded 90% for all Illumina-based workflows with classification accuracy from Illumina-based workflows surpassing 91% (except for Kraken2; 85.3% classification accuracy) compared to substantially lower taxonomic resolution and accuracy for consensus assignments from 16S rRNA gene sequencing and phenotypic profiling under conservative reporting thresholds (48.8% and 79.4%, respectively). These differences were statistically significant and indicate that the advantages of WGS arise from genome-scale data rather than incremental improvements in workflow design or individual biomarker.

These findings support the study hypothesis that modernization of bacterial identification with WGS-based approaches has the potential to enhance confirmatory identification and diagnostic accuracy for rare and low-prevalence enteric pathogens compared to the two traditional *gold-standard* methods evaluated in this study. The results directly address the study objectives by demonstrating improved performance of genome-based tools, quantifying limitations of traditional and WGS-based approaches, and informing implementation strategies for clinical and public health laboratories.

The limited performance of 16S rRNA gene sequencing at the species level highlights a well-recognized constraint of single-locus identification. Conservative sequence identity and coverage thresholds frequently resulted in genus-level assignments without species-level resolution, with only 14.6% of isolates receiving confident species-level identifications (Fig. 14, Fig. A1, Table A4). Type strain analysis likewise demonstrated low species-level accuracy of only 20.6% classification accuracy under these reporting criteria (Fig. 18). This outcome does not reflect methodological error, but rather the intrinsic conservation of the 16S rRNA gene among closely related taxa, which reduces discriminatory power in groups with recent divergence or complex taxonomy (67–74). In contrast, genome-wide comparisons incorporate thousands of loci, enabling resolution of subtle but diagnostically relevant differences that are not detectable within the 16S locus alone.

Phenotypic profiling demonstrated different but equally important limitations. Only 69.7% of isolates achieved a species-level identification, and 26.3% failed to receive any confident identification. *Campylobacter* isolates represented the clearest example of this limitation, with Biolog Gen III failing to identify *Campylobacter* in 49 of 54 isolates (90.7%) despite extended incubation and appropriate growth media, as defined by Biolog. These data likely reflect both the restricted representation of rare taxa in the commercial Biolog Gen III reference database, which cannot be locally curated or updated by end users, and the biological plasticity of metabolic traits, which can vary with growth conditions, gene regulation, or horizontal gene transfer (75). As a result, phenotype-based systems may be inherently disadvantaged when applied to uncommon organisms whose biochemical profiles overlap with those of more prevalent taxa.

Importantly, the enhanced performance of WGS-based identification compared to the two traditional methods was supported by both taxonomic resolution metrics (Fig. 21, Table A7) and independent type-strain accuracy assessment (Fig. 27) where five of six Illumina-based workflows achieved $\geq 91\%$ species-level classification accuracy (91.2-97.1%), compared with significantly lower performance for the Nanopore workflows (67.6% classification accuracy) and the traditional methods (20.6-79.4% classification accuracy). The only Illumina-based workflow below this threshold was Kraken2 (85.3% classification accuracy), although this still exceeded the performance of traditional approaches. The consistency of these findings across k-mer-based (Kraken2, Mash, and RefSeq Masher), ANI-based (FastANI and skANI), and genome-distance and phylogenetic classification (TYGS) workflows indicates that the observed improvement is not attributable to a single algorithm or similarity measurement, but rather the greater discriminatory information contained within whole genomes. This is consistent with previous work supporting WGS for bacterial identification and surveillance, including its adoption in routine workflows by the CDC (164, 166–168) and the European Centre for Disease Prevention and Control (154, 158), and extend this work to the particularly challenging context of rare and low-prevalence enteric taxa (196, 198, 203).

4.2 Structural Limitations of Traditional Identification Methods

The reduced performance of both traditional identification methods was consistent with the inherent methodological limitations (67–74) of each approach rather than isolated failures within this dataset. Although 16S rRNA gene sequencing and phenotypic profiling failed for different reasons, both demonstrated systemic reductions in species-level resolution and classification accuracy compared with WGS-based workflows.

Single-locus identification imposes an inherent ceiling on species-level resolution because closely related organisms frequently share highly conserved 16S rRNA gene sequences (74). This limitation was reflected in the high proportion of genus- and family-level assignments (43.1% and 33.7%, respectively) produced under our identity thresholds and the comparatively low type strain classification accuracy observed for 16S-based identification (20.6%). These findings are consistent with previous studies demonstrating that 16S rRNA sequencing is often insufficient for distinguishing recently diverged or taxonomically complex bacterial species (67–74).

Phenotypic profiling exhibited different limitations. Biolog Gen III showed reduced identification success for uncommon organisms and particularly poor performance for *Campylobacter*, where 90.7% of *Campylobacter* isolates identified by 16S rRNA gene sequencing failed to receive a *Campylobacter* identification despite the inclusion of *Campylobacter* species within the commercial reference database. This suggests the limitations extend beyond database representation alone and likely reflect the dependence of phenotype-based identification on reproducible metabolic expression under standardized laboratory conditions. Previous studies have similarly shown that biochemical identification systems become less reliable when applied to uncommon organisms or taxa with variable phenotypic characteristics (75).

These data indicate that the limitations of traditional approaches arise from fundamental methodological constraints rather than analytical implementation. In contrast, WGS-based workflows evaluate genome-wide sequence information, allowing discrimination among closely related organisms even when more conserved genetic markers or phenotypic traits provide insufficient resolution. The improved performance of WGS-based methods observed throughout

this study reflects a shift from inherently limited identification targets toward comprehensive genome-scale comparison rather than simply the adoption of newer technology (67–75).

4.3 Effects of Sequencing Platform on Taxonomic Classification

Although both Illumina and Nanopore sequencing generated high-quality genome assemblies for the majority of retained isolates (Fig. 19-20, Table 17, Table A7), sequencing platform had a measurable influence on downstream taxonomic classification performance. Illumina-based workflows consistently achieved higher species-level resolution (Fig. 21, Table A7), stronger concordance among workflows (Fig. 22-25, Table A8), and significantly higher type-strain classification accuracy (Fig 27, Table 10) than Nanopore-based workflows. These data indicate that sequencing platform influenced taxonomic classification outcomes, particularly at the species-level, but its effect was secondary to reference database composition, taxonomic framework, and workflow design (Fig. 26, Table 18-19, Table A10).

Species-level classification accuracy differed significantly between platforms. When evaluated using 34 type strains with known identities, Illumina-based workflows correctly identified 85.3-97.1% the type strains, whereas all evaluated Nanopore-based workflows correctly identified 67.6% of the type strains (Fig. 27, Table 20). Likewise, Illumina-based workflows demonstrated stronger concordance with one another than comparisons involving Nanopore-derived classifications (Fig. 22, Fig. 24, Table A8). This indicates that the observed platform effect primarily influenced species-level precision and consistency rather than the ability to generate a species assignment at all.

Retained assemblies from both sequencing platforms demonstrated similarly high completeness, contamination, and sequencing coverage, and platform-consistent contiguity

following quality filtering. Once assemblies passed predefined QC thresholds, assembly quality metrics did not differ significantly between successfully classified and unclassified isolates (Table A12). This suggests that assembly quality alone did not explain differences in taxonomic classification performance. Instead, once minimum assembly quality standards had been achieved, reference database completeness, taxonomic instability, workflow-specific analytical approaches, and residual sequencing error became the dominant determinants of classification success (Fig. 26, Table 18-19, Table A10).

The lower species-level performance observed among Nanopore-based workflows is therefore unlikely to reflect poor-quality retained assemblies alone. Rather, it most likely reflects the combined influence of higher per-base sequencing error, variable assembly quality among difficult-to-characterize isolates, and the sensitivity of k-mer- and ANI-based similarity methods to residual sequence error (175, 240–243). Although Nanopore assemblies generally exhibited superior contiguity metrics (measured by N50) than Illumina assemblies, assembly-related limitations accounted for 46.4% of all Nanopore-based *no identity* classifications compared with only 7.9% among Illumina-based workflows (Table 19), which was also confirmed with standardized residuals (Table A10-A11). This emphasizes that assembly contiguity should not be interpreted as a surrogate for taxonomic classification reliability. Highly contiguous assemblies may still contain residual sequencing errors, misassemblies, or contamination that influences downstream similarity calculations despite satisfying conventional QC metrics.

Failure mode analysis further supports this interpretation. Although the overall proportions of classified versus unclassified (*no identity*) retained assemblies differed only modestly between platforms (11.0% unclassified for Illumina and 19.2% unclassified for Nanopore), the underlying causes of classification failure differed significantly. Illumina-based

workflows were most likely to fail because of reference database limitations (29.7% of failures) or invalid taxonomy (51.4% of failures), whereas Nanopore-based workflows were disproportionately affected by assembly-related limitations (46.4%) and algorithmic or confidence threshold filtering (20.7%) (Fig. 20, Table 18). These data show that Illumina-derived genomes more often reached the analytical limits imposed by current reference databases and taxonomic frameworks, whereas Nanopore-derived genomes more frequently encountered limitations associated with sequence quality and downstream similarity calculations.

Recent improvements in ONT sequencing have primarily increased raw read accuracy rather than fundamentally altering the analytical framework of long-read sequencing for bacterial identification (175, 240–243). These advances, while substantial, are not uniform across taxa or sequencing contexts. Error profiles remain influenced by sequence composition, including GC content, homopolymer regions, and methylation sites, and vary across taxonomic groups (179, 189, 244–246). As a result, improvements in accuracy do not translate equally across all organisms or workflows, and classification performance remains dependent on both taxon-specific sequence characteristics and downstream analytical methods. Variability was observed in this dataset, and these factors may contribute to the platform-associated differences observed in this study, particularly for similarity-based classification approaches that are sensitive to residual errors.

Therefore, these findings support the use of Illumina short-read WGS as the preferred platform for routine species-level taxonomic identification of rare and low-prevalence enteric pathogens in clinical public health reference laboratories. Its combination of high species-level classification accuracy, strong concordance among workflows, and low susceptibility to assembly-related classification failure makes it well suited to confirmatory diagnostic

applications where precise species identification directly informs biosafety assessment, surveillance, and public-health decision making. ONT long-read sequencing remains highly valuable for complementary applications including structural genome characterization, plasmid analysis, and hybrid genome assembly. Furthermore, hybrid Illumina-Nanopore assemblies may provide an effective strategy for resolving particularly challenging or high-consequence isolates by combining the base-level accuracy of short-read sequencing with the structural contiguity of long-read sequencing. Although hybrid assemblies were excluded from this study to evaluate independently deployable workflows, their potential to improve taxonomic classification warrants future investigation, particularly for uncommon organisms that remain difficult to classify using either platform alone.

4.4 Workflow-dependent Variation and Genomic Taxonomic Classification

Variation among the evaluated bioinformatic workflows was observed throughout the analyses performed in this study, demonstrating that taxonomic classification performance depends not only on sequencing data but also on algorithm design, reference database curation, and taxonomic framework. Although Illumina-based workflows achieved similarly high type strain classification accuracy (85.3-97.1%), they differed in species-level resolution (Fig. 21), concordance (Figs. 22-25), classification failure profiles (Fig. 26), and susceptibility to taxonomic inconsistencies. No single workflow consistently optimized taxonomic resolution, concordance, and classification robustness across all isolates. Therefore, a single platform or taxonomic classifier is not likely to be a uniform standard for all enteric bacterial isolates, especially given the genomic differences across taxa.

Failure profile analysis clearly demonstrated that different workflows were limited by different analytical constraints. For example, Illumina-based RefSeq Masher exhibited significant overrepresentation of reference database limitations (9.6% of Illumina-based workflow failures) and skANI disproportionately produced invalid taxonomic assignments (10.9% of Illumina-based workflow failures). Nanopore-derived workflow failures were more frequently affected by assembly-related limitations (46.4% of Nanopore-based workflow failures) (Fig. 26, Table 18-19, Table A10-A11). This indicates that classification outcomes are shaped as much by the architecture, completeness, and taxonomic framework of the underlying reference databases as by the classification algorithms themselves.

These observations suggest that discordance amongst workflows should not automatically be interpreted as analytical error. Instead, discordant classifications frequently reflected differences in database representation, taxonomic interpretation, or workflow-specific confidence criteria despite broadly similar genomic data. Therefore, the performance of any individual workflow must be interpreted within the context of both its analytical methodology and its reference database.

The strong concordance observed among several genome similarity-based approaches further supports this interpretation. Mash (Mikrokondu module), FastANI (GDB-Tk module), and skANI (GTDB-Tk module) demonstrated consistently high taxonomic agreement for most isolates (Table A8) from both Illumina- and ONT-derived assemblies, suggesting that genome similarity approaches capture comparable biological relationships despite employing different computational methods. However, these same workflows also shared similar vulnerabilities. Notably, these three workflows were responsible for the *Y. pestis* misclassification (Table 21) all relied on GTDB-derived reference databases with similar curation and taxonomic frameworks

(Table 10). This suggests that shared database composition may contribute as much to concordant classifications (and misclassification) as the underlying similarity algorithms themselves.

Similar variability across tools and dependence on database composition has been demonstrated in comparative benchmarking studies, highlighting that taxonomic classification outputs are inherently shaped by both algorithm design and reference database structure (63–66). These findings, therefore, support a tiered genomic classification strategy, consensus-based interpretation, or combinations of both, in which complementary workflows are used to capitalize on their respective strengths rather than reliance on any single workflow. Rapid, genome-wide screening methods (e.g., k-mer screening) provide efficient initial classification, whereas genome similarity methods (e.g. ANI or whole-genome comparisons), provide valuable confirmation for species-level assignments. When discordant or clinically important classifications occur, comparison across multiple workflows allows disagreements to be recognized and investigated rather than automatically accepted.

Such an approach is particularly relevant for clinical and public health laboratories, where false positive or false negative identifications may have important biosafety or surveillance implications. Rather than selecting a single “best” workflow, consensus across complementary analytical approaches pay provide greater confidence for difficult or high-consequence isolates. Accordingly, the presented findings suggest that future reference laboratory workflows should emphasize complementary analytical evidence rather than exclusive reliance on a single classifier.

4.5 Taxonomic Instability and Nomenclatural Discordance

A substantial proportion of apparent discordance observed in this study reflected taxonomic and nomenclatural instability rather than genuine biological disagreement. Prior to standardization of all assignments according to the LPSN (accessed 25 January 2026) (101), 21.9% of isolates were associated with a homotypic synonym set. These findings demonstrate that a considerable proportion of apparent disagreement among workflows simply reflected differences in accepted nomenclature rather than genomic evidence. Importantly, all classifications were standardized prior to concordance analyses using curated homotypic synonym sets (Table A13) so that these nomenclatural differences did not influence the concordance analyses presented throughout this thesis. Instead, these results highlight a practical challenge for data interpretation: identical organisms may legitimately receive different names depending on the reference database version or taxonomic framework used. Without careful standardization, these differences may be incorrectly interpreted as biological discordance.

Taxonomic instability was particularly evident among members of the Enterobacterales (101) where recent reclassification has altered family and genus boundaries without changing underlying genomic relationships among organisms (7, 101, 110). Examples observed in this study included *Raoultella*, *Yersinia*, *Erwinia*, and *Hafnia*, among others. Such revisions are an expected consequence of advances in microbial systematics as genome-scale analyses continue to redefine bacterial taxonomy.

Legacy taxonomy remained evident in some genomic workflows. Mash, using the GTDB Mash Sketch reference database, reported Enterobacteriaceae family names that corresponded to genera now assigned to Budviciaceae, Hafniaceae, Erwiniaceae, Morganellaceae, and Yersiniaceae under current taxonomy (101). Although these assignments did not alter genus or

species identification, they illustrate how legacy taxonomic frameworks embedded within the reference databases can influence broader-level classifications despite otherwise acceptable genomic identification. This represents yet another manifestation of taxonomic instability rather than classification error (7, 101, 110).

The practical implications of these observations were illustrated by discordant *Yersinia* assignments. Three isolates produced inconsistent assignments between *Y. pseudotuberculosis* and *Y. pestis*, despite independent confirmatory testing confirming that none represented *Y. pestis* (Table 21). No evidence from this study suggested that these three isolates were phenotypically unusual or exhibited consistently poor assembly quality that would explain the observed discordance. Instead, the findings are biologically consistent with the exceptionally high genomic similarity shared between *Y. pestis* and *Y. pseudotuberculosis*. Notably, the discordant assignments occurred exclusively within workflows using GTDB-derived reference databases. This pattern strongly suggests that reference database composition and representation of extremely closely related taxa, rather than poor sequence quality, contributed substantially to discordant *Yersinia* classifications. These observations emphasize that closely related pathogens with markedly different biosafety implications may require additional confirmatory analyses when classified using genome similarity approaches.

These findings reflect the continuing transition from historical phenotype-based and single locus-based taxonomy towards whole genome-based microbial systematics. Genome-informed taxonomic frameworks, such as those proposed by LPSN (101) and GTDB (63), increasingly define species relationships using whole-genome similarity and phylogenetic evidence rather than phenotypic characteristics or single-locus criteria, leading to widespread reclassification of established taxa (226). Maintaining current nomenclature, standardized

synonym mapping, and regularly curated reference databases will become integral components of implementing WGS-based identification within clinical and public health laboratories (7, 110).

4.6 Implications for Public Health Reference Laboratories

The findings of this study have direct implications for implementation of bacterial identification workflows in public health reference laboratories. The consistent improvement in species-level resolution, concordance, and type strain classification accuracy observed with Illumina-based approaches support their use as the primary approach for confirmatory identification of rare and low-prevalence enteric bacterial pathogens. In contrast, 16S rRNA gene sequencing and Biolog Gen III phenotypic profiling, the two traditional identification approaches evaluated in this study, demonstrated significantly lower species-level resolution (14.6% and 69.7% species assigned, respectively) and greater discordance, particularly for uncommon taxa, and diagnostically challenging genera such as *Campylobacter* (Table A6). These data support ongoing transitions towards genome-based identification within public health systems internationally, where WGS has replaced or supplemented traditional typing methods for multiple pathogens (164, 166–168, 203, 240).

Adoption of genomic workflows, however, requires consideration of operational factors beyond analytical performance. As discussed in Section 4.3, Illumina-based sequencing platforms consistently provided more stable species-level classifications than Nanopore-based workflows. Long-read sequencing-based approaches remain valuable for applications extending beyond routine taxonomic classification, including structural genome analysis, plasmid characterization, complete genome assembly, and hybrid assembly workflows but require further

optimization for routine diagnostic speciation. Platform selection should therefore align with the intended analytical endpoint.

Workflow design is equally important. The variability in failure patterns identified in this study (Fig. 26; Table 18-19) demonstrate that reliance on a single classifier increases susceptibility to database gaps, taxonomy conflicts, or algorithm-specific thresholds. A tiered or consensus building strategy combining rapid screening methods followed by genome similarity confirmation and expert review of ambiguous classifications would provide a balanced approach that leverages complementary strengths while mitigating tool-specific weaknesses and remaining computationally practical for routine implementation. Such strategies are particularly valuable for high-consequence organisms where incorrect species assignments may alter biosafety procedures or public health response, as illustrated by the discordant *Yersinia* classifications.

Finally, successful implementation increasingly depends less on sequencing technology itself than on the surrounding analytical infrastructure. Sustained attention to database curation, taxonomic frameworks, computational infrastructure, and personnel expertise remain essential for accurate interpretation of genomic data. As sequencing technologies continue to advance, these supporting components are likely to become the primary determinants of successful implementation in clinical and public health laboratories.

4.7 Integrated Interpretation of Taxonomic Classification Performance

The findings of this study demonstrate that bacterial identification performance is shaped by an interaction of sequencing data quality, reference database structure, taxonomic stability, and algorithmic design rather than from any single methodological component. Although Illumina-based workflows consistently achieved the highest species-level accuracy (85.3-97.1%)

and concordance (Figs. 22-25, Table A8), workflow-specific discordance persisted primarily where reference database representation or taxonomic interpretation differed rather than where genomic signal itself conflicted.

The shift is evident throughout the results presented in Chapter 3. Discordant *Yersinia* assignments arose because several GTDB-derived reference databases lacked appropriate representation of *Y. pseudotuberculosis*, resulting in high-similarity matches to *Y. pestis* (Table 21). Likewise, 21.9% of isolates were associated with homotypic synonym sets (Table A13), and Mash-based taxonomic classification produced legacy Enterobacteriaceae assignments. These examples demonstrate that many remaining sources of discordance originate from reference infrastructure rather than limitations in genome sequencing itself.

As WGS becomes increasingly routine, discordance is more likely to arise from inconsistencies in reference database composition. Future improvements in taxonomic classification are therefore likely to depend less on advances in sequencing technology than on coordinated management of reference resources. Continued curation of representative genomes, harmonization of taxonomic frameworks, standardized handling of homotypic synonyms, and routine database updates will likely have a greater impact on classification consistency rather than incremental improvements in sequencing accuracy. Because these isolates were initially submitted from multiple clinical laboratories across Canada, coordinated national efforts involving reference laboratories, taxonomic authorities, and pathogen surveillance networks may ultimately be required to ensure consistent interpretations across jurisdictions.

4.8 Limitations of the Study

4.8.1 Reference Database Coverage and Taxonomic Stability

All evaluated workflows depend on the completeness and taxonomic structure of their underlying reference databases. Limited representation of rare or recently revised taxa contributed to unresolved classifications and, in some cases, similarity-driven mislabeling to closely related but incorrect species. The discordant *Yersinia* classifications (Table 21) provide a clear example where absence of certain closely related taxa in some databases contributed to high similarity matches to *Y. pestis*. Independent confirmatory testing excluded the high-risk organisms, indicating that these cases reflected database structure rather than sequencing or analytical error.

Taxonomic instability during the study period further complicated cross-workflow comparisons. Ongoing nomenclatural revisions and synonymy produced biologically concordant assignments reported under different valid species names. To minimize this source of apparent discordance, all classifications were standardized against the LPSN as of 25 January 2026 (101) (Table A13). Although standardization improved comparability, it also illustrates that maintaining current taxonomy remains an ongoing requirement.

4.8.2 Sequencing Platform Comparison Constraints

Illumina and Nanopore WGS were performed on DNA extracted from separate extraction batches over time using the same extraction methodology. The interval between platform sequencing necessitated new extractions for Nanopore processing and some Nanopore libraries required additional gDNA concentration steps prior to sequencing, introducing the possibility of minor batch-related variation in DNA quality. However, platform-associated trends across

hundreds of isolates strongly suggest that the observed differences primarily reflect platform characteristics rather than batch effects.

Multiplexed Nanopore sequencing also exhibited uneven read distribution among samples in some sequencing runs. Although this phenomenon was not formally investigated, unequal read distribution may have contributed to reduced sequencing depth and increased assembly fragmentation for some isolates, which aligns with an anecdotal pattern observed in our laboratory. Potential contributors include DNA fragmentation, variability in high-molecular-weight gDNA recovery, or biases introduced during library preparation. Because these factors were not experimentally evaluated, their contribution to the observed classification differences cannot be determined from the present study and warrants further investigation.

4.8.3 Type Strain Sample Size and Study Scope

Type strain classification accuracy analysis was used in this study as an independent benchmark for assessing species-level classification accuracy across workflows. A total of 34 type strains were included among 365 total isolates analyzed. Although this type strain subset provided an objective reference point for evaluating classification accuracy, they represent only a small proportion of the taxonomic diversity of the whole sample set and may limit the breadth of species-level validation. Expanding future validation datasets to include additional type strains spanning a broader range of rare enteric taxa would strengthen estimates of classification accuracy across diverse bacterial groups. Future benchmarking could also incorporate well-characterized plasmids and other mobile genetic elements to evaluate how accurately integrated genomic workflows characterize clinically important accessory genomes alongside taxonomic identity.

The study focused on rare and low-prevalence enteric bacteria, archived within the Canadian NML reference collection, which are underrepresented in traditional diagnostic databases and present unique classification challenges. Therefore, the findings are directly applicable to reference laboratory investigations involving diagnostically challenging organisms but should not automatically be generalized to common bacterial pathogens with extensive reference representation. Future Canadian studies incorporating both common and uncommon organisms would provide useful context for determining how database representation influences classification performance across the spectrum of organisms routinely encountered in national surveillance programs.

4.8.4 Scope of Evaluation and Baseline Study Design

This study evaluated taxonomic classification performance rather than downstream clinical, epidemiological, or operational outcomes. While accurate identification underpins public health practice, evaluation of clinical impact, treatment implications, risk assessment, turnaround time, implementation cost, and decision making was beyond the scope of this study.

Likewise, the WGS-based workflows evaluated in this study were assessed under standardized baseline analytical parameters rather than platform- and tool-specific optimization. This design allowed differences in performance to be primarily attributed to workflow components and reference database characteristics rather than individualized optimization strategies. The results of this study represent comparative baseline performance under practical implication conditions rather than theoretical best-case performance and identify which approaches warrant further refinement rather than defining theoretical best-case limits. Furthermore, the data presented in this thesis indicate that additional optimization is likely to be

most beneficial for specific problematic taxa, particularly *Yersinia*, *Enterobacter*, *Providencia*, *Serratia*, and *Pantoea*, among others, which accounted for a disproportionate share of discordant classifications observed throughout the study (Tables A9, 21).

Taken together, these findings demonstrate that reliable taxonomic classification of rare and low-prevalence enteric bacteria depends on coordinated performance across sequencing data quality, analytical workflow design, reference database representation, and taxonomic framework, rather than any single methodological component. While WGS substantially improves species-level identification compared to 16S rRNA gene sequencing and phenotypic profiling, the principal barriers to further improvement increasingly arise from the supporting reference infrastructure rather than from sequencing technology itself.

As sequencing technologies continue to advance, implementation of WGS-based identification likely to become progressively less constrained by laboratory instrumentation and increasingly dependent on the capacity of diagnostic and reference laboratories, sustained funding, coordinated national and international implementation strategies, standardized and maintained taxonomic frameworks, and access to highly trained laboratory and bioinformatics personnel. These components were not directly evaluated in this study but represent critical determinants for successful integration of WGS-based identification into routine public health practice.

Despite remaining challenges, the consistent performance advantages demonstrated by Illumina WGS-based workflows, support their adoption as the primary strategy for confirmatory identification of uncommon enteric bacterial pathogens in reference laboratory settings. The

following chapter translates these findings into practical recommendations and priorities for future implementation and research.

Chapter 5: Conclusions and Future Directions

5.1 Study Conclusions

This study demonstrates that WGS-based approaches provide more reliable species-level identification for rare and low-prevalence enteric pathogens than 16S rRNA gene sequencing and phenotypic profiling, the two traditional confirmatory methods evaluated in this study. Whole genome-based workflows achieved higher species-level resolution, stronger concordance, and greater classification accuracy while limitations of traditional methods reflected inherent methodological constraints of those approaches. Among the evaluated workflows, Illumina-based analyses consistently produced the most stable and reliable species-level assignments, whereas Nanopore-based approaches showed greater variability and require further optimization for routine diagnostic speciation. Taken together, these findings support adoption of Illumina-based WGS as the primary confirmatory identification strategy for rare and low-prevalence enteric bacterial pathogens in Canadian public health reference laboratories. This study highlights that successful implementation depends equally on continued improvement of reference databases, taxonomic harmonization, and standardized analytical workflows and emphasizes the need for continued development of supporting reference resources to maximize its diagnostic usefulness.

5.2 Implications for Diagnostic Workflows

5.2.1 Role of Traditional Methods

The results of this study indicate that 16S rRNA sequencing is no longer sufficient as a confirmatory identification method for rare and low-prevalence enteric pathogens in reference laboratory contexts. Although useful for broad genus- and family-level placement or preliminary assessment, its limited discriminatory power and dependence on a single conserved locus restrict

reliability for species-level confirmation of clinically or epidemiologically significant taxa. Similarly, phenotypic profiling demonstrated variable performance, frequent non-identifications, and poor agreement with 16S rRNA gene sequencing for several clinically important taxa, particularly *Campylobacter*. Phenotypic profiling limitations reflected both limitations of the commercial reference database and the biological plasticity inherent to phenotype-based identification. Therefore, traditional methods should be regarded primarily as complementary or preliminary approaches rather than definitive methods for confirmatory identification of uncommon enteric bacteria in reference laboratory settings.

5.2.2 Recommended Sequencing Platform

Illumina short-read sequencing currently represents the most readily implementable platform for routine genomic identification of rare and low-prevalence enteric bacterial pathogens. Its low per-base error rates support stable performance of k-mer- and ANI-based classifiers. ONT long-read sequencing remains promising for complementary applications, including structural genome characterization, complete genome assembly, and investigation of mobile genetic elements. However, the lower species-level classification accuracy observed in this study indicates that additional optimization of laboratory workflows, sequencing chemistry, and downstream analytical pipelines is required before long-read sequencing can reliably replace Illumina for routine taxonomic confirmation.

For Canadian public health reference laboratories, these findings support Illumina sequencing as the preferred platform for routine species-level confirmation and its integration into existing public health sequencing workflows. For reference laboratories currently implementing genomic identification workflows, this facilitates adoption without major

infrastructure changes. Nanopore sequencing can serve a complementary role where long-read information provides additional value, but further optimization and validation is needed.

5.2.3 Bioinformatic Workflow Considerations

No single classifier uniformly optimized resolution, concordance, and taxonomic stability. However, integrated workflows that combine QC, assembly, and taxonomic classification offer practical advantages for diagnostic laboratories.

The Mikrokondo pipeline, which incorporates Mash for rapid k-mer-based speciation, performed comparably to other high-performing genome-based tools while providing an end-to-end analytical framework. Its integration of assembly, quality assessment and control, speciation, and other non-evaluated downstream analyses such as multi-locus sequence typing and antimicrobial resistance detection offers operational efficiency. Recent availability within a graphical user interface via IRIDA Next, developed in-house at the NML, further reduces barriers to implementation. Similarly, the GTDB-Tk pipeline, incorporating skANI, demonstrated strong performance consistent with genome similarity-based approaches and represents a suitable option for laboratories with command-line bioinformatics capacity. Nevertheless, legacy taxonomic outputs and dependence on GTDB-derived reference databases highlight the need for curated Mash and skANI reference databases. Selection of workflows should therefore consider both analytical performance and operational feasibility, including user expertise, computational infrastructure, and the need for integrated reporting.

Additionally, these findings reinforce that bioinformatic workflows are closely coupled to specific database releases and taxonomic schemas. Many non-commercial or open-source databases may lag or diverge from current nomenclature standards as incorporation of newly

proposed taxonomic revisions follows publication, external validation, and release schedules. As a result, identical genomes can be assigned different names that simply reflects different update schedules despite concordant genome sequences. As taxonomic revision continues, maintaining synchronized and well-curated reference databases will become increasingly important for ensuring consistent interpretation across laboratories.

Taken together, these findings support implementation of tiered genomic classification strategies, consensus-based interpretation, or combinations of both, in which complementary workflows are used to capitalize on their respective strengths while reducing dependence on the limitations of any single algorithm or reference database. For example, rapid k-mer-based screening may be followed by ANI-based confirmation, or concordant classifications across multiple high-performing workflows may be used to increase confidence in species-level assignments while flagging discordant results or high-consequence taxa for expert review. Such approaches have the potential to improve performance for uncommon taxa, particularly where database representation is incomplete or taxonomy remains unstable.

5.3 Future Directions

The findings of this study indicate that continued advancement in genomic taxonomic identification depend increasingly on refinement of reference infrastructure and workflow implementation. A central priority is improved curation and representation of rare and recently revised taxa within reference databases. Similarity-based mislabelling observed in this study, including *Yersinia* assignments associated with incomplete database coverage, demonstrates that classification accuracy is fundamentally constrained by available reference genomes and associated taxonomy. Targeted expansion and expert curation of databases for clinically relevant

but low-prevalence organisms would substantially improve reliability of genomic diagnostics. Coordinated expansion and curation of reference databases should therefore occur at institutional, regional, national, and international levels to ensure consistent genomic identification of clinically relevant but uncommon organisms.

Harmonization of taxonomic frameworks across databases represents a related need. Discordance arising from legacy nomenclature, homotypic synonymy, and ongoing taxonomic revision highlights that consistent interpretation requires collaboration among nomenclature authorities, database developers, clinical and public health agencies, and diagnostic laboratories. Greater alignment between genomic classification tools and authoritative taxonomic resources would reduce interpretative variability that is unrelated to underlying biological differences.

Further optimization of long-read sequencing workflows also represents an important area for development. While Nanopore sequencing offers advantages in portability and read length, the observed variability associated with read accuracy, assembly quality, and multiplexing currently limits its reliability for routine species-level classification. Continued improvements in library preparation, sequencing chemistry, basecalling, hybrid assembly strategies, and workflow standardization are expected to improve species-level classification while preserving the advantages of long-read sequencing for structural genomic analyses which may allow long-read platforms to achieve performance comparable to short-read systems in diagnostic settings.

Operational evaluation of genomic workflows is another necessary step toward broader implementation. Although this study focused on taxonomic performance, future work should evaluate turnaround time, computational requirements, cost efficiency, scalability, and workforce training within Canadian public health laboratory networks to help define scalable models for

integrating WGS-based identification into routine diagnostic pipelines. In addition, future studies should compare single-workflow, tiered, and consensus-based classification strategies to determine whether combining complementary tools improves diagnostic confidence, reduces false-positive and false-negative classifications, and provides a practical balance between analytical robustness and computational efficiency for routine reference laboratory implementation and will influence adoption in public health laboratories.

Finally, integration of high-resolution WGS-based identification into surveillance programs should proceed alongside continued advancements in reference databases, taxonomy, and standardized analytical pipelines. As these supporting resources mature, genomic classification can more effectively be linked with epidemiological surveillance systems, strengthening detection of emerging pathogens, improving national surveillance capacity, and supporting coordinated responses to rare and low-prevalence enteric bacterial pathogens.

This study demonstrates that WGS-based identification provides a robust and reliable framework for taxonomic classification of rare and low-prevalence enteric bacterial pathogens. Across a large, taxonomically diverse collection of clinical isolates submitted to Canada's National Microbiology Laboratory, together with type strains, Illumina-based genomic workflows consistently outperformed traditional confirmatory methods while demonstrating that much of the remaining diagnostic discordance arises from reference database composition and taxonomic instability rather than limitations of genome sequencing itself.

The future of genomic diagnostics depends not only on generating sequence data, but on how reference laboratories standardize, interpret, and apply it. Collectively, these findings support implementation of Illumina-based WGS as the primary confirmatory identification

approach for rare and low-prevalence enteric bacterial pathogens within Canadian public health reference laboratories. As Canadian public health laboratories continue transitioning toward genome-based diagnostics, investment should increasingly focus not only on sequencing technologies, but also on the supporting infrastructure required for their successful implementation, including database curation, harmonized taxonomy, sequence analysis standardization, and sustained computational and personnel capacity. Together, these developments will enable more accurate, reproducible, and nationally consistent identification of rare enteric bacterial pathogens while strengthening genomic surveillance and public health response.

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Appendices

Appendix A: Per-isolate taxonomic classification outputs from WGS-based identification workflows

Table A1. Raw taxonomic outputs from Illumina WGS-based workflows. Unfiltered taxonomic assignments returned by each Illumina-based classification tool prior to reconciliation, standardization, or exclusion. Entries include valid taxon names, synonymous or outdated nomenclature, provisional or non-standard labels, and subspecies assignments. Cells left blank indicate that the tool did not return a taxonomic assignment and instances where analysis was not performed are explicitly indicated. These raw outputs were subsequently reconciled by consolidating synonyms under a single accepted name (Table A13), removing invalid taxa, and truncating subspecies designations to genus-species level for downstream analysis in Section 3.2.

Isolate	Mikrokon Kraken2	Mikrokon Mash	RefSeq Masher	GTDB-Tk FastANI	GTDB-Tk - skANI	TYGS
JDID-01	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i> subsp. <i>polarctica</i> <i>PhRBD_Ye1</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>
JDID-02	<i>Yersinia pseudotuberculosis</i>	<i>Yersinia pestis</i>	<i>Yersinia pseudotuberculosis</i> B-7194	<i>Yersinia pestis</i>	<i>Yersinia pestis</i>	<i>Yersinia pseudotuberculosis</i>
JDID-03	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>
JDID-04	<i>Campylobacter curvus</i>	<i>Campylobacter_A curvus</i>	<i>Campylobacter</i> sp. <i>FOBRC14</i>	<i>Campylobacter_A curvus</i>	<i>Campylobacter_A curvus</i>	potential new species
JDID-05	<i>Serratia entomophila</i>	<i>Serratia entomophila</i>	<i>Serratia marcescens</i>	<i>Serratia</i> sp	<i>Serratia</i> sp	potential new species
JDID-06	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella oxytoca</i> 10-5242	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>
JDID-07	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter freundii</i> UCI 32	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>

JDID-08	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i> GTC 09479	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>
JDID-09	<i>Tatumella ptyseos</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>
JDID-10	<i>Providencia rettgeri</i>	<i>Providencia rettgeri_A</i>	<i>Providencia rettgeri</i>	<i>Providencia rettgeri_A</i>	<i>Providencia xianensis</i>	<i>Providencia huashanensis</i>
JDID-11	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>
JDID-12	<i>Campylobacter sputorum</i>	<i>Campylobacter_B sputorum</i>	<i>Campylobacter sputorum</i> biovar <i>sputorum</i>	<i>Campylobacter_B sputorum</i>	<i>Campylobacter_F sputorum</i>	<i>Campylobacter sputorum</i>
JDID-13	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Morganella morganii</i>	Unclassified	Unclassified	<i>Proteus mirabilis</i>
JDID-14	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-15	<i>Yersinia intermedia</i>	<i>Yersinia rochesterensis</i>	<i>Yersinia kristensenii</i>	<i>Yersinia rochesterensis</i>	<i>Yersinia rochesterensis</i>	<i>Yersinia rochesterensis</i>
JDID-16	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i> subsp. <i>venerealis</i> NCTC 10354	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>
JDID-17	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i> subsp. <i>venerealis</i> NCTC 10354	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>
JDID-18	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i> subsp. <i>fetus</i> 82-40	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>
JDID-19	<i>Salmonella enterica</i>	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter upsaliensis</i> JV21	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	potential new species
JDID-20	<i>Campylobacter</i> sp. RM8964	<i>Campylobacter</i> sp002139875	<i>Campylobacter concisus</i> UNSWCD	<i>Campylobacter</i> sp002139875	<i>Campylobacter vicugnae</i>	<i>Campylobacter vicugnae</i>
JDID-21	<i>Campylobacter upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter upsaliensis</i> JV21	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	potential new species
JDID-22	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i> ATCC 29909	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-23	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i> subsp. <i>hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>
JDID-24	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i> CCUG 53443	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis_A</i>	potential new species
JDID-25	<i>Cutibacterium acnes</i>	<i>Campylobacter_D helveticus</i>	<i>Propionibacterium acnes</i> hdn-1	<i>Campylobacter_D helveticus</i>	<i>Campylobacter_D helveticus</i>	<i>Cutibacterium acnes</i>
JDID-26	<i>Campylobacter peloridis</i>	<i>Campylobacter_D peloridis</i>	<i>Campylobacter peloridis</i> LMG 23910	<i>Campylobacter_D peloridis</i>	<i>Campylobacter_D peloridis</i>	<i>Campylobacter peloridis</i>
JDID-27	<i>Campylobacter lari</i>	<i>Campylobacter_D lari_C</i>	<i>Campylobacter lari</i> RM16701	<i>Campylobacter_D lari_C</i>	<i>Campylobacter_D lari_C</i>	potential new species
JDID-28	<i>Campylobacter upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter upsaliensis</i> JV21	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	potential new species

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JDID-29	<i>Campylobacter upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter upsaliensis</i> JV21	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	potential new species
JDID-30	<i>Campylobacter helveticus</i>	<i>Campylobacter_D helveticus</i>	<i>Campylobacter upsaliensis</i> DSM 5365	<i>Campylobacter_D helveticus</i>	<i>Campylobacter_D helveticus</i>	<i>Campylobacter helveticus</i>
JDID-31	<i>Campylobacter concisus</i>	<i>Campylobacter_A concisus_Y</i>	<i>Campylobacter concisus</i> ATCC 51562	<i>Campylobacter_A concisus_Y</i>	<i>Campylobacter_A concisus_Y</i>	potential new species
JDID-32	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	<i>Yersinia enterocolitica</i> NFO	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>
JDID-33	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	<i>Yersinia enterocolitica</i> NFO	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>
JDID-34	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter concisus</i> ATCC 51562	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>
JDID-35	<i>Campylobacter upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter upsaliensis</i> JV21	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	potential new species
JDID-36	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter fetus</i> subsp. <i>venerealis</i> 642-21	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>	<i>Campylobacter lanienae</i>
JDID-37	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia frederiksenii</i> ATCC 33641	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>
JDID-38	<i>Campylobacter lari</i>	<i>Campylobacter_D lari_D</i>	<i>Campylobacter lari</i> CCUG 22395	<i>Campylobacter_D lari_D</i>	<i>Campylobacter_D lari_D</i>	potential new species
JDID-39	<i>Campylobacter lari</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter lari</i> RM2100	<i>Campylobacter_D lari</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter lari</i>
JDID-40	<i>Campylobacter lari</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter lari</i> RM2100	<i>Campylobacter_D lari</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter lari</i>
JDID-41	<i>Yersinia pseudotuberculosis</i>	<i>Yersinia pestis</i>	<i>Yersinia pseudotuberculosis</i> YPIII	<i>Yersinia pestis</i>	<i>Yersinia pestis</i>	<i>Yersinia pseudotuberculosis</i>
JDID-42	<i>Campylobacter insulaenigrae</i>	<i>Campylobacter_D insulaenigrae</i>	<i>Campylobacter insulaenigrae</i> NCTC 12927	<i>Campylobacter_D insulaenigrae</i>	<i>Campylobacter_D insulaenigrae</i>	potential new species
JDID-43	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>
JDID-44	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> 2008-872	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i>
JDID-45	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i>
JDID-46	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i> subsp. <i>fetus</i> 82-40	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>
JDID-47	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i> subsp. <i>hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>
JDID-48	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> 81-176	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i>

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JDID-49	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> LMG 9872	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i>
JDID-50	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> 1854	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i>
JDID-51	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> 1798	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i>
JDID-52	<i>Campylobacter coli</i>	<i>Campylobacter_D coli</i>	<i>Campylobacter coli</i>	<i>Campylobacter_D coli</i>	<i>Campylobacter_D coli</i>	<i>Campylobacter coli</i>
JDID-53	<i>Campylobacter upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter upsaliensis</i> JV21	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	potential new species
JDID-54	<i>Campylobacter coli</i>	<i>Campylobacter_D coli</i>	<i>Campylobacter coli</i> K7	<i>Campylobacter_D coli</i>	<i>Campylobacter_D coli</i>	<i>Campylobacter coli</i>
JDID-55	<i>Campylobacter coli</i>	<i>Campylobacter_D coli</i>	<i>Campylobacter coli</i> 1148	<i>Campylobacter_D coli</i>	<i>Campylobacter_D coli</i>	<i>Campylobacter coli</i>
JDID-56	<i>Campylobacter sp.</i> RM8964	<i>Campylobacter sp002139875</i>	<i>Campylobacter fetus</i> subsp. <i>testudinum</i>	<i>Campylobacter sp002139875</i>	<i>Campylobacter vicugnae</i>	<i>Campylobacter vicugnae</i>
JDID-57	<i>Pantoea rwandensis</i>	<i>Pantoea cancerogena_A</i>	<i>Enterobacter cancerogenus</i>	<i>Pantoea cancerogena_A</i>	<i>Pantoea communis</i>	<i>Candidatus Pantoea communis</i>
JDID-58	<i>Pantoea rwandensis</i>	<i>Pantoea cancerogena_A</i>	<i>Enterobacter cancerogenus</i>	<i>Pantoea cancerogena_A</i>	<i>Pantoea communis</i>	<i>Candidatus Pantoea communis</i>
JDID-59	<i>Buttiauxella agrestis</i>	No Species Identified	<i>Klebsiella oxytoca</i> SA2	<i>Buttiauxella sp</i>	<i>Dryocola sp</i>	potential new species
JDID-60	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>	<i>Kluyvera ascorbata</i> ATCC 33433	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>
JDID-61	<i>Serratia liquefaciens</i>	<i>Serratia_J liquefaciens</i>	<i>Serratia liquefaciens</i> ATCC 27592	<i>Serratia_J liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>
JDID-62	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter cloacae</i> UCI 50	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter intestinhominis</i>	<i>Enterobacter hormaechei</i>
JDID-63	<i>Citrobacter farmeri</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter farmeri</i> GTC 1319	<i>Citrobacter_A farmeri</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter farmeri</i>
JDID-64	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i> AER397	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	potential new species
JDID-65	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-66	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-67	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-68	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-69	<i>Aeromonas media</i>	<i>Aeromonas rivipollensis</i>	<i>Aeromonas media</i> WS	<i>Aeromonas rivipollensis</i>	<i>Aeromonas sp023093515</i>	potential new species
JDID-70	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-71	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i> Ae398	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-72	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i> AMC35	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	potential new species

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JDID-73	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>
JDID-74	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-75	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-76	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i> AMC35	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-77	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i> Finland 1998	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-78	analysis not performed					
JDID-79	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Hartford str. 06-0676	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella typhi</i>
JDID-80	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea</i> sp. NGS-ED- 1003	<i>Pantoea septica</i>	<i>Pantoea septica</i>	potential new species
JDID-81	<i>Klebsiella variicola</i>	<i>Klebsiella variicola</i>	<i>Klebsiella variicola</i>	<i>Klebsiella variicola</i>	<i>Klebsiella variicola</i>	<i>Klebsiella variicola</i>
JDID-82	<i>Salmonella enterica</i>	No Species Identified	<i>Enterobacter</i> sp. BispH2	<i>Phytobacter</i> sp	<i>Phytobacter</i> sp	potential new species
JDID-83	<i>Citrobacter</i> sp. BDA59-3	No Species Identified	<i>Enterobacter</i> sp. BispH2	<i>Phytobacter</i> sp	<i>Phytobacter</i> sp	potential new species
JDID-84	<i>Citrobacter</i> sp. BDA59-3	No Species Identified	<i>Enterobacter</i> sp. BispH2	<i>Phytobacter</i> sp	<i>Phytobacter</i> sp	potential new species
JDID-85	<i>Pseudocitrobacter</i> <i>corydidari</i>	<i>Pseudocitrobacter</i> <i>corydidari</i>	<i>Enterobacteriaceae</i> <i>bacterium</i> strain FGI 57	<i>Pseudocitrobacter</i> <i>corydidari</i>	<i>Pseudocitrobacter</i> <i>corydidari</i>	potential new species
JDID-86	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter cloacae</i> subsp. <i>dissolvens</i> SDM	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter</i> <i>oligotrophicus</i>
JDID-87	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter</i> <i>oligotrophicus</i>
JDID-88	<i>Enterobacter cloacae</i>	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter mori</i> LMG 25706	<i>Enterobacter</i> sp	<i>Enterobacter</i> sp	potential new species
JDID-89	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i> MS 115-1	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-90	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter cloacae</i> UCI 49	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae</i>
JDID-91	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i> GTC 09479	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>
JDID-92	<i>Citrobacter cronae</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter freundii</i> CFNIH1	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-93	<i>Kluyvera</i> sp. CRP	<i>Kluyvera georgiana_A</i>	<i>Kluyvera ascorbata</i> ATCC 33433	<i>Kluyvera georgiana_A</i>	<i>Kluyvera georgiana_A</i>	potential new species
JDID-94	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i> NBRC 105721	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-95	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella typhi</i>

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			<i>Enteritidis str.</i> <i>EC20110223</i>			
JDID-96	<i>Superficieibacter sp.</i> <i>HKU1</i>	<i>Superficieibacter</i> <i>sp002421005</i>	<i>Citrobacter rodentium</i>	<i>Superficieibacter</i> <i>sp002421005</i>	<i>Superficieibacter</i> <i>sp002421005</i>	potential new species
JDID-97	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i> <i>MGH 77</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>
JDID-98	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-99	<i>Klebsiella</i> <i>quasipneumoniae</i>	<i>Klebsiella</i> <i>quasipneumoniae</i>	<i>Klebsiella</i> <i>quasipneumoniae</i> subsp. <i>similipneumoniae</i>	<i>Klebsiella</i> <i>quasipneumoniae</i>	<i>Klebsiella</i> <i>quasipneumoniae</i>	<i>Klebsiella</i> <i>quasipneumoniae</i>
JDID-100	<i>Klebsiella</i> <i>quasipneumoniae</i>	<i>Klebsiella</i> <i>quasipneumoniae</i>	<i>Klebsiella</i> <i>quasipneumoniae</i> subsp. <i>similipneumoniae</i>	<i>Klebsiella</i> <i>quasipneumoniae</i>	<i>Klebsiella</i> <i>quasipneumoniae</i>	<i>Klebsiella</i> <i>quasipneumoniae</i>
JDID-101	<i>Raoultella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Raoultella ornithinolytica</i> <i>2-156-04_S1_C1</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-102	<i>Raoultella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Raoultella ornithinolytica</i> <i>B6</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-103	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-104	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-105	<i>Raoultella terrigena</i>	<i>Klebsiella terrigena</i>	<i>Raoultella ornithinolytica</i>	<i>Klebsiella terrigena</i>	<i>Klebsiella terrigena</i>	<i>Klebsiella terrigena</i>
JDID-106	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>
JDID-107	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter sp. BIDMC</i> <i>26</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>
JDID-108	<i>Lelliottia sp. AC1</i>	<i>Lelliottia nimipressuralis</i>	<i>Enterobacter cloacae</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>
JDID-109	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-110	<i>Scandinavium</i> <i>goeteborgense</i>	<i>Scandinavium</i> <i>goeteborgense</i>	<i>Enterobacter mori</i> LMG <i>25706</i>	<i>Scandinavium</i> <i>goeteborgense</i>	<i>Scandinavium</i> <i>goeteborgense</i>	potential new species
JDID-111	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-112	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-113	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i> <i>ATCC 49162</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-114	<i>Kluyvera sp. CRP</i>	<i>Kluyvera georgiana_A</i>	<i>Kluyvera ascorbata</i> ATCC <i>33433</i>	<i>Kluyvera georgiana_A</i>	<i>Kluyvera georgiana_A</i>	potential new species
JDID-115	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Enterobacter sp. Bisph2</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>
JDID-116	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i> <i>BIDMC 52</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i> ⁵¹

⁵¹ Continuation of Table A1, part 6 of 18

JDID-117	<i>Serratia quinivorans</i>	<i>Serratia_J quinivorans</i>	<i>Serratia proteamaculans</i> 568	<i>Serratia_J quinivorans</i>	<i>Serratia quinivorans</i>	<i>Serratia quinivorans</i>
JDID-118	<i>Serratia marcescens</i>	<i>Serratia ureilytica</i>	<i>Serratia marcescens</i> BIDMC 81	<i>Serratia ureilytica</i>	<i>Serratia ureilytica</i>	<i>Serratia ureilytica</i>
JDID-119	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i> ATCC 33433	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>
JDID-120	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea</i> sp. NGS-ED- 1003	<i>Pantoea septica</i>	<i>Pantoea septica</i>	potential new species
JDID-121	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea</i> sp. NGS-ED- 1003	<i>Pantoea septica</i>	<i>Pantoea septica</i>	potential new species
JDID-122	<i>Leclercia pneumoniae</i>	UBA7405 sp000755535	<i>Enterobacteriaceae</i> bacterium ATCC 29904	UBA7405 sp000755535	<i>Leclercia_A pneumoniae</i>	<i>Leclercia pneumoniae</i>
JDID-123	<i>Serratia marcescens</i>	<i>Serratia marcescens_K</i>	<i>Serratia marcescens</i>	<i>Serratia marcescens_K</i>	<i>Serratia sarumanii</i>	<i>Serratia sarumanii</i>
JDID-124	<i>Serratia marcescens</i>	<i>Serratia marcescens_K</i>	<i>Serratia marcescens</i>	<i>Serratia marcescens_K</i>	<i>Serratia sarumanii</i>	<i>Serratia sarumanii</i>
JDID-125	<i>Serratia liquefaciens</i>	<i>Serratia_J liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia_J liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>
JDID-126	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea</i> sp. NGS-ED- 1003	<i>Pantoea septica</i>	<i>Pantoea septica</i>	potential new species
JDID-127	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Pantoea</i> sp. PSNIH2	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>
JDID-128	<i>Kluyvera</i> sp. CRP	<i>Kluyvera georgiana_A</i>	<i>Kluyvera ascorbata</i> ATCC 33433	<i>Kluyvera georgiana_A</i>	<i>Kluyvera georgiana_A</i>	potential new species
JDID-129	<i>Mixta calida</i>	<i>Kluyvera georgiana_A</i>	<i>Kluyvera ascorbata</i> ATCC 33433	<i>Kluyvera georgiana_A</i>	<i>Kluyvera georgiana_A</i>	potential new species
JDID-130	<i>Serratia liquefaciens</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i> ATCC 33433	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>
JDID-131	<i>Serratia liquefaciens</i>	<i>Serratia_J liquefaciens</i>	<i>Serratia liquefaciens</i> ATCC 27592	<i>Serratia_J liquefaciens</i>	<i>Serratia liquefaciens</i>	<i>Serratia liquefaciens</i>
JDID-132	<i>Enterobacter</i> <i>roggenkampii</i>	<i>Enterobacter</i> <i>roggenkampii</i>	<i>Enterobacter cloacae</i> MGH 54	<i>Enterobacter</i> <i>roggenkampii</i>	<i>Enterobacter</i> <i>roggenkampii</i>	<i>Enterobacter</i> <i>roggenkampii</i>
JDID-133	<i>Enterobacter</i> <i>roggenkampii</i>	<i>Enterobacter</i> <i>roggenkampii</i>	<i>Enterobacter asburiae</i>	<i>Proteus</i> sp	<i>Proteus</i> sp	<i>Enterobacter</i> <i>roggenkampii</i>
JDID-134	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i> MGH 77	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>
JDID-135	<i>Citrobacter sedlakii</i>	<i>Citrobacter_A sedlakii</i>	<i>Citrobacter sedlakii</i> NBRC 105722	<i>Citrobacter_A sedlakii</i>	<i>Citrobacter_A sedlakii</i>	<i>Citrobacter sedlakii</i>
JDID-136	<i>Citrobacter</i> sp. RHB25- C09	<i>Citrobacter_A sedlakii</i>	<i>Citrobacter sedlakii</i> NBRC 105722	<i>Citrobacter_A sedlakii</i>	<i>Citrobacter_A sedlakii</i>	<i>Citrobacter sedlakii</i>
JDID-137	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>
JDID-138	<i>Proteus columbae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i> BIDMC 52	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>

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JDID-139	<i>Proteus columbae</i>	<i>Proteus</i> sp003144505	<i>Proteus hauseri</i> ZMd44	<i>Proteus</i> sp003144505	<i>Proteus</i> sp003144505	potential new species
JDID-140	<i>Proteus columbae</i>	<i>Proteus myxofaciens</i>	<i>Proteus mirabilis</i>	<i>Proteus</i> sp	<i>Proteus</i> sp	potential new species
JDID-141	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-142	<i>Raoultella planticola</i>	<i>Klebsiella planticola</i>	<i>Raoultella planticola</i> ATCC 33531	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-143	<i>Enterobacter hormaechei</i>	<i>Enterobacter cloacae_Q</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter hormaechei_C</i>	<i>Enterobacter hormaechei</i>
JDID-144	<i>Serratia marcescens</i>	<i>Serratia nevei</i>	<i>Serratia marcescens</i> AB42556419-isolate1	<i>Serratia nevei</i>	<i>Serratia nevei</i>	potential new species
JDID-145	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i> BIDMC 72	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-146	<i>Buttiauxella agrestis</i>	<i>Buttiauxella massiliensis</i>	<i>Buttiauxella agrestis</i>	<i>Buttiauxella gaviniae</i>	<i>Buttiauxella gaviniae</i>	potential new species
JDID-147	<i>Enterobacter asburiae</i>	<i>Enterobacter cloacae_M</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter cloacae_M</i>	<i>Enterobacter cloacae_M</i>	<i>Enterobacter asburiae</i>
JDID-148	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_D</i>	<i>Enterobacter asburiae</i> LI	<i>Enterobacter asburiae_D</i>	<i>Enterobacter asburiae_D</i>	potential new species
JDID-149	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter cloacae</i> UCI 49	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae</i>
JDID-150	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter freundii</i> UCI 32	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-151	<i>Citrobacter amalonaticus</i>	<i>Citrobacter_A amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter_A amalonaticus</i>	<i>Citrobacter_A amalonaticus_F</i>	potential new species
JDID-152	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i> 907700	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-153	<i>Citrobacter amalonaticus</i>	<i>Citrobacter_A amalonaticus</i>	<i>Citrobacter</i> sp. MGH 55	<i>Citrobacter_A amalonaticus</i>	<i>Citrobacter_A amalonaticus</i>	<i>Citrobacter amalonaticus</i>
JDID-154	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae</i>
JDID-155	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i> G54	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>
JDID-156	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter freundii</i> 4_7_47CFAA	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-157	<i>Citrobacter cronae</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter freundii</i> CFNIH1	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-158	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter cloacae</i> UCI 49	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae</i>
JDID-159	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter intestinihominis</i>	<i>Enterobacter hormaechei</i>
JDID-160	<i>Duffyella gerundensis</i>	<i>Erwinia_B gerundensis</i>	<i>Pantoea agglomerans</i>	<i>Erwinia_B gerundensis</i>	<i>Duffyella gerundensis</i>	<i>Duffyella gerundensis</i>
JDID-161	<i>Duffyella gerundensis</i>	<i>Erwinia_B gerundensis</i>	<i>Pantoea agglomerans</i>	<i>Erwinia_B gerundensis</i>	<i>Duffyella gerundensis</i>	<i>Duffyella gerundensis</i>
JDID-162	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>

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JDID-163	<i>Providencia heimbachae</i>	<i>Providencia</i> sp003533305	<i>Providencia alcalifaciens</i> F90-2004	<i>Providencia</i> sp003533305	<i>Providencia</i> sp003533305	potential new species
JDID-164	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i> ATCC 29909	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-165	<i>Klebsiella huaxiensis</i>	<i>Klebsiella spallanzanii</i>	<i>Klebsiella michiganensis</i> KCTC 1686	<i>Klebsiella spallanzanii</i>	<i>Klebsiella spallanzanii</i>	<i>Klebsiella spallanzanii</i>
JDID-166	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-167	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter</i> sp. 30_2	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-168	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter freundii</i> 4_7_47CFAA	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-169	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-170	<i>Enterobacter</i> sp. SA187	<i>Enterobacter_D kobei_A</i>	<i>Leclercia adecarboxylata</i>	<i>Enterobacter_D kobei_A</i>	<i>Enterobacter_D kobei_A</i>	<i>Enterobacter kobei</i>
JDID-171	<i>Raoultella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Raoultella ornithinolytica</i> B6	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-172	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea</i> sp. FF5	<i>Pantoea septica</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>
JDID-173	<i>Leclercia</i> sp. 29361	<i>Leclercia</i> sp003024485	<i>Leclercia adecarboxylata</i> ATCC 23216 = NBRC 102595	<i>Leclercia</i> sp003024485	<i>Leclercia tamurae</i>	<i>Leclercia tamurae</i>
JDID-174	<i>Helicobacter winghamensis</i>	<i>Helicobacter_D winghamensis</i>	<i>Helicobacter winghamensis</i> ATCC BAA-430	<i>Helicobacter_D winghamensis</i>	<i>Helicobacter_D winghamensis</i>	<i>Helicobacter winghamensis</i>
JDID-175	<i>Raoultella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Raoultella ornithinolytica</i> 2-156-04_S1_C2	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-176	<i>Raoultella planticola</i>	<i>Klebsiella planticola</i>	<i>Raoultella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-177	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i> NBRC 105721	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-178	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter freundii</i> UCI 32	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-179	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter cloacae</i> UCI 49	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae</i>
JDID-180	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter hormaechei_C</i>	<i>Enterobacter hormaechei</i>
JDID-181	<i>Leclercia adecarboxylata</i>	<i>Leclercia</i> sp002902985	<i>Leclercia adecarboxylata</i>	<i>Leclercia</i> sp002902985	<i>Leclercia</i> sp002902985	potential new species
JDID-182	<i>Cedecea neteri</i>	<i>Cedecea neteri_A</i>	<i>Cedecea neteri</i>	<i>Cedecea neteri_A</i>	<i>Cedecea neteri_A</i>	potential new species
JDID-183	<i>Leclercia adecarboxylata</i>	<i>Leclercia adecarboxylata_D</i>	<i>Leclercia adecarboxylata</i>	<i>Leclercia</i> sp	<i>Leclercia</i> sp	potential new species

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JDID-184	<i>Helicobacter winghamensis</i>	<i>Helicobacter_D winghamensis</i>	<i>Helicobacter winghamensis</i> ATCC BAA-430	<i>Helicobacter_D winghamensis</i>	<i>Helicobacter_D winghamensis</i>	<i>Helicobacter winghamensis</i>
JDID-185	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i> ATCC BAA-894	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Klebsiella ornithinolytica</i>
JDID-186	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Serratia marcescens</i> BIDMC 50	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>
JDID-187	<i>Citrobacter portucalensis</i>	<i>Yersinia alsatica</i>	<i>Citrobacter freundii</i> UCI 32	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Citrobacter portucalensis</i>
JDID-188	<i>Raoultella planticola</i>	<i>Klebsiella planticola</i>	<i>Raoultella planticola</i> ATCC 33531	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-189	<i>Leminorella richardii</i>	<i>Leminorella richardii</i>	<i>Leminorella grimontii</i> ATCC 33999 = DSM 5078	<i>Leminorella richardii</i>	<i>Leminorella richardii</i>	<i>Leminorella richardii</i>
JDID-190	<i>Citrobacter farmeri</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter farmeri</i> GTC 1319	<i>Citrobacter_A farmeri</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter farmeri</i>
JDID-191	<i>Helicobacter cinaedi</i>	<i>Helicobacter_C cinaedi</i>	<i>Helicobacter cinaedi</i> PAGU611	<i>Helicobacter_C cinaedi</i>	<i>Helicobacter_C cinaedi</i>	<i>Helicobacter cinaedi</i>
JDID-192	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i> subsp. <i>hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>
JDID-193	<i>Helicobacter cinaedi</i>	<i>Helicobacter_C labetoulli</i>	<i>Helicobacter cinaedi</i> CCUG 18818 = ATCC BAA-847	<i>Helicobacter_C labetoulli</i>	<i>Helicobacter_C labetoulli</i>	<i>Helicobacter labetoulli</i>
JDID-194	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i> UMEA 3317-1	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-195	<i>Campylobacter lari</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter lari</i> RM2100	<i>Campylobacter_D lari</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter lari</i>
JDID-196	<i>Pseudocitrobacter corydidari</i>	<i>Pseudocitrobacter faecalis</i>	<i>Enterobacteriaceae bacterium</i> strain FGI 57	<i>Pseudocitrobacter faecalis</i>	<i>Pseudocitrobacter faecalis</i>	<i>Pseudocitrobacter faecalis</i>
JDID-197	<i>Lelliottia sp. WB101</i>	<i>Lelliottia nimipressuralis</i>	<i>Leclercia adecarboxylata</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>
JDID-198	<i>Lelliottia sp. AC1</i>	<i>Lelliottia nimipressuralis</i>	<i>Enterobacter asburiae</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>
JDID-199	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter sp.</i> MGH 38	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter hormaechei_C</i>	<i>Enterobacter hormaechei</i>
JDID-200	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter cloacae</i> CHS 79	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-201	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter sp.</i> MGH 38	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter hormaechei_C</i>	<i>Enterobacter hormaechei</i>
JDID-202	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter sp.</i> 5-4	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>

JDID-203	<i>Leclercia</i> sp. 29361	<i>Leclercia</i> sp003024485	<i>Leclercia</i> adecarboxylata ATCC 23216 = NBRC 102595	<i>Leclercia</i> sp003024485	<i>Leclercia</i> tamurae	<i>Leclercia</i> tamurae
JDID-204	<i>Leclercia</i> sp. 29361	<i>Leclercia</i> sp003024485	<i>Leclercia</i> adecarboxylata ATCC 23216 = NBRC 102595	<i>Leclercia</i> sp003024485	<i>Leclercia</i> tamurae	<i>Leclercia</i> tamurae
JDID-205	<i>Helicobacter pullorum</i>	<i>Campylobacter</i> _D upsaliensis	<i>Campylobacter</i> upsaliensis JV21	<i>Campylobacter</i> _D upsaliensis	<i>Campylobacter</i> _D upsaliensis	potential new species
JDID-206	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Serratia marcescens</i> subsp. <i>marcescens</i> Db11	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>
JDID-207	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter rongchengensis</i>
JDID-208	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter rongchengensis</i>
JDID-209	<i>Serratia plymuthica</i>	<i>Serratia</i> _J <i>plymuthica</i>	<i>Serratia plymuthica</i> S13	<i>Serratia</i> _J <i>plymuthica</i>	<i>Serratia plymuthica</i>	<i>Serratia plymuthica</i>
JDID-210	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter</i> sp. 5-4	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-211	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	<i>Enterobacter</i> sp. MGH 25	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>
JDID-212	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>	<i>Enterobacter</i> sp. BIDMC 29	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>
JDID-213	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i> subsp. <i>hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>
JDID-214	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter</i> sp. 5-4	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-215	<i>Helicobacter pullorum</i>	<i>Helicobacter</i> _D <i>pullorum</i>	<i>Helicobacter pullorum</i> MIT 98-5489	<i>Helicobacter</i> _D <i>pullorum</i>	<i>Helicobacter</i> _D <i>pullorum</i>	<i>Helicobacter pullorum</i>
JDID-216	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i> BIDMC 47	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-217	<i>Raoultella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Raoultella ornithinolytica</i> 2-156-04_S1_C2	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-218	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter cancerogenus</i> YZ1	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>
JDID-219	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>	<i>Enterobacter asburiae</i> LF7a	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>
JDID-220	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i> _A	<i>Enterobacter cloacae</i>	<i>Enterobacter hormaechei</i> _A	<i>Enterobacter intestinihominis</i>	<i>Enterobacter hormaechei</i>
JDID-221	<i>Sodalis ligni</i>	No Species Identified	<i>Pluralibacter gergoviae</i>	<i>Acerihibitans</i> sp	<i>Acerihibitans</i> sp	potential new species
JDID-222	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i> BIDMC 78	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>

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JDID-223	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i> _CK	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i> _CY	potential new species
JDID-224	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i> oki422	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i> _CY	potential new species
JDID-225	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i> 5-172-05_S1_C1	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>
JDID-226	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-227	<i>Campylobacter lari</i>	<i>Campylobacter</i> _D lari	<i>Campylobacter lari</i> RM2100	<i>Campylobacter</i> _D lari	<i>Campylobacter</i> _D lari	<i>Campylobacter lari</i>
JDID-228	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i> ATCC BAA-894	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-229	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i> oki422	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i> _CY	potential new species
JDID-230	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i> _CK	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i> _CX	potential new species
JDID-231	<i>Providencia</i> sp. R33	<i>Providencia vermicola</i>	<i>Providencia rettgeri</i> DSM 1131	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>	<i>Providencia xihuensis</i>
JDID-232	<i>Providencia</i> sp. R33	<i>Hafnia paralvei</i>	<i>Hafnia alvei</i> ATCC 51873	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	potential new species
JDID-233	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-234	<i>Salmonella enterica</i>	<i>Phytobacter diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-235	<i>Campylobacter jejuni</i>	<i>Campylobacter</i> _D jejuni	<i>Campylobacter jejuni</i> subsp. jejuni 1854	<i>Campylobacter</i> _D jejuni	<i>Campylobacter</i> _D jejuni	<i>Campylobacter jejuni</i>
JDID-236	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i> ES35	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-237	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-238	<i>Salmonella enterica</i>	<i>Pantoea eucrina</i>	<i>Pantoea</i> sp. PSNIH1	<i>Pantoea eucrina</i>	<i>Pantoea eucrina</i>	<i>Pantoea eucrina</i>
JDID-239	<i>Providencia</i> sp. R33	<i>Buttiauxella</i> sp002321695	<i>Pluralibacter gergoviae</i>	<i>Buttiauxella</i> sp002321695	<i>Dryocola</i> sp002321695	potential new species
JDID-240	<i>Cedecea neteri</i>	<i>Cedecea neteri</i> _A	<i>Cedecea neteri</i>	<i>Cedecea neteri</i> _A	<i>Cedecea neteri</i> _A	potential new species
JDID-241	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i> ATCC 33433	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>
JDID-242	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i> _A	<i>Enterobacter cloacae</i> MGH 53	<i>Enterobacter hormaechei</i> _A	<i>Enterobacter hormaechei</i> _C	<i>Enterobacter hormaechei</i>
JDID-243	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter freundii</i> UCI 32	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-244	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>

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JDID-245	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia</i> <i>sp002918705</i>	<i>Pseudescherichia vulneris</i> <i>NBRC 102420</i>	<i>Pseudescherichia</i> <i>sp002918705</i>	<i>Pseudescherichia</i> <i>sp002918705</i>	potential new species
JDID-246	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>
JDID-247	<i>Providencia</i> sp. R33	<i>Providencia vermicola</i>	<i>Providencia rettgeri</i>	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>	<i>Providencia xihuensis</i>
JDID-248	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter hormaechei</i> <i>ATCC 49162</i>	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter</i> <i>oligotrophicus</i>	<i>Enterobacter</i> <i>oligotrophicus</i>
JDID-249	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i> <i>subsp. enterica serovar</i> <i>Enteritidis str. PT23</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella typhi</i>
JDID-250	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>
JDID-251	<i>Raoultella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Raoultella ornithinolytica</i> <i>B6</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-252	<i>Enterobacter</i> <i>roggenkampii</i>	<i>Enterobacter</i> <i>roggenkampii</i>	<i>Enterobacter cloacae</i> <i>UCICRE 12</i>	<i>Enterobacter</i> <i>roggenkampii</i>	<i>Enterobacter</i> <i>roggenkampii</i>	<i>Enterobacter</i> <i>roggenkampii</i>
JDID-253	<i>Campylobacter</i> <i>upsaliensis</i>	<i>Campylobacter_D</i> <i>upsaliensis</i>	<i>Campylobacter</i> <i>upsaliensis JV21</i>	<i>Campylobacter_D</i> <i>upsaliensis</i>	<i>Campylobacter_D</i> <i>upsaliensis</i>	potential new species
JDID-254	<i>Salmonella enterica</i>	<i>Mixta calida</i>	<i>Pantoea</i> sp. PSNIH2	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>
JDID-255	<i>Staphylococcus</i> <i>pseudintermedius</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i> ATCC 29909	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-256	<i>Yersinia intermedia</i>	<i>Yersinia alsatica</i>	<i>Yersinia frederiksenii</i> <i>ATCC 33641</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>
JDID-257	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i> ATCC 29909	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-258	<i>Yersinia intermedia</i>	<i>Yersinia enterocolitica_E</i>	<i>Yersinia intermedia</i> ATCC 29909	<i>Yersinia enterocolitica_E</i>	<i>Yersinia enterocolitica_E</i>	potential new species
JDID-259	<i>Scandinavium</i> <i>goeteborgense</i>	No Species Identified	<i>Trabulsiella guamensis</i> <i>ATCC 49490</i>	<i>Scandinavium</i> sp	<i>Scandinavium</i> sp	potential new species
JDID-260	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>
JDID-261	<i>Escherichia coli</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>
JDID-262	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>	<i>Phytobacter</i> <i>diazotrophicus</i>
JDID-263	<i>Serratia grimesii</i>	<i>Serratia_J</i> sp017832355	<i>Serratia grimesii</i>	<i>Serratia_J</i> sp017832355	<i>Serratia</i> sp017832355	potential new species
JDID-264	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Pantoea</i> sp. PSNIH2	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>
JDID-265	<i>Enterobacter hormaechei</i>	<i>Enterobacter</i> <i>hormaechei_A</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter</i> <i>hormaechei_A</i>	<i>Enterobacter</i> <i>intestinihominis</i>	<i>Enterobacter hormaechei</i>
JDID-266	<i>Providencia rettgeri</i>	<i>Providencia_C</i> <i>manganoxydans</i>	<i>Providencia stuartii</i> <i>ATCC 25827</i>	<i>Providencia_C</i> <i>manganoxydans</i>	<i>Providencia</i> <i>manganoxydans</i>	<i>Providencia</i> <i>manganoxydans</i>

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JDID-267	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>
JDID-268	<i>Helicobacter canadensis</i>	<i>Helicobacter_D valdiviensis</i>	<i>Campylobacter lari</i> subsp. <i>concheus</i> LMG 11760	<i>Helicobacter_D valdiviensis</i>	<i>Helicobacter_D valdiviensis</i>	<i>Helicobacter valdiviensis</i>
JDID-269	<i>Helicobacter pylori</i>	<i>Helicobacter pylori_CK</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori_CX</i>	potential new species
JDID-270	<i>Helicobacter pylori</i>	<i>Helicobacter pylori_CK</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori_CX</i>	potential new species
JDID-271	<i>Campylobacter coli</i>	<i>Campylobacter_D coli_A</i>	<i>Campylobacter coli</i> BIGS0006	<i>Campylobacter_D coli_A</i>	<i>Campylobacter_D coli_A</i>	potential new species
JDID-272	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i> subsp. <i>fetus</i> 82-40	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>
JDID-273	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i> subsp. <i>fetus</i> 82-40	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>
JDID-274	<i>Campylobacter upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter upsaliensis</i> JV21	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	potential new species
JDID-275	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> ATCC 33560	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i>
JDID-276	<i>Cutibacterium acnes</i>	No Species Identified	<i>Campylobacter cuniculorum</i> DSM 23162 = LMG 24588	<i>Campylobacter_B sp</i>	<i>Campylobacter_B sp</i>	potential new species
JDID-277	<i>Campylobacter showae</i>	<i>Campylobacter_A showae_E</i>	<i>Campylobacter showae</i> RM3277	<i>Campylobacter_A sp</i>	<i>Campylobacter_A sp</i> 963517705	potential new species
JDID-278	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter cloacae</i> str. <i>Hanford</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>
JDID-279	<i>Pantoea anthophila</i>	<i>Pantoea anthophila</i>	<i>Pantoea</i> sp. <i>Sc1</i>	<i>Pantoea anthophila</i>	<i>Pantoea anthophila</i>	<i>Pantoea anthophila</i>
JDID-280	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Stanley</i> str. 06-0538	<i>Pantoea septica</i>	<i>Pantoea septica</i>	potential new species
JDID-281	<i>Bacillus velezensis</i>	<i>Bacillus velezensis</i>	<i>Bacillus velezensis</i> AS43.3	<i>Bacillus velezensis</i>	<i>Bacillus velezensis</i>	<i>Bacillus velezensis</i>
JDID-282	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella oxytoca</i> KONIH1	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>
JDID-283	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Pantoea</i> sp. <i>PSNIH2</i>	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i>
JDID-284	<i>Serratia marcescens</i>	<i>Serratia nematodiphila</i>	<i>Serratia nematodiphila</i>	<i>Serratia nematodiphila</i>	<i>Serratia nematodiphila</i>	<i>Serratia marcescens</i>
JDID-285	<i>Pantoea</i> sp. <i>CCBC3-3-1</i>	<i>Erwinia</i> sp003937915	<i>Erwinia typographi</i>	<i>Erwinia</i> sp003937915	<i>Erwinia</i> sp003937915	<i>Erwinia aeris</i>
JDID-286	<i>Pantoea piersonii</i>	<i>Pantoea piersonii</i>	<i>Pantoea</i> sp. <i>NGS-ED-1003</i>	<i>Pantoea piersonii</i>	<i>Pantoea piersonii</i>	<i>Pantoea piersonii</i>
JDID-287	<i>Campylobacter lari</i>	<i>Campylobacter_D lari_D</i>	<i>Campylobacter lari</i> CCUG 22395	<i>Campylobacter_D lari_D</i>	<i>Campylobacter_D lari_D</i>	potential new species
JDID-288	<i>Salmonella enterica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i> subsp. <i>palaearctica</i> YE-P4	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>

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JDID-289	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter intestinihominis</i>	<i>Enterobacter hormaechei</i>
JDID-290	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>
JDID-291	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>
JDID-292	<i>Campylobacter lari</i>	<i>Campylobacter_D concheus</i>	<i>Campylobacter lari</i> subsp. <i>concheus</i> LMG 11760	<i>Campylobacter_D concheus</i>	<i>Campylobacter_D concheus</i>	<i>Campylobacter lari</i>
JDID-293	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-294	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i> Lm25180	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-295	<i>Phytobacter</i> sp. SCO41	<i>Phytobacter diazotrophicus</i>	<i>Enterobacter</i> sp. Bisph2	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-296	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i> LMG 20103	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>	<i>Pantoea ananatis</i>
JDID-297	<i>Kytococcus sedentarius</i>	<i>Kytococcus sedentarius</i>	<i>Campylobacter showae</i> RM3277	<i>Campylobacter_A</i> sp	<i>Campylobacter_A</i> sp963519915	<i>Kytococcus sedentarius</i>
JDID-298	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia bercovieri</i> ATCC 43970	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>
JDID-299	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia bercovieri</i> ATCC 43970	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>	<i>Yersinia aleksiciae</i>
JDID-300	<i>Salmonella enterica</i>	<i>Pantoea septica</i>	<i>Pantoea</i> sp. NGS-ED-1003	<i>Pantoea septica</i>	<i>Pantoea septica</i>	potential new species
JDID-301	<i>Escherichia coli</i>	<i>Escherichia</i> sp002965065	<i>Escherichia coli</i>	<i>Escherichia</i> sp002965065	<i>Escherichia</i> sp002965065	potential new species
JDID-302	<i>Campylobacter lari</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter lari</i> RM2100	<i>Campylobacter_D lari</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter lari</i>
JDID-303	<i>Aliarcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>	<i>Arcobacter butzleri</i> RM4018	<i>Aliarcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>	<i>Arcobacter butzleri</i>
JDID-304	<i>Campylobacter upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter upsaliensis</i> JV21	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>	potential new species
JDID-305	<i>Helicobacter pylori</i>	<i>Helicobacter pylori_CK</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori_CX</i>	potential new species
JDID-306	<i>Helicobacter pylori</i>	<i>Helicobacter pylori_CK</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori_CX</i>	potential new species
JDID-307	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> D2600	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter jejuni</i>
JDID-308	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i> ATCC 29909	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-309	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>
JDID-310	<i>Helicobacter pullorum</i>	<i>Helicobacter_D pullorum</i>	<i>Helicobacter pullorum</i> MIT 98-5489	<i>Helicobacter_D pullorum</i>	<i>Helicobacter_D pullorum</i>	<i>Helicobacter pullorum</i>
JDID-311	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>

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JDID-312	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae</i>
JDID-313	<i>Phytobacter</i> sp. SCO41	<i>Phytobacter diazotrophicus</i>	<i>Enterobacter</i> sp. BispH2	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-314	<i>Citrobacter freundii</i>	<i>Citrobacter murlinae</i>	<i>Citrobacter</i> sp. S-77	<i>Citrobacter murlinae</i>	<i>Citrobacter murlinae</i>	potential new species
JDID-315	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-316	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i> Lm25180	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-317	analysis not performed					
JDID-318	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i> (type O:5) str. YE53/03	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	potential new species
JDID-319	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i> Hp H-45	<i>Helicobacter pylori</i>	<i>Helicobacter pylori</i>	potential new species
JDID-320	<i>Helicobacter winghamensis</i>	<i>Helicobacter_D winghamensis</i>	<i>Helicobacter winghamensis</i> ATCC BAA-430	<i>Helicobacter_D winghamensis</i>	<i>Helicobacter_D winghamensis</i>	<i>Helicobacter cinaedi</i>
JDID-321	analysis not performed					
JDID-322	<i>Proteus mirabilis</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>
JDID-323	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i> KCTC 2190	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>
JDID-324	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i> BRL6-2	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>
JDID-325	<i>Proteus mirabilis</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i> ATCC 13337	Unclassified	JDID-325.final.filtered.assembly	<i>Proteus mirabilis</i>
JDID-326	<i>Citrobacter amalonaticus</i>	<i>Citrobacter_A amalonaticus</i>	<i>Citrobacter amalonaticus</i>	<i>Citrobacter_A amalonaticus</i>	<i>Citrobacter_A amalonaticus</i>	<i>Citrobacter amalonaticus</i>
JDID-327	<i>Citrobacter koseri</i>	<i>Citrobacter_B koseri</i>	<i>Escherichia coli</i> HVH 154 (4-5636698)	<i>Citrobacter_B koseri</i>	<i>Citrobacter_B koseri</i>	<i>Citrobacter koseri</i>
JDID-328	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i> BB2000	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-329	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i> NBRC 102416	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-330	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i> ATCC 29906	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-331	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i> DSM 4481 = NBRC 105725	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>
JDID-332	<i>Enterobacter</i> sp. C2	<i>Pseudescherichia</i> sp002298805	<i>Pseudescherichia vulneris</i> NBRC 102420	<i>Pseudescherichia</i> sp002298805	<i>Pseudescherichia</i> sp002298805	potential new species
JDID-333	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i> ATCC 35316	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>

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JDID-334	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i> ATCC 33301	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>
JDID-335	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i> ATCC 33301	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>
JDID-336	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i> DSM 4481 = NBRC 105725	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>
JDID-337	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i> DSM 4481 = NBRC 105725	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>
JDID-338	<i>Proteus penneri</i>	<i>Proteus penneri</i>	<i>Proteus hauseri</i> ZMd44	<i>Proteus penneri</i>	<i>Proteus penneri</i>	<i>Proteus penneri</i>
JDID-339	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i> NBRC 105704	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Escherichia hermannii</i>
JDID-340	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i> NBRC 105704	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Escherichia hermannii</i>
JDID-341	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i> NBRC 105704	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Escherichia hermannii</i>
JDID-342	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i> NBRC 105704	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Escherichia hermannii</i>
JDID-343	<i>Pseudoescherichia vulneris</i>	<i>Pseudoescherichia vulneris</i>	<i>Pseudoescherichia vulneris</i> NBRC 102420	<i>Pseudoescherichia vulneris</i>	<i>Pseudoescherichia vulneris</i>	<i>Pseudoescherichia vulneris</i>
JDID-344	<i>Enterobacter</i> sp. C2	<i>Pseudoescherichia vulneris</i>	<i>Pseudoescherichia vulneris</i> NBRC 102420	<i>Pseudoescherichia vulneris</i>	<i>Pseudoescherichia vulneris</i>	<i>Pseudoescherichia vulneris</i>
JDID-345	<i>Enterobacter</i> sp. C2	<i>Pseudoescherichia vulneris</i>	<i>Pseudoescherichia vulneris</i> NBRC 102420	<i>Pseudoescherichia vulneris</i>	<i>Pseudoescherichia vulneris</i>	<i>Pseudoescherichia vulneris</i>
JDID-346	<i>Ewingella americana</i>	<i>Ewingella americana</i>	<i>Ewingella americana</i> ATCC 33852	<i>Ewingella americana</i>	<i>Ewingella americana</i>	<i>Ewingella americana</i>
JDID-347	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i> A35218R	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-348	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-349	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-350	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-351	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i> ECD227	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-352	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i> ECD227	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-353	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i> LI	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>
JDID-354	<i>Yersinia mollaretii</i>	<i>Yersinia mollaretii</i>	<i>Yersinia mollaretii</i> ATCC 43969	<i>Yersinia mollaretii</i>	<i>Yersinia mollaretii</i>	<i>Yersinia mollaretii</i>
JDID-355	<i>Citrobacter farmeri</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter farmeri</i> GTC 1319	<i>Citrobacter_A farmeri</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter farmeri</i>

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JDID-356	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i> ATCC 33301	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>
JDID-357	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i> ATCC 33301	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>
JDID-358	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i> ATCC 33301	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>	<i>Tatumella pyseos</i>
JDID-359	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i> ES713	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-360	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i> subsp. <i>lactaridi</i> LMG 23825	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>
JDID-361	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>	<i>Citrobacter malonaticus</i>
JDID-362	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i> ATCC 51329	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i>
JDID-363	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-364	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i> ATCC 29906	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-365	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i> ATCC 29906	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>

Table A2. Raw taxonomic outputs from ONT WGS-based workflows. Unfiltered taxonomic assignments returned by each ONT-based classification tool prior to reconciliation, standardization, or exclusion. Entries include valid taxon names, synonymous or outdated nomenclature, provisional or non-standard labels, and subspecies assignments. Cells left blank indicate that the tool did not return a taxonomic assignment and instances where analysis was not performed are explicitly indicated. These raw outputs were subsequently reconciled by consolidating synonyms under a single accepted name (Table A13), removing invalid taxa, and truncating subspecies designations to genus-species level for downstream analysis in Section 3.2.

Isolate	Mikrokonodo - Kraken2	Mikrokonodo - Mash	GTDB-Tk - skANI
JDID-01	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter hormaechei_C</i>
JDID-02	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-03	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>
JDID-04		analysis not performed	
JDID-05	<i>Morganella morganii</i>	<i>Morganella morganii</i>	<i>Morganella morganii</i>
JDID-06	<i>Providencia rettgeri</i>	<i>Providencia rettgeri_A</i>	<i>Providencia xianensis</i>
JDID-07	<i>Lelliottia sp. AC1</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>
JDID-08	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>
JDID-09	<i>Tatumella ptyseos</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>
JDID-10	<i>Pantoea piersonii</i>	<i>Erwinia sp003937915</i>	<i>Erwinia sp003937915</i>
JDID-11	<i>Serratia entomophila</i>	<i>Serratia entomophila</i>	<i>Serratia sp</i>
JDID-12	<i>Campylobacter sputorum</i>	<i>Campylobacter_B sputorum</i>	<i>Campylobacter_F sputorum</i>
JDID-13	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>
JDID-14	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>
JDID-15	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>
JDID-16		analysis not performed	
JDID-17		analysis not performed	
JDID-18	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-19	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-20	<i>Klebsiella pneumoniae</i>	<i>Citrobacter werkmanii</i>	Unclassified
JDID-21	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>
JDID-22	<i>Serratia marcescens</i>	<i>Serratia nematodiphila</i>	<i>Serratia nematodiphila</i>
JDID-23	<i>Campylobacter peloridis</i>	<i>Campylobacter_D lari_C</i>	<i>Campylobacter_D lari_C</i>
JDID-24	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-25	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>

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JDID-26	<i>Enterobacter hormaechei</i>	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>
JDID-27	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>	<i>Campylobacter hyointestinalis</i>
JDID-28	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-29		analysis not performed	
JDID-30		analysis not performed	
JDID-31		analysis not performed	
JDID-32	<i>Hafnia paralvei</i>	<i>Hafnia alvei</i>	<i>Hafnia alvei</i>
JDID-33	<i>Serratia entomophila</i>	<i>Serratia entomophila</i>	<i>Serratia sp</i>
JDID-34	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis_A</i>
JDID-35		analysis not performed	
JDID-36	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>
JDID-37	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter intestinihominis</i>
JDID-38	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>
JDID-39	<i>Campylobacter lari</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter_D lari</i>
JDID-40		analysis not performed	
JDID-41	<i>Serratia liquefaciens</i>	<i>Serratia_J liquefaciens</i>	<i>Serratia liquefaciens</i>
JDID-42	analysis not performed		
JDID-43	<i>Klebsiella pneumoniae</i>	<i>Kluyvera cryocrescens</i>	<i>Kluyvera cryocrescens</i>
JDID-44		analysis not performed	
JDID-45		analysis not performed	
JDID-46	<i>Providencia rettgeri</i>	<i>Campylobacter fetus</i>	<i>Campylobacter fetus</i>
JDID-47	<i>Campylobacter hyointestinalis</i>	<i>Citrobacter_B koseri</i>	<i>Unclassified</i>
JDID-48	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Unclassified</i>
JDID-49		analysis not performed	
JDID-50		analysis not performed	
JDID-51		analysis not performed	
JDID-52		analysis not performed	
JDID-53		analysis not performed	
JDID-54		analysis not performed	
JDID-55		analysis not performed	
JDID-56	<i>Klebsiella pneumoniae</i>	<i>Enterobacter roggkampii</i>	<i>Unclassified</i>
JDID-57	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>
JDID-58	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-59	<i>Enterobacter hormaechei</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-60	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-61	<i>Yersinia pseudotuberculosis</i>	<i>Yersinia pestis</i>	<i>Yersinia pestis</i>
JDID-62	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>
JDID-63	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis_A</i>
JDID-64		analysis not performed	
JDID-65	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	<i>Yersinia proxima</i>
JDID-66	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis</i>	<i>Yersinia massiliensis_A</i>
JDID-67	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>
JDID-68	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>

JDID-69	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-70	<i>Escherichia coli</i>	<i>Escherichia coli</i>	Unclassified
JDID-71	<i>Klebsiella pneumoniae</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>
JDID-72	<i>Escherichia coli</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-73	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>
JDID-74	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-75	<i>Aeromonas hydrophila</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-76	<i>Tatumella ptyseos</i>	<i>Tatumella saanichensis</i>	<i>Tatumella saanichensis</i>
JDID-77	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-78	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-79	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-80	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>
JDID-81	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-82	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-83	<i>Citrobacter freundii</i>	No Species Identified	Unclassified
JDID-84	<i>Klebsiella pneumoniae</i>	<i>Superficieibacter sp002421005</i>	<i>Superficieibacter sp002421005</i>
JDID-85	<i>Yersinia enterocolitica</i>	<i>Yersinia proxima</i>	Unclassified
JDID-86	<i>Klebsiella pneumoniae</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter_A farmeri</i>
JDID-87		analysis not performed	
JDID-88	<i>Pantoea sp. At-9b</i>	<i>Pantoea cancerogena_A</i>	<i>Pantoea communis</i>
JDID-89	<i>Kosakonia radicincitans</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-90	<i>Escherichia coli</i>	<i>Kluyvera georgiana_A</i>	<i>Kluyvera georgiana_A</i>
JDID-91		analysis not performed	
JDID-92		analysis not performed	
JDID-93	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>
JDID-94	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-95	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-96	<i>Klebsiella pneumoniae</i>	<i>Serratia_J liquefaciens</i>	analysis not performed
JDID-97	<i>Phytobacter sp. MRY16-398</i>	No Species Identified	<i>Phytobacter sp</i>
JDID-98	<i>Sodalis ligni</i>	No Species Identified	<i>Acerihabitans sp</i>
JDID-99	<i>Hafnia alvei</i>	No Species Identified	Unclassified
JDID-100	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>	<i>Enterobacter soli</i>
JDID-101	<i>Klebsiella quasipneumoniae</i>	<i>Citrobacter freundii</i>	<i>Citrobacter freundii</i>
JDID-102	<i>Escherichia coli</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-103	<i>Klebsiella pneumoniae</i>	<i>Serratia_J liquefaciens</i>	analysis not performed
JDID-104	<i>Klebsiella michiganensis</i>	<i>Klebsiella terrigena</i>	<i>Klebsiella terrigena</i>
JDID-105	<i>Kluyvera sp. CRP</i>	<i>Kluyvera georgiana_A</i>	<i>Kluyvera georgiana_A</i>
JDID-106	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-107	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>	<i>Aeromonas hydrophila</i>
JDID-108	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>
JDID-109	<i>Klebsiella quasipneumoniae</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>
JDID-110	<i>Enterobacter kobei</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-111	<i>Aeromonas media</i>	<i>Aeromonas rivipollensis</i>	<i>Aeromonas sp023093515</i>

JDID-112	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-113	<i>Aeromonas hydrophila</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-114	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>
JDID-115	<i>Leclercia</i> sp. 29361	<i>Leclercia</i> sp003024485	<i>Leclercia tamurae</i>
JDID-116	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-117	<i>Proteus mirabilis</i>	<i>Proteus myxofaciens</i>	<i>Proteus</i> sp
JDID-118	analysis not performed		
JDID-119	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-120	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-121	<i>Kluyvera ascorbata</i>	<i>Kluyvera georgiana_A</i>	<i>Kluyvera georgiana_A</i>
JDID-122	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-123	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-124	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-125	<i>Serratia liquefaciens</i>	<i>Serratia_J liquefaciens</i>	<i>Serratia liquefaciens</i>
JDID-126	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-127	<i>Serratia marcescens</i>	<i>Serratia marcescens_K</i>	<i>Serratia sarumanii</i>
JDID-128	<i>Kluyvera</i> sp. CRP	<i>Kluyvera georgiana_A</i>	<i>Kluyvera georgiana_A</i>
JDID-129	<i>Serratia marcescens</i>	<i>Serratia_J quinivorans</i>	<i>Serratia quinivorans</i>
JDID-130	<i>Serratia marcescens</i>	No Species Identified	<i>Serratia ureilytica</i>
JDID-131	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-132	<i>Klebsiella pneumoniae</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>
JDID-133	<i>Klebsiella quasipneumoniae</i>	<i>Kluyvera ascorbata</i>	<i>Kluyvera ascorbata</i>
JDID-134	<i>Enterobacter ludwigii</i>	<i>Enterobacter asburiae_D</i>	<i>Enterobacter</i> sp
JDID-135	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>
JDID-136	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-137	<i>Proteus mirabilis</i>	<i>Proteus myxofaciens</i>	<i>Proteus</i> sp
JDID-138	analysis not performed		
JDID-139	<i>Proteus columbae</i>	<i>Proteus</i> sp003144505	<i>Proteus</i> sp003144505
JDID-140	<i>Proteus mirabilis</i>	<i>Proteus myxofaciens</i>	<i>Proteus</i> sp
JDID-141	analysis not performed		
JDID-142	<i>Citrobacter</i> sp. RHB25-C09	<i>Citrobacter_A sedlakii</i>	<i>Citrobacter_A sedlakii</i>
JDID-143	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>
JDID-144	<i>Proteus mirabilis</i>	<i>Proteus myxofaciens</i>	<i>Proteus</i> sp
JDID-145	<i>Escherichia coli</i>	<i>Citrobacter_A amalonaticus</i>	<i>Citrobacter portucalensis</i>
JDID-146	<i>Klebsiella pneumoniae</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>
JDID-147	<i>Enterobacter roggenkampii</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>
JDID-148	<i>Pantoea rwandensis</i>	<i>Pantoea cancerogena_A</i>	<i>Pantoea communis</i>
JDID-149	<i>Leclercia pneumoniae</i>	UBA7405 sp000755535	<i>Leclercia_A pneumoniae</i>
JDID-150	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-151	<i>Klebsiella pneumoniae</i>	<i>Pseudocitrobacter corydidari</i>	<i>Pseudocitrobacter corydidari</i>
JDID-152	<i>Escherichia coli</i>	<i>Salmonella enterica</i>	<i>Escherichia coli</i>
JDID-153	<i>Enterobacter ludwigii</i>	<i>Enterobacter asburiae_D</i>	<i>Enterobacter</i> sp
JDID-154	<i>Escherichia coli</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter_A farmeri</i>

JDID-155	<i>Buttiauxella agrestis</i>	<i>Buttiauxella massiliensis</i>	<i>Buttiauxella gaviniae</i>
JDID-156	<i>Serratia marcescens</i>	<i>Serratia marcescens_K</i>	<i>Serratia sarumanii</i>
JDID-157	<i>Citrobacter cronae</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-158	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>
JDID-159	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter intestinihominis</i>
JDID-160	<i>Duffyella gerundensis</i>	<i>Erwinia_B gerundensis</i>	<i>Duffyella gerundensis</i>
JDID-161	<i>Klebsiella pneumoniae</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-162	analysis not performed		
JDID-163	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-164	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-165	<i>Klebsiella pneumoniae</i>	<i>Citrobacter werkmanii</i>	<i>Citrobacter werkmanii</i>
JDID-166	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-167	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-168	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-169	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-170	<i>Enterobacter sp. SA187</i>	<i>Enterobacter_D kobei_A</i>	<i>Enterobacter_D kobei_A</i>
JDID-171	<i>Klebsiella pneumoniae</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-172	<i>Pantoea agglomerans</i>	<i>Pantoea septica</i>	<i>Pantoea septica</i>
JDID-173	<i>Leclercia sp. 29361</i>	<i>Leclercia sp003024485</i>	<i>Leclercia tamurae</i>
JDID-174	analysis not performed		
JDID-175	<i>Klebsiella pneumoniae</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-176	<i>Raoultella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-177	analysis not performed		
JDID-178	<i>Escherichia coli</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-179	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>
JDID-180	analysis not performed		
JDID-181	<i>Leclercia adecarboxylata</i>	No Species Identified	Unclassified
JDID-182	<i>Cedecea neteri</i>	<i>Cedecea neteri_A</i>	<i>Cedecea neteri_A</i>
JDID-183	<i>Leclercia sp. W17</i>	<i>Leclercia adecarboxylata_D</i>	<i>Leclercia sp</i>
JDID-184	<i>Klebsiella pneumoniae</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-185	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-186	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>	<i>Chimaeribacter arupi</i>
JDID-187	<i>Raoultella planticola</i>	<i>Yersinia alsatica</i>	Unclassified
JDID-188	<i>Raoultella planticola</i>	<i>Klebsiella planticola</i>	<i>Klebsiella planticola</i>
JDID-189	analysis not performed		
JDID-190	<i>Enterobacter roggenkampii</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>
JDID-191	analysis not performed		
JDID-192	<i>Phytobacter sp. SCO41</i>	<i>Salmonella enterica</i>	Unclassified
JDID-193	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-194	<i>Chimaeribacter arupi</i>	<i>Leminorella richardii</i>	Unclassified
JDID-195	<i>Enterobacter roggenkampii</i>	<i>Enterobacter asburiae_B</i>	<i>Enterobacter asburiae_B</i>
JDID-196	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>
JDID-197	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i>	<i>Listeria monocytogenes</i> ⁶⁸

JDID-198	analysis not performed		
JDID-199	analysis not performed		
JDID-200	<i>Campylobacter sputorum</i>	<i>Campylobacter_B sputorum</i>	<i>Campylobacter_F sputorum</i>
JDID-201	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-202	<i>Leclercia sp. 29361</i>	<i>Leclercia sp003024485</i>	<i>Leclercia tamurae</i>
JDID-203	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-204	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-205	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-206	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter hormaechei_C</i>
JDID-207	<i>Enterobacter kobei</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>
JDID-208	<i>Enterobacter roggenkampii</i>	<i>Enterobacter chengduensis</i>	<i>Enterobacter chengduensis</i>
JDID-209	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-210	<i>Serratia plymuthica</i>	<i>Serratia_J plymuthica</i>	<i>Serratia plymuthica</i>
JDID-211	<i>Enterobacter asburiae</i>	<i>Enterobacter kobei</i>	<i>Enterobacter kobei</i>
JDID-212	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>	<i>Enterobacter chuandaensis</i>
JDID-213	analysis not performed		
JDID-214	<i>Salmonella enterica</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-215	<i>Escherichia coli</i>	<i>Escherichia sp002965065</i>	<i>Escherichia sp002965065</i>
JDID-216	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-217	<i>Raoultella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-218	<i>Enterobacter hormaechei</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>
JDID-219	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>
JDID-220	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter intestinhominis</i>
JDID-221	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i>
JDID-222	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-223	<i>Campylobacter jejuni</i>	<i>Phytobacter diazotrophicus</i>	Unclassified
JDID-224	<i>Phytobacter sp. SCO41</i>	<i>Phytobacter diazotrophicus</i>	Unclassified
JDID-225	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>	<i>Aeromonas caviae</i>
JDID-226	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-227	<i>Aeromonas media</i>	<i>Aeromonas rivipollensis</i>	<i>Aeromonas sp023093515</i>
JDID-228	<i>Salmonella enterica</i>	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>
JDID-229	analysis not performed		
JDID-230	analysis not performed		
JDID-231	<i>Campylobacter peloridis</i>	<i>Campylobacter_D peloridis</i>	<i>Campylobacter_D peloridis</i>
JDID-232	<i>Hafnia alvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>
JDID-233	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-234	<i>Phytobacter sp. MRY16-398</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-235	<i>Klebsiella oxytoca</i>	<i>Citrobacter_B koseri</i>	<i>Citrobacter_B koseri</i>
JDID-236	analysis not performed		
JDID-237	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-238	<i>Pantoea eucrina</i>	<i>Pantoea eucrina</i>	Unclassified
JDID-239	<i>Enterobacter hormaechei</i>	<i>Buttiauxella sp002321695</i>	<i>Dryocola sp002321695</i>
JDID-240	<i>Cedecea neteri</i>	<i>Cedecea neteri_A</i>	<i>Cedecea neteri_A</i>

JDID-241	<i>Hafnia alvei</i>	<i>Kluyvera ascorbata</i>	Unclassified
JDID-242		analysis not performed	
JDID-243	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>	<i>Citrobacter portucalensis</i>
JDID-244	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter intestinihominis</i>
JDID-245	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia</i> sp002918705	<i>Pseudescherichia</i> sp002918705
JDID-246	<i>Phytobacter</i> sp. MRY16-398	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-247	<i>Providencia alcalifaciens</i>	<i>Providencia vermicola</i>	<i>Providencia vermicola</i>
JDID-248	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-249	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>	<i>Salmonella enterica</i>
JDID-250	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>
JDID-251	<i>Raoultella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>	<i>Klebsiella ornithinolytica</i>
JDID-252	<i>Salmonella enterica</i>	<i>Enterobacter roggenkampii</i>	<i>Enterobacter roggenkampii</i>
JDID-253	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>
JDID-254	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>
JDID-255	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-256	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>	<i>Yersinia alsatica</i>
JDID-257	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>	<i>Yersinia intermedia</i>
JDID-258	<i>Yersinia intermedia</i>	<i>Yersinia enterocolitica_E</i>	<i>Yersinia enterocolitica_E</i>
JDID-259	<i>Scandinavium goeteborgense</i>	No Species Identified	<i>Scandinavium</i> sp033843285
JDID-260	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-261	<i>Escherichia coli</i>	<i>Phytobacter diazotrophicus</i>	Unclassified
JDID-262	<i>Escherichia coli</i>	<i>Phytobacter diazotrophicus</i>	Unclassified
JDID-263	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-264	<i>Pantoea eucrina</i>	<i>Mixta calida</i>	<i>Mixta calida</i>
JDID-265	<i>Enterobacter hormaechei</i>	No Species Identified	Unclassified
JDID-266	<i>Salmonella enterica</i>	<i>Providencia_C manganoxydans</i>	<i>Providencia manganoxydans</i>
JDID-267	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>
JDID-268	<i>Scandinavium goeteborgense</i>	<i>Hafnia paralvei</i>	Unclassified
JDID-269		analysis not performed	
JDID-270		analysis not performed	
JDID-271	<i>Enterobacter</i> sp. C2	<i>Pseudescherichia</i> sp002298805	<i>Pseudescherichia</i> sp002298805
JDID-272	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-273		analysis not performed	
JDID-274	<i>Campylobacter lari</i>	<i>Campylobacter_D lari_D</i>	<i>Campylobacter_D lari_D</i>
JDID-275	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>
JDID-276	<i>Providencia stuartii</i>	<i>Providencia_C manganoxydans</i>	<i>Providencia manganoxydans</i>
JDID-277		analysis not performed	
JDID-278	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>	<i>Enterobacter ludwigii</i>
JDID-279	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>
JDID-280	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>	<i>Aeromonas veronii</i>
JDID-281	<i>Enterobacter cloacae</i>	<i>Enterobacter oligotrophicus</i>	<i>Enterobacter oligotrophicus</i>
JDID-282	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>
JDID-283	<i>Mixta calida</i>	<i>Mixta calida</i>	<i>Mixta calida</i> ⁷⁰

JDID-284	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>	<i>Klebsiella michiganensis</i>
JDID-285	<i>Providencia rettgeri</i>	<i>Providencia rettgeri_A</i>	<i>Providencia xianensis</i>
JDID-286	<i>Pantoea agglomerans</i>	<i>Pantoea piersonii</i>	<i>Pantoea piersonii</i>
JDID-287	<i>Serratia proteamaculans</i>	<i>Serratia_J sp017832355</i>	<i>Serratia sp017832355</i>
JDID-288	<i>Yersinia enterocolitica</i>	<i>Salmonella enterica</i>	Unclassified
JDID-289	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei_A</i>	<i>Enterobacter intestinihominis</i>
JDID-290	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>
JDID-291	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>	<i>Pantoea agglomerans</i>
JDID-292	<i>Pantoea agglomerans</i>	No Species Identified	Unclassified
JDID-293	<i>Phytobacter diazotrophicus</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>
JDID-294	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>
JDID-295	<i>Phytobacter sp. SCO41</i>	<i>Phytobacter diazotrophicus</i>	<i>Phytobacter diazotrophicus</i>
JDID-296		analysis not performed	
JDID-297		analysis not performed	
JDID-298	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>
JDID-299	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>	<i>Klebsiella quasipneumoniae</i>
JDID-300	<i>Pantoea agglomerans</i>	<i>Salmonella enterica</i>	Unclassified
JDID-301	<i>Escherichia coli</i>	<i>Escherichia sp002965065</i>	<i>Escherichia sp002965065</i>
JDID-302	<i>Enterobacter cloacae</i>	No Species Identified	Unclassified
JDID-303	<i>Aliarcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>	<i>Aliarcobacter butzleri</i>
JDID-304		analysis not performed	
JDID-305	<i>Citrobacter koseri</i>	<i>Yersinia enterocolitica</i>	<i>Yersinia enterocolitica</i>
JDID-306		analysis not performed	
JDID-307	<i>Escherichia coli</i>	<i>Citrobacter_B koseri</i>	<i>Citrobacter_B koseri</i>
JDID-308		analysis not performed	
JDID-309		analysis not performed	
JDID-310		analysis not performed	
JDID-311		analysis not performed	
JDID-312	<i>Campylobacter lari</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter_D lari</i>
JDID-313		analysis not performed	
JDID-314		analysis not performed	
JDID-315	<i>Lelliottia sp. AC1</i>	<i>Lelliottia nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>
JDID-316	<i>Pseudocitrobacter corydidari</i>	<i>Pseudocitrobacter faecalis</i>	<i>Pseudocitrobacter faecalis</i>
JDID-317		analysis not performed	
JDID-318	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>	<i>Tatumella ptyseos</i>
JDID-319		analysis not performed	
JDID-320	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-321	<i>Helicobacter winghamensis</i>	<i>Helicobacter_D winghamensis</i>	<i>Helicobacter_D winghamensis</i>
JDID-322	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter cloacae</i>
JDID-323	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>	<i>Klebsiella aerogenes</i>
JDID-324	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>	<i>Klebsiella oxytoca</i>
JDID-325	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-326	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>

JDID-327	<i>Citrobacter koseri</i>	<i>Citrobacter_B koseri</i>	<i>Citrobacter_B koseri</i>
JDID-328	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-329	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-330	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-331	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>	<i>Shimwellia blattae</i>
JDID-332	<i>Enterobacter sp. C2</i>	<i>Pseudescherichia sp002298805</i>	<i>Pseudescherichia sp002298805</i>
JDID-333	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>	<i>Enterobacter cancerogenus</i>
JDID-334	<i>Tatumella tyseos</i>	<i>Tatumella tyseos</i>	<i>Tatumella tyseos</i>
JDID-335	<i>Tatumella tyseos</i>	<i>Tatumella tyseos</i>	<i>Tatumella tyseos</i>
JDID-336	<i>Campylobacter jejuni</i>	<i>Campylobacter_D jejuni</i>	<i>Campylobacter_D jejuni</i>
JDID-337	<i>Campylobacter armoricus</i>	<i>Campylobacter_D lari</i>	<i>Campylobacter_D lari</i>
JDID-338	analysis not performed		
JDID-339	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>
JDID-340	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>
JDID-341	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>
JDID-342	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>
JDID-343	<i>Klebsiella pneumoniae</i>	<i>Hafnia paralvei</i>	<i>Hafnia paralvei</i>
JDID-344	<i>Cronobacter sakazakii</i>	<i>Klebsiella oxytoca</i>	Unclassified
JDID-345	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>	<i>Pseudescherichia vulneris</i>
JDID-346	<i>Ewingella americana</i>	<i>Ewingella americana</i>	<i>Ewingella americana</i>
JDID-347	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Escherichia coli</i>
JDID-348	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-349	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>	<i>Atlantibacter hermannii</i>
JDID-350	<i>Campylobacter fetus</i>	<i>Hafnia alvei</i>	Unclassified
JDID-351	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-352	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>	<i>Escherichia fergusonii</i>
JDID-353	<i>Enterobacter roggenkampii</i>	<i>Enterobacter asburiae</i>	<i>Enterobacter asburiae</i>
JDID-354	<i>Citrobacter farmeri</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter_A farmeri</i>
JDID-355	<i>Citrobacter farmeri</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter_A farmeri</i>
JDID-356	<i>Citrobacter farmeri</i>	<i>Citrobacter_A farmeri</i>	<i>Citrobacter_A farmeri</i>
JDID-357	<i>Citrobacter koseri</i>	<i>Campylobacter_D upsaliensis</i>	<i>Campylobacter_D upsaliensis</i>
JDID-358	<i>Tatumella tyseos</i>	<i>Tatumella tyseos</i>	<i>Tatumella tyseos</i>
JDID-359	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>	<i>Cronobacter sakazakii</i>
JDID-360	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>	<i>Cronobacter dublinensis</i>
JDID-361	<i>Cronobacter sp. JZ38</i>	<i>Cronobacter muytjensii</i>	<i>Cronobacter muytjensii</i>
JDID-362	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>	<i>Cronobacter malonaticus</i>
JDID-363	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>	<i>Enterobacter hormaechei</i>
JDID-364	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>
JDID-365	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>	<i>Proteus mirabilis</i>

Appendix B: Genome Assembly Statistics and Quality Control Metrics

Table A3. Per-isolate genome assembly and QC metrics for Illumina and ONT WGS data.

QC metrics were generated by Mikrokondo sub-workflows (Section 2.4.1 and 2.4.2), including estimated genome completeness, contamination, sequencing coverage, N50, total genome size, assembly status, and overall QC pass or fail designation. Dataset-level QC trends and summary statistics are described in Section 3.2.2.

Sample	Platform	Completeness	Contamination	Coverage	N50	Genome Size (bps)	Assembly Status	QC Pass
JDID-01	Illumina	100	0	100	57791	4392965	passed	TRUE
JDID-02	Illumina	99.87	0.33	100	72867	4739046	passed	TRUE
JDID-03	Illumina	99.92	0.28	100	257123	4613910	passed	TRUE
JDID-04	Illumina	99.88	0	100	126087	2128672	passed	TRUE
JDID-05	Illumina	99.88	0.15	99.99	242073	4973419	passed	TRUE
JDID-06	Illumina	100	0.89	100	325928	5850820	passed	TRUE
JDID-07	Illumina	99.97	0	100	467493	4861254	passed	TRUE
JDID-08	Illumina	99.7	0.82	100	233547	5355961	passed	TRUE
JDID-09	Illumina	94.24	0.4	100	130829	3310951	passed	TRUE
JDID-10	Illumina	100	1.08	100	31269	4478203	passed	TRUE
JDID-11	Illumina	100	0	100	216967	4081384	passed	TRUE
JDID-12	Illumina	99.14	0.18	100	44139	1714773	passed	TRUE
JDID-13	Illumina	100	100	100	58758	7872408	passed	TRUE
JDID-14	Illumina	100	0	100	47319	3936616	passed	TRUE
JDID-15	Illumina	99.95	0.16	100	180724	4385410	passed	TRUE
JDID-16	Illumina	99.69	0.18	100	94908	1875139	passed	TRUE
JDID-17	Illumina	99.69	0.18	100	36327	1867775	passed	TRUE
JDID-18	Illumina	99.69	0	99.99	51047	1726957	passed	TRUE
JDID-19	Illumina	99.88	0	99.99	46475	1661740	passed	TRUE
JDID-20	Illumina	99.88	0	100	53720	1509883	passed	TRUE
JDID-21	Illumina	99.88	0.37	100	40541	1711446	passed	TRUE
JDID-22	Illumina	99.95	0.59	100	39147	5147123	passed	TRUE
JDID-23	Illumina	99.88	0	99.98	43921	1741480	passed	TRUE
JDID-24	Illumina	99.84	0.2	100	238221	5010886	passed	TRUE
JDID-25	Illumina	99.69	34.45	100	25373	2852608	passed	TRUE

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JDID-26	Illumina	98.78	0	99.98	34691	1642093	passed	TRUE
JDID-27	Illumina	98.78	0	100	44376	1534313	passed	TRUE
JDID-28	Illumina	99.69	0.05	99.99	52639	1618680	passed	TRUE
JDID-29	Illumina	99.88	0	100	45993	1706656	passed	TRUE
JDID-30	Illumina	99.69	0	99.99	64321	1833046	passed	TRUE
JDID-31	Illumina	99.88	0.57	100	151076	1844959	passed	TRUE
JDID-32	Illumina	99.89	1.02	100	49944	4591880	passed	TRUE
JDID-33	Illumina	99.95	0.33	100	133096	4572814	passed	TRUE
JDID-34	Illumina	99.88	0.07	99.99	39692	1580743	passed	TRUE
JDID-35	Illumina	99.51	0	100	67445	1604273	passed	TRUE
JDID-36	Illumina	99.88	0	100	61755	1567779	passed	TRUE
JDID-37	Illumina	99.95	0.16	100	210234	5259313	passed	TRUE
JDID-38	Illumina	98.78	0	99.99	33724	1678518	passed	TRUE
JDID-39	Illumina	98.78	0	100	65064	1449286	passed	TRUE
JDID-40	Illumina	98.78	0	99.99	36451	1501676	passed	TRUE
JDID-41	Illumina	99.54	0.8	100	77165	4645109	passed	TRUE
JDID-42	Illumina	98.66	0.37	99.96	27341	1457633	passed	TRUE
JDID-43	Illumina	100	0	100	366810	4001690	passed	TRUE
JDID-44	Illumina	99.81	0.11	100	42148	1717554	passed	TRUE
JDID-45	Illumina	99.59	0.16	99.99	37691	1811369	passed	TRUE
JDID-46	Illumina	99.69	0	100	75444	1709665	passed	TRUE
JDID-47	Illumina	99.51	0	100	89229	1749133	passed	TRUE
JDID-48	Illumina	99.8	0.31	100	69143	1650035	passed	TRUE
JDID-49	Illumina	99.66	0.11	100	43684	1582619	passed	TRUE
JDID-50	Illumina	99.38	0.11	100	39315	1663368	passed	TRUE
JDID-51	Illumina	99.33	0.11	99.99	34047	1627280	passed	TRUE
JDID-52	Illumina	99.44	0.11	99.99	37214	1838965	passed	TRUE
JDID-53	Illumina	99.88	0	100	40879	1729341	passed	TRUE
JDID-54	Illumina	99.37	0.11	100	57933	1785978	passed	TRUE
JDID-55	Illumina	98.8	0.11	100	79983	1699124	passed	TRUE
JDID-56	Illumina	99.88	1	99.99	53978	1694587	passed	TRUE
JDID-57	Illumina	100	1.36	100	284212	5399914	passed	TRUE
JDID-58	Illumina	100	1.36	100	284067	5407656	passed	TRUE
JDID-59	Illumina	99.99	0.49	100	460943	4906480	passed	TRUE
JDID-60	Illumina	99.28	1.61	100	452307	5270993	passed	TRUE
JDID-61	Illumina	99.51	0.89	100	551312	5140436	passed	TRUE
JDID-62	Illumina	99.05	0.37	100	60419	4598104	passed	TRUE
JDID-63	Illumina	99.97	1.25	100	192657	5609233	passed	TRUE
JDID-64	Illumina	100	0	100	279873	4407739	passed	TRUE
JDID-65	Illumina	99.67	0	100	318197	4323375	passed	TRUE
JDID-66	Illumina	100	0	100	313486	4547931	passed	TRUE

Continuation of Table A3, part 2 of 19

JDID-67	Illumina	99.97	0	100	139557	4416926	passed	TRUE
JDID-68	Illumina	99.97	0	100	257042	4421366	passed	TRUE
JDID-69	Illumina	99.97	0	100	280626	4667428	passed	TRUE
JDID-70	Illumina	99.97	0	100	160012	4413451	passed	TRUE
JDID-71	Illumina	99.97	0.29	100	134243	4438090	passed	TRUE
JDID-72	Illumina	100	0	100	292592	4592786	passed	TRUE
JDID-73	Illumina	99.97	0	99.99	388771	4804014	passed	TRUE
JDID-74	Illumina	99.97	0	100	122508	4468342	passed	TRUE
JDID-75	Illumina	99.97	0	100	168442	4541594	passed	TRUE
JDID-76	Illumina	100	0	100	484282	4343012	passed	TRUE
JDID-77	Illumina	99.45	0.18	100	247771	2973809	passed	TRUE
JDID-78	Illumina	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-79	Illumina	99.41	0.11	100	207304	4794982	passed	TRUE
JDID-80	Illumina	99.95	0.19	100	152095	4827376	passed	TRUE
JDID-81	Illumina	100	1.09	100	413305	5594446	passed	TRUE
JDID-82	Illumina	99.69	1.17	100	110145	5344491	passed	TRUE
JDID-83	Illumina	99.69	1.17	100	141819	5321759	passed	TRUE
JDID-84	Illumina	99.69	1.17	100	137981	5324123	passed	TRUE
JDID-85	Illumina	100	0.21	100	331864	5383596	passed	TRUE
JDID-86	Illumina	99.67	0.63	100	540783	4509902	passed	TRUE
JDID-87	Illumina	99.97	0.33	100	231829	4439163	passed	TRUE
JDID-88	Illumina	99.59	0.23	100	236335	4910860	passed	TRUE
JDID-89	Illumina	99.62	1.43	100	79938	5027078	passed	TRUE
JDID-90	Illumina	99.82	0.59	100	239962	5005782	passed	TRUE
JDID-91	Illumina	99.6	0.71	100	190781	5320711	passed	TRUE
JDID-92	Illumina	99.6	0.32	100	743278	4930814	passed	TRUE
JDID-93	Illumina	99.59	0.69	100	108052	5375937	passed	TRUE
JDID-94	Illumina	99.87	0.92	100	163453	5262808	passed	TRUE
JDID-95	Illumina	100	0.04	100	401205	4693342	passed	TRUE
JDID-96	Illumina	99.75	0.86	100	177906	4827262	passed	TRUE
JDID-97	Illumina	99.87	0.6	100	446894	5201537	passed	TRUE
JDID-98	Illumina	100	1.87	100	129186	5539668	passed	TRUE
JDID-99	Illumina	99.99	0.14	100	394603	5138484	passed	TRUE
JDID-100	Illumina	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-101	Illumina	99.99	0.14	100	467424	5137658	passed	TRUE
JDID-102	Illumina	99.99	1.63	100	229266	6198360	passed	TRUE
JDID-103	Illumina	99.99	1.46	100	276744	5683937	passed	TRUE
JDID-104	Illumina	99.9	0.97	100	92667	5495308	passed	TRUE
JDID-105	Illumina	99.4	0.74	100	86683	5241080	passed	TRUE
JDID-106	Illumina	99.99	1.2	100	351572	5674883	passed	TRUE
JDID-107	Illumina	99.7	0.52	100	190432	5431088	passed	TRUE

Continuation of Table A3, part 3 of 19

JDID-108	Illumina	99.97	0.3	100	449724	4779907	passed	TRUE
JDID-109	Illumina	99.35	0.67	100	133344	4935357	passed	TRUE
JDID-110	Illumina	99.9	0.46	100	149010	4924967	passed	TRUE
JDID-111	Illumina	100	0.7	100	598796	4887650	passed	TRUE
JDID-112	Illumina	99.97	0.58	100	205917	4648235	passed	TRUE
JDID-113	Illumina	99.97	0.43	100	139085	4711926	passed	TRUE
JDID-114	Illumina	99.87	0.04	100	258603	4530681	passed	TRUE
JDID-115	Illumina	99.59	0.39	100	380314	5212030	passed	TRUE
JDID-116	Illumina	99.38	1.21	100	171157	5694349	passed	TRUE
JDID-117	Illumina	100	1.11	100	247676	5252211	passed	TRUE
JDID-118	Illumina	100	0	100	365816	5589771	passed	TRUE
JDID-119	Illumina	99.86	0	100	416062	5236966	passed	TRUE
JDID-120	Illumina	99.69	0.73	100	259839	5147671	passed	TRUE
JDID-121	Illumina	99.99	0.24	100	168859	4875523	passed	TRUE
JDID-122	Illumina	99.95	0.24	100	163981	4680870	passed	TRUE
JDID-123	Illumina	99.37	0.24	100	169514	4615496	passed	TRUE
JDID-124	Illumina	99.8	0	100	327306	5084541	passed	TRUE
JDID-125	Illumina	99.31	0	100	1120869	4912550	passed	TRUE
JDID-126	Illumina	100	0.5	100	224141	5161714	passed	TRUE
JDID-127	Illumina	99.99	0.15	100	584216	5065476	passed	TRUE
JDID-128	Illumina	99.95	0.41	100	309395	4364341	passed	TRUE
JDID-129	Illumina	99.59	1.08	100	282534	5013224	passed	TRUE
JDID-130	Illumina	99.59	0.9	100	250088	5021960	passed	TRUE
JDID-131	Illumina	99.69	1.05	100	504901	5133654	passed	TRUE
JDID-132	Illumina	100	0.45	100	132167	5489567	passed	TRUE
JDID-133	Illumina	99.03	0.52	100	106274	4845549	passed	TRUE
JDID-134	Illumina	100	36.59	99.99	19082	5303844	passed	TRUE
JDID-135	Illumina	99.62	1.1	100	131257	5204091	passed	TRUE
JDID-136	Illumina	99.32	0.68	99.99	23104	4381269	passed	TRUE
JDID-137	Illumina	100	0.09	100	212336	4429955	passed	TRUE
JDID-138	Illumina	100	0.46	100	47821	5406082	passed	TRUE
JDID-139	Illumina	100	1.11	100	273845	5251908	passed	TRUE
JDID-140	Illumina	100	0	100	99914	4003024	passed	TRUE
JDID-141	Illumina	100	0	99.99	58563	3884690	passed	TRUE
JDID-142	Illumina	99.28	1.58	100	188136	5515673	passed	TRUE
JDID-143	Illumina	99.99	3.53	100	252826	6145737	passed	TRUE
JDID-144	Illumina	99.41	0.64	100	353476	5055242	passed	TRUE
JDID-145	Illumina	99.86	0.11	100	104628	5480046	passed	TRUE
JDID-146	Illumina	99.97	0.39	100	323423	4954985	passed	TRUE
JDID-147	Illumina	99.84	0.67	100	44267	4889999	passed	TRUE
JDID-148	Illumina	99.67	0.94	100	158197	4872357	passed	TRUE

Continuation of Table A3, part 4 of 19

JDID-149	Illumina	98.78	0.43	100	371255	4703638	passed	TRUE
JDID-150	Illumina	99.82	0.59	100	225489	4986183	passed	TRUE
JDID-151	Illumina	99.87	1.33	100	240004	5167735	passed	TRUE
JDID-152	Illumina	99.97	0.23	100	947480	4960021	passed	TRUE
JDID-153	Illumina	99.97	0.33	100	192959	5063727	passed	TRUE
JDID-154	Illumina	99.5	0.82	100	53548	4760359	passed	TRUE
JDID-155	Illumina	99.97	0.43	100	472374	4876813	passed	TRUE
JDID-156	Illumina	100	0.77	100	301661	6337229	passed	TRUE
JDID-157	Illumina	98.68	2.43	100	65415	5724975	passed	TRUE
JDID-158	Illumina	99.57	0.63	100	276003	5241883	passed	TRUE
JDID-159	Illumina	99.97	0.48	100	194613	4935824	passed	TRUE
JDID-160	Illumina	99.97	1.19	100	161631	4716738	passed	TRUE
JDID-161	Illumina	100	0.33	100	193970	4470904	passed	TRUE
JDID-162	Illumina	100	0.33	100	193877	4476600	passed	TRUE
JDID-163	Illumina	99.38	1.33	100	223381	5763558	passed	TRUE
JDID-164	Illumina	100	0	100	160553	4605871	passed	TRUE
JDID-165	Illumina	100	0.16	100	239591	5310672	passed	TRUE
JDID-166	Illumina	91.65	3.92	99.99	5096	5585426	passed	TRUE
JDID-167	Illumina	99.87	0.76	100	203652	4802461	passed	TRUE
JDID-168	Illumina	98.97	0.6	100	345967	5296394	passed	TRUE
JDID-169	Illumina	99.9	0.3	100	267173	5128317	passed	TRUE
JDID-170	Illumina	99.38	1.72	100	229179	5820250	passed	TRUE
JDID-171	Illumina	98.64	0.2	100	208846	4824431	passed	TRUE
JDID-172	Illumina	99.99	3.04	100	108963	5683160	passed	TRUE
JDID-173	Illumina	99.99	0.49	100	257347	4810174	passed	TRUE
JDID-174	Illumina	99.7	0.56	100	576190	4748095	passed	TRUE
JDID-175	Illumina	99.71	0	100	98799	1624176	passed	TRUE
JDID-176	Illumina	99.84	2.3	100	371868	5948132	passed	TRUE
JDID-177	Illumina	99.99	2.09	100	331454	5687426	passed	TRUE
JDID-178	Illumina	99.9	0.09	100	549926	5058174	passed	TRUE
JDID-179	Illumina	98.97	0.33	100	423902	5053325	passed	TRUE
JDID-180	Illumina	99.97	0.75	100	210957	4878114	passed	TRUE
JDID-181	Illumina	99.65	0.04	100	181249	4654531	passed	TRUE
JDID-182	Illumina	99.65	0.35	100	281364	4683211	passed	TRUE
JDID-183	Illumina	99.99	0.26	100	196622	4980795	passed	TRUE
JDID-184	Illumina	99.7	0.82	100	347261	4713448	passed	TRUE
JDID-185	Illumina	99.47	0	100	102270	1655459	passed	TRUE
JDID-186	Illumina	99.69	0.51	100	525754	4594823	passed	TRUE
JDID-187	Illumina	99.98	0.16	100	369550	5040999	passed	TRUE
JDID-188	Illumina	100	82.46	100	13274	8893711	passed	TRUE
JDID-189	Illumina	99.99	2.2	100	379952	5701463	passed	TRUE

Continuation of Table A3, part 5 of 19

JDID-190	Illumina	100	0.14	100	394578	4124743	passed	TRUE
JDID-191	Illumina	99.97	0.69	100	497214	5114750	passed	TRUE
JDID-192	Illumina	99.23	0.94	100	112329	2190464	passed	TRUE
JDID-193	Illumina	99.88	0	100	192195	1718382	passed	TRUE
JDID-194	Illumina	99.71	0.35	100	82671	2010092	passed	TRUE
JDID-195	Illumina	99.88	0.04	100	58448	4971523	passed	TRUE
JDID-196	Illumina	98.78	0	100	98366	1497299	passed	TRUE
JDID-197	Illumina	100	0.12	100	574272	4840294	passed	TRUE
JDID-198	Illumina	99.35	0.33	100	502407	4462485	passed	TRUE
JDID-199	Illumina	99.35	0.68	100	146748	4799817	passed	TRUE
JDID-200	Illumina	99.77	0.21	100	502808	4669824	passed	TRUE
JDID-201	Illumina	99.07	0.73	100	143164	5221316	passed	TRUE
JDID-202	Illumina	99.77	0.21	100	502808	4671566	passed	TRUE
JDID-203	Illumina	99.07	0.33	100	225527	4818301	passed	TRUE
JDID-204	Illumina	99.66	0.56	100	260490	4721888	passed	TRUE
JDID-205	Illumina	99.7	0.56	100	299188	4724758	passed	TRUE
JDID-206	Illumina	99.88	0.55	99.99	55898	1672953	passed	TRUE
JDID-207	Illumina	99.98	0.77	100	482245	4971374	passed	TRUE
JDID-208	Illumina	99.06	0.63	100	186775	4879013	passed	TRUE
JDID-209	Illumina	99	0.83	100	81975	4890571	passed	TRUE
JDID-210	Illumina	99.98	0	100	488855	5462191	passed	TRUE
JDID-211	Illumina	99.07	0.33	100	188822	5012983	passed	TRUE
JDID-212	Illumina	99.67	0.48	100	206433	5008199	passed	TRUE
JDID-213	Illumina	99.97	0.26	100	152746	4655275	passed	TRUE
JDID-214	Illumina	99.88	0	99.99	89492	1789431	passed	TRUE
JDID-215	Illumina	99.07	0.33	100	210155	4881927	passed	TRUE
JDID-216	Illumina	99.82	0.35	100	137719	1714076	passed	TRUE
JDID-217	Illumina	99.85	0.63	100	167445	5446313	passed	TRUE
JDID-218	Illumina	99.99	2.02	100	427374	5637312	passed	TRUE
JDID-219	Illumina	99.97	0.43	100	780356	4466253	passed	TRUE
JDID-220	Illumina	99.61	1.38	100	474494	4812956	passed	TRUE
JDID-221	Illumina	99.97	0.44	100	201609	4874880	passed	TRUE
JDID-222	Illumina	98.9	0	100	267939	5117527	passed	TRUE
JDID-223	Illumina	99.97	0.33	100	229855	5102982	passed	TRUE
JDID-224	Illumina	99.42	0	100	83811	1633826	passed	TRUE
JDID-225	Illumina	99.42	0.41	100	98910	1572353	passed	TRUE
JDID-226	Illumina	97.62	0.41	100	171386	4990374	passed	TRUE
JDID-227	Illumina	99.38	1.85	100	384822	5793582	passed	TRUE
JDID-228	Illumina	98.78	0.37	99.99	101782	1503407	passed	TRUE
JDID-229	Illumina	99.69	0.15	100	77615	4497071	passed	TRUE
JDID-230	Illumina	99.22	0.41	100	73020	1572027	passed	TRUE

Continuation of Table A3, part 6 of 19

JDID-231	Illumina	99.42	0	100	83666	1634300	passed	TRUE
JDID-232	Illumina	100	0.54	100	55844	4416178	passed	TRUE
JDID-233	Illumina	99.86	0.28	100	346061	4665656	passed	TRUE
JDID-234	Illumina	99.31	1.05	100	679591	5614652	passed	TRUE
JDID-235	Illumina	99.38	1.6	100	96574	5662044	passed	TRUE
JDID-236	Illumina	99.38	0.11	100	58834	1626015	passed	TRUE
JDID-237	Illumina	99.69	0.2	100	162474	4430711	passed	TRUE
JDID-238	Illumina	99.04	1	100	143432	5087470	passed	TRUE
JDID-239	Illumina	99.28	5.02	100	442769	4254352	passed	TRUE
JDID-240	Illumina	100	0.08	100	729513	4232612	passed	TRUE
JDID-241	Illumina	99.99	0.26	100	218876	4749118	passed	TRUE
JDID-242	Illumina	99.69	0.45	100	101992	4971876	passed	TRUE
JDID-243	Illumina	99.06	0.04	100	86340	4566421	passed	TRUE
JDID-244	Illumina	99.87	0	100	2546199	4850724	passed	TRUE
JDID-245	Illumina	99.92	0.58	100	106336	5028547	passed	TRUE
JDID-246	Illumina	97.9	1.82	100	402851	4516860	passed	TRUE
JDID-247	Illumina	99.31	1.35	100	126276	5830614	passed	TRUE
JDID-248	Illumina	100	0.54	100	72177	4585868	passed	TRUE
JDID-249	Illumina	99.57	0.33	100	263063	4296989	passed	TRUE
JDID-250	Illumina	100	0.04	100	494392	4694629	passed	TRUE
JDID-251	Illumina	100	0.04	100	519036	5146603	passed	TRUE
JDID-252	Illumina	99.99	1.31	100	177502	5430823	passed	TRUE
JDID-253	Illumina	99.07	0.04	100	133432	4918744	passed	TRUE
JDID-254	Illumina	99.88	0.37	99.98	51178	1599763	passed	TRUE
JDID-255	Illumina	99.95	15.18	100	132257	4905390	passed	TRUE
JDID-256	Illumina	99.95	0.89	100	248972	5231520	passed	TRUE
JDID-257	Illumina	99.95	0.33	100	184916	4991309	passed	TRUE
JDID-258	Illumina	99.95	0.16	100	183802	5160037	passed	TRUE
JDID-259	Illumina	99.63	0	100	161002	4999852	passed	TRUE
JDID-260	Illumina	100	0.19	100	366820	4565740	passed	TRUE
JDID-261	Illumina	99.2	1.23	100	84586	5645072	passed	TRUE
JDID-262	Illumina	99.38	1.04	100	127376	5659305	passed	TRUE
JDID-263	Illumina	99.38	1.14	100	89767	5550592	passed	TRUE
JDID-264	Illumina	100	0.07	100	142622	5643139	passed	TRUE
JDID-265	Illumina	99.95	0.47	100	245865	4541657	passed	TRUE
JDID-266	Illumina	99.97	0.24	100	287549	4695783	passed	TRUE
JDID-267	Illumina	100	0.54	100	14467	4371803	passed	TRUE
JDID-268	Illumina	99.86	0.45	100	394148	4662030	passed	TRUE
JDID-269	Illumina	99.71	0	99.99	40106	2002589	passed	TRUE
JDID-270	Illumina	99.42	0	100	65446	1634442	passed	TRUE
JDID-271	Illumina	99.42	0	99.99	76913	1634018	passed	TRUE

Continuation of Table A3, part 7 of 19

JDID-272	Illumina	98.14	0.4	100	136235	1567228	passed	TRUE
JDID-273	Illumina	99.69	0	100	109816	1739496	passed	TRUE
JDID-274	Illumina	99.69	0	100	79325	1735600	passed	TRUE
JDID-275	Illumina	99.88	0	99.98	79166	1636416	passed	TRUE
JDID-276	Illumina	99.57	0.11	100	83184	1724699	passed	TRUE
JDID-277	Illumina	99.14	0.69	100	40124	1405359	passed	TRUE
JDID-278	Illumina	99.88	0.57	100	115718	2390568	passed	TRUE
JDID-279	Illumina	99.97	0.14	100	149260	4797456	passed	TRUE
JDID-280	Illumina	100	0.08	100	581391	4595480	passed	TRUE
JDID-281	Illumina	98.28	59.46	99.99	129842	8105039	passed	TRUE
JDID-282	Illumina	99.63	0	100	379921	3933932	passed	TRUE
JDID-283	Illumina	99.33	0.44	100	152467	6024976	passed	TRUE
JDID-284	Illumina	99.91	0.41	100	226281	4247154	passed	TRUE
JDID-285	Illumina	99.81	1	100	644063	5137088	passed	TRUE
JDID-286	Illumina	99.99	0	100	335935	4626982	passed	TRUE
JDID-287	Illumina	100	0.34	100	248894	4928760	passed	TRUE
JDID-288	Illumina	98.78	0	100	46836	1532619	passed	TRUE
JDID-289	Illumina	100	0	100	72774	4463999	passed	TRUE
JDID-290	Illumina	99.87	0.45	100	231355	4914171	passed	TRUE
JDID-291	Illumina	100	0.36	100	587466	4732832	passed	TRUE
JDID-292	Illumina	100	0.36	100	520281	4730964	passed	TRUE
JDID-293	Illumina	98.78	0	100	70164	1479285	passed	TRUE
JDID-294	Illumina	77.92	2.71	100	2292	2109463	passed	TRUE
JDID-295	Illumina	99.45	0	100	490534	2847384	passed	TRUE
JDID-296	Illumina	99.38	1.31	100	349926	5618845	passed	TRUE
JDID-297	Illumina	100	0.74	100	605112	4702422	passed	TRUE
JDID-298	Illumina	96.55	26.76	99.98	8236	2961787	passed	TRUE
JDID-299	Illumina	99.95	0.46	99.99	70220	4514516	passed	TRUE
JDID-300	Illumina	99.95	0	100	155692	4220124	passed	TRUE
JDID-301	Illumina	99.95	0.49	100	190284	4768764	passed	TRUE
JDID-302	Illumina	98.93	0.53	100	58258	4560229	passed	TRUE
JDID-303	Illumina	98.78	0	100	48646	1487046	passed	TRUE
JDID-304	Illumina	100	0.41	99.99	50494	2298786	passed	TRUE
JDID-305	Illumina	99.88	0.05	100	46769	1628140	passed	TRUE
JDID-306	Illumina	99.42	0	99.99	82448	1633775	passed	TRUE
JDID-307	Illumina	99.42	0.2	99.98	100568	1633740	passed	TRUE
JDID-308	Illumina	99.38	0.11	99.99	97731	1597774	passed	TRUE
JDID-309	Illumina	99.95	0.25	100	261622	5031348	passed	TRUE
JDID-310	Illumina	99.86	0.57	100	513212	4857558	passed	TRUE
JDID-311	Illumina	99.82	0	100	104696	1725817	passed	TRUE
JDID-312	Illumina	100	0.45	100	728804	5530900	passed	TRUE

Continuation of Table A3, part 8 of 19

JDID-313	Illumina	99.97	0.35	100	285516	4705475	passed	TRUE
JDID-314	Illumina	99.07	1.31	100	92201	5650489	passed	TRUE
JDID-315	Illumina	99.94	0.4	100	418094	4983759	passed	TRUE
JDID-316	Illumina	77.92	2.71	100	2292	2109463	passed	TRUE
JDID-317	Illumina	99.45	0	100	490534	2847384	passed	TRUE
JDID-318	Illumina	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-319	Illumina	99.95	0.13	100	70652	5055502	passed	TRUE
JDID-320	Illumina	99.36	0	100	45324	1597340	passed	TRUE
JDID-321	Illumina	99.71	0	99.99	86032	1661962	passed	TRUE
JDID-322	Illumina	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-323	Illumina	100	1.24	100	111099	5464429	passed	TRUE
JDID-324	Illumina	100	0.39	100	558658	5243060	passed	TRUE
JDID-325	Illumina	100	0.07	100	374905	5802446	passed	TRUE
JDID-326	Illumina	100	100	100	57617	8609604	passed	TRUE
JDID-327	Illumina	99.97	0.05	100	358474	5033924	passed	TRUE
JDID-328	Illumina	99.88	0.32	100	939213	4867042	passed	TRUE
JDID-329	Illumina	100	0	100	48944	4018613	passed	TRUE
JDID-330	Illumina	99.99	0.2	100	92360	4554739	passed	TRUE
JDID-331	Illumina	100	0	100	31145	3951784	passed	TRUE
JDID-332	Illumina	99.98	0.74	100	133353	4068910	passed	TRUE
JDID-333	Illumina	97.81	0.89	100	433775	4326897	passed	TRUE
JDID-334	Illumina	100	0.29	100	724097	4782615	passed	TRUE
JDID-335	Illumina	95.87	0.46	100	122157	3538291	passed	TRUE
JDID-336	Illumina	95.87	0.38	100	195213	3438062	passed	TRUE
JDID-337	Illumina	99.87	0.74	100	151264	4157246	passed	TRUE
JDID-338	Illumina	99.98	0.77	100	216438	4206372	passed	TRUE
JDID-339	Illumina	100	0	100	33973	3740698	passed	TRUE
JDID-340	Illumina	99.1	0.92	100	200877	4508209	passed	TRUE
JDID-341	Illumina	99.1	0.92	100	218825	4508486	passed	TRUE
JDID-342	Illumina	99.2	0.87	100	409916	4280241	passed	TRUE
JDID-343	Illumina	99.23	0.92	100	238255	4585001	passed	TRUE
JDID-344	Illumina	98.02	0.77	100	308117	4380521	passed	TRUE
JDID-345	Illumina	97.96	0.71	100	560293	4330762	passed	TRUE
JDID-346	Illumina	98.02	0.71	100	492343	4274523	passed	TRUE
JDID-347	Illumina	99.66	0.16	100	660039	4877456	passed	TRUE
JDID-348	Illumina	99.97	0.07	100	287347	5080411	passed	TRUE
JDID-349	Illumina	100	0.04	100	207110	4598522	passed	TRUE
JDID-350	Illumina	99.9	0.27	100	183375	4593737	passed	TRUE
JDID-351	Illumina	99.9	0.37	100	310901	4565361	passed	TRUE
JDID-352	Illumina	100	0.37	100	443692	4426615	passed	TRUE
JDID-353	Illumina	100	0.52	100	215978	4683247	passed	TRUE

Continuation of Table A3, part 9 of 19

JDID-354	Illumina	99.07	0.65	100	94011	4784134	passed	TRUE
JDID-355	Illumina	99.84	0.19	100	368820	4566981	passed	TRUE
JDID-356	Illumina	99.97	0.25	100	599179	4931808	passed	TRUE
JDID-357	Illumina	95.87	0.38	100	214118	3441055	passed	TRUE
JDID-358	Illumina	95.87	0.51	100	171892	3525567	passed	TRUE
JDID-359	Illumina	95.87	0.46	100	184895	3542779	passed	TRUE
JDID-360	Illumina	99.4	0.29	100	324485	4573136	passed	TRUE
JDID-361	Illumina	99.62	0.2	100	384092	4214603	passed	TRUE
JDID-362	Illumina	99.97	0.85	100	529459	4596429	passed	TRUE
JDID-363	Illumina	99.38	0.19	100	355819	4471504	passed	TRUE
JDID-364	Illumina	99.97	0.47	100	233448	4891894	passed	TRUE
JDID-365	Illumina	100	0	100	41220	4073914	passed	TRUE
JDID-01	Nanopore	99.77	0.21	100	4722324	4722324	passed	TRUE
JDID-02	Nanopore	100	0	100	4017704	4017704	passed	TRUE
JDID-03	Nanopore	100	0	100	4150256	4150256	passed	TRUE
JDID-04	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-05	Nanopore	100	0	100	4105567	4105567	passed	TRUE
JDID-06	Nanopore	100	1.08	100	4487569	4572435	passed	TRUE
JDID-07	Nanopore	99.35	0.68	100	4820512	4879761	passed	TRUE
JDID-08	Nanopore	99.97	0	100	4878798	4878798	passed	TRUE
JDID-09	Nanopore	94.35	0.4	100	3372934	3372934	passed	TRUE
JDID-10	Nanopore	99.99	0	100	4606001	4665745	passed	TRUE
JDID-11	Nanopore	99.88	0.15	100	5024103	5024103	passed	TRUE
JDID-12	Nanopore	99.14	0.18	100	1754119	1754119	passed	TRUE
JDID-13	Nanopore	99.92	0.28	100	4552810	4660782	passed	TRUE
JDID-14	Nanopore	99.92	0.33	100	4532045	4532045	passed	TRUE
JDID-15	Nanopore	100	0	100	4542027	4542027	passed	TRUE
JDID-16	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-17	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-18	Nanopore	99.99	0.51	100	4695099	4695099	passed	TRUE
JDID-19	Nanopore	99.93	0	100	4901357	4901357	passed	TRUE
JDID-20	Nanopore	100	100	100	6312469	11484366	passed	TRUE
JDID-21	Nanopore	99.89	0.28	100	4552825	4660798	passed	TRUE
JDID-22	Nanopore	99.81	1	100	5167112	5167112	passed	TRUE
JDID-23	Nanopore	98.78	0	100	1525311	1586688	passed	TRUE
JDID-24	Nanopore	99.97	0	100	4901652	4901652	passed	TRUE
JDID-25	Nanopore	99.69	0.2	100	4298210	4480221	passed	TRUE
JDID-26	Nanopore	100	0.54	100	4444254	4496634	passed	TRUE
JDID-27	Nanopore	99.88	0	100	1766673	1766673	passed	TRUE
JDID-28	Nanopore	99.69	0.15	100	4177652	4607530	passed	TRUE
JDID-29	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE

Continuation of Table A3, part 10 of 19

JDID-30	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-31	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-32	Nanopore	100	0.28	100	4552802	4660773	passed	TRUE
JDID-33	Nanopore	99.88	0.15	100	5024103	5024103	passed	TRUE
JDID-34	Nanopore	99.84	0.2	100	4971096	5060893	passed	TRUE
JDID-35	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-36	Nanopore	99.07	0.65	100	4774118	4965722	passed	TRUE
JDID-37	Nanopore	99.07	0.48	100	4652545	4762583	passed	TRUE
JDID-38	Nanopore	99.33	0.44	100	6104717	6104717	passed	TRUE
JDID-39	Nanopore	98.41	0	100	803860	1470794	passed	TRUE
JDID-40	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-41	Nanopore	99.51	0.89	100	5178329	5178329	passed	TRUE
JDID-42	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-43	Nanopore	99.28	1.61	100	4734399	5335593	passed	TRUE
JDID-44	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-45	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-46	Nanopore	100	82.13	100	234905	5617240	passed	TRUE
JDID-47	Nanopore	100	100	100	4800981	6685315	passed	TRUE
JDID-48	Nanopore	100	100	100	2144745	6308182	passed	TRUE
JDID-49	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-50	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-51	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-52	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-53	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-54	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-55	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-56	Nanopore	98.96	98.96	100	4831155	10299009	passed	TRUE
JDID-57	Nanopore	99.95	0.33	100	4616906	4616906	passed	TRUE
JDID-58	Nanopore	99.97	0	100	4900678	4900678	passed	TRUE
JDID-59	Nanopore	99.47	0.25	100	5150383	5211908	passed	TRUE
JDID-60	Nanopore	99.66	0.04	100	4571692	4571692	passed	TRUE
JDID-61	Nanopore	99.5	0.08	100	4704497	4704497	passed	TRUE
JDID-62	Nanopore	99.95	0.16	100	5287646	5330268	passed	TRUE
JDID-63	Nanopore	99.52	0.2	100	4971140	5060930	passed	TRUE
JDID-64	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-65	Nanopore	99.95	0.33	100	4616933	4616933	passed	TRUE
JDID-66	Nanopore	99.84	0.2	100	4971177	5060968	passed	TRUE
JDID-67	Nanopore	99.97	0.15	100	3953499	4834706	passed	TRUE
JDID-68	Nanopore	100	10.34	99.89	191902	7105476	passed	TRUE
JDID-69	Nanopore	99.87	0.62	100	4877331	5277736	passed	TRUE
JDID-70	Nanopore	100	100	100	2299156	9683489	passed	TRUE

Continuation of Table A3, part 11 of 19

JDID-71	Nanopore	97.62	0.41	100	4977608	5079782	passed	TRUE
JDID-72	Nanopore	100	91.67	100	3707123	9399996	passed	TRUE
JDID-73	Nanopore	99.97	0.3	100	4810672	4810672	passed	TRUE
JDID-74	Nanopore	100	0	100	4663816	4663816	passed	TRUE
JDID-75	Nanopore	99.97	0.29	100	4437806	4561203	passed	TRUE
JDID-76	Nanopore	94.35	0.4	100	3372919	3372919	passed	TRUE
JDID-77	Nanopore	88.71	0.27	100	722340	2911078	passed	TRUE
JDID-78	Nanopore	99.45	0	100	3005345	3005345	passed	TRUE
JDID-79	Nanopore	99.97	0	100	4509778	4509778	passed	TRUE
JDID-80	Nanopore	99.95	0.19	100	4083515	4884880	passed	TRUE
JDID-81	Nanopore	99.97	0	100	4488334	4488334	passed	TRUE
JDID-82	Nanopore	99.97	0	100	4528643	4528643	passed	TRUE
JDID-83	Nanopore	0	0	100	40406	320896	passed	TRUE
JDID-84	Nanopore	99.75	0.86	100	4708837	4874016	passed	TRUE
JDID-85	Nanopore	100	100	100	5268643	9885330	passed	TRUE
JDID-86	Nanopore	99.83	1.25	100	5208574	5685313	passed	TRUE
JDID-87	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-88	Nanopore	100	1.36	100	4229613	5463027	passed	TRUE
JDID-89	Nanopore	99.87	0.92	100	4874397	5348627	passed	TRUE
JDID-90	Nanopore	99.59	0.69	100	5173252	5506617	passed	TRUE
JDID-91	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-92	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-93	Nanopore	99.82	0.59	100	4855004	5117507	passed	TRUE
JDID-94	Nanopore	99.62	1.73	100	4930744	5228309	passed	TRUE
JDID-95	Nanopore	98.81	0.91	100	822108	5200110	passed	TRUE
JDID-96	Nanopore	100	100	100	4703590	10996904	passed	TRUE
JDID-97	Nanopore	99.69	1.41	100	5288486	5419977	passed	TRUE
JDID-98	Nanopore	98.9	0	100	5158017	5158017	passed	TRUE
JDID-99	Nanopore	0	0	100	28342	43839	passed	TRUE
JDID-100	Nanopore	99.61	1.38	100	4855787	4855787	passed	TRUE
JDID-101	Nanopore	99.7	0.52	100	5120858	5491547	passed	TRUE
JDID-102	Nanopore	99.99	1.46	100	5604049	5737947	passed	TRUE
JDID-103	Nanopore	100	100	100	5483075	10915693	passed	TRUE
JDID-104	Nanopore	99.99	1.2	100	5590741	5724941	passed	TRUE
JDID-105	Nanopore	99.59	0.39	100	5126315	5257279	passed	TRUE
JDID-106	Nanopore	99.42	0	100	4485316	4485316	passed	TRUE
JDID-107	Nanopore	99.38	0	100	4878858	4878858	passed	TRUE
JDID-108	Nanopore	99.99	0.14	100	5173806	5173806	passed	TRUE
JDID-109	Nanopore	99.69	0.73	100	5195766	5202799	passed	TRUE
JDID-110	Nanopore	99.03	0.52	100	4703583	4926373	passed	TRUE
JDID-111	Nanopore	99.97	0	100	4756605	4756605	passed	TRUE

Continuation of Table A3, part 12 of 19

JDID-112	Nanopore	99.97	0.43	100	4719698	4791257	passed	TRUE
JDID-113	Nanopore	99.97	0.88	100	4437814	4561210	passed	TRUE
JDID-114	Nanopore	99.69	1.26	100	5053282	5188173	passed	TRUE
JDID-115	Nanopore	99.7	0.56	100	4759550	4759550	passed	TRUE
JDID-116	Nanopore	100	1.11	100	5309646	5309646	passed	TRUE
JDID-117	Nanopore	100	0	100	3967327	3977541	passed	TRUE
JDID-118	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-119	Nanopore	100	0	100	4413972	4413972	passed	TRUE
JDID-120	Nanopore	100	0	100	3957609	4419131	passed	TRUE
JDID-121	Nanopore	99.59	0.39	100	5009697	5027552	passed	TRUE
JDID-122	Nanopore	99.9	1.11	100	5309584	5309584	passed	TRUE
JDID-123	Nanopore	99.97	0.33	100	2938301	5805679	passed	TRUE
JDID-124	Nanopore	99.07	0.73	100	5131012	5353925	passed	TRUE
JDID-125	Nanopore	100	0.45	100	5186796	5204235	passed	TRUE
JDID-126	Nanopore	100	1.11	100	5308956	5308956	passed	TRUE
JDID-127	Nanopore	99.01	0	100	5115755	5115755	passed	TRUE
JDID-128	Nanopore	99.59	1.08	100	5030326	5105395	passed	TRUE
JDID-129	Nanopore	99.66	91.55	100	773496	10895628	passed	TRUE
JDID-130	Nanopore	4.71	0	100	53312	331402	passed	TRUE
JDID-131	Nanopore	99.97	0.43	100	4719224	4719224	passed	TRUE
JDID-132	Nanopore	99.69	0.73	100	5195744	5203121	passed	TRUE
JDID-133	Nanopore	99.67	0.73	100	5195678	5202262	passed	TRUE
JDID-134	Nanopore	98.78	0.43	100	4628117	4748466	passed	TRUE
JDID-135	Nanopore	99.82	0.59	100	4833781	5050067	passed	TRUE
JDID-136	Nanopore	99.28	1.58	100	5446520	5570508	passed	TRUE
JDID-137	Nanopore	100	0	100	3966018	3966018	passed	TRUE
JDID-138	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-139	Nanopore	100	0	100	4066916	4078140	passed	TRUE
JDID-140	Nanopore	100	7.02	100	3966883	4013197	passed	TRUE
JDID-141	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-142	Nanopore	100	0.09	100	4478572	4478572	passed	TRUE
JDID-143	Nanopore	99.62	0.6	100	5232525	5241822	passed	TRUE
JDID-144	Nanopore	100	0	100	3967315	3967315	passed	TRUE
JDID-145	Nanopore	100	93.1	100	1932002	10823364	passed	TRUE
JDID-146	Nanopore	100	0.77	100	5988026	6404429	passed	TRUE
JDID-147	Nanopore	99.97	0.43	100	4694643	4969912	passed	TRUE
JDID-148	Nanopore	97.48	0.98	100	3004556	5231364	passed	TRUE
JDID-149	Nanopore	99.37	0.24	100	4570809	4698386	passed	TRUE
JDID-150	Nanopore	99.87	1.33	100	5033336	5238718	passed	TRUE
JDID-151	Nanopore	99.69	0.21	100	5064784	5474513	passed	TRUE
JDID-152	Nanopore	100	100	100	4987807	9801230	passed	TRUE

Continuation of Table A3, part 13 of 19

JDID-153	Nanopore	98.78	0.43	100	4628141	4748490	passed	TRUE
JDID-154	Nanopore	99.97	0.69	100	5070947	5186220	passed	TRUE
JDID-155	Nanopore	100	0.8	100	4940326	5011355	passed	TRUE
JDID-156	Nanopore	98.16	0	100	5113349	5113349	passed	TRUE
JDID-157	Nanopore	99.57	0.63	100	5117525	5311980	passed	TRUE
JDID-158	Nanopore	99.97	0.48	100	4773838	4963656	passed	TRUE
JDID-159	Nanopore	99.97	1.19	100	4666031	4782632	passed	TRUE
JDID-160	Nanopore	100	0.33	100	3746704	4583462	passed	TRUE
JDID-161	Nanopore	99.99	2.34	100	5563582	5755096	passed	TRUE
JDID-162	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-163	Nanopore	99.93	0.43	100	4717549	4717549	passed	TRUE
JDID-164	Nanopore	100	0.16	100	4616066	5381448	passed	TRUE
JDID-165	Nanopore	99.9	0.09	100	4958040	5104410	passed	TRUE
JDID-166	Nanopore	99.87	0.76	100	4666577	4866596	passed	TRUE
JDID-167	Nanopore	98.97	0.6	100	4980631	5343711	passed	TRUE
JDID-168	Nanopore	100	0.6	100	4899967	5216593	passed	TRUE
JDID-169	Nanopore	100	94.48	100	5703553	10691363	passed	TRUE
JDID-170	Nanopore	98.64	0.14	100	4061395	5031424	passed	TRUE
JDID-171	Nanopore	99.99	3.04	100	5160155	5822873	passed	TRUE
JDID-172	Nanopore	99.99	0.41	100	4117514	4854747	passed	TRUE
JDID-173	Nanopore	99.7	0.56	100	4790792	4790792	passed	TRUE
JDID-174	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-175	Nanopore	99.99	2.3	100	5732862	6004680	passed	TRUE
JDID-176	Nanopore	99.99	2.09	100	5670253	5733823	passed	TRUE
JDID-177	Nanopore						passed	TRUE
JDID-178	Nanopore	98.97	0.33	100	4980628	5123233	passed	TRUE
JDID-179	Nanopore	99.97	0.75	100	4736622	4993272	passed	TRUE
JDID-180	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-181	Nanopore	0	0	100	5072	7550	passed	TRUE
JDID-182	Nanopore	99.99	0.26	100	5086607	5126243	passed	TRUE
JDID-183	Nanopore	99.7	0.82	100	4699396	4756428	passed	TRUE
JDID-184	Nanopore	99.99	2.34	100	5616268	5807782	passed	TRUE
JDID-185	Nanopore	99.69	0.51	100	2348670	4660156	passed	TRUE
JDID-186	Nanopore	99.97	0.16	100	4243109	4984562	passed	TRUE
JDID-187	Nanopore	100	91.38	99.94	1061157	10609879	passed	TRUE
JDID-188	Nanopore	99.99	2.34	100	5593751	5785265	passed	TRUE
JDID-189	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-190	Nanopore	99.97	0.43	100	4689737	4981471	passed	TRUE
JDID-191	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-192	Nanopore	100	97.93	100	5542995	10484462	passed	TRUE
JDID-193	Nanopore	99.89	0.43	100	2493913	4856727	passed	TRUE

Continuation of Table A3, part 14 of 19

JDID-194	Nanopore	98.96	98.96	100	4040711	9261081	passed	TRUE
JDID-195	Nanopore	99.93	0.35	100	4641444	4781449	passed	TRUE
JDID-196	Nanopore	99.45	0	100	2879198	2885219	passed	TRUE
JDID-197	Nanopore	99.45	0	100	2879201	2885222	passed	TRUE
JDID-198	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-199	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-200	Nanopore	99.14	0.18	100	1754117	1754117	passed	TRUE
JDID-201	Nanopore	100	0.04	100	4782330	4782330	passed	TRUE
JDID-202	Nanopore	99.7	0.56	100	4759722	4759722	passed	TRUE
JDID-203	Nanopore	99.38	1.52	100	5631636	5787986	passed	TRUE
JDID-204	Nanopore	98.37	0.33	100	4800352	4886063	passed	TRUE
JDID-205	Nanopore	100	0.04	100	4782204	4782204	passed	TRUE
JDID-206	Nanopore	99.77	0.21	100	4722319	4722319	passed	TRUE
JDID-207	Nanopore	99.07	0.63	100	4787604	4960487	passed	TRUE
JDID-208	Nanopore	99.07	0.65	100	4775735	4967348	passed	TRUE
JDID-209	Nanopore	98.58	0.33	100	4868632	5088295	passed	TRUE
JDID-210	Nanopore	99.98	0	100	5499131	5499131	passed	TRUE
JDID-211	Nanopore	99.67	0.48	100	4953654	5049855	passed	TRUE
JDID-212	Nanopore	99.97	0.26	100	4723763	4723763	passed	TRUE
JDID-213	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-214	Nanopore	98.83	22.62	100	4843032	6023088	passed	TRUE
JDID-215	Nanopore	98.93	0.53	100	4672536	4736813	passed	TRUE
JDID-216	Nanopore	99.85	0.57	100	5375695	5383847	passed	TRUE
JDID-217	Nanopore	99.99	2.02	100	5505872	5690642	passed	TRUE
JDID-218	Nanopore	99.97	0.3	100	4810682	4821462	passed	TRUE
JDID-219	Nanopore	99.99	0.14	100	5173788	5173788	passed	TRUE
JDID-220	Nanopore	99.97	0.44	100	4786510	4940929	passed	TRUE
JDID-221	Nanopore	100	2.85	100	4013134	5814244	passed	TRUE
JDID-222	Nanopore	99.45	0.33	100	5098951	5132872	passed	TRUE
JDID-223	Nanopore	100	100	100	4114077	7288281	passed	TRUE
JDID-224	Nanopore	98.96	98.96	100	5665750	10608069	passed	TRUE
JDID-225	Nanopore	99.97	0.29	100	4437821	4561145	passed	TRUE
JDID-226	Nanopore	99.38	1.85	100	5701800	5844529	passed	TRUE
JDID-227	Nanopore	99.97	0	100	4756570	4756570	passed	TRUE
JDID-228	Nanopore	100	76.58	100	107255	6009958	passed	TRUE
JDID-229	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-230	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-231	Nanopore	98.78	0	100	1715011	1741725	passed	TRUE
JDID-232	Nanopore	99.86	0.28	100	4705730	4705730	passed	TRUE
JDID-233	Nanopore	99.38	1.28	100	5536787	5652238	passed	TRUE
JDID-234	Nanopore	99.38	1.29	100	5530836	5715994	passed	TRUE

JDID-235	Nanopore	97.93	62.38	100	490166	8497577	passed	TRUE
JDID-236	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-237	Nanopore	99.38	1.29	100	5530829	5715994	passed	TRUE
JDID-238	Nanopore	100	97.93	100	4679462	8863940	passed	TRUE
JDID-239	Nanopore	100	0.08	100	4266146	4266146	passed	TRUE
JDID-240	Nanopore	99.99	0.26	100	4811351	4811351	passed	TRUE
JDID-241	Nanopore	100	100	100	5104723	9816657	passed	TRUE
JDID-242	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-243	Nanopore	99.97	0	100	4839817	4888563	passed	TRUE
JDID-244	Nanopore	99.97	0.44	100	4786505	4940926	passed	TRUE
JDID-245	Nanopore	97.9	1.82	100	4380115	4575317	passed	TRUE
JDID-246	Nanopore	99.38	1.53	100	5771454	5905740	passed	TRUE
JDID-247	Nanopore	100	0.54	100	4424055	4646237	passed	TRUE
JDID-248	Nanopore	100	0.04	100	4679562	4738922	passed	TRUE
JDID-249	Nanopore	100	0.04	100	4679656	4744829	passed	TRUE
JDID-250	Nanopore	99.94	0.04	100	5189746	5189746	passed	TRUE
JDID-251	Nanopore	99.54	1.31	100	5458905	5458905	passed	TRUE
JDID-252	Nanopore	99.07	5.92	100	4984488	5276631	passed	TRUE
JDID-253	Nanopore	99.61	0.29	100	4821726	4821726	passed	TRUE
JDID-254	Nanopore	28.64	0.11	100	50154	1795979	passed	TRUE
JDID-255	Nanopore	99.95	0.16	100	5209040	5264811	passed	TRUE
JDID-256	Nanopore	99.95	0.16	100	4998972	4998972	passed	TRUE
JDID-257	Nanopore	99.95	0.16	100	4290277	5334936	passed	TRUE
JDID-258	Nanopore	99.63	0	100	5042262	5042262	passed	TRUE
JDID-259	Nanopore	99.66	0.19	100	4597591	4597591	passed	TRUE
JDID-260	Nanopore	99.38	1.27	100	5571346	5739198	passed	TRUE
JDID-261	Nanopore	100	100	99.98	1770318	11405751	passed	TRUE
JDID-262	Nanopore	100	100	99.98	1060141	11837740	passed	TRUE
JDID-263	Nanopore	99.85	0.08	100	4237574	5325693	passed	TRUE
JDID-264	Nanopore	99.92	0.47	100	4348932	4585425	passed	TRUE
JDID-265	Nanopore	0	0	100	31883	39172	passed	TRUE
JDID-266	Nanopore	100	12.51	100	4635810	5263990	passed	TRUE
JDID-267	Nanopore	99.86	0.45	100	4567520	4700584	passed	TRUE
JDID-268	Nanopore	100	193.06	100	4257762	13594317	passed	TRUE
JDID-269	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-270	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-271	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-272	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-273	Nanopore	97.81	0.89	100	4361332	4361332	passed	TRUE
JDID-274	Nanopore	100	0	100	3662227	4066060	passed	TRUE ⁸⁸
JDID-275	Nanopore	98.78	0	100	1717859	1717859	passed	TRUE

Continuation of Table A3, part 16 of 19

JDID-276	Nanopore	99.61	0.32	100	935811	5832638	passed	TRUE
JDID-277	Nanopore	100	0.54	100	4635787	4641513	passed	TRUE
JDID-278	Nanopore	99.97	0.14	100	4832453	4832453	passed	TRUE
JDID-279	Nanopore	99.04	0.11	100	1617132	1617132	passed	TRUE
JDID-280	Nanopore	100	0	100	3509847	4663998	passed	TRUE
JDID-281	Nanopore	99.97	0.33	100	4520794	4567525	passed	TRUE
JDID-282	Nanopore	99.33	0.47	100	6104710	6104710	passed	TRUE
JDID-283	Nanopore	99.55	0.41	100	3037338	4294427	passed	TRUE
JDID-284	Nanopore	99.33	0.44	100	6104695	6104695	passed	TRUE
JDID-285	Nanopore	100	1.08	100	4487562	4580439	passed	TRUE
JDID-286	Nanopore	100	0.34	100	3984252	4979268	passed	TRUE
JDID-287	Nanopore	100	0.07	100	5599368	5739832	passed	TRUE
JDID-288	Nanopore	100	93.97	100	126601	9020481	passed	TRUE
JDID-289	Nanopore	99.87	0.45	100	4770503	4965905	passed	TRUE
JDID-290	Nanopore	100	0.36	100	4044351	4770055	passed	TRUE
JDID-291	Nanopore	100	0.36	100	4044366	4770071	passed	TRUE
JDID-292	Nanopore	4.25	0	100	36799	433821	passed	TRUE
JDID-293	Nanopore	99.38	0.14	100	1652176	1665701	passed	TRUE
JDID-294	Nanopore	98.71	0.11	100	1653300	1653300	passed	TRUE
JDID-295	Nanopore	99.38	1.31	100	5665744	5665744	passed	TRUE
JDID-296	Nanopore	99.53	0.21	100	1634048	1634048	passed	TRUE
JDID-297	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-298	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-299	Nanopore	99.99	0.14	100	5173816	5173816	passed	TRUE
JDID-300	Nanopore	98.28	97.07	100	4661172	8564100	passed	TRUE
JDID-301	Nanopore	98.93	0.53	100	4672553	4736831	passed	TRUE
JDID-302	Nanopore	8.33	0	100	46481	373240	passed	TRUE
JDID-303	Nanopore	100	0	100	2342969	2342969	passed	TRUE
JDID-304	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-305	Nanopore	100	19.54	100	4224611	5700029	passed	TRUE
JDID-306	Nanopore	NA	NA	NA	NA	NA	not_sequenced	NA
JDID-307	Nanopore	99.88	0.32	100	4800987	4915208	passed	TRUE
JDID-308	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-309	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-310	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-311	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-312	Nanopore	98.78	0	100	1516333	1516333	passed	TRUE
JDID-313	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-314	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-315	Nanopore	99.35	0.33	100	4503230	4503230	passed	TRUE
JDID-316	Nanopore	99.92	0.12	100	4893578	4893578	passed	TRUE

JDID-317	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-318	Nanopore	95.87	0.51	100	3563330	3563330	passed	TRUE
JDID-319	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-320	Nanopore	99.99	0.2	100	2409664	4726231	passed	TRUE
JDID-321	Nanopore	99.65	0.35	100	1702311	1702311	passed	TRUE
JDID-322	Nanopore	100	0.77	100	5316610	5602488	passed	TRUE
JDID-323	Nanopore	100	0.39	100	5286304	5286304	passed	TRUE
JDID-324	Nanopore	100	0.07	100	5856470	5856470	passed	TRUE
JDID-325	Nanopore	99.9	0.37	100	4605123	4605123	passed	TRUE
JDID-326	Nanopore	98.02	0.77	100	4426908	4426908	passed	TRUE
JDID-327	Nanopore	99.88	0.32	100	4800972	4915201	passed	TRUE
JDID-328	Nanopore	100	0	100	2316958	4099161	passed	TRUE
JDID-329	Nanopore	99.97	0.2	100	4509699	4657060	passed	TRUE
JDID-330	Nanopore	100	0	100	4056279	4056279	passed	TRUE
JDID-331	Nanopore	99.98	0.74	100	4156707	4156707	passed	TRUE
JDID-332	Nanopore	97.81	0.89	100	4361312	4361312	passed	TRUE
JDID-333	Nanopore	100	0.29	100	4821716	4821716	passed	TRUE
JDID-334	Nanopore	95.87	0.46	100	3589257	3592940	passed	TRUE
JDID-335	Nanopore	95.87	0.38	100	3489203	3489203	passed	TRUE
JDID-336	Nanopore	99.16	0.11	100	1653362	1653362	passed	TRUE
JDID-337	Nanopore	98.41	0	100	1493934	1547583	passed	TRUE
JDID-338	Nanopore	NA	NA	NA	NA	NA	fail_assembly	FALSE
JDID-339	Nanopore	99.1	0.92	100	4554422	4554422	passed	TRUE
JDID-340	Nanopore	99.1	0.92	100	4554431	4554431	passed	TRUE
JDID-341	Nanopore	99.1	0.87	100	4315320	4315320	passed	TRUE
JDID-342	Nanopore	99.23	0.92	100	4630041	4630041	passed	TRUE
JDID-343	Nanopore	99.53	0.57	100	4847280	4896374	passed	TRUE
JDID-344	Nanopore	98.96	197.54	100	4361806	14800850	passed	TRUE
JDID-345	Nanopore	98.02	1.01	100	4306163	4306163	passed	TRUE
JDID-346	Nanopore	99.66	0.16	100	4558238	4908936	passed	TRUE
JDID-347	Nanopore	99.97	0.07	100	5114762	5150548	passed	TRUE
JDID-348	Nanopore	99.9	0.1	100	4588703	4645917	passed	TRUE
JDID-349	Nanopore	99.1	0.92	100	4555649	4555649	passed	TRUE
JDID-350	Nanopore	100	200	100	4730752	11744821	passed	TRUE
JDID-351	Nanopore	100	0.04	100	4593667	4650872	passed	TRUE
JDID-352	Nanopore	99.75	0.52	100	4727110	4727110	passed	TRUE
JDID-353	Nanopore	99.07	0.65	100	4732694	4849804	passed	TRUE
JDID-354	Nanopore	99.94	0.25	100	4876003	4964907	passed	TRUE
JDID-355	Nanopore	99.97	0.25	100	4876134	4965038	passed	TRUE
JDID-356	Nanopore	99.94	0.25	100	4876024	4964923	passed	TRUE
JDID-357	Nanopore	98.23	1.71	100	1588149	1733027	passed	TRUE

Continuation of Table A3, part 18 of 19

JDID-358	Nanopore	95.87	0.46	100	3590171	3590171	passed	TRUE
JDID-359	Nanopore	99.4	0.29	100	4491289	4609161	passed	TRUE
JDID-360	Nanopore	99.67	0.2	100	4249029	4249029	passed	TRUE
JDID-361	Nanopore	99.38	0.19	100	4301149	4539657	passed	TRUE
JDID-362	Nanopore	99.97	0.85	100	4244287	4627068	passed	TRUE
JDID-363	Nanopore	99.97	0.47	100	4802310	4959496	passed	TRUE
JDID-364	Nanopore	100	0	100	2914725	4167618	passed	TRUE
JDID-365	Nanopore	100	0	100	3033803	4051971	passed	TRUE

Note. QC statistics are shown only for isolates with retained assemblies (Illumina, n=362; Nanopore; n=310) and downstream taxonomic classification. Isolate datasets falling below thresholds were not retained in the data set or marked as “no identity” id carried forward.

Appendix C: Supplementary Figure

Figure A1. Per-isolate taxonomic resolution across traditional and WGS-based identification methods. Heatmap of the taxonomic rank assigned to each isolate by each identification method. Rows represent isolates (JDID-01-JDID-365) and columns represent classification method. Rank is colour-coded: species (blue), genus (green), family (pink), order (yellow), and no identity (red). When *a no identity* classification is assigned for all workflows under an isolate, its genome assembly was not retained in the dataset and did not undergo taxonomic classification. White cells indicate that a given method was not applied to that isolate. Method prefixes denote sequencing platform: “I:” indicating Illumina-based workflows and “N:” indicating Nanopore-based workflows. This figure provides isolate-level resolution detail corresponding to the aggregated resolution summaries presented in Chapter 3.2 and 3.3.

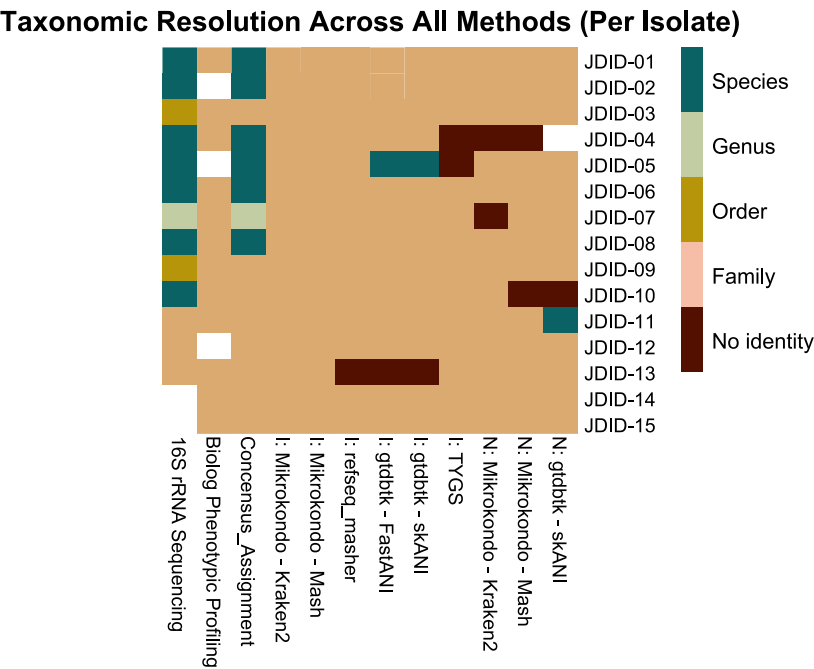
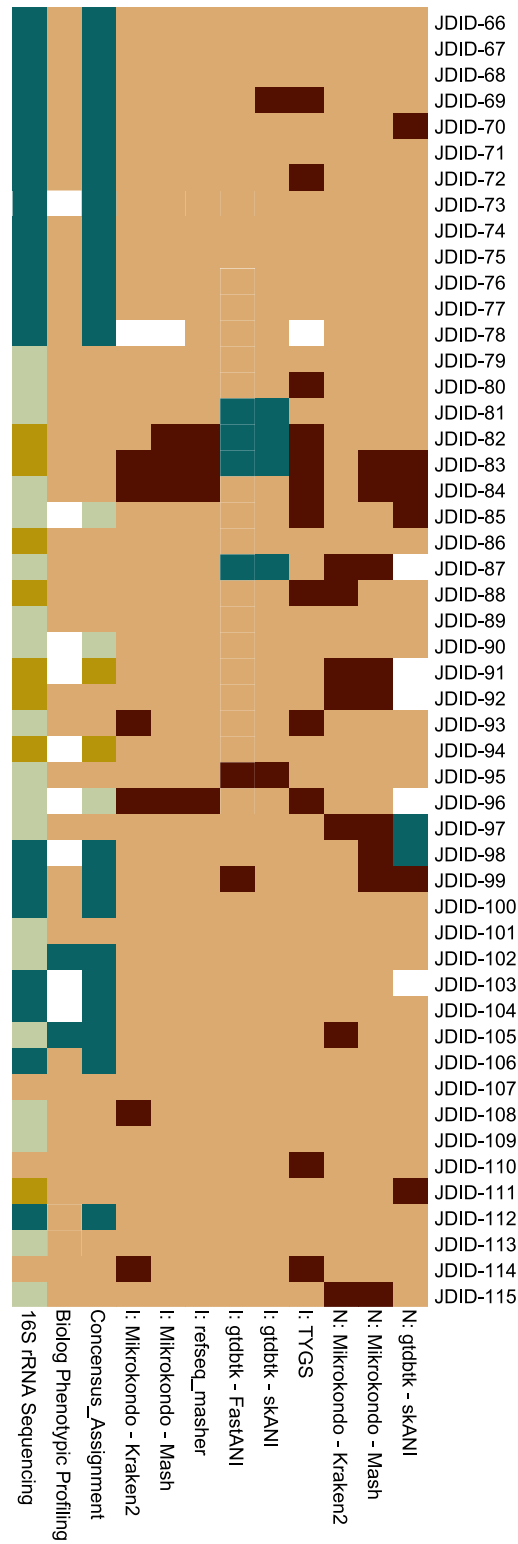
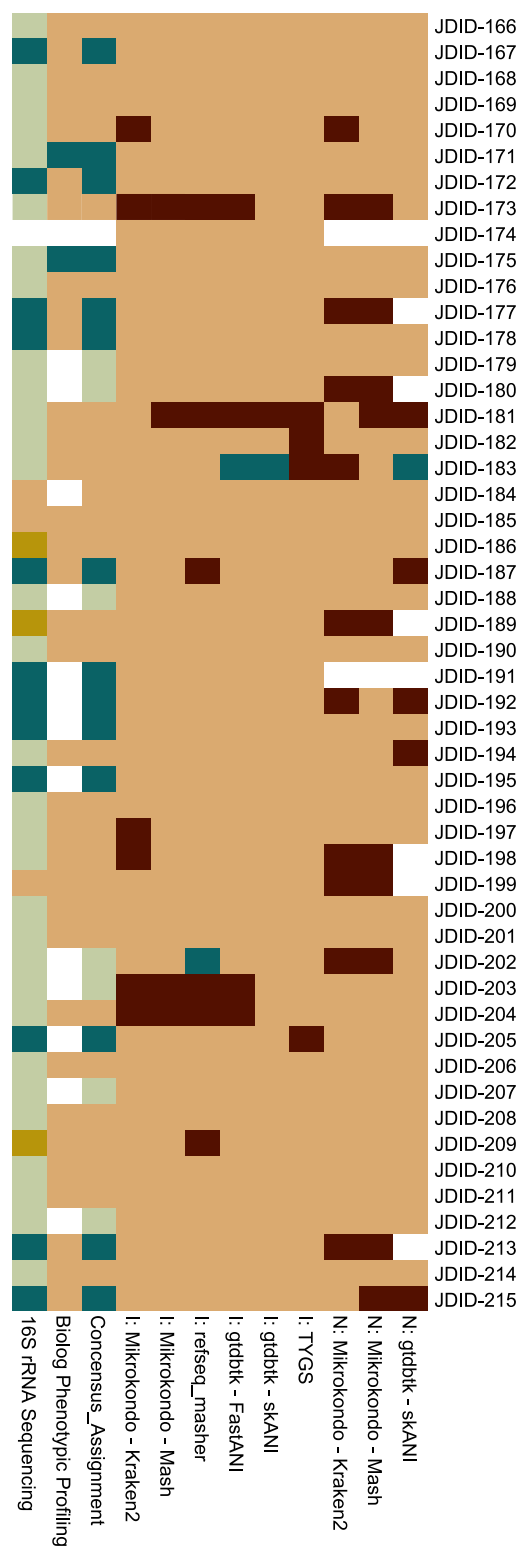
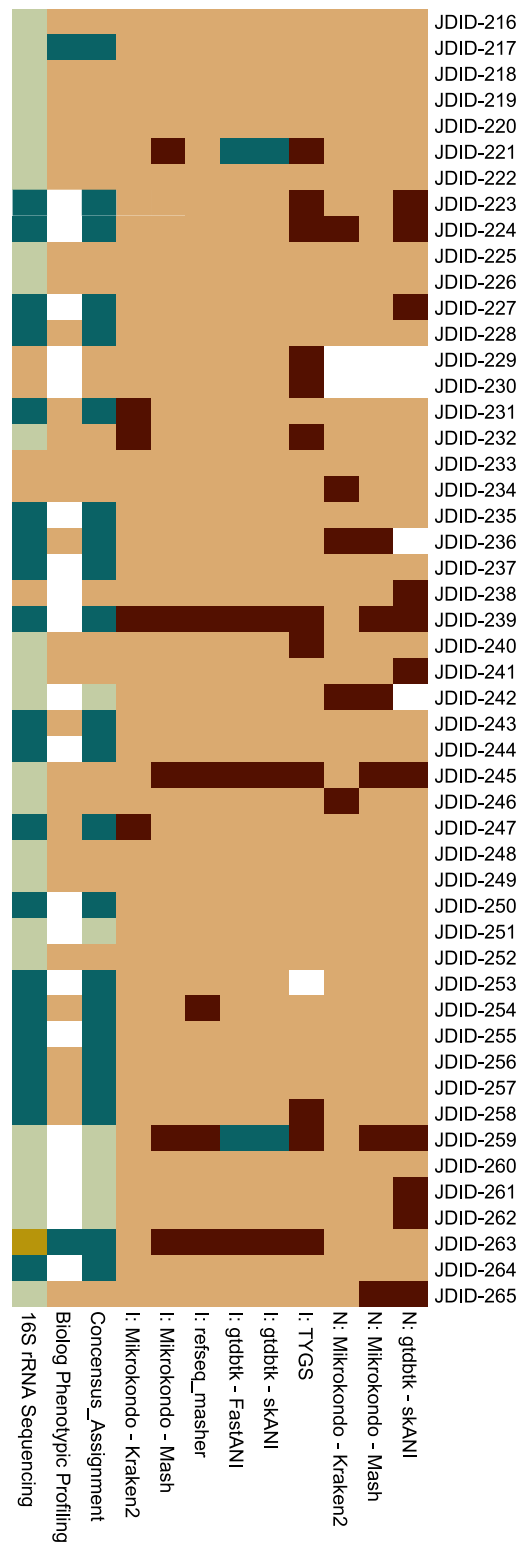
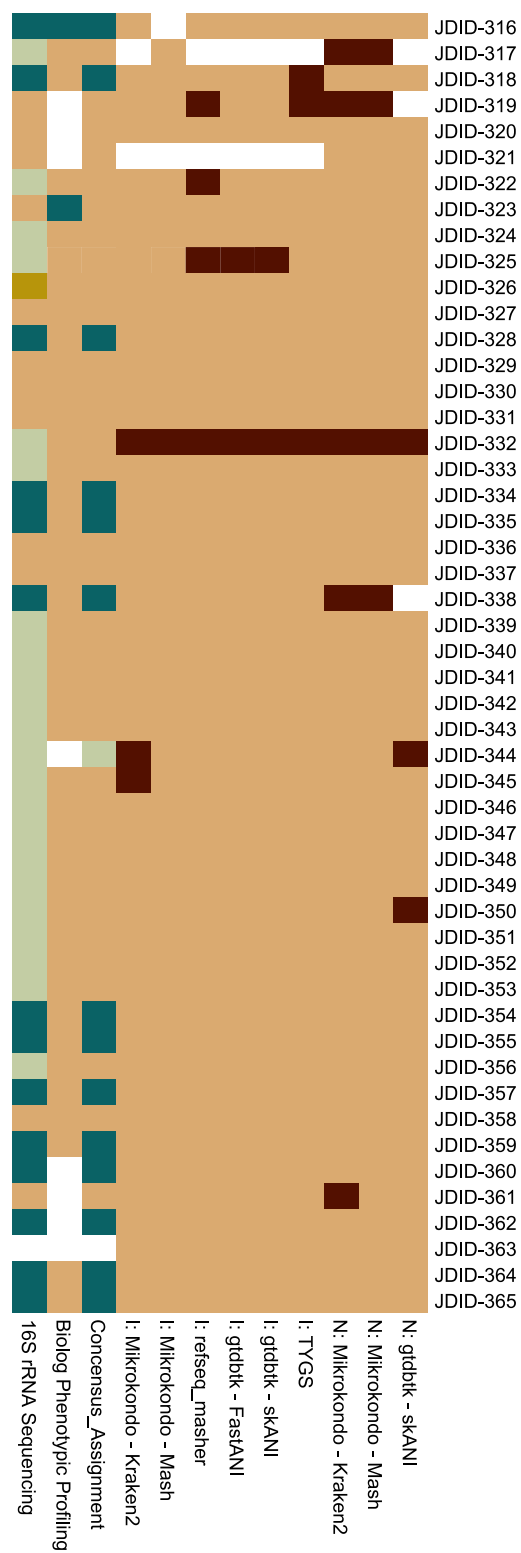


Figure A1, part 1 of 8









Appendix D: Statistics of Taxonomic Resolution, Concordance, and Failure Patterns

Across Traditional and WGS Methods

Table A4. Standardized residuals for taxonomic resolution across traditional identification

methods. Standardized residuals from a chi-square test comparing taxonomic resolution outcomes across 16S rRNA sequencing, Biolog phenotypic profiling, and reconciled consensus assignments. Positive residuals indicate overrepresentation of a given taxonomic rank, while negative residuals indicate underrepresentation. Residual magnitudes highlight ranks contributing most strongly to the overall association.

Method	species	genus	family	order	phylum	no identity
Consensus Assignment	1.904733872	6.844823336	-5.055608659	-2.113600017	-0.715340145	-6.976490252
Genotypic Assignment	-13.71547863	6.241074474	13.93899744	6.005957622	1.405065998	-6.496582334
Phenotypic Assignment	11.90922647	-13.2072342	-8.952516649	-3.92278539	-0.69465252	13.59790228

Table A5. Standardized residuals for failure and agreement outcomes across traditional

methods. Standardized residuals from a chi-square test evaluating failure and agreement outcomes from traditional methods (16S rRNA sequencing and Biolog phenotypic profiling) across taxonomic levels. Residuals quantify deviations from the null hypothesis of independence, in which failure and agreement outcome are assumed to occur proportionately across taxonomic levels. Positive values indicate outcome categories observed more frequently than predicted under independence, while negative values indicate fewer observations than expected.

Taxonomic Level	Outcome	Standardized Residual
family	16S only	8.144855137
	Biolog only	-0.445740444
	Both fail	-0.256624458
	Concordant	-1.082699776
	Discordant	-6.969167403
genus	16S only	2.414038426
	Biolog only	-1.576442036
	Both fail	-0.907599006
	Concordant	-0.832427043
	Discordant	-1.442409133
species	16S only	-6.321646437
	Biolog only	1.783791233
	Both fail	1.026975374
	Concordant	1.34956497
	Discordant	4.788769452

Table A6. Taxon-specific contributions to discordance between traditional identification methods. Standardized residuals from a chi-square test identifying the taxonomic groups that disproportionately contribute to discordance between 16S rRNA sequencing and Biolog phenotypic profiling. Residuals reflect deviations from expected counts calculated under the null hypothesis that discordance is evenly distributed across taxa. Larger absolute residuals indicate taxa that most strongly drive the overall association.

<i>Taxon</i>	<i>Standardized Residual</i>
<i>Aeromonas</i>	2.058822475
<i>Arcobacter</i>	-1.412043109
<i>Bacillus</i>	0.712619887
<i>Buttiauxella</i>	0.712619887
<i>Campylobacter</i>	-5.122702033
<i>Citrobacter</i>	2.193397731
<i>Cronobacter</i>	0.651483417
<i>Enterobacter</i>	-0.243334471
<i>Enterobacteriales</i>	0.712619887
<i>Enterobacteriaceae</i>	1.613766263
<i>Erwinia</i>	0.712619887
<i>Helicobacter</i>	1.10325149
<i>Klebsiella</i>	-0.867090948
<i>Listeria</i>	-1.751590872
<i>Micrococcus</i>	-1.412043109
<i>Mixta</i>	0.366359145
<i>Pantoea</i>	1.438792279
<i>Phytobacter</i>	-1.412043109
<i>Proteus</i>	1.613766263
<i>Providencia</i>	1.438792279
<i>Serratia</i>	-1.439699334
<i>Tatumella</i>	1.24208127
<i>Yersinia</i>	2.138618181

Table A7. WGS workflow- and platform-specific deviations in taxonomic resolution.

Standardized residuals from a chi-square test assessing the association between WGS-based workflows, sequencing platforms, and taxonomic resolution outcomes. Expected values were calculated among independence between platform-workflow combinations and resolution category. Residual magnitudes identify combinations that produce significantly higher or lower frequencies of species-level, genus-level, or unresolved assignments (NI) assignments than predicted under the null model.

<i>Workflow</i>	<i>Platform</i>	<i>no identity</i>	<i>species</i>	<i>genus</i>
<i>Mikrokonko - Kraken2</i>	Illumina	-2.346060968	2.986528367	-2.225922384
<i>Mikrokonko - Mash</i>		-2.88620217	3.502426638	-2.225922384
<i>TYGS</i>		5.397590467	-4.417731781	-2.201555532
<i>gtdbtk - FastANI</i>		-3.621449608	1.801201807	4.947846191
<i>gtdbtk - skANI</i>		-4.340773204	2.83175955	3.922526526
<i>refseq_masher</i>		-1.463478822	1.972961431	-1.716731634
<i>Mikrokonko - Kraken2</i>	Nanopore	3.751322195	-2.853566276	-2.17703879
<i>Mikrokonko - Mash</i>		4.667208433	-3.728345176	-2.17703879
<i>gtdbtk - skANI</i>		1.1198372	-2.419528588	4.029273259

Table A8. Concordance between WGS sequencing workflows. Cohen's kappa statistics

quantifying pairwise agreement between taxonomic assignments generated by Illumina- (I:) and ONT-based (N:) workflows, stratified by sequencing platforms. κ values range from 0 (no agreement) to 1 (perfect agreement). Values ≥ 0.80 indicate strong concordance, 0.60-0.79 moderate concordance, 0.40-0.59 weak concordance, and < 0.40 minimal agreement (Landis and Koch, 1977). Sample sizes (n) indicate the number of isolates compared for each workflow pair.

Method 1	Method 2	Kappa	n
I: Mikrokondo - Kraken2	I: Mikrokondo - Mash	0.854791	315
I: Mikrokondo - Kraken2	I: gtdbtk - skANI	0.775868	317
I: Mikrokondo - Kraken2	I: gtdbtk - FastANI	0.792384	318
I: Mikrokondo - Kraken2	I: refseq_masher	0.865116	309
I: Mikrokondo - Kraken2	I: TYGS	0.873578	266
I: Mikrokondo - Kraken2	N: Mikrokondo - Kraken2	0.309545	267
I: Mikrokondo - Kraken2	N: Mikrokondo - Mash	0.339208	260
I: Mikrokondo - Kraken2	N: gtdbtk - skANI	0.330367	247
I: Mikrokondo - Mash	I: gtdbtk - skANI	0.91222	324
I: Mikrokondo - Mash	I: gtdbtk - FastANI	0.93142	326
I: Mikrokondo - Mash	I: refseq_masher	0.984117	320
I: Mikrokondo - Mash	I: TYGS	0.925655	274
I: Mikrokondo - Mash	N: Mikrokondo - Kraken2	0.301866	259
I: Mikrokondo - Mash	N: Mikrokondo - Mash	0.404643	261
I: Mikrokondo - Mash	N: gtdbtk - skANI	0.392212	247
I: gtdbtk - skANI	I: gtdbtk - FastANI	0.972562	333
I: gtdbtk - skANI	I: refseq_masher	0.892073	320
I: gtdbtk - skANI	I: TYGS	0.889848	277
I: gtdbtk - skANI	N: Mikrokondo - Kraken2	0.275697	270
I: gtdbtk - skANI	N: Mikrokondo - Mash	0.370535	269
I: gtdbtk - skANI	N: gtdbtk - skANI	0.40282	253
I: gtdbtk - FastANI	I: refseq_masher	0.91451	321
I: gtdbtk - FastANI	I: TYGS	0.894757	271
I: gtdbtk - FastANI	N: Mikrokondo - Kraken2	0.295457	265
I: gtdbtk - FastANI	N: Mikrokondo - Mash	0.387292	265
I: gtdbtk - FastANI	N: gtdbtk - skANI	0.391619	250
I: refseq_masher	I: TYGS	0.927207	266
I: refseq_masher	N: Mikrokondo - Kraken2	0.302811	255
I: refseq_masher	N: Mikrokondo - Mash	0.403208	257
I: refseq_masher	N: gtdbtk - skANI	0.393056	244
I: TYGS	N: Mikrokondo - Kraken2	0.32042	232
I: TYGS	N: Mikrokondo - Mash	0.399758	232
I: TYGS	N: gtdbtk - skANI	0.398083	221
N: Mikrokondo - Kraken2	N: Mikrokondo - Mash	0.643663	269
N: Mikrokondo - Kraken2	N: gtdbtk - skANI	0.643034	251
N: Mikrokondo - Mash	N: gtdbtk - skANI	0.92113	258

Landis JR, Koch GG. The measurement of observer agreement for categorical data. *Biometrics*. 1977 Mar; 33(1): 159-74. PMID: 843571.

Table A9. Genus-level concordance and discordance across WGS-based workflows.

Standardized residuals from a chi-square analysis evaluating the association between genus and concordance among WGS-based workflows. Expected counts were calculated under the null hypothesis (agreement outcomes occur independently of genus). Residuals indicate the direction of magnitude of deviation from this null model, identifying genera that disproportionately contribute to agreement or disagreement.

Genus	Concordant	Discordant
<i>Acerihabitans</i>	0.680486	-0.68049
<i>Aeromonas</i>	-0.57776	0.577755
<i>Aliarcobacter</i>	0.48078	-0.48078
<i>Atlantibacter</i>	1.078617	-1.07862
<i>Bacillus</i>	0.48078	-0.48078
<i>Buttiauxella</i>	-3.61448	3.61448
<i>Campylobacter</i>	2.600185	-2.60019
<i>Cedecea</i>	0.680486	-0.68049
<i>Chimaeribacter</i>	0.834111	-0.83411
<i>Citrobacter</i>	1.654685	-1.65469
<i>Cronobacter</i>	0.314259	-0.31426
<i>Cutibacterium</i>	0.680486	-0.68049
<i>Dryocola</i>	0.48078	-0.48078
<i>Enterobacter</i>	-2.8392	2.839196
<i>Erwinia</i>	0.834111	-0.83411
<i>Escherichia</i>	2.650943	-2.65094
<i>Ewingella</i>	0.48078	-0.48078
<i>Hafnia</i>	0.314259	-0.31426
<i>Helicobacter</i>	1.214072	-1.21407
<i>Klebsiella</i>	-0.2613	0.261297
<i>Khuyvera</i>	0.64911	-0.64911
<i>Kosakonia</i>	0.48078	-0.48078
<i>Kytococcus</i>	0.48078	-0.48078
<i>Leclercia</i>	0.591531	-0.59153
<i>Lelliottia</i>	1.078617	-1.07862
<i>Leminorella</i>	0.680486	-0.68049
<i>Listeria</i>	1.367761	-1.36776
<i>Mixta</i>	1.078617	-1.07862
<i>Morganella</i>	0.963945	-0.96395
<i>Pantoea</i>	-1.8933	1.893299
<i>Phytobacter</i>	2.348696	-2.3487
<i>Pluralibacter</i>	0.48078	-0.48078
<i>Proteus</i>	-0.38314	0.38314
<i>Providencia</i>	-5.00374	5.003743
<i>Pseudescherichia</i>	1.078617	-1.07862
<i>Pseudocitrobacter</i>	-1.22243	1.222432
<i>Salmonella</i>	0.800421	-0.80042
<i>Scandinavium</i>	-0.64875	0.648753
<i>Serratia</i>	-4.53572	4.535721
<i>Shimwellia</i>	0.834111	-0.83411
<i>Sodalis</i>	0.680486	-0.68049
<i>Staphylococcus</i>	0.48078	-0.48078
<i>Tatumella</i>	-0.45592	0.45592
<i>Yersinia</i>	-2.32661	2.326608
<i>Acerihabitans</i>	0.680486	-0.68049

Table A10. Failure category bias by workflow and sequencing platform. Standardized residuals from a chi-square analysis assessing the distribution of failure categories among classified isolates across WGS-based workflows and sequencing platforms. Residual values identify workflow-platform combinations disproportionately associated with specific failure categories.

Failure Category	MikroKondo Kraken2	MikroKondo Mash	RefSeq Masher	TYGS	GTDB-Tk FastANI	GTDB-Tk skANI	MikroKondo Kraken2	MikroKondo Mash	GTDB-Tk skANI
	Illumina						Nanopore		
Reference database limitations	-2.337663521	-2.423102268	4.800320163	-4.417203205	-1.580894091	-1.196463425	-3.469380788	0.112087699	10.05342906
Invalid taxonomy	-2.946428407	-0.794584377	-3.461195144	-1.50465901	-2.721873392	-2.891505841	8.545934003	6.803046361	-4.329686726
Assembly related Limitations	6.316074704	3.914606978	1.999577427	-7.867217233	5.003571677	5.410004357	-1.376276896	-3.124184522	-2.685939824
Algorithmic or confidence threshold filtering	-2.740478612	-1.89748478	-3.219264123	15.41450377	-2.010476419	-2.68939503	-4.067208031	-3.282258288	-1.168487951

Table A11. Platform-specific failure category bias. Standardized residuals from a chi-square test comparing failure category distributions between Illumina and Nanopore sequencing platforms. Positive and negative residuals indicate over or underrepresentation of specific failure categories relative to expected platform-independent distributions.

Failure Category	Illumina	Nanopore
Reference database limitations	-4.641710812	4.641710812
Invalid taxonomy	-7.932518993	7.932518993
Assembly related limitations	5.10814945	-5.10814945
Algorithmic or confidence threshold filtering	6.052657864	-6.052657864

Note. Because the contingency table contains only two platform categories (Illumina and Nanopore), residuals are mathematically equal in magnitude and opposite in sign for each failure category. Positive residuals indicate that a failure category occurred more frequently than expected for that platform under the null hypothesis of independence, whereas negative residuals indicate fewer occurrences than expected.

Table A12. Assembly and QC metrics associated with classification status. Wilcoxon rank-sum test results comparing assembly and QC metrics between classified and unclassified WGS assemblies. Reported W statistics and p-values identify with metrics significantly associated with classification failure. Assembly contiguity (N50) is evaluated separately from QC measures.

Metric	Type	W	<i>p</i>
Genome Size (bps)	Quality Control	102336	0.9387
Contamination (%)		100488	0.7052
Completeness (%)		104120	0.6047
Coverage (%)		103742	0.3183
N50 (bps)	Assembly	110207	0.4443

Appendix E: Homotypic Synonym Sets

Table A13. Homotypic synonym sets observed in this study and normalized taxon names used for downstream analysis of WGS data. Homotypic synonym sets are shown where at least one name was observed across WGS-based or traditional method-based outputs and assignments. The normalized taxon name represents the name used to reconcile classifications and reduce nomenclature- and reference database-driven discordance. Synonym relationships were validated against the LPSN (26 January 2026). Blank cells indicate that no additional homotypic synonym was observed for that taxon in this study.

Observed Synonym (variant 1)	Observed Synonym (variant 2)	Observed Synonym (variant 3)	Normalized Taxon Name (used in analysis)
<i>Cronobacter sakazakii</i>	<i>Enterobacter sakazakii</i>		<i>Cronobacter sakazakii</i>
<i>Escherichia blattae</i>	<i>Shimwellia blattae</i>		<i>Shimwellia blattae</i>
<i>Morganella morganii</i>	<i>Proteus morganii</i>		<i>Morganella morganii</i>
<i>Pantoea stewartii</i>	<i>Erwinia stewartii</i>		<i>Pantoea stewartii</i>
<i>Proteus myxofaciens</i>	<i>Cosenzaea myxofaciens</i>		<i>Proteus myxofaciens</i>
<i>Klebsiella aerogenes</i>	<i>Klebsiella mobilis</i>	<i>Enterobacter aerogenes</i>	<i>Klebsiella aerogenes</i>
<i>Aeromonas caviae</i>	<i>Aeromonas punctata</i>		<i>Aeromonas caviae</i>
<i>Enterobacter asburiae</i>	<i>Enterobacter muelleri</i>		<i>Enterobacter asburiae</i>
<i>Escherichia hermannii</i>	<i>Atlantibacter hermannii</i>		<i>Atlantibacter hermannii</i>
<i>Escherichia vulneris</i>	<i>Pseudescherichia vulneris</i>		<i>Pseudescherichia vulneris</i>
<i>Kosakonia cowanii</i>	<i>Enterobacter cowanii</i>		<i>Kosakonia cowanii</i>
<i>Kytococcus sedentarius</i>	<i>Micrococcus sedentarius</i>		<i>Kytococcus sedentarius</i>
<i>Lactobacillus paracasei</i>	<i>Lactacaseibacillus paracasei</i>		<i>Lactacaseibacillus paracasei</i>
<i>Leclercia adecarboxylata</i>	<i>Escherichia adecarboxylata</i>		<i>Leclercia adecarboxylata</i>
<i>Lelliottia nimipressuralis</i>	<i>Erwinia nimipressuralis</i>	<i>Enterobacter nimipressuralis</i>	<i>Lelliottia nimipressuralis</i>
<i>Methylobacterium extorquens</i>	<i>Methylorubrum extorquens</i>		<i>Methylobacterium extorquens</i>
<i>Salmonella enterica</i>	<i>Salmonella typhimurium</i>		<i>Salmonella enterica</i>
<i>Siccibacter turicensis</i>	<i>Cronobacter zurichensis</i>	<i>Enterobacter turicensis</i>	<i>Siccibacter turicensis</i>
<i>Tatumella punctata</i>	<i>Pantoea punctata</i>		<i>Tatumella punctata</i>
<i>Aliarcobacter butzleri</i>	<i>Arcobacter butzleri</i>	<i>Campylobacter butzleri</i>	<i>Aliarcobacter butzleri</i>
<i>Duffyella gerundensis</i>	<i>Erwinia gerundensis</i>		<i>Erwinia gerundensis</i>
<i>Klebsiella ornithinolytica</i>	<i>Raoultella ornithinolytica</i>		<i>Klebsiella ornithinolytica</i>
<i>Klebsiella planticola</i>	<i>Raoultella planticola</i>		<i>Klebsiella planticola</i>
<i>Klebsiella terrigena</i>	<i>Raoultella terrigena</i>		<i>Klebsiella terrigena</i>
<i>Mixta calida</i>	<i>Pantoea calida</i>		<i>Mixta calida</i>
<i>Cutibacterium acnes</i>	<i>Propionibacterium acnes</i>		<i>Cutibacterium acnes</i>

Appendix F: Classification Failure Definitions

Appendix E provides operational definitions for the classification failure categories used to describe unclassified WGS-based taxonomic outputs (Section 3.2.1). These categories were applied uniformly across sequencing platforms and bioinformatic workflows to support consistent interpretation and analysis of classification failures (Section 3.2.6).

Table A14. Definitions of classification failure categories used in concordance performance analyses.

Category	Definition	Examples
Reference database limitations	Failure to assign a taxonomic assignment due to absence, incomplete representation, or insufficient resolution of the relevant taxon in the reference database used by the workflow.	• No close match present in the reference database • Taxon present only at higher rank • Outdated or missing type strain representation
Assembly-related limitations	Failure attributable to inadequate assembly quality preventing reliable taxonomic classification, despite sufficient raw sequencing data.	• Highly fragmented assemblies • Low N50 • Excessive contig counts • Low read quality • Insufficient coverage per base • Insufficient breadth of sequence coverage
Algorithmic or confidence threshold filtering	Failure resulting from tool-specific decision rules, confidence thresholds, or scoring criteria that prevent assignment despite detectable similarity to reference sequences.	• Similarity scores below tool-defined cutoffs • Conflicting top hits filtered by algorithm • Conservative confidence thresholds excluding borderline matches
Invalid taxonomy	Output taxon names that are no longer valid, no recognized under current nomenclature, or incompatible with downstream normalization rules, resulting in classification as <i>no identity</i> .	• Deprecated species names • Provisional or non-standard labels • Conflicting synonyms not resolvable to a valid species name